# Detailed Protein Report

## Project Info

**Name:** teeth-151208 **Date:** Dec 8, 2015

**Note:**

## Sample Info & Protocols

**Name:** id-UP **Date:** Dec 10, 2015

**Fraction:**

**Volume:** **Concentration:**

**Note:**

**Buffer:** **Organism:**

## Search Result Info

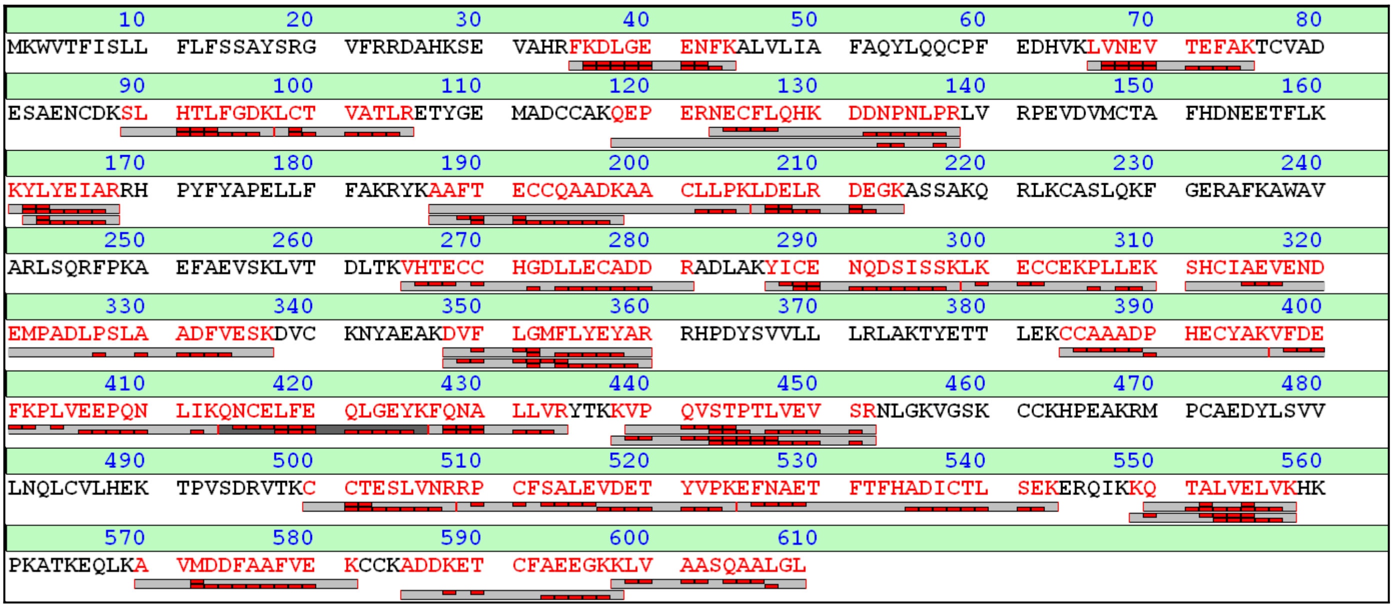
| Search Result | Location | Search Engine | Database |
|---|---|---|---|
| ZT_human_PE_2015-12-10 16:24:42 | /teeth-151208/id-UP/"Combined MS/MS spectra" | Mascot | refseq_human |

## Protein 1: serum albumin preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4502027 | **Score:** | 1475.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 54.5 |
| | | **No. of unique Peptides:** | 31 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.11 | **CV:** | 102.80 % | **No. of Peptides:** | 15 |
| ***WUP:QUP*** | **Median:** | 0.82 | **CV:** | 70.70 % | **No. of Peptides:** | 17 |



```
        10         20         30         40         50         60         70         80
MKWVTFISLL FLFSSAYSRG VFRRDAHKSE VAHRFKDLGE ENFKALVLIA FAQYLQQCPF EDHVKLVNEV TEFAKTCVAD
        90        100        110        120        130        140        150        160
ESAENCDKSL HTLFGDKLCT VATLRETYGE MADCCAKQEP ERNECFLQHK DDNPNLPRLV RPEVDVMCTA FHDNEETFLK
       170        180        190        200        210        220        230        240
KYLYEIARRH PYFYAPELLF FAKRYKAAFT ECCQAADKAA CLLPKLDELR DEGKASSAKQ RLKCASLQKF GERAFKAWAV
       250        260        270        280        290        300        310        320
ARLSQRFPKA EFAEVSKLVT DLTKVHTECC HGDLLECADD RADLAKYICE NQDSISSKLK ECCEKPLLEK SHCIAEVEND
       330        340        350        360        370        380        390        400
EMPADLPSLA ADFVESKDVC KNYAEAKDVF LGMFLYEYAR RHPDYSVVLL LRLAKTYETT LEKCCAAADP HECYAKVFDE
       410        420        430        440        450        460        470        480
FKPLVEEPQN LIKQNCELFE QLGEYKFQNA LLVRYTKKVP QVSTPTLVEV SRNLGKVGSK CCKHPEAKRM PCAEDYLSVV
       490        500        510        520        530        540        550        560
LNQLCVLHEK TPVSDRVTKC CTESLVNRRP CFSALEVDET YVPKEFNAET FTFHADICTL SEKERQIKKQ TALVELVKHK
       570        580        590        600        610
PKATKEQLKA VMDDFAAFVE KCCKADDKET CFAEEGKKLV AASQAALGL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 250 | 12 | 613.8261 | 32.39 | 2 | 33.1 | 70.4 | 1 | 35-44 | R.FKDLGEENFK.A | | WUP:QUP 1.90<br>QU:MU 1.13 |
| 514 | 15 | 575.2390 | -125.46 | 2 | 34.9 | 63.4 | 0 | 66-75 | K.LVNEVTEFAK.T | | |
| 529 | 11 | 509.2667 | -10.16 | 2 | 36.6 | 49.5 | 0 | 89-97 | K.SLHTLFGDK.L | | QU:MU 0.23 |
| 299 | 2 | 467.2609 | -4.27 | 2 | 33.7 | 52.0 | 0 | 98-105 | K.LCTVATLR.E | Carbamidomethyl: 2 | |
| 265 | 3 | 879.3978 | -18.24 | 3 | 33.3 | 25.7 | 2 | 118-138 | K.QEPERNECFLQHKDDNPNLPR.L | Carbamidomethyl: 8 | WUP:QUP 1.09<br>QU:MU 1.47 |
| 279 | 2 | 666.3028 | -17.84 | 3 | 33.5 | 40.0 | 1 | 123-138 | R.NECFLQHKDDNPNLPR.L | Carbamidomethyl: 3 | WUP:QUP 0.81<br>QU:MU 1.34 |
| | | | | | | | | | | | WUP:QUP 2.55 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 350 | 3 | 528.2959 | -3.73 | 2 | 34.4 | 39.6 | 1 | 161-168 | K.KYLYEIAR.R |  | QU:MU 0.82 |
| 326 | 11 | 464.1239 | -272.44 | 2 | 32.8 | 30.1 | 0 | 162-168 | K.YLYEIAR.R |  | WUP:QUP 0.87<br>QU:MU 1.39 |
| 18 | 2 | 686.2378 | -71.67 | 2 | 29.2 | 64.2 | 0 | 187-198 | K.AAFTECCQAADK.A | Carbamidomethyl: 6, 7 |  |
| 1590 | 1 | 977.4188 | -47.42 | 2 | 50.1 | 11.8 | 1 | 187-205 | K.AAFTECCQAADKAACLLPK.L |  |  |
| 31 | 4 | 537.7767 | 3.24 | 2 | 30.1 | 45.4 | 1 | 206-214 | K.LDELRDEGK.A |  | QU:MU 2.86<br>WUP:QUP 0.31 |
| 143 | 2 | 696.2767 | -10.48 | 3 | 31.5 | 53.1 | 0 | 265-281 | K.VHTECCHGDLLECADDR.A | Carbamidomethyl: 5, 6, 13 | WUP:QUP 0.63<br>QU:MU 1.67 |
| 45 | 8 | 722.3225 | -3.01 | 2 | 30.4 | 77.4 | 0 | 287-298 | K.YICENQDSISSK.L | Carbamidomethyl: 3 | WUP:QUP 0.50<br>QU:MU 1.82 |
| 104 | 1 | 773.8655 | -47.15 | 2 | 31.0 | 20.6 | 1 | 299-310 | K.LKECCEKPLLEK.S | Carbamidomethyl: 4, 5 | WUP:QUP 0.64 |
| 2459 | 1 | 997.4538 | 2.48 | 3 | 59.0 | 27.7 | 0 | 311-337 | K.<br>SHCIAEVENDEMPADLPSLAADFV<br>D | Carbamidomethyl: 3;<br>Oxidation: 12 |  |
| 2841 | 5 | 812.4044 | 8.52 | 2 | 65.9 | 42.2 | 0 | 348-360 | K.DVFLGMFLYEYAR.R |  |  |
| 2516 | 10 | 820.4094 | 17.73 | 2 | 59.7 | 54.5 | 0 | 348-360 | K.DVFLGMFLYEYAR.R | Oxidation: 6 | WUP:QUP 2.21 |
| 8 | 5 | 776.7890 | -17.37 | 2 | 29.1 | 42.3 | 0 | 384-396 | K.CCAAADPHECYAK.V | Carbamidomethyl: 1, 2, 10 |  |
| 2964 | 40 | 682.3684 | -2.26 | 3 | 65.8 | 51.0 | 0 | 397-413 | K.VFDEFKPLVEEPQNLIK.Q |  |  |
| 1272 | 12 | 829.3522 | -33.47 | 2 | 45.5 | 60.5 | 0 | 414-426 | K.QNCELFEQLGEYK.F | Carbamidomethyl: 3 | WUP:QUP 0.90<br>QU:MU 1.12 |
| 742 | 18 | 480.7783 | -13.77 | 2 | 39.3 | 53.1 | 0 | 427-434 | K.FQNALLVR.Y |  | QU:MU 1.46 |
| 694 | 1 | 547.3131 | -7.95 | 3 | 37.1 | 59.0 | 1 | 438-452 | K.KVPQVSTPTLVEVSR.N |  | WUP:QUP 0.50<br>QU:MU 1.51 |
| 930 | 1 | 756.4093 | -20.82 | 2 | 40.0 | 32.0 | 0 | 439-452 | K.VPQVSTPTLVEVSR.N |  | WUP:QUP 0.70 |
| 78 | 4 | 569.7455 | -12.45 | 2 | 30.7 | 62.5 | 0 | 500-508 | K.CCTESLVNR.R | Carbamidomethyl: 1, 2 | WUP:QUP 0.31<br>QU:MU 3.50 |
| 1168 | 1 | 637.6405 | -12.97 | 3 | 44.2 | 54.8 | 0 | 509-524 | R.RPCFSALEVDETYVPK.E | Carbamidomethyl: 3 | WUP:QUP 0.36 |
| 2419 | 11 | 753.9221 | -119.82 | 3 | 58.5 | 64.2 | 0 | 525-543 | K.EFNAETFTFHADICTLSEK.E | Carbamidomethyl: 14 | WUP:QUP 1.24 |
| 628 | 1 | 564.7514 | -179.84 | 2 | 37.9 | 25.5 | 1 | 549-558 | K.KQTALVELVK.H |  | QU:MU 1.02<br>WUP:QUP 1.60 |
| 807 | 12 | 500.7995 | -11.94 | 2 | 38.5 | 46.8 | 0 | 550-558 | K.QTALVELVK.H |  |  |
| 2104 | 14 | 671.7654 | -82.73 | 2 | 56.7 | 98.0 | 0 | 570-581 | K.AVMDDFAAFVEK.C |  | QU:MU 0.11 |
| 27 | 1 | 543.2457 | -2.64 | 3 | 30.0 | 35.7 | 2 | 585-598 | K.ADDKETCFAEEGKK.L | Carbamidomethyl: 7 |  |
| 895 | 1 | 571.3207 | -52.32 | 2 | 39.6 | 22.1 | 1 | 598-609 | K.KLVAASQAALGL.- |  |  |

BRUKER

# Detailed Protein Report

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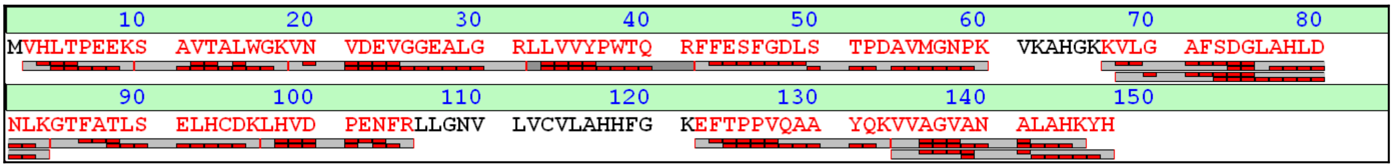
## **Protein 2:** hemoglobin subunit beta [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4504349 | **Score:** | 703.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 16.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 84.4 |
| | | **No. of unique Peptides:** | 12 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.65 | **CV:** | 69.99 % | **No. of Peptides:** | 7 |
| ***WUP:QUP*** | **Median:** | 0.51 | **CV:** | 49.14 % | **No. of Peptides:** | 10 |



| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 63 | 3 | 476.7531 | -11.35 | 2 | 30.5 | 38.7 | 0 | 2-9 | M.VHLTPEEK.S | | QU:MU 1.43<br>WUP:QUP 0.36 |
| 629 | 13 | 466.7591 | -9.74 | 2 | 36.3 | 58.8 | 0 | 10-18 | K.SAVTALWGK.V | | WUP:QUP 1.66<br>QU:MU 0.23 |
| 496 | 9 | 657.8496 | 20.65 | 2 | 36.2 | 81.3 | 0 | 19-31 | K.VNVDEVGGEALGR.L | | WUP:QUP 0.57 |
| 2284 | 26 | 637.8143 | -81.79 | 2 | 56.9 | 61.8 | 0 | 32-41 | R.LLVVYPWTQR.F | | WUP:QUP 0.46<br>QU:MU 0.52 |
| 2107 | 7 | 1029.8517 | -122.16 | 2 | 56.7 | 64.9 | 0 | 42-60 | R.FFESFGDLSTPDAVMGNPK.V | | |
| 2980 | 23 | 599.9999 | -0.41 | 3 | 66.0 | 82.5 | 1 | 67-83 | K.KVLGAFSDGLAHLDNLK.G | | WUP:QUP 0.28 |
| 2515 | 57 | 835.4601 | 13.21 | 2 | 59.7 | 95.3 | 0 | 68-83 | K.VLGAFSDGLAHLDNLK.G | | WUP:QUP 0.75 |
| 527 | 3 | 739.8504 | -0.54 | 2 | 35.0 | 36.5 | 0 | 84-96 | K.GTFATLSELHCDK.L | Carbamidomethyl: 11 | WUP:QUP 0.38<br>QU:MU 0.70 |
| 187 | 13 | 563.6579 | -226.49 | 2 | 31.2 | 45.5 | 0 | 97-105 | K.LHVDPENFR.L | | QU:MU 1.24<br>WUP:QUP 0.42 |
| 532 | 2 | 689.8492 | -6.46 | 2 | 36.6 | 44.0 | 0 | 122-133 | K.EFTPPVQAAYQK.V | | WUP:QUP 0.46<br>QU:MU 0.97 |
| 307 | 6 | 575.3418 | 2.06 | 2 | 33.8 | 76.7 | 0 | 134-145 | K.VVAGVANALAHK.Y | | QU:MU 0.32 |
| 430 | 1 | 725.3587 | -59.21 | 2 | 35.4 | 17.7 | 1 | 134-147 | K.VVAGVANALAHKYH.- | | WUP:QUP 0.49 |

# Detailed Protein Report

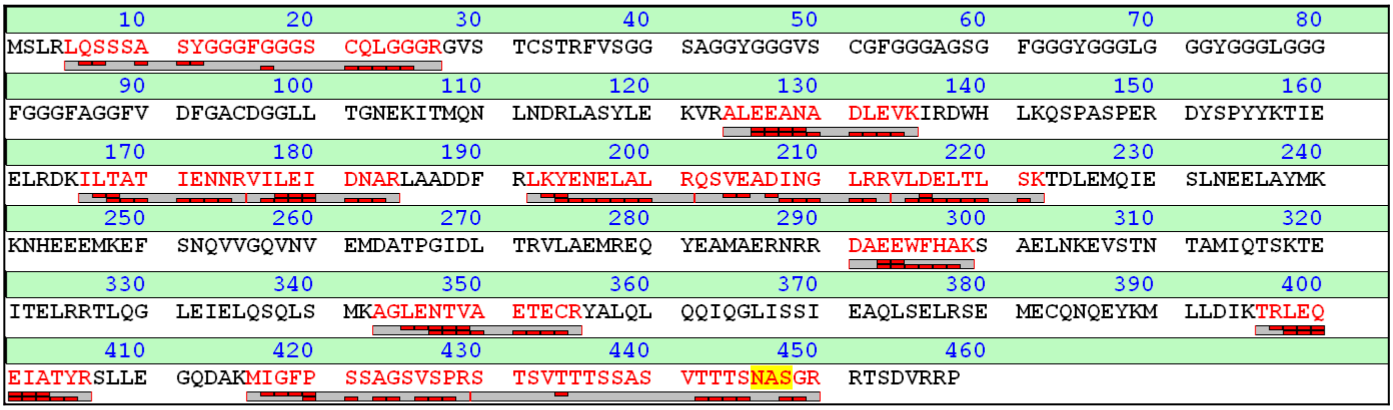
## Protein 3: keratin, type I cytoskeletal 13 isoform a [Homo sapiens]

**Accession:** gi|131412225
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 575.0
**MW [kDa]:** 49.5
**pI:** 4.8
**Sequence Coverage [%]:** 33.4
**No. of unique Peptides:** 12

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.04 | **CV:** | 25.84 % | **No. of Peptides:** | 7 |
| ***WUP:QUP*** | **Median:** | 1.09 | **CV:** | 110.84 % | **No. of Peptides:** | 8 |



```
        10         20         30         40         50         60         70         80
MSLRLQSSSA SYGGGFGGGS CQLGGGRGVS TCSTRFVSGG SAGGYGGGVS CGFGGGAGSG FGGGYGGGLG GGYGGGLGGG
        90        100        110        120        130        140        150        160
FGGGFAGGFV DFGACDGGLL TGNEKITMQN LNDRLASYLE KVRALEEANA DLEVKIRDWH LKQSPASPER DYSPYYKTIE
       170        180        190        200        210        220        230        240
ELRDKILTAT IENNRVILEI DNARLAADDF RLKYENELAL RQSVEADING LRRVLDELTL SKTDLEMQIE SLNEELAYMK
       250        260        270        280        290        300        310        320
KNHEEEMKEF SNQVVGQVNV EMDATPGIDL TRVLAEMREQ YEAMAERNRR DAEEWFHAKS AELNKEVSTN TAMIQTSKTE
       330        340        350        360        370        380        390        400
ITELRRTLQG LEIELQSQLS MKAGLENTVA ETECRYALQL QQIQGLISSI EAQLSELRSE MECQNQEYKM LLDIKTRLEQ
       410        420        430        440        450        460
EIATYRSLLE GQDAKMIGFP SSAGSVSPRS TSVTTTSSAS VTTTSNASGR RTSDVRRP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 337 | 2 | 1073.9554 | -24.90 | 2 | 34.2 | 51.4 | 0 | 5-27 | R. LQSSSASYGGGFGGGSCQLGGG G | Carbamidomethyl: 17 | WUP:QUP 1.88<br>QU:MU 0.75 |
| 323 | 3 | 651.3296 | -4.86 | 2 | 34.0 | 78.4 | 0 | 124-135 | R.ALEEANADLEVK.I | | |
| 264 | 4 | 572.8011 | -32.35 | 2 | 33.3 | 62.0 | 0 | 166-175 | K.ILTATIENNR.V | | WUP:QUP 0.13 |
| 547 | 1 | 521.6684 | -248.82 | 2 | 36.4 | 53.1 | 0 | 176-184 | R.VILEIDNAR.L | | QU:MU 1.21<br>WUP:QUP 2.66 |
| 518 | 1 | 624.8405 | -16.71 | 2 | 36.5 | 46.5 | 1 | 192-201 | R.LKYENELALR.Q | | WUP:QUP 1.23 |
| 322 | 1 | 679.3584 | -6.47 | 2 | 34.0 | 14.0 | 1 | 202-213 | R.QSVEADINGLRR.V | | WUP:QUP 1.52<br>QU:MU 1.32 |
| 727 | 1 | 509.2783 | -32.74 | 2 | 39.1 | 53.0 | 0 | 214-222 | R.VLDELTLSK.T | | |
| 434 | 2 | 566.7484 | -14.34 | 2 | 35.4 | 31.5 | 0 | 291-299 | R.DAEEWFHAK.S | | QU:MU 0.74 |
| 153 | 4 | 725.3478 | 16.83 | 2 | 31.6 | 68.8 | 0 | 343-355 | K.AGLENTVAETECR.Y | Carbamidomethyl: 12 | WUP:QUP 1.76<br>QU:MU 1.13 |
| 269 | 3 | 690.3609 | -9.58 | 2 | 33.1 | 55.3 | 1 | 396-406 | K.TRLEQEIATYR.S | | WUP:QUP 1.45<br>QU:MU 1.45 |
| 942 | 3 | 696.8484 | -3.18 | 2 | 41.8 | 28.0 | 0 | 416-429 | K.MIGFPSSAGSVSPR.S | | |
| 38 | 3 | 1001.9629 | -16.86 | 2 | 30.2 | 32.9 | 0 | 430-450 | R.STSVTTTSSASVTTTSNASGR. R | | WUP:QUP 0.63<br>QU:MU 0.88 |

# Detailed Protein Report

## Protein 4: apolipoprotein A-I preproprotein [Homo sapiens]

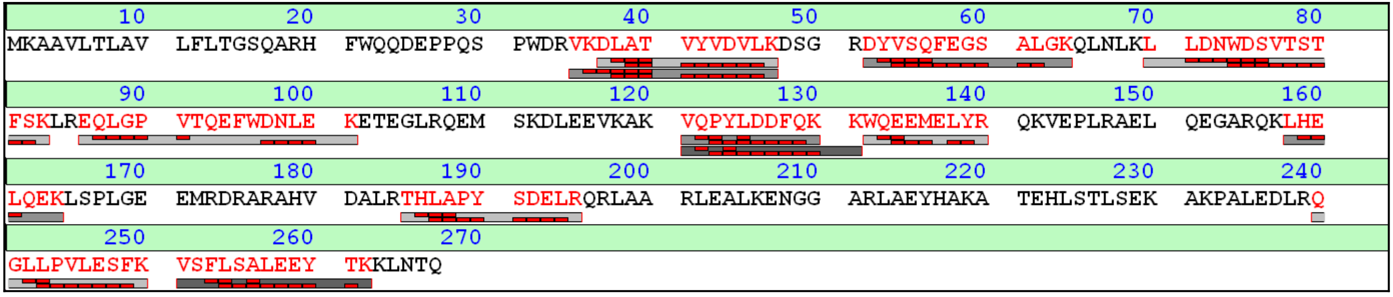
| | | | |
|---|---|---|---|
| **Accession:** | gi\|4557321 | **Score:** | 524.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 30.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| | | **Sequence Coverage [%]:** | 43.8 |
| | | **No. of unique Peptides:** | 12 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.32 | **CV:** | 17.55 % | **No. of Peptides:** | 7 |
| ***WUP:QUP*** | **Median:** | 1.01 | **CV:** | 24.03 % | **No. of Peptides:** | 6 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530398069 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: apolipoprotein A-I isoform X2 [Homo sapiens] |
| gi\|530398067 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: apolipoprotein A-I isoform X1 [Homo sapiens] |



| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKAAVLTLAV | LFLTGSQARH | FWQQDEPPQS | PWDRVKDLAT | VYVDVLKDSG | RDYVSQFEGS | ALGKQLNLKL | LDNWDSVTST |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| FSKLREQLGP | VTQEFWDNLE | KETEGLRQEM | SKDLEEVKAK | VQPYLDDFQK | KWQEEMELYR | QKVEPLRAEL | QEGARQKLHE |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| LQEKLSPLGE | EMRDRARAHV | DALRTHLAPY | SDELRQRLAA | RLEALKENGG | ARLAEYHAKA | TEHLSTLSEK | AKPALEDLRQ |
| **250** | **260** | **270** | | | | | |
| GLLPVLESFK | VSFLSALEEY | TKKLNTQ | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2017 | 8 | 731.8316 | -133.68 | 2 | 53.6 | 39.6 | 1 | 35-47 | R.VKDLATVYVDVLK.D | | |
| 2150 | 1 | 618.2001 | -238.81 | 2 | 55.2 | 52.2 | 0 | 37-47 | K.DLATVYVDVLK.D | | WUP:QUP 0.79<br>QU:MU 1.39 |
| 893 | 2 | 700.8159 | -31.87 | 2 | 39.6 | 45.2 | 0 | 52-64 | R.DYVSQFEGSALGK.Q | | QU:MU 1.22 |
| 1864 | 18 | 806.8865 | -12.14 | 2 | 51.7 | 89.9 | 0 | 70-83 | K.LLDNWDSVTSTFSK.L | | WUP:QUP 0.78<br>QU:MU 1.13 |
| 2426 | 2 | 966.9435 | -27.92 | 2 | 58.6 | 21.1 | 0 | 86-101 | R.EQLGPVTQEFWDNLEK.E | | |
| 497 | 2 | 626.6875 | -201.93 | 2 | 34.7 | 29.3 | 0 | 121-130 | K.VQPYLDDFQK.K | | QU:MU 1.15<br>WUP:QUP 1.02 |
| 257 | 4 | 690.8471 | -20.89 | 2 | 32.0 | 53.5 | 1 | 121-131 | K.VQPYLDDFQKK.W | | QU:MU 1.36<br>WUP:QUP 0.91 |
| 774 | 1 | 642.2953 | 8.43 | 2 | 39.7 | 17.4 | 0 | 132-140 | K.WQEEMELYR.Q | | QU:MU 1.94<br>WUP:QUP 1.54 |
| 1475 | 3 | 896.3833 | -111.83 | 1 | 48.6 | 11.9 | 0 | 158-164 | K.LHELQEK.L | | |
| 283 | 3 | 651.3276 | -0.37 | 2 | 33.5 | 58.6 | 0 | 185-195 | R.THLAPYSDELR.Q | | WUP:QUP 1.18<br>QU:MU 1.19 |
| 2876 | 19 | 615.8555 | -4.42 | 2 | 64.7 | 47.2 | 0 | 240-250 | R.QGLLPVLESFK.V | | |
| 2827 | 22 | 693.8609 | -0.42 | 2 | 65.8 | 57.9 | 0 | 251-262 | K.VSFLSALEEYTK.K | | |

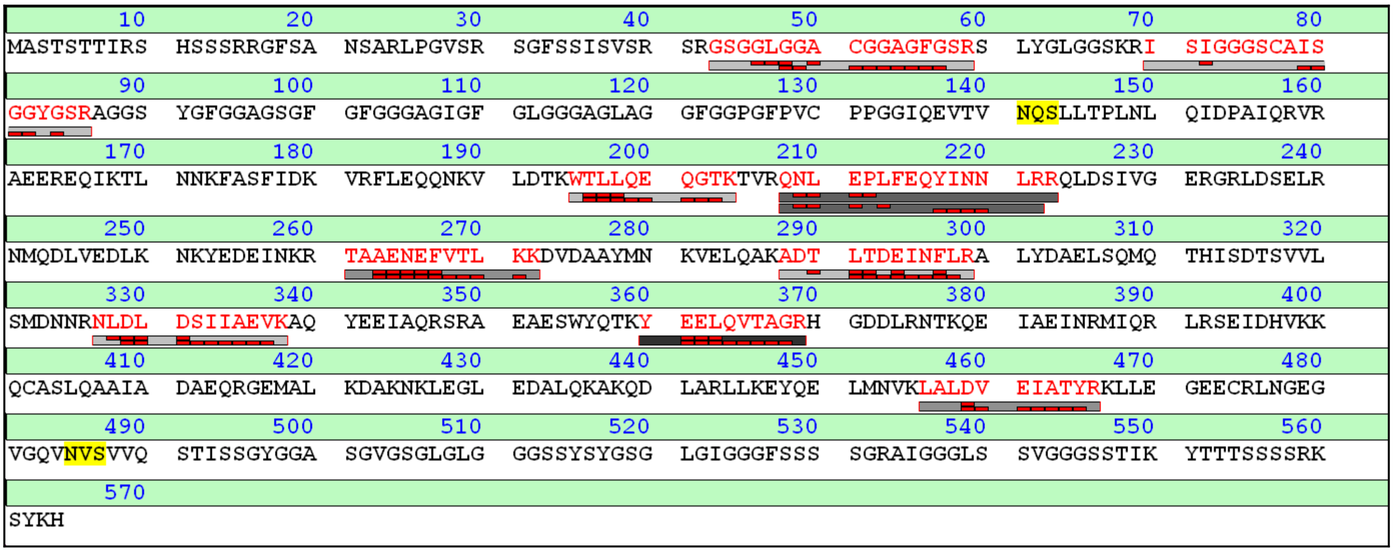
# Detailed Protein Report

## Protein 5: keratin, type II cytoskeletal 6C [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|155969697 | **Score:** | 467.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 60.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 20.7 |
| | | **No. of unique Peptides:** | 10 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.28 | **CV:** | 85.94 % | **No. of Peptides:** | 4 |
| ***WUP:QUP*** | **Median:** | 1.38 | **CV:** | 64.36 % | **No. of Peptides:** | 5 |



```
        10         20         30         40         50         60         70         80
MASTSTTIRS HSSSRRGFSA NSARLPGVSR SGFSSISVSR SRGSGGLGGA CGGAGFGSRS LYGLGGSKRI SIGGGSCAIS
        90        100        110        120        130        140        150        160
GGYGSRAGGS YGFGGAGSGF GFGGGAGIGF GLGGGAGLAG GFGGPGFPVC PPGGIQEVTV NQSLLTPLNL QIDPAIQRVR
       170        180        190        200        210        220        230        240
AEEREQIKTL NNKFASFIDK VRFLEQQNKV LDTKWTLLQE QGTKTVRQNL EPLFEQYINN LRRQLDSIVG ERGRLDSELR
       250        260        270        280        290        300        310        320
NMQDLVEDLK NKYEDEINKR TAAENEFVTL KKDVDAAYMN KVELQAKADT LTDEINFLRA LYDAELSQMQ THISDTSVVL
       330        340        350        360        370        380        390        400
SMDNNRNLDL DSIIAEVKAQ YEEIAQRSRA EAESWYQTKY EELQVTAGRH GDDLRNTKQE IAEINRMIQR LRSEIDHVKK
       410        420        430        440        450        460        470        480
QCASLQAAIA DAEQRGEMAL KDAKNKLEGL EDALQKAKQD LARLLKEYQE LMNVKLALDV EIATYRKLLE GEECRLNGEG
       490        500        510        520        530        540        550        560
VGQVNVSVVQ STISSGYGGA SGVGSGLGLG GGSSYSYGSG LGIGGGFSSS SGRAIGGGLS SVGGGSSTIK YTTTSSSSRK
       570
SYKH
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 152 | 1 | 712.8348 | 20.14 | 2 | 31.9 | 14.7 | 0 | 43-59 | R.GSGGLGGACGGAGFGSR.S | Carbamidomethyl: 9 | |
| 470 | 1 | 799.8881 | 6.12 | 2 | 35.9 | 18.2 | 0 | 70-86 | R.ISIGGGSCAISGGYGSR.A | Carbamidomethyl: 8 | WUP:QUP 2.01 |
| 808 | 1 | 602.3214 | -1.12 | 2 | 40.1 | 44.0 | 0 | 195-204 | K.WTLLQEQGTK.T | | |
| 2908 | 8 | 945.9990 | 10.55 | 2 | 65.1 | 35.8 | 0 | 208-222 | R.QNLEPLFEQYINNLR.R | | |
| 2813 | 2 | 682.9825 | -67.79 | 3 | 65.6 | 26.1 | 1 | 208-223 | R.QNLEPLFEQYINNLRR.Q | | |
| 328 | 2 | 675.8743 | 11.03 | 2 | 34.1 | 67.2 | 1 | 261-272 | R.TAAENEFVTLKK.D | | WUP:QUP 1.73<br>QU:MU 0.56 |
| 1975 | 11 | 704.2826 | -108.99 | 2 | 55.1 | 74.7 | 0 | 288-299 | K.ADTLTDEINFLR.A | | QU:MU 0.74<br>WUP:QUP 2.35 |
| 2923 | 15 | 665.3592 | -11.18 | 2 | 65.3 | 86.6 | 0 | 327-338 | R.NLDLDSIIAEVK.A | | |
| 167 | 4 | 583.1671 | -220.95 | 2 | 31.8 | 56.5 | 0 | 360-369 | K.YEELQVTAGR.H | | WUP:QUP 1.38<br>QU:MU 1.71 |
| 1633 | 4 | 632.2990 | -81.98 | 2 | 50.2 | 43.1 | 0 | 456-466 | K.LALDVEIATYR.K | | WUP:QUP 0.45<br>QU:MU 3.73 |

BRUKER

# Detailed Protein Report

## **Protein 6:** hemoglobin subunit delta [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4504351 | **Score:** | 461.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 16.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| | | **Sequence Coverage [%]:** | 48.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.14 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.16 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MVHLTPEEKT AVNALWGKVN VDAVGGEALG RLLVVYPWTQ RFFESFGDLS SPDAVMGNPK VKAHGKKVLG AFSDGLAHLD
        90        100        110        120        130        140        150
NLKGTFSQLS ELHCDKLHVD PENFRLLGNV LVCVLARNFG KEFTPQMQAA YQKVVAGVAN ALAHKYH
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 467 | 1 | 628.8213 | -19.13 | 2 | 35.8 | 42.8 | 0 | 19-31 | K.VNVDAVGGEALGR.L | | QU:MU 1.14<br>WUP:QUP 0.16 |

# Detailed Protein Report

## Protein 7: hemoglobin subunit alpha [Homo sapiens]

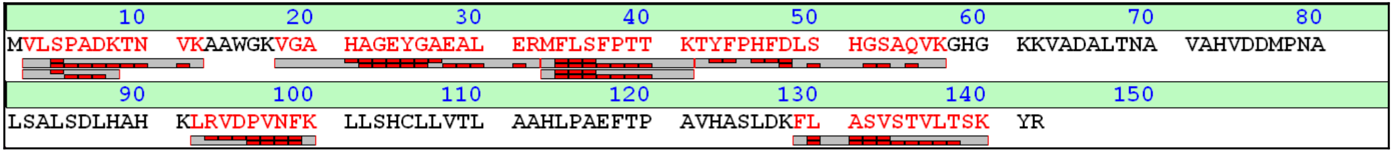
| | | | |
|---|---|---|---|
| **Accession:** | gi\|4504345 | **Score:** | 438.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 15.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 50.7 |
| | | **No. of unique Peptides:** | 8 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.55 | **CV:** | 45.17 % | **No. of Peptides:** | 3 |
| ***WUP:QUP*** | **Median:** | 0.28 | **CV:** | 94.03 % | **No. of Peptides:** | 5 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|4504347 | refseq_human<br>(refseq_human_20140103.fasta) | hemoglobin subunit alpha [Homo sapiens] |



| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 4 | 1 | 729.4098 | -5.99 | 1 | 29.0 | 28.6 | 0 | 2-8 | M.VLSPADK.T | | |
| 31 | 2 | 586.3232 | -24.65 | 2 | 29.3 | 50.8 | 1 | 2-12 | M.VLSPADKTNVK.A | | WUP:QUP 0.72 |
| 146 | 11 | 765.3477 | -30.12 | 2 | 31.6 | 78.8 | 0 | 18-32 | K.VGAHAGEYGAEALER.M | | WUP:QUP 0.74<br>QU:MU 0.96 |
| 1126 | 1 | 544.1344 | -264.30 | 2 | 42.3 | 39.7 | 0 | 33-41 | R.MFLSFPTTK.T | Oxidation: 1 | WUP:QUP 0.19 |
| 1845 | 38 | 536.1590 | -227.09 | 2 | 51.4 | 57.9 | 0 | 33-41 | R.MFLSFPTTK.T | | |
| 1189 | 4 | 917.4299 | -21.44 | 2 | 45.0 | 51.1 | 0 | 42-57 | K.TYFPHFDLSHGSAQVK.G | | QU:MU 0.50 |
| 592 | 6 | 544.3095 | -13.04 | 2 | 37.4 | 51.7 | 1 | 92-100 | K.LRVDPVNFK.L | | WUP:QUP 0.13<br>QU:MU 0.34 |
| 1648 | 39 | 626.8403 | -33.03 | 2 | 48.9 | 80.4 | 0 | 129-140 | K.FLASVSTVLTSK.Y | | WUP:QUP 0.13 |

# Detailed Protein Report

## **Protein 8:** keratin, type I cytoskeletal 15 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|24430190 | **Score:** | 385.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| | | **Sequence Coverage [%]:** | 16.0 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.36 | **CV:** | 29.32 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 3.83 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MTTTFLQTSS STFGGGSTRG GSLLAGGGGF GGGSLSGGGG SRSISASSAR FVSSGSGGGY GGGMRVCGFG GGAGSVFGGG
        90        100        110        120        130        140        150        160
FGGGVGGGFG GGFGGGDGGL LSGNEKITMQ NLNDRLASYL DKVRALEEAN ADLEVKIHDW YQKQTPTSPE CDYSQYFKTI
       170        180        190        200        210        220        230        240
EELRDKIMAT TIDNSRVILE IDNARLAADD FRLKYENELA LRQGVEADIN GLRRVLDELT LARTDLEMQI EGLNEELAYL
       250        260        270        280        290        300        310        320
KKNHEEEMKE FSSQLAGQVN VEMDAAPGVD LTRVLAEMRE QYEAMAEKNR RDVEAWFFSK TEELNKEVAS NTEMIQTSKT
       330        340        350        360        370        380        390        400
EITDLRRTMQ ELEIELQSQL SMKAGLENSL AETECRYATQ LQQIQGLIGG LEAQLSELRC EMEAQNQEYK MLLDIKTRLE
       410        420        430        440        450        460
QEIATYRSLL EGQDAKMAGI GIREASSGGG GSSSNFHINV EESVDGQVVS SHKREI
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 296 | 1 | 532.8004 | -15.38 | 2 | 33.7 | 58.7 | 1 | 116-124 | R.LASYLDKVR.A | | QU:MU 0.27 |
| 853 | 1 | 515.2848 | -30.68 | 2 | 40.2 | 40.1 | 0 | 215-223 | R.VLDELTLAR.T | | QU:MU 0.48<br>WUP:QUP 3.83 |

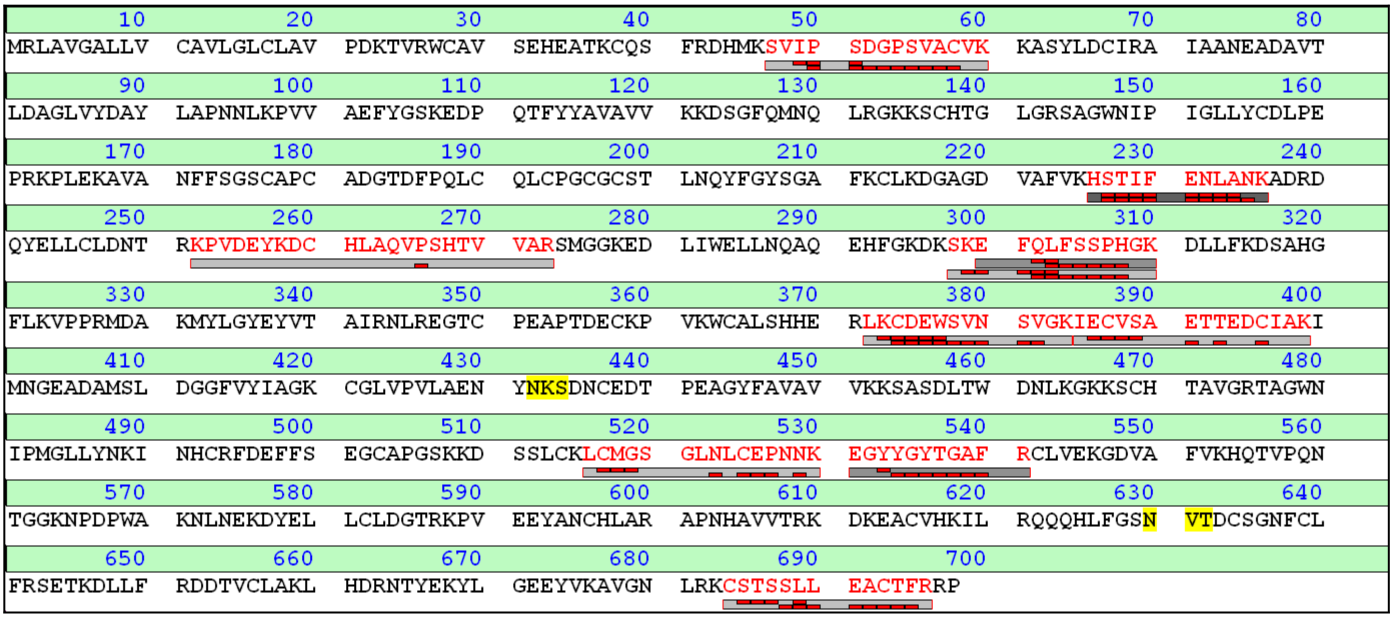
# Detailed Protein Report

## Protein 9: serotransferrin precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4557871 | **Score:** | 352.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 77.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 18.2 |
| | | **No. of unique Peptides:** | 10 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.30 | **CV:** | 33.87 % | **No. of Peptides:** | 7 |
| ***WUP:QUP*** | **Median:** | 0.94 | **CV:** | 38.12 % | **No. of Peptides:** | 6 |



```
        10         20         30         40         50         60         70         80
MRLAVGALLV CAVLGLCLAV PDKTVRWCAV SEHEATKCQS FRDHMKSVIP SDGPSVACVK KASYLDCIRA IAANEADAVT
        90        100        110        120        130        140        150        160
LDAGLVYDAY LAPNNLKPVV AEFYGSKEDP QTFYYAVAVV KKDSGFQMNQ LRGKKSCHTG LGRSAGWNIP IGLLYCDLPE
       170        180        190        200        210        220        230        240
PRKPLEKAVA NFFSGSCAPC ADGTDFPQLC QLCPGCGCST LNQYFGYSGA FKCLKDGAGD VAFVKHSTIF ENLANKADRD
       250        260        270        280        290        300        310        320
QYELLCLDNT RKPVDEYKDC HLAQVPSHTV VARSMGGKED LIWELLNQAQ EHFGKDKSKE FQLFSSPHGK DLLFKDSAHG
       330        340        350        360        370        380        390        400
FLKVPPRMDA KMYLGYEYVT AIRNLREGTC PEAPTDECKP VKWCALSHHE RLKCDEWSVN SVGKIECVSA ETTEDCIAKI
       410        420        430        440        450        460        470        480
MNGEADAMSL DGGFVYIAGK CGLVPVLAEN YNKSDNCEDT PEAGYFAVAV VKKSASDLTW DNLKGKKSCH TAVGRTAGWN
       490        500        510        520        530        540        550        560
IPMGLLYNKI NHCRFDEFFS EGCAPGSKKD SSLCKLCMGS GLNLCEPNNK EGYYGYTGAF RCLVEKGDVA FVKHQTVPQN
       570        580        590        600        610        620        630        640
TGGKNPDPWA KNLNEKDYEL LCLDGTRKPV EEYANCHLAR APNHAVVTRK DKEACVHKIL RQQQHLFGSN VTDCSGNFCL
       650        660        670        680        690        700
FRSETKDLLF RDDTVCLAKL HDRNTYEKYL GEEYVKAVGN LRKCSTSSLL EACTFRRP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 568 | 2 | 708.3474 | -22.90 | 2 | 37.1 | 42.7 | 0 | 47-60 | K.SVIPSDGPSVACVK.K | Carbamidomethyl: 12 | WUP:QUP<br>QU:MU | 1.25<br>1.10 |
| 431 | 2 | 637.3141 | -25.64 | 2 | 35.0 | 51.8 | 0 | 226-236 | K.HSTIFENLANK.A | | WUP:QUP<br>QU:MU | 0.82<br>1.39 |
| 302 | 1 | 850.4388 | 3.54 | 3 | 33.8 | 10.5 | 1 | 252-273 | R.KPVDEYKDCHLAQVPSHTVVAR.S | Carbamidomethyl: 9 | WUP:QUP | 0.63 |
| 498 | 1 | 746.3968 | 18.25 | 2 | 36.2 | 42.7 | 1 | 298-310 | K.SKEFQLFSSPHGK.D | | QU:MU | 0.82 |
| 678 | 2 | 638.8051 | -22.74 | 2 | 38.0 | 31.2 | 0 | 300-310 | K.EFQLFSSPHGK.D | | QU:MU | 2.12 |
| 172 | 3 | 761.3492 | -29.85 | 2 | 31.0 | 78.7 | 1 | 372-384 | R.LKCDEWSVNSVGK.I | Carbamidomethyl: 3 | QU:MU<br>WUP:QUP | 1.29<br>0.57 |
| 255 | 1 | 863.4074 | 23.48 | 2 | 33.2 | 14.5 | 0 | 385-399 | K.IECVSAETTEDCIAK.I | Carbamidomethyl: 3, 12 | WUP:QUP<br>QU:MU | 1.20<br>0.93 |
| 840 | 1 | 853.8816 | -5.85 | 2 | 40.5 | 22.5 | 0 | 516-530 | K.LCMGSGLNLCEPNNK.E | Carbamidomethyl: 2, 10 | | |
| 448 | 1 | 642.1562 | -205.50 | 2 | 34.1 | 34.3 | 0 | 531-541 | K.EGYYGYTGAFR.C | | QU:MU<br>WUP:QUP | 1.94<br>1.54 |
| 845 | 1 | 766.3399 | -10.08 | 2 | 39.0 | 23.0 | 0 | 684-696 | K.CSTSSLLEACTFR.R | Carbamidomethyl: 1, 10 | | |

## Protein 10: PREDICTED: alpha-2-macroglobulin isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578822814 | **Score:** | 332.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 167.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 10.3 |
| | | **No. of unique Peptides:** | 12 |

### Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.75 | **CV:** | 37.08 % | **No. of Peptides:** | 5 |
| ***WUP:QUP*** | **Median:** | 0.63 | **CV:** | 31.85 % | **No. of Peptides:** | 4 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGKNKLLHPS | LVLLLLVLLP | TDASVSGKPQ | YMVLVPSLLH | TETTEKGCVL | LSYLNETVTV | SASLESVRGN | RSLFTDLEAE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NDVLHCVAFA | VPKSSSNEEV | MFLTVQVKGP | TQEFKKRTTV | MVKNEDSLVF | VQTDKSIYKP | GQTVKFRVVS | MDENFHPLNE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LIPLVYIQDP | KGNRIAQWQS | FQLEGGLKQF | SFPLSSEPFQ | GSYKVVVQKK | SGGRTEHPFT | VEEFVLPKFE | VQVTVPKIIT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ILEEEMNVSV | CGLYTYGKPV | PGHVTVSICR | KYSDASDCHG | EDSQAFCEKF | SGQLNSHGCF | YQQVKTKVFQ | LKRKEYEMKL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HTEAQIQEEG | TVVELTGRQS | SEITRTITKL | SFVKVDSHFR | QGIPFFGQVR | LVDGKGVPIP | NKVIFIRGNE | ANYYSNATTD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EHGLVQFSIN | TTNVMGTSLT | VRVNYKDRSP | CYGYQWVSEE | HEEAHHTAYL | VFSPSKSFVH | LEPMSHELPC | GHTQTVQAHY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ILNGGTLLGL | KKLSFYYLIM | AKGGIVRTGT | HGLLVKQEDM | KGHFSISIPV | KSDIAPVARL | LIYAVLPTGD | VIGDSAKYDV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ENCLANKVDL | SFSPSQSLPA | SHAHLRVTAA | PQSVCALRAV | DQSVLLMKPD | AELSASSVYN | LLPEKDLTGF | PGPLNDQDNE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DCINRHNVYI | NGITYTPVSS | TNEKDMYSFL | EDMGLKAFTN | SKIRKPKMCP | QLQQYEMHGP | EGLRVGFYES | DVMGRGHARL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VHVEEPHTET | VRKYFPETWI | WDLVVVNSAG | VAEVGVTVPD | TITEWKAGAF | CLSEDAGLGI | SSTASLRAFQ | PFFVELTMPY |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SVIRGEAFTL | KATVLNYLPK | CIRVSVQLEA | SPAFLAVPVE | KEQAPHCICA | NGRQTVSWAV | TPKSLGNVNF | TVSAEALESQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ELCGTEVPSV | PEHGRKDTVI | KPLLVEPEGL | EKETTFNSLL | CPSGGEVSEE | LSLKLPPNVV | EESARASVSV | LGDILGSAMQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NTQNLLQMPY | GCGEQNMVLF | APNIYVLDYL | NETQQLTPEI | KSKAIGYLNT | GYQRQLNYKH | YDGSYSTFGE | RYGRNQGNTW |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LTAFVLKTFA | QARAYIFIDE | AHITQALIWL | SQRQKDNGCF | RSSGSLLNNA | IKGGVEDEVT | LSAYITIALL | EIPLTVTHPV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| VRNALFCLES | AWKTAQEGDH | GSHVYTKALL | AYAFALAGNQ | DKRKEVLKSL | NEEAVKKDNS | VHWERPQKPK | APVGHFYEPQ |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| APSAEVEMTS | YVLLAYLTAQ | PAPTSEDLTS | ATNIVKWITK | QQNAQGGFSS | TQDTVVALHA | LSKYGAATFT | RTGKAAQVTI |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| QSSGTFSSKF | QVDNNNRLLL | QQVSLPELPG | EYSMKVTGEG | CVYLQTSLKY | NILPEKEEFP | FALGVQTLPQ | TCDEPKAHTS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| FQISLSVSYT | GSRSASNMAI | VDVKMVSGFI | PLKPTVKMLE | RSNHVSRTEV | SSNHVLIYLD | KVSNQTLSLF | FTVLQDVPVR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DLKPAIVKVY | DYYETDEFAI | AEYNAPCSKG | KPLTLLQKAV | RAPSACPPNL | LLHKTLGKYL | SKTSNYSHCT | LL |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 743 | 1 | 697.8370 | -9.33 | 2 | 39.3 | 19.9 | 0 | 124-135 | K.NEDSLVFVQTDK.S | | |
| 1703 | 3 | 802.9034 | -27.20 | 2 | 49.6 | 35.7 | 0 | 175-188 | R.IAQWQSFQLEGGLK.Q | | WUP:QUP 1.07<br>QU:MU 1.50 |
| 2299 | 2 | 924.9110 | -35.46 | 2 | 57.0 | 20.1 | 0 | 189-204 | K.QFSFPLSSEPFQGSYK.V | | WUP:QUP 0.55<br>QU:MU 1.41 |
| 2052 | 5 | 574.7391 | -130.69 | 2 | 54.0 | 26.2 | 0 | 361-370 | R.QGIPFFGQVR.L | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 898 | 1 | 542.6752 | -250.41 | 2 | 39.6 | 25.9 | 0 | 522-531 | K.GHFSISIPVK.S | | |
| 276 | 2 | 636.8299 | -16.03 | 2 | 33.4 | 30.1 | 0 | 587-598 | R.VTAAPQSVCALR.A | Carbamidomethyl: 9 | QU:MU 1.12 |
| 2461 | 2 | 942.5232 | -4.52 | 2 | 59.1 | 21.9 | 0 | 824-841 | R.VSVQLEASPAFLAVPVEK.E | | |
| 305 | 2 | 558.6600 | -261.38 | 2 | 32.5 | 48.3 | 0 | 854-863 | R.QTVSWAVTPK.S | | WUP:QUP 0.48<br>QU:MU 2.34 |
| 189 | 1 | 605.6838 | -232.96 | 2 | 31.2 | 17.9 | 0 | 935-945 | K.LPPNVVEESAR.A | | WUP:QUP 0.55<br>QU:MU 2.98 |
| 2462 | 1 | 669.8332 | 5.93 | 2 | 59.1 | 43.0 | 0 | 1123-1133 | R.NALFCLESAWK.T | Carbamidomethyl: 5 | |
| 2729 | 1 | 783.4212 | 1.90 | 2 | 65.2 | 28.1 | 0 | 1148-1162 | K.ALLAYAFALAGNQDK.R | | |
| 2649 | 1 | 973.5082 | -44.93 | 2 | 64.0 | 15.9 | 1 | 1385-1401 | K.MVSGFIPLKPTVKMLER.S | | |

# Detailed Protein Report

## Protein 11: keratin, type I cytoskeletal 14 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|15431310 | **Score:** | 315.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 51.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| | | **Sequence Coverage [%]:** | 14.2 |
| | | **No. of unique Peptides:** | 3 |

```
        10         20         30         40         50         60         70         80
MTTCSRQFTS SSSMKGSCGI GGGIGGGSSR ISSVLAGGSC RAPSTYGGGL SVSSSRFSSG GAYGLGGGYG GGFSSSSSSF
        90        100        110        120        130        140        150        160
GSGFGGGYGG GLGAGLGGGF GGGFAGGDGL LVGSEKVTMQ NLNDRLASYL DKVRALEEAN ADLEVKIRDW YQRQRPAEIK
       170        180        190        200        210        220        230        240
DYSPYFKTIE DLRNKILTAT VDNANVLLQI DNARLAADDF RTKYETELNL RMSVEADING LRRVLDELTL ARADLEMQIE
       250        260        270        280        290        300        310        320
SLKEELAYLK KNHEEEMNAL RGQVGGDVNV EMDAAPGVDL SRILNEMRDQ YEKMAEKNRK DAEEWFFTKT EELNREVATN
       330        340        350        360        370        380        390        400
SELVQSGKSE ISELRRTMQN LEIELQSQLS MKASLENSLE ETKGRYCMQL AQIQEMIGSV EEQLAQLRCE MEQQNQEYKI
       410        420        430        440        450        460        470        480
LLDVKTRLEQ EIATYRRLLE GEDAHLSSSQ FSSGSQSSRD VTSSSRQIRT KVMDVHDGKV VSTHEQVLRT KN
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 88 | 1 | 713.3252 | -37.61 | 2 | 30.0 | 39.9 | 0 | 42-56 | R.APSTYGGGLSVSSSR.F | |
| 282 | 1 | 633.8578 | 31.13 | 2 | 33.5 | 20.5 | 1 | 202-211 | R.TKYETELNLR.M | |
| 246 | 2 | 512.5147 | -194.60 | 3 | 33.1 | 22.6 | 2 | 406-417 | K.TRLEQEIATYRR.L | |

# Detailed Protein Report

---

## Protein 12: titin isoform N2-A [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|291045225 | **Score:** | 283.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 3711.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 18 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.93 | **CV:** | 119.44 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 0.85 | **CV:** | 65.88 % | **No. of Peptides:** | 5 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTTQAPTFTQ | PLQSVVVLEG | STATFEAHIS | GFPVPEVSWF | RDGQVISTST | LPGVQISFSD | GRAKLTIPAV | TKANSGRYSL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KATNGSGQAT | STAELLVKAE | TAPPNFVQRL | QSMTVRQGSQ | VRLQVRVTGI | PTPVVKFYRD | GAEIQSSLDF | QISQEGDLYS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLIAEAYPED | SGTYSVNATN | SVGRATSTAE | LLVQGEEEVP | AKKTKTIVST | AQISESRQTR | IEKKIEAHFD | ARSIATVEMV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IDGAAGQQLP | HKTPPRIPPK | PKSRSPTPPS | IAAKAQLARQ | QSPSPIRHSP | SPVRHVRAPT | PSPVRSVSPA | ARISTSPIRS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VRSPLLMRKT | QASTVATGPE | VPPPWKQEGY | VASSSEAEMR | ETTLTTSTQI | RTEERWEGRY | GVQEQVTISG | AAGAAASVSA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SASYAAEAVA | TGAKEVKQDA | DKSAAVATVV | AAVDMARVRE | PVISAVEQTA | QRTTTTAVHI | QPAQEQVRKE | AEKTAVTKVV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VAADKAKEQE | LKSRTKEVIT | TKQEQMHVTH | EQIRKETEKT | FVPKVVISAA | KAKEQETRIS | EEITKKQKQV | TQEAIRQETE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ITAASMVVVA | TAKSTKLETV | PGAQEETTTQ | QDQMHLSYEK | IMKETRKTVV | PKVIVATPKV | KEQDLVSRGR | EGITTKREQV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QITQEKMRKE | AEKTALSTIA | VATAKAKEQE | TILRTRETMA | TRQEQIQVTH | GKVDVGKKAE | AVATVVAAVD | QARVREPREP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GHLEESYAQQ | TTLEYGYKER | ISAAKVAEPP | QRPASEPHVV | PKAVKPRVIQ | APSETHIKTT | DQKGMHISSQ | IKKTTDLTTE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RLVHVDKRPR | TASPHFTVSK | ISVPKTEHGY | EASIAGSAIA | TLQKELSATS | SAQKITKSVK | APTVKPSETR | VRAEPTPLPQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| FPFADTPDTY | KSEAGVEVKK | EVGVSITGTT | VREERFEVLH | GREAKVTETA | RVPAPVEIPV | TPPTLVSGLK | NVTVIEGESV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TLECHISGYP | SPTVTWYRED | YQIESSIDFQ | ITFQSGIARL | MIREAFAEDS | GRFTCSAVNE | AGTVSTSCYL | AVQVSEEFEK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ETTAVTEKFT | TEEKRFVESR | DVVMTDTSLT | EEQAGPGEPA | APYFITKPVV | QKLVEGGSVV | FGCQVGGNPK | PHVYWKKSGV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PLTTGYRYKV | SYNKQTGECK | LVISMTFADD | AGEYTIVVRN | KHGETSASAS | LLEEADYELL | MKSQQEMLYQ | TQVTAFVQEP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KVGETAPGFV | YSEYEKEYEK | EQALIRKKMA | KDTVVVRTYV | EDQEFHISSF | EERLIKEIEY | RIIKTTLEEL | LEEDGEEKMA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VDISESEAVE | SGFDSRIKNY | RILEGMGVTF | HCKMSGYPLP | KIAWYKDGKR | IKHGERYQMD | FLQDGRASLR | IPVVLPEDEG |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| IYTAFASNIK | GNAICSGKLY | VEPAAPLGAP | TYIPTLEPVS | RIRSLSPRSV | SRSPIRMSPA | RMSPARMSPA | RMSPARMSPG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| RRLEETDESQ | LERLYKPVFV | LKPVSFKCLE | GQTARFDLKV | VGRPMPETFW | FHDGQQIVND | YTHKVVIKED | GTQSLIIVPA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| TPSDSGEWTV | VAQNRAGRSS | ISVILTVEAV | EHQVKPMFVE | KLKNVNIKEG | SRLEMKVRAT | GNPNPDIVWL | KNSDIIVPHK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| YPKIRIEGTK | GEAALKIDST | VSQDSAWYTA | TAINKAGRDT | TRCKVNVEVE | FAEPEPERKL | IIPRGTYRAK | EIAAPELEPL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| HLRYGQEQWE | EGDLYDKEKQ | QKPFFKKKLT | SLRLKRFGPA | HFECRLTPIG | DPTMVVEWLH | DGKPLEAANR | LRMINEFGYC |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SLDYGVAYSR | DSGIITCRAT | NKYGTDHTSA | TLIVKDEKSL | VEESQLPEGR | KGLQRIEELE | RMAHEGALTG | VTTDQKEKQK |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| PDIVLYPEPV | RVLEGETARF | RCRVTGYPQP | KVNWYLNGQL | IRKSKRFRVR | YDGIHYLDIV | DCKSYDTGEV | KVTAENPEGV |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| IEHKVKLEIQ | QREDFRSVLR | RAPEPRPEFH | VHEPGKLQFE | VQKVDRPVDT | TETKEVVKLK | RAERITHEKV | PEESEELRSK |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| FKRRTEEGYY | EAITAVELKS | RKKDESYEEL | LRKTKDELLH | WTKELTEEEK | KALAEEGKIT | IPTFKPDKIE | LSPSMEAPKI |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| FERIQSQTVG | QGSDAHFRVR | VVGKPDPECE | WYKNGVKIER | SDRIYWYWPE | DNVCELVIRD | VTAEDSASIM | VKAINIAGET |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 619 | 1 | 690.3860 | 77.00 | 2 | 37.3 | 10.5 | 0 | 4467-4479 | R.VTNEVGSSICSAR.V | Carbamidomethyl: 10 | |
| 2868 | 1 | 805.9212 | 74.64 | 2 | 66.3 | 17.2 | 0 | 5591-5605 | K.AQNEVGSDTCVCTVK.L | Carbamidomethyl: 10 | |
| 2735 | 1 | 1045.0652 | 51.04 | 2 | 64.6 | 11.1 | 1 | 6628-6646 | K.NDAGMRECSAVLTVLEPAR.I | Carbamidomethyl: 8 | |
| 1761 | 1 | 785.8716 | -131.54 | 2 | 51.8 | 13.2 | 2 | 9274-9287 | K.IHVAISKRVEPPPK.V | | |
| 1331 | 1 | 640.2131 | -156.95 | 2 | 45.0 | 10.2 | 1 | 9719-9728 | K.EVTIMEEKER.A | Oxidation: 5 | WUP:QUP 1.16 |
| 1495 | 1 | 620.4184 | 75.49 | 3 | 48.4 | 11.8 | 2 | 10442-10458 | K.GPEISEKIIPPKKPPTK.V | | |
| 1106 | 7 | 555.2011 | -153.95 | 2 | 43.9 | 16.9 | 0 | 11321-11331 | K.GTAIFACDIAK.D | | |
| 1925 | 1 | 661.3041 | -146.74 | 2 | 54.4 | 13.5 | 1 | 12630-12641 | R.AAAHLTVIEKLR.I | | WUP:QUP 0.93 |
| 958 | 10 | 481.1097 | -309.72 | 2 | 41.5 | 15.0 | 0 | 13135-13142 | K.TWVLATDR.A | | |
| 1842 | 1 | 740.3191 | -71.84 | 2 | 53.4 | 15.5 | 2 | 13621-13633 | K.GYIVERCPRGSDK.W | | WUP:QUP 2.11<br>QU:MU 0.75 |
| 2512 | 3 | 813.3358 | -60.53 | 2 | 61.3 | 13.8 | 0 | 17073-17085 | R.VPDLLEGCQYEFR.V | Carbamidomethyl: 8 | |
| 2614 | 2 | 701.8585 | 19.90 | 2 | 62.7 | 22.1 | 1 | 27706-27717 | K.MVCSSVARTTFK.V | Carbamidomethyl: 3;<br>Oxidation: 1 | |
| 69 | 1 | 731.7932 | -168.95 | 2 | 30.8 | 10.2 | 1 | 28600-28611 | K.QLTFTVERLVEK.T | | |
| 560 | 1 | 607.8375 | 45.47 | 2 | 37.0 | 10.1 | 1 | 29711-29721 | R.AQNEKGVSEPR.E | | WUP:QUP 0.40 |
| 658 | 1 | 677.6643 | -16.40 | 3 | 38.2 | 11.8 | 2 | 31095-31112 | K.DAGFYVVCAKNRFGIDQK.T | | |
| 2593 | 1 | 616.1731 | -223.16 | 2 | 60.7 | 11.0 | 1 | 31970-31979 | R.MPYDVPEPRK.Y | | |
| 2811 | 1 | 1052.5183 | -55.98 | 2 | 65.6 | 16.6 | 0 | 32274-32291 | R.SLSPTYIELMRPVSELIR.S | | |
| 27 | 1 | 731.6483 | -99.39 | 3 | 29.3 | 11.9 | 2 | 32802-32820 | K.TNLQFMGQAFKSIHEKVSK.I | | WUP:QUP 0.49<br>QU:MU 4.95 |

# Detailed Protein Report

## Protein 13: keratin, type II cytoskeletal 5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|119395754 | **Score:** | 273.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 62.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 13.7 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.06 | **CV:** | 13.88 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 1.54 | **CV:** | 18.38 % | **No. of Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSRQSSVSFR | SGGSRSFSTA | SAITPSVSRT | SFTSVSRSGG | GGGGGFGRVS | LAGACGVGGY | GSRSLYNLGG | SKRISISTSG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GSFRNRFGAG | AGGGYGFGGG | AGSGFGFGGG | AGGGFGLGGG | AGFGGGFGGP | GFPVCPPGGI | QEVTVNQSLL | TPLNLQIDPS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IQRVRTEERE | QIKTLNNKFA | SFIDKVRFLE | QQNKVLDTKW | TLLQEQGTKT | VRQNLEPLFE | QYINNLRRQL | DSIVGERGRL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DSELRNMQDL | VEDFKNKYED | EINKRTTAEN | EFVMLKKDVD | AAYMNKVELE | AKVDALMDEI | NFMKMFFDAE | LSQMQTHVSD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TSVVLSMDNN | RNLDLDSIIA | EVKAQYEEIA | NRSRTEAESW | YQTKYEELQQ | TAGRHGDDLR | NTKHEISEMN | RMIQRLRAEI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DNVKKQCANL | QNAIADAEQR | GELALKDARN | KLAELEEALQ | KAKQDMARLL | REYQELMNTK | LALDVEIATY | RKLLEGEECR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LSGEGVGPVN | ISVVTSSVSS | GYGSGSGYGG | GLGGGLGGGL | GGGLAGGSSG | SYYSSSSGGV | GLGGGLSVGG | SGFSASSGRG |
| 570 | 580 | 590 | 600 | | | | |
| LGVGFGSGGG | SSSSVKFVST | TSSSRKSFKS | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 585 | 1 | 851.2523 | -176.11 | 2 | 36.9 | 23.4 | 0 | 406-420 | K.QCANLQNAIADAEQR.G | Carbamidomethyl: 2 | WUP:QUP 1.85<br>QU:MU 0.92 |
| 455 | 1 | 720.3680 | 11.23 | 2 | 35.7 | 13.9 | 0 | 560-576 | R.GLGVGFGSGGGSSSSVK.F | | WUP:QUP 1.28<br>QU:MU 1.21 |

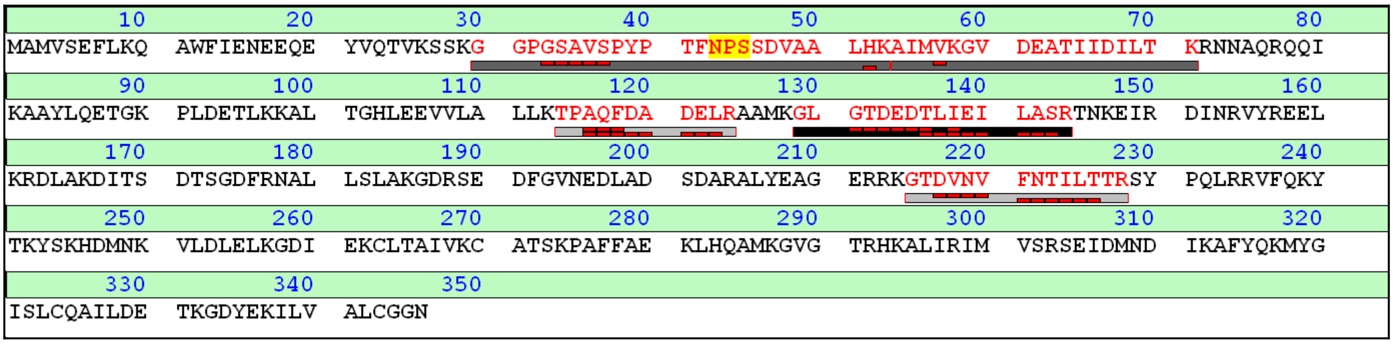
# Detailed Protein Report

## Protein 14: annexin A1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4502101 | **Score:** | 224.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 24.0 |
| | | **No. of unique Peptides:** | 5 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.79 | **CV:** | 25.20 % | **No. of Peptides:** | 3 |
| ***WUP:QUP*** | **Median:** | 1.22 | **CV:** | 0.79 % | **No. of Peptides:** | 2 |



```
        10         20         30         40         50         60         70         80
MAMVSEFLKQ AWFIENEEQE YVQTVKSSKG GPGSAVSPYP TFNPSSDVAA LHKAIMVKGV DEATIIDILT KRNNAQRQQI
        90        100        110        120        130        140        150        160
KAAYLQETGK PLDETLKKAL TGHLEEVVLA LLKTPAQFDA DELRAAMKGL GTDEDTLIEI LASRTNKEIR DINRVYREEL
       170        180        190        200        210        220        230        240
KRDLAKDITS DTSGDFRNAL LSLAKGDRSE DFGVNEDLAD SDARALYEAG ERRKGTDVNV FNTILTTRSY PQLRRVFQKY
       250        260        270        280        290        300        310        320
TKYSKHDMNK VLDLELKGDI EKCLTAIVKC ATSKPAFFAE KLHQAMKGVG TRHKALIRIM VSRSEIDMND IKAFYQKMYG
       330        340        350
ISLCQAILDE TKGDYEKILV ALCGGN
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1254 | 2 | 786.0316 | -32.49 | 3 | 45.3 | 18.2 | 0 | 30-53 | K.GGPGSAVSPYPTFNPSSDVAALHA | | QU:MU 0.59 |
| 2994 | 1 | 973.5095 | -39.14 | 2 | 66.2 | 10.2 | 1 | 54-71 | K.AIMVKGVDEATIIDILTK.R | Oxidation: 3 | |
| 422 | 1 | 631.7779 | -41.67 | 2 | 35.3 | 82.8 | 0 | 114-124 | K.TPAQFDADELR.A | | QU:MU 0.78<br>WUP:QUP 1.21 |
| 2959 | 4 | 851.9284 | -21.25 | 2 | 65.8 | 81.3 | 0 | 129-144 | K.GLGTDEDTLIEILASR.T | | |
| 2421 | 1 | 775.8147 | -125.84 | 2 | 58.5 | 32.3 | 0 | 215-228 | K.GTDVNVFNTILTTR.S | | QU:MU 1.08<br>WUP:QUP 1.23 |

# Detailed Protein Report

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## Protein 15: actin, cytoplasmic 2 [Homo sapiens]

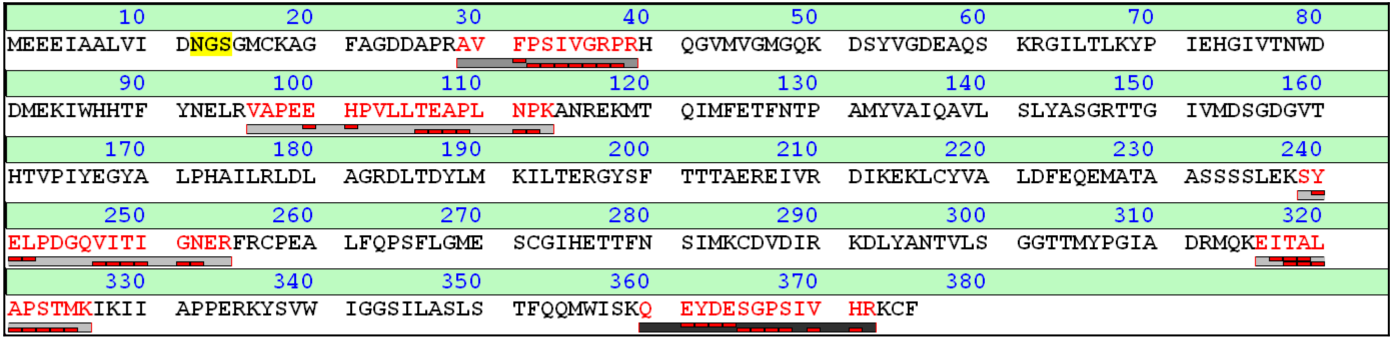
| | | | |
|---|---|---|---|
| **Accession:** | gi\|4501887 | **Score:** | 217.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| | | **Sequence Coverage [%]:** | 18.4 |
| | | **No. of unique Peptides:** | 5 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.66 | **CV:** | 11.30 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 2.75 | **CV:** | 23.69 % | **No. of Peptides:** | 4 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|316659409 | refseq_human (refseq_human_20140103.fasta) | actin, cytoplasmic 2 [Homo sapiens] |



```
        10         20         30         40         50         60         70         80
MEEEIAALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD
        90        100        110        120        130        140        150        160
DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT
       170        180        190        200        210        220        230        240
HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY
       250        260        270        280        290        300        310        320
ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL
       330        340        350        360        370        380
APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 962 | 2 | 599.7074 | -248.44 | 2 | 42.1 | 46.8 | 0 | 29-39 | R.AVFPSIVGRPR.H | | WUP:QUP 3.30 |
| 1159 | 2 | 651.9980 | -43.48 | 3 | 44.1 | 29.5 | 0 | 96-113 | R.VAPEEHPVLLTEAPLNPK.A | | |
| 1450 | 4 | 895.8455 | -116.24 | 2 | 48.3 | 44.3 | 0 | 239-254 | K.SYELPDGQVITIGNER.F | | WUP:QUP 3.60<br>QU:MU 0.59 |
| 563 | 1 | 581.2929 | -34.36 | 2 | 37.0 | 51.0 | 0 | 316-326 | K.EITALAPSTMK.I | | WUP:QUP 2.03 |
| 102 | 3 | 758.7219 | -175.32 | 2 | 31.0 | 46.3 | 0 | 360-372 | K.QEYDESGPSIVHR.K | | WUP:QUP 2.39<br>QU:MU 0.74 |

# Detailed Protein Report

## Protein 16: keratin, type II cytoskeletal 2 epidermal [Homo sapiens]

**Accession:** gi|47132620
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 200.1
**MW [kDa]:** 65.4
**pI:** 8.9
**Sequence Coverage [%]:** 5.5
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSCQISCKSR | GRGGGGGGFR | GFSSGSAVVS | GGSRRSTSSF | SCLSRHGGGG | GGFGGGGFGS | RSLVGLGGTK | SISISVAGGG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GGFGAAGGFG | GRGGGFGGGS | SFGGGSGFSG | GGFGGGGFGG | GRFGGFGGPG | GVGGLGGPGG | FGPGGYPGGI | HEVSVNQSLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QPLNVKVDPE | IQNVKAQERE | QIKTLNNKFA | SFIDKVRFLE | QQNQVLQTKW | ELLQQMNVGT | RPINLEPIFQ | GYIDSLKRYL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DGLTAERTSQ | NSELNNMQDL | VEDYKKKYED | EINKRTAAEN | DFVTLKKDVD | NAYMIKVELQ | SKVDLLNQEI | EFLKVLYDAE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ISQIHQSVTD | TNVILSMDNS | RNLDLDSIIA | EVKAQYEEIA | QRSKEEAEAL | YHSKYEELQV | TVGRHGDSLK | EIKIEISELN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RVIQRLQGEI | AHVKKQCKNV | QDAIADAEQR | GEHALKDARN | KLNDLEEALQ | QAKEDLARLL | RDYQELMNVK | LALDVEIATY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RKLLEGEECR | MSGDLSSNVT | VSVTSSTISS | NVASKAAFGG | SGGRGSSSGG | GYSSGSSSYG | SGGRQSGSRG | GSGGGGSISG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GGYGSGGGSG | GRYGSGGGSK | GGSISGGGYG | SGGGKHSSGG | GSRGGSSSGG | GYGSGGGGSS | SVKGSSGEAF | GSSVTFSFR |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 412 | 1 | 738.3807 | -21.14 | 2 | 35.1 | 70.4 | 0 | 198-209 | R.FLEQQNQVLQTK.W | |

# Detailed Protein Report

---

## Protein 17: keratin, type II cytoskeletal 75 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|153791158 | **Score:** | 197.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| | | **Sequence Coverage [%]:** | 8.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSRQSSITFQ | SGSRRGFSTT | SAITPAAGRS | RFSSVSVARS | AAGSGGLGRI | SSAGASFGSR | SLYNLGGAKR | VSINGCGSSC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RSGFGGRASN | RFGVNSGFGY | GGGVGGGFSG | PSFPVCPPGG | IQEVTVNQSL | LTPLHLQIDP | TIQRVRAEER | EQIKTLNNKF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ASFIDKVRFL | EQQNKVLETK | WALLQEQGSR | TVRQNLEPLF | DSYTSELRRQ | LESITTERGR | LEAELRNMQD | VVEDFKVRYE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DEINKRTAAE | NEFVALKKDV | DAAYMNKVEL | EAKVKSLPEE | INFIHSVFDA | ELSQLQTQVG | DTSVVLSMDN | NRNLDLDSII |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AEVKAQYEDI | ANRSRAEAES | WYQTKYEELQ | VTAGRHGDDL | RNTKQEISEM | NRMIQRLRAE | IDSVKKQCSS | LQTAIADAEQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RGELALKDAR | AKLVDLEEAL | QKAKQDMARL | LREYQELMNI | KLALDVEIAT | YRKLLEGEEC | RLSGEGVSPV | NISVVTSTLS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SGYGSGSSIG | GGNLGLGGGS | GYSFTTSGGH | SLGAGLGGSG | FSATSNRGLG | GSGSSVKFVS | TTSSSQKSYT | H |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 300 | 1 | 678.9411 | 74.83 | 2 | 32.5 | 11.4 | 1 | 413-424 | K.LVDLEEALQKAK.Q | |

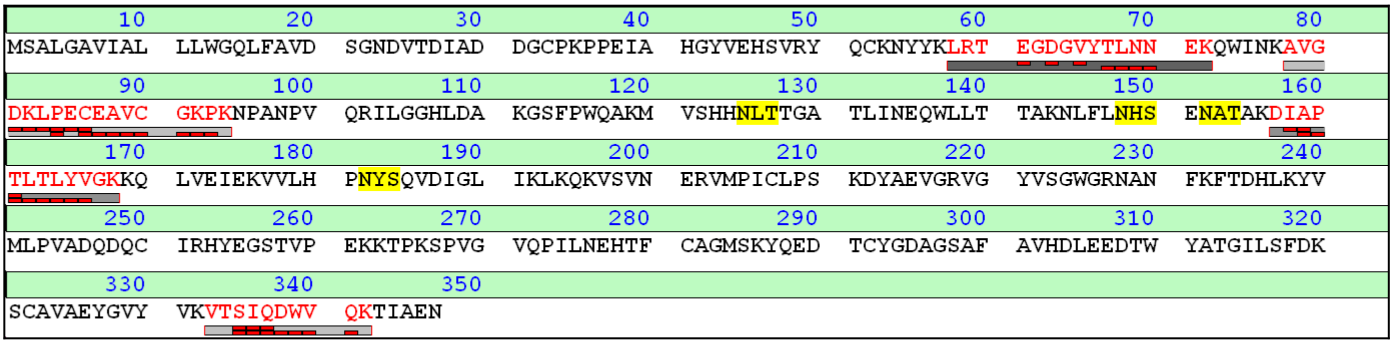
# Detailed Protein Report

## Protein 18: haptoglobin isoform 2 preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|186910296 | **Score:** | 190.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 15.6 |
| | | **No. of unique Peptides:** | 4 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.99 | **CV:** | 43.43 % | **No. of Peptides:** | 4 |
| ***WUP:QUP*** | **Median:** | 0.74 | **CV:** | 66.89 % | **No. of Peptides:** | 4 |



```
        10         20         30         40         50         60         70         80
MSALGAVIAL LLWGQLFAVD SGNDVTDIAD DGCPKPPEIA HGYVEHSVRY QCKNYYKLRT EGDGVYTLNN EKQWINKAVG
        90        100        110        120        130        140        150        160
DKLPECEAVC GKPKNPANPV QRILGGHLDA KGSFPWQAKM VSHHNLTTGA TLINEQWLLT TAKNLFLNHS ENATAKDIAP
       170        180        190        200        210        220        230        240
TLTLYVGKKQ LVEIEKVVLH PNYSQVDIGL IKLKQKVSVN ERVMPICLPS KDYAEVGRVG YVSGWGRNAN FKFTDHLKYV
       250        260        270        280        290        300        310        320
MLPVADQDQC IRHYEGSTVP EKKTPKSPVG VQPILNEHTF CAGMSKYQED TCYGDAGSAF AVHDLEEDTW YATGILSFDK
       330        340        350
SCAVAEYGVY VKVTSIQDWV QKTIAEN
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 107 | 1 | 854.9264 | -2.66 | 2 | 30.3 | 16.6 | 1 | 58-72 | K.LRTEGDGVYTLNNEK.Q | | WUP:QUP 0.74<br>QU:MU 1.81 |
| 73 | 2 | 619.9745 | -5.86 | 3 | 29.9 | 61.3 | 1 | 78-94 | K.AVGDKLPECEAVCGKPK.N | Carbamidomethyl: 9, 13 | WUP:QUP 0.73<br>QU:MU 1.02 |
| 1754 | 7 | 645.8334 | -54.84 | 2 | 50.3 | 65.3 | 0 | 157-168 | K.DIAPTLTLYVGK.K | | QU:MU 0.94<br>WUP:QUP 0.32 |
| 741 | 2 | 602.2951 | -44.79 | 2 | 39.2 | 47.7 | 0 | 333-342 | K.VTSIQDWVQK.T | | QU:MU 0.56<br>WUP:QUP 1.76 |

BRUKER

# Detailed Protein Report

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## Protein 19: actin, aortic smooth muscle [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4501883 | **Score:** | 174.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 42.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 19.9 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|213688375 | refseq_huma (refseq_human_20140103.fasta) | actin, aortic smooth muscle [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MCEEEDSTAL VCDNGSGLCK AGFAGDDAPR AVFPSIVGRP RHQGVMVGMG QKDSYVGDEA QSKRGILTLK YPIEHGIITN
        90        100        110        120        130        140        150        160
WDDMEKIWHH SFYNELRVAP EEHPTLLTEA PLNPKANREK MTQIMFETFN VPAMYVAIQA VLSLYASGRT TGIVLDSGDG
       170        180        190        200        210        220        230        240
VTHNVPIYEG YALPHAIMRL DLAGRDLTDY LMKILTERGY SFVTTAEREI VRDIKEKLCY VALDFENEMA TAASSSSLEK
       250        260        270        280        290        300        310        320
SYELPDGQVI TIGNERFRCP ETLFQPSFIG MESAGIHETT YNSIMKCDID IRKDLYANNV LSGGTTMYPG IADRMQKEIT
       330        340        350        360        370        380
ALAPSTMKIK IIAPPERKYS VWIGGSILAS LSTFQQMWIS KQEYDEAGPS IVHRKCF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2365 | 1 | 1015.4376 | 26.15 | 2 | 60.0 | 17.3 | 0 | 2-20 | M.CEEEDSTALVCDNGSGLCK.A | Carbamidomethyl: 11 |
| 1391 | 1 | 652.6877 | 2.54 | 3 | 47.5 | 15.3 | 0 | 98-115 | R.VAPEEHPTLLTEAPLNPK.A | |

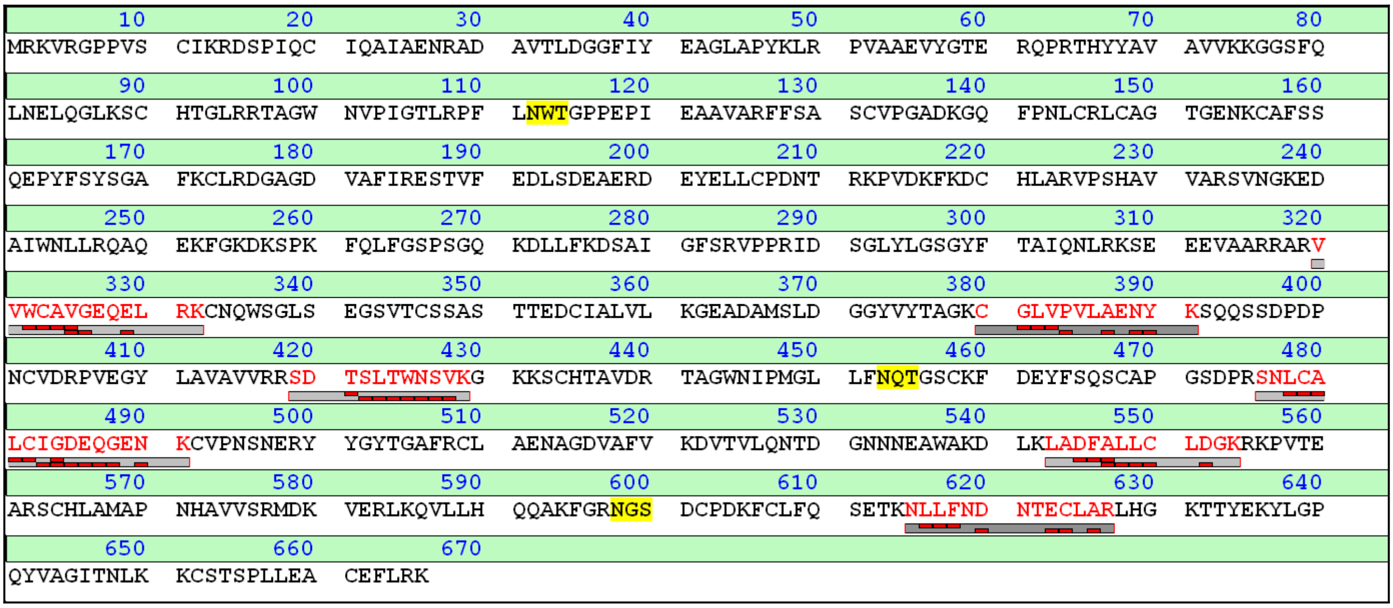
# Detailed Protein Report

## Protein 20: lactotransferrin isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|312433998 | **Score:** | 170.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 73.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 11.6 |
| | | **No. of unique Peptides:** | 6 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.73 | **CV:** | 42.10 % | **No. of Peptides:** | 3 |
| ***WUP:QUP*** | **Median:** | 3.59 | **CV:** | 25.66 % | **No. of Peptides:** | 2 |



```
        10         20         30         40         50         60         70         80
MRKVRGPPVS CIKRDSPIQC IQAIAENRAD AVTLDGGFIY EAGLAPYKLR PVAAEVYGTE RQPRTHYYAV AVVKKGGSFQ
        90        100        110        120        130        140        150        160
LNELQGLKSC HTGLRRTAGW NVPIGTLRPF LNWTGPPEPI EAAVARFFSA SCVPGADKGQ FPNLCRLCAG TGENKCAFSS
       170        180        190        200        210        220        230        240
QEPYFSYSGA FKCLRDGAGD VAFIRESTVF EDLSDEAERD EYELLCPDNT RKPVDKFKDC HLARVPSHAV VARSVNGKED
       250        260        270        280        290        300        310        320
AIWNLLRQAQ EKFGKDKSPK FQLFGSPSGQ KDLLFKDSAI GFSRVPPRID SGLYLGSGYF TAIQNLRKSE EEVAARRARV
       330        340        350        360        370        380        390        400
VWCAVGEQEL RKCNQWSGLS EGSVTCSSAS TTEDCIALVL KGEADAMSLD GGYVYTAGKC GLVPVLAENY KSQQSSDPDP
       410        420        430        440        450        460        470        480
NCVDRPVEGY LAVAVVRRSD TSLTWNSVKG KKSCHTAVDR TAGWNIPMGL LFNQTGSCKF DEYFSQSCAP GSDPRSNLCA
       490        500        510        520        530        540        550        560
LCIGDEQGEN KCVPNSNERY YGYTGAFRCL AENAGDVAFV KDVTVLQNTD GNNNEAWAKD LKLADFALLC LDGKRKPVTE
       570        580        590        600        610        620        630        640
ARSCHLAMAP NHAVVSRMDK VERLKQVLLH QQAKFGRNGS DCPDKFCLFQ SETKNLLFND NTECLARLHG KTTYEKYLGP
       650        660        670
QYVAGITNLK KCSTSPLLEA CEFLRK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 739 | 1 | 787.3768 | -43.94 | 2 | 39.2 | 13.3 | 1 | 320-332 | R.VVWCAVGEQELRK.C | Carbamidomethyl: 4 | |
| 1575 | 3 | 681.8469 | -16.13 | 2 | 49.9 | 23.1 | 0 | 380-391 | K.CGLVPVLAENYK.S | Carbamidomethyl: 1 | |
| 458 | 1 | 619.2938 | -20.74 | 2 | 35.7 | 45.8 | 0 | 419-429 | R.SDTSLTWNSVK.G | | QU:MU 1.20 |
| 593 | 1 | 904.3991 | -2.21 | 2 | 37.4 | 38.9 | 0 | 476-491 | R.SNLCALCIGDEQGENK.C | Carbamidomethyl: 4, 7 | |
| 2333 | 1 | 668.3646 | 18.05 | 2 | 59.0 | 28.6 | 0 | 543-554 | K.LADFALLCLDGK.R | Carbamidomethyl: 8 | QU:MU 0.73<br>WUP:QUP 2.79 |
| 1229 | 1 | 790.3991 | 23.83 | 2 | 45.5 | 20.9 | 0 | 615-627 | K.NLLFNDNTECLAR.L | Carbamidomethyl: 10 | WUP:QUP 4.62<br>QU:MU 0.44 |

# Detailed Protein Report

## Protein 21: POTE ankyrin domain family member F [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|153791352 | **Score:** | 148.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 121.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| | | **Sequence Coverage [%]:** | 4.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVVEVDSMPA | ASSVKKPFGL | RSKMGKWCCR | CFPCCRESGK | SNVGTSGDHD | DSAMKTLRSK | MGKWCRHCFP | CCRGSGKSNV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GASGDHDDSA | MKTLRNKMGK | WCCHCFPCCR | GSSKSKVGAW | GDYDDSAFME | PRYHVRGEDL | DKLHRAAWWG | KVPRKDLIVM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LRDTDVNKQD | KQKRTALHLA | SANGNSEVVK | LLLDRRCQLN | VLDNKKRTAL | IKAVQCQEDE | CALMLLEHGT | DPNIPDEYGN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TTLHYAIYNE | DKLMAKALLL | YGADIESKNK | HGLTPLLLGV | HEQKQQVVKF | LIKKKANLNA | LDRYGRTALI | LAVCCGSASI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VSLLLEQNID | VSSQDLSGQT | AREYAVSSHH | HVICQLLSDY | KEKQMLKISS | ENSNPEQDLK | LTSEEESQRF | KGSENSQPEK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MSQEPEINKD | GDREVEEEMK | KHESNNVGLL | ENLTNGVTAG | NGDNGLIPQR | KSRTPENQQF | PDNESEEYHR | ICELLSDYKE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KQMPKYSSEN | SNPEQDLKLT | SEEESQRLKG | SENGQPEKRS | QEPEINKDGD | RELENFMAIE | EMKKHRSTHV | GFPENLTNGA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TAGNGDDGLI | PPRKSRTPES | QQFPDTENEE | YHSDEQNDTQ | KQFCEEQNTG | ILHDEILIHE | EKQIEVVEKM | NSELSLSCKK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EKDILHENST | LREEIAMLRL | ELDTMKHQSQ | LREKKYLEDI | ESVKKRNDNL | LKALQLNELT | MDDDTAVLVI | DNGSGMCKAG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| FAGDDAPRAV | FPSIVGRPRQ | QGMMGGMHQK | ESYVGKEAQS | KRGILTLKYP | MEHGIITNWD | DMEKIWHHTF | YNELRVAPEE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| HPVLLTEATL | NPKANREKMT | QIMFETFNTP | AMYVAIQAVL | SLYTSGRTTG | IVMDSGDGVT | HTVPIYEGNA | LPHATLRLDL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| AGRELPDYLM | KILTEHGYRF | TTMAEREIVR | DIKEKLCYVA | LDFEQEMATV | ASSSSLEKSY | ELPDGQVITI | GNERFRCPEA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LFQPCFLGME | SCGIHETTFN | SIMKSDVDIR | KDLYTNTVLS | GGTTMYPGMA | HRMQKEIAAL | APSMMKIRII | APPKRKYSVW |
| 1050 | 1060 | 1070 | 1080 | | | | |
| VGGSILASLS | TFQQMWISKQ | EYDESGPSIV | HRKCL | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1070 | 1 | 670.5538 | 205.94 | 2 | 43.5 | 10.8 | 2 | 152-162 | K.VPRKDLIVMLR.D | |

# Detailed Protein Report

## Protein 22: alpha-1-antitrypsin precursor [Homo sapiens]

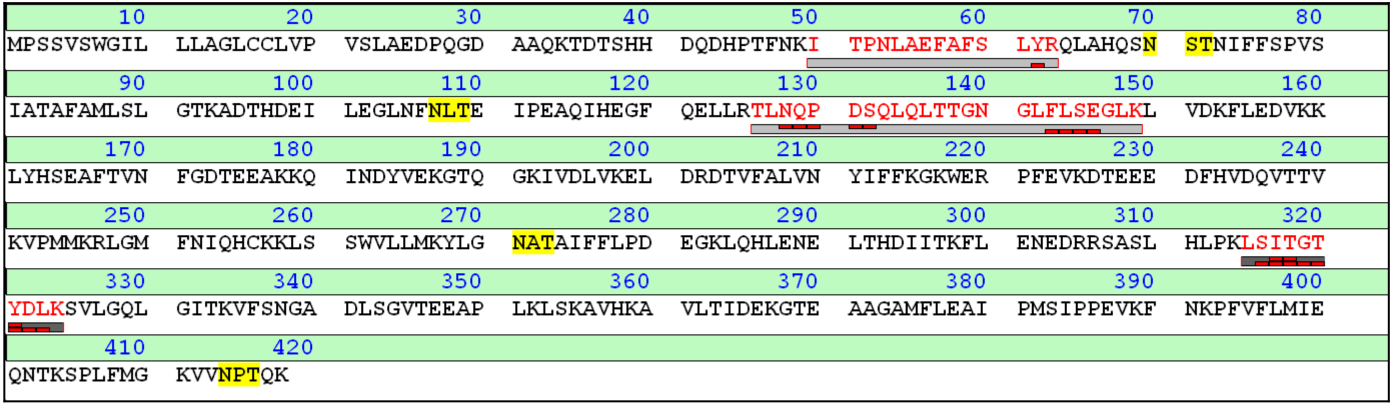
| | | | |
|---|---|---|---|
| **Accession:** | gi\|50363217 | **Score:** | 141.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 15.8 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.56 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.71 | **CV:** | 28.96 % | **No. of Peptides:** | 2 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|189163542 | refseq_huma (refseq_human_20140103.fasta) | alpha-1-antitrypsin precursor [Homo sapiens] |
| gi\|189163540 | refseq_huma (refseq_human_20140103.fasta) | alpha-1-antitrypsin precursor [Homo sapiens] |
| gi\|189163538 | refseq_huma (refseq_human_20140103.fasta) | alpha-1-antitrypsin precursor [Homo sapiens] |
| gi\|189163536 | refseq_huma (refseq_human_20140103.fasta) | alpha-1-antitrypsin precursor [Homo sapiens] |
| gi\|189163534 | refseq_huma (refseq_human_20140103.fasta) | alpha-1-antitrypsin precursor [Homo sapiens] |
| gi\|189163532 | refseq_huma (refseq_human_20140103.fasta) | alpha-1-antitrypsin precursor [Homo sapiens] |
| gi\|189163530 | refseq_huma (refseq_human_20140103.fasta) | alpha-1-antitrypsin precursor [Homo sapiens] |
| gi\|189163528 | refseq_huma (refseq_human_20140103.fasta) | alpha-1-antitrypsin precursor [Homo sapiens] |
| gi\|50363221 | refseq_huma (refseq_human_20140103.fasta) | alpha-1-antitrypsin precursor [Homo sapiens] |
| gi\|50363219 | refseq_huma (refseq_human_20140103.fasta) | alpha-1-antitrypsin precursor [Homo sapiens] |



```
        10         20         30         40         50         60         70         80
MPSSVSWGIL LLAGLCCLVP VSLAEDPQGD AAQKTDTSHH DQDHPTFNKI TPNLAEFAFS LYRQLAHQSN STNIFFSPVS
        90        100        110        120        130        140        150        160
IATAFAMLSL GTKADTHDEI LEGLNFNLTE IPEAQIHEGF QELLRTLNQP DSQLQLTTGN GLFLSEGLKL VDKFLEDVKK
       170        180        190        200        210        220        230        240
LYHSEAFTVN FGDTEEAKKQ INDYVEKGTQ GKIVDLVKEL DRDTVFALVN YIFFKGKWER PFEVKDTEEE DFHVDQVTTV
       250        260        270        280        290        300        310        320
KVPMMKRLGM FNIQHCKKLS SWVLLMKYLG NATAIFFLPD EGKLQHLENE LTHDIITKFL ENEDRRSASL HLPKLSITGT
       330        340        350        360        370        380        390        400
YDLKSVLGQL GITKVFSNGA DLSGVTEEAP LKLSKAVHKA VLTIDEKGTE AAGAMFLEAI PMSIPPEVKF NKPFVFLMIE
       410        420
QNTKSPLFMG KVVNPTQK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2521 | 1 | 821.3964 | -47.50 | 2 | 61.5 | 24.3 | 0 | 50-63 | K.ITPNLAEFAFSLYR.Q | | |
| 2391 | 1 | 1287.6505 | -18.34 | 2 | 58.2 | 20.0 | 0 | 126-149 | R.<br>TLNQPDSQLQLTTGNGLFLSEGLK<br>L | | WUP:QUP 0.94 |
| 677 | 3 | 555.6562 | -269.06 | 2 | 36.9 | 69.2 | 0 | 315-324 | K.LSITGTYDLK.S | | QU:MU 2.56<br>WUP:QUP 0.53 |

# Detailed Protein Report

## Protein 23: keratin, type II cytoskeletal 79 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|32567786 | **Score:** | 140.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.66 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRSSVSRQTY | STKGGFSSNS | ASGGSGSQAR | TSFSSVTVSR | SSGSGGGAHC | GPGTGGFGSR | SLYNLGGHKS | ISVSVAGGAL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LGRALGGFGF | GSRAFMGQGA | GRQTFGPACP | PGGIQEVTVN | QSLLTPLHVE | IDPEIQRVRT | QEREQIKTLN | NKFASFIDKV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RFLEQQNKVL | ETKWALLQEQ | GQNLGVTRNN | LEPLFEAYLG | SMRSTLDRLQ | SERGRLDSEL | RNVQDLVEDF | KNKYEDEINK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HTAAENEFVV | LKKDVDAAYM | GRMDLHGKVG | TLTQEIDFLQ | QLYEMELSQV | QTHVSNTNVV | LSMDNNRNLD | LDSIIAEVKA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QYELIAQRSR | AEAEAWYQTK | YEELQVTAGK | HGDNLRDTKN | EIAELTRTIQ | RLQGEADAAK | KQCQQLQTAI | AEAEQRGELA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LKDAQKKLGD | LDVALHQAKE | DLTRLLRDYQ | ELMNVKLALD | VEIATYRKLL | ESEESRMSGE | CPSAVSISVT | GNSTTVCGGG |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| AASFGGGISL | GGSGGATKGG | FSTNVGYSTV | KGGPVSAGTS | ILRKTTTVKT | SSQRY | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 140 | 1 | 773.9092 | 30.36 | 2 | 31.7 | 10.7 | 2 | 1-13 | -.MRSSVSRQTYSTK.G | Oxidation: 1 | QU:MU | 0.66 |

# Detailed Protein Report

## **Protein 24:** fibrinogen gamma chain isoform gamma-A precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|70906437 | **Score:** | 122.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 10.8 |
| | | **No. of unique Peptides:** | 4 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.76 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.36 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSWSLHPRNL | ILYFYALLFL | SSTCVAYVAT | RDNCCILDER | FGSYCPTTCG | IADFLSTYQT | KVDKDLQSLE | DILHQVENKT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SEVKQLIKAI | QLTYNPDESS | KPNMIDAATL | KSRKMLEEIM | KYEASILTHD | SSIRYLQEIY | NSNNQKIVNL | KEKVAQLEAQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CQEPCKDTVQ | IHDITGKDCQ | DIANKGAKQS | GLYFIKPLKA | NQQFLVYCEI | DGSGNGWTVF | QKRLDGSVDF | KKNWIQYKEG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FGHLSPTGTT | EFWLGNEKIH | LISTQSAIPY | ALRVELEDWN | GRTSTADYAM | FKVGPEADKY | RLTYAYFAGG | DAGDAFDGFD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FGDDPSDKFF | TSHNGMQFST | WDNDNDKFEG | NCAEQDGSGW | WMNKCHAGHL | NGVYYQGGTY | SKASTPNGYD | NGIIWATWKT |
| 410 | 420 | 430 | 440 | | | | |
| RWYSMKKTTM | KIIPFNRLTI | GEGQQHHLGG | AKQAGDV | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 127 | 1 | 757.2233 | -190.62 | 2 | 30.5 | 61.4 | 0 | 135-146 | R.YLQEIYNSNNQK.I | | QU:MU 1.76<br>WUP:QUP 0.36 |
| 1191 | 1 | 647.3732 | -13.52 | 2 | 43.1 | 26.2 | 0 | 189-199 | K.QSGLYFIKPLK.A | | |
| 2104 | 2 | 841.8525 | -155.05 | 2 | 54.7 | 23.4 | 0 | 259-273 | K.IHLISTQSAIPYALR.V | | |
| 353 | 1 | 559.1708 | -172.44 | 2 | 34.1 | 11.9 | 0 | 274-282 | R.VELEDWNGR.T | | |

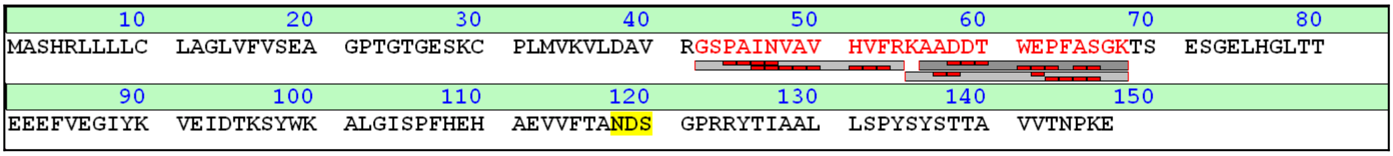
# Detailed Protein Report

**Protein 25:** **transthyretin precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4507725 | **Score:** | 120.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 15.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 18.4 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

***QU:MU*** **Median:** 1.43 **CV:** 0.00 % **No. of Peptides:** 1



```
        10        20        30        40        50        60        70        80
MASHRLLLLC LAGLVFVSEA GPTGTGESKC PLMVKVLDAV RGSPAINVAV HVFRKAADDT WEPFASGKTS ESGELHGLTT
        90       100       110       120       130       140       150
EEEFVEGIYK VEIDTKSYWK ALGISPFHEH AEVVFTANDS GPRRYTIAAL LSPYSYSTTA VVTNPKE
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1401 | 2 | 683.8722 | -15.95 | 2 | 45.9 | 76.1 | 0 | 42-54 | R.GSPAINVAVHVFR.K | | |
| 594 | 2 | 761.8596 | -3.46 | 2 | 37.4 | 15.4 | 1 | 55-68 | R.KAADDTWEPFASGK.T | | QU:MU 1.43 |
| 810 | 1 | 697.8221 | 10.50 | 2 | 40.1 | 29.0 | 0 | 56-68 | K.AADDTWEPFASGK.T | | |

# Detailed Protein Report

**Protein 26:** **neutrophil defensin 1 preproprotein [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4758146 | **Score:** | 108.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 10.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 19.1 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.71 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.65 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|124248516 | refseq_huma<br>(refseq_human_20140103.fasta) | neutrophil defensin 1 precursor [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MRTLAILAAI LLVALQAQAE PLQARADEVA AAPEQIAADI PEVVVSLAWD ESLAPKHPGS RKNMACYCRI PACIAGERRY
        90        100
GTCIYQGRLW AFCC
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 147 | 1 | 493.7604 | 4.77 | 2 | 31.8 | 52.9 | 0 | 70-78 | R.IPACIAGER.R | Carbamidomethyl: 4 | QU:MU 0.71 |
| 108 | 3 | 559.2630 | 8.21 | 2 | 31.3 | 55.9 | 0 | 80-88 | R.YGTCIYQGR.L | Carbamidomethyl: 4 | WUP:QUP 1.65 |

# Detailed Protein Report

## Protein 27: laminin subunit alpha-2 isoform a precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|28559088 | **Score:** | 104.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 343.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 8 |

### Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.80 | **CV:** | 107.92 % | **No. of Peptides:** | 3 |
| ***WUP:QUP*** | **Median:** | 1.64 | **CV:** | 49.37 % | **No. of Peptides:** | 2 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPGAAGVLLL | LLLSGGLGGV | QAQRPQQQRQ | SQAHQQRGLF | PAVLNLASNA | LITTNATCGE | KGPEMYCKLV | EHVPGQPVRN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PQCRICNQNS | SNPNQRHPIT | NAIDGKNTWW | QSPSIKNGIE | YHYVTITLDL | QQVFQIAYVI | VKAANSPRPG | NWILERSLDD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VEYKPWQYHA | VTDTECLTLY | NIYPRTGPPS | YAKDDEVICT | SFYSKIHPLE | NGEIHISLIN | GRPSADDPSP | ELLEFTSARY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IRLRFQRIRT | LNADLMMFAH | KDPREIDPIV | TRRYYYSVKD | ISVGGMCICY | GHARACPLDP | ATNKSRCECE | HNTCGDSCDQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CCPGFHQKPW | RAGTFLTKTE | CEACNCHGKA | EECYYDENVA | RRNLSLNIRG | KYIGGGVCIN | CTQNTAGINC | ETCTDGFFRP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KGVSPNYPRP | CQPCHCDPIG | SLNEVCVKDE | KHARRGLAPG | SCHCKTGFGG | VSCDRCARGY | TGYPDCKACN | CSGLGSKNED |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PCFGPCICKE | NVEGGDCSRC | KSGFFNLQED | NWKGCDECFC | SGVSNRCQSS | YWTYGKIQDM | SGWYLTDLPG | RIRVAPQQDD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LDSPQQISIS | NAEARQALPH | SYYWSAPAPY | LGNKLPAVGG | QLTFTISYDL | EEEEEDTERV | LQLMIILEGN | DLSISTAQDE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VYLHPSEEHT | NVLLLKEESF | TIHGTHFPVR | RKEFMTVLAN | LKRVLLQITY | SFGMDAIFRL | SSVNLESAVS | YPTDGSIAAA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VEVCQCPPGY | TGSSCESCWP | RHRRVNGTIF | GGICEPCQCF | GHAESCDDVT | GECLNCKDHT | GGPYCDKCLP | GFYGEPTKGT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SEDCQPCACP | LNIPSNNFSP | TCHLDRSLGL | ICDGCPVGYT | GPRCERCAEG | YFGQPSVPGG | SCQPCQCNDN | LDFSIPGSCD |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SLSGSCLICK | PGTTGRYCEL | CADGYFGDAV | DAKNCQPCRC | NAGGSFSEVC | HSQTGQCECR | ANVQGQRCDK | CKAGTFGLQS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ARGCVPCNCN | SFGSKSFDCE | ESGQCWCQPG | VTGKKCDRCA | HGYFNFQEGG | CTACECSHLG | NNCDPKTGRC | ICPPNTIGEK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| CSKCAPNTWG | HSITTGCKAC | NCSTVGSLDF | QCNVNTGQCN | CHPKFSGAKC | TECSRGHWNY | PRCNLCDCFL | PGTDATTCDS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ETKKCSCSDQ | TGQCTCKVNV | EGIHCDRCRP | GKFGLDAKNP | LGCSSCYCFG | TTTQCSEAKG | LIRTWVTLKA | EQTILPLVDE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ALQHTTTKGI | VFQHPEIVAH | MDLMREDLHL | EPFYWKLPEQ | FEGKKLMAYG | GKLKYAIYFE | AREETGFSTY | NPQVIIRGGT |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PTHARIIVRH | MAAPLIGQLT | RHEIEMTEKE | WKYYGDDPRV | HRTVTREDFL | DILYDIHYIL | IKATYGNFMR | QSRISEISME |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VAEQGRGTTM | TPPADLIEKC | DCPLGYSGLS | CEACLPGFYR | LRSQPGGRTP | GPTLGTCVPC | QCNGHSSLCD | PETSICQNCQ |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| HHTAGDFCER | CALGYYGIVK | GLPNDCQQCA | CPLISSSNNF | SPSCVAEGLD | DYRCTACPRG | YEGQYCERCA | PGYTGSPGNP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| GGSCQECECD | PYGSLPVPCD | PVTGFCTCRP | GATGRKCDGC | KHWHAREGWE | CVFCGDECTG | LLLGDLARLE | QMVMSINLTG |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| PLPAPYKMLY | GLENMTQELK | HLLSPQRAPE | RLIQLAEGNL | NTLVTEMNEL | LTRATKVTAD | GEQTGQDAER | TNTRAKSLGE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| FIKELARDAE | AVNEKAIKLN | ETLGTRDEAF | ERNLEGLQKE | IDQMIKELRR | KNLETQKEIA | EDELVAAEAL | LKKVKKLFGE |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SRGENEEMEK | DLREKLADYK | NKVDDAWDLL | REATDKIREA | NRLFAVNQKN | MTALEKKKEA | VESGKRQIEN | TLKEGNDILD |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| EANRLADEIN | SIIDYVEDIQ | TKLPPMSEEL | NDKIDDLSQE | IKDRKLAEKV | SQAESHAAQL | NDSSAVLDGI | LDEAKNISFN |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| ATAAFKAYSN | IKDYIDEAEK | VAKEAKDLAH | EATKLATGPR | GLLKEDAKGC | LQKSFRILNE | AKKLANDVKE | NEDHLNGLKT |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| RIENADARNG | DLLRTLNDTL | GKLSAIPNDT | AAKLQAVKDK | ARQANDTAKD | VLAQITELHQ | NLDGLKKNYN | KLADSVAKTN |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| AVVKDPSKNK | IIADADATVK | NLEQEADRLI | DKLKPIKELE | DNLKKNISEI | KELINQARKQ | ANSIKVSVSS | GGDCIRTYKP |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2885 | 1 | 1023.0269 | 2.26 | 2 | 64.8 | 14.8 | 2 | 248-264 | R.IRTLNADLMMFAHKDPR.E | Oxidation: 9 | |
| 2021 | 1 | 665.3031 | -44.41 | 2 | 55.2 | 14.0 | 1 | 295-306 | R.ACPLDPATNKSR.C | Carbamidomethyl: 2 | QU:MU 0.31 |
| 892 | 1 | 739.3524 | 121.81 | 2 | 39.5 | 10.1 | 0 | 1125-1137 | K.CSCSDQTGQCTCK.V | Carbamidomethyl: 1, 10 | |
| 1065 | 1 | 836.1966 | -317.81 | 1 | 42.9 | 11.8 | 1 | 1756-1762 | K.KLFGESR.G | | |
| 445 | 1 | 475.6547 | -205.40 | 2 | 34.1 | 10.7 | 1 | 1810-1817 | K.NMTALEKK.K | Oxidation: 2 | WUP:QUP 1.03<br>QU:MU 2.57 |
| 1656 | 1 | 803.8745 | -81.91 | 2 | 50.5 | 10.4 | 2 | 1969-1982 | K.GCLQKSFRILNEAK.K | | |
| 1760 | 1 | 568.7537 | -31.99 | 2 | 52.3 | 14.8 | 0 | 2146-2156 | K.VSVSSGGDCIR.T | Carbamidomethyl: 9 | |
| 2430 | 1 | 531.0471 | -454.49 | 1 | 60.8 | 17.8 | 0 | 2291-2295 | K.ADAVR.V | | WUP:QUP 2.62<br>QU:MU 0.65 |

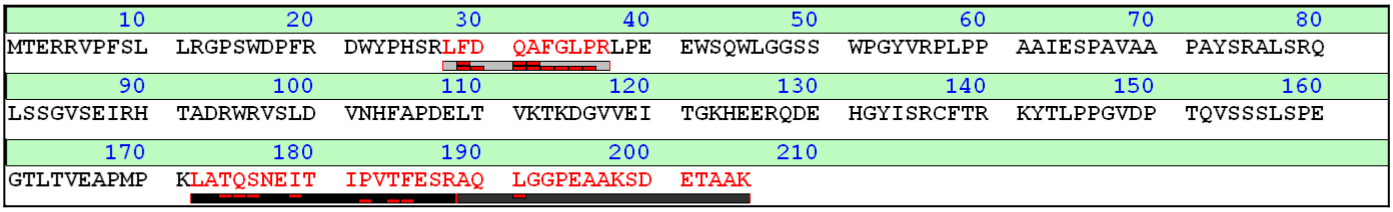
# Detailed Protein Report

## Protein 28: heat shock protein beta-1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4504517 | **Score:** | 97.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 22.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 21.5 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | |
|---|---|---|---|---|
| ***QU:MU*** | **Median:** 0.88 | **CV:** 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** 2.40 | **CV:** 0.00 % | **No. of Peptides:** | 1 |



```
         10         20         30         40         50         60         70         80
MTERRVPFSL LRGPSWDPFR DWYPHSRLFD QAFGLPRLPE EWSQWLGGSS WPGYVRPLPP AAIESPAVAA PAYSRALSRQ
         90        100        110        120        130        140        150        160
LSSGVSEIRH TADRWRVSLD VNHFAPDELT VKTKDGVVEI TGKHEERQDE HGYISRCFTR KYTLPPGVDP TQVSSSLSPE
        170        180        190        200        210
GTLTVEAPMP KLATQSNEIT IPVTFESRAQ LGGPEAAKSD ETAAK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1772 | 7 | 582.3088 | -9.00 | 2 | 50.5 | 62.7 | 0 | 28-37 | R.LFDQAFGLPR.L | | |
| 1635 | 1 | 953.4046 | -99.49 | 2 | 50.2 | 22.4 | 0 | 172-188 | K.LATQSNEITIPVTFESR.A | | WUP:QUP 2.40<br>QU:MU 0.88 |
| 2630 | 2 | 822.4504 | 42.56 | 2 | 63.7 | 12.6 | 1 | 189-205 | R.AQLGGPEAAKSDETAAK.- | | |

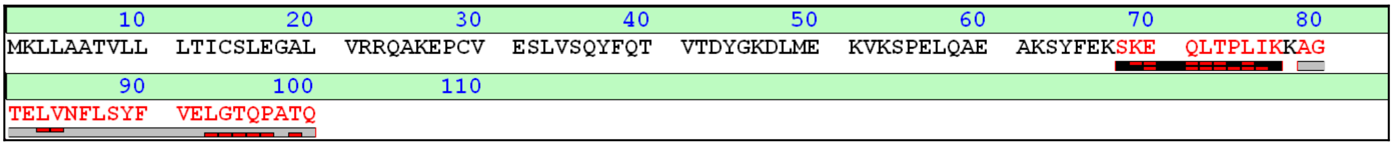
# Detailed Protein Report

---

## Protein 29: apolipoprotein A-II preproprotein [Homo sapiens]

**Accession:** gi|4502149
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 97.3
**MW [kDa]:** 11.2
**pI:** 7.1
**Sequence Coverage [%]:** 32.0
**No. of unique Peptides:** 2



```
         10         20         30         40         50         60         70         80
MKLLAATVLL LTICSLEGAL VRRQAKEPCV ESLVSQYFQT VTDYGKDLME KVKSPELQAE AKSYFEKSKE QLTPLIKKAG
         90        100        110
TELVNFLSYF VELGTQPATQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 457 | 3 | 578.8364 | -24.29 | 2 | 35.7 | 60.5 | 1 | 68-77 | K.SKEQLTPLIK.K | |
| 2890 | 1 | 1193.0548 | -39.81 | 2 | 64.9 | 36.7 | 0 | 79-100 | K.AGTELVNFLSYFVELGTQPATQ.- | |

# Detailed Protein Report

## Protein 30: keratin, type II cytoskeletal 1 [Homo sapiens]

**Accession:** gi|119395750
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 94.9
**MW [kDa]:** 66.0
**pI:** 8.8
**Sequence Coverage [%]:** 3.7
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSRQFSSRSG | YRSGGGFSSG | SAGIINYQRR | TTSSSTRRSG | GGGGRFSSCG | GGGGSFGAGG | GFGSRSLVNL | GGSKSISISV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ARGGGRGSGF | GGGYGGGGFG | GGGFGGGGFG | GGGIGGGGFG | GFGSGGGGFG | GGGFGGGGYG | GGYGPVCPPG | GIQEVTINQS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLQPLNVEID | PEIQKVKSRE | REQIKSLNNQ | FASFIDKVRF | LEQQNQVLQT | KWELLQQVDT | STRTHNLEPY | FESFINNLRR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RVDQLKSDQS | RLDSELKNMQ | DMVEDYRNKY | EDEINKRTNA | ENEFVTIKKD | VDGAYMTKVD | LQAKLDNLQQ | EIDFLTALYQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AELSQMQTQI | SETNVILSMD | NNRSLDLDSI | IAEVKAQYED | IAQKSKAEAE | SLYQSKYEEL | QITAGRHGDS | VRNSKIEISE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LNRVIQRLRS | EIDNVKKQIS | NLQQSISDAE | QRGENALKDA | KNKLNDLEDA | LQQAKEDLAR | LLRDYQELMN | TKLALDLEIA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TYRTLLEGEE | SRMSGECAPN | VSVSVSTSHT | TISGGGSRGG | GGGGYGSGGS | SYGSGGGSYG | SGGGGGGGRG | SYGSGGSSYG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SGGGSYGSGG | GGGGHGSYGS | GSSSGGYRGG | SGGGGGGSSG | GRGSGGGSSG | GSIGGRGSSS | GGVKSSGGSS | SVKFVSTTYS |
| 650 | | | | | | | |
| GVTR | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1554 | 1 | 692.3258 | -33.18 | 2 | 49.6 | 24.5 | 0 | 186-197 | K.SLNNQFASFIDK.V | |

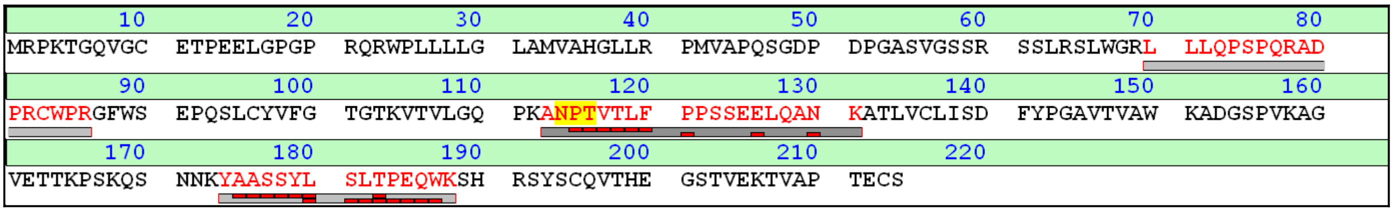
# Detailed Protein Report

## Protein 31: immunoglobulin lambda-like polypeptide 5 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|295986608 | **Score:** | 94.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 23.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 23.8 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

***WUP:QUP*** **Median:** 0.90 **CV:** 0.00 % **No. of Peptides:** 1



```
        10         20         30         40         50         60         70         80
MRPKTGQVGC ETPEELGPGP RQRWPLLLLG LAMVAHGLLR PMVAPQSGDP DPGASVGSSR SSLRSLWGRL LLQPSPQRAD
        90        100        110        120        130        140        150        160
PRCWPRGFWS EPQSLCYVFG TGTKVTVLGQ PKANPTVTLF PPSSEELQAN KATLVCLISD FYPGAVTAW KADGSPVKAG
       170        180        190        200        210        220
VETTKPSKQS NNKYAASSYL SLTPEQWKSH RSYSCQVTHE GSTVEKTVAP TECS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2042 | 1 | 1045.4503 | -102.49 | 2 | 55.9 | 14.4 | 2 | 70-86 | R.LLLQPSPQRADPRCWPR.G | Carbamidomethyl: 14 | |
| 1468 | 2 | 1022.0062 | -16.69 | 2 | 48.0 | 16.1 | 0 | 113-131 | K.ANPTVTLFPPSSEELQANK.A | | |
| 1789 | 12 | 872.4180 | -17.25 | 2 | 50.7 | 64.0 | 0 | 174-188 | K.YAASSYLSLTPEQWK.S | | WUP:QUP 0.90 |

# Detailed Protein Report

## Protein 32: PREDICTED: nesprin-2 isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578825626 | **Score:** | 91.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 553.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 7 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.75 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 6.20 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASSPELPTE | DEQGSWGIDD | LHISLQAEQE | DTQKKAFTCW | INSQLARHTS | PSVISDLFTD | IKKGHVLLDL | LEVLSGQQLP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RDKGSNTFQC | RINIEHALTF | LRNRSIKLIN | IHVTDIIDGN | PSIILGLIWT | IILHFHIEKL | AQTLSCNYNQ | PSLDDVSVVD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SSPASSPPAK | KCSKVQARWQ | MSARKALLLW | AQEQCATYES | VNVTDFKSSW | RNGMAFLAII | HALRPDLIDM | KSVKHRSNKD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NLREAFRIAE | QELKIPRLLE | PEDVDVVDPD | EKSIMTYVAQ | FLQYSKDAPG | TGEEAQGKVK | DAMGWLTLQK | EKLQKLLKDS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ENDTYFKKYN | SLLSFMESFN | EEKKSFLDVL | SIKRDLDELD | KDHLQLREAW | DGLDHQINAW | KIKLNYALPP | PLHQTEAWLQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EVEELMDEDL | SASQDHSQAV | TLIQEKMTLF | KSLMDRFEHH | SNILLTFENK | DENHLPLVPP | NKLEEMKRRI | NNILEKKFIL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LLEFHYYKCL | VLGLVDEVKS | KLDIWNIKYG | SRESVELLLE | DWHKFIEEKE | FLARLDTSFQ | KCGEIYKNLA | GECQNINKQY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MMVKSDVCMY | RKNIYNVKST | LQKVLACWAT | YVENLRLLRA | CFEETKKEEI | KEVPFETLAQ | WNLEHATLNE | AGNFLVEVSN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DVVGSSISKE | LRRLNKRWRK | LVSKTQLEMN | LPLMIKKQDQ | PTFDNSGNIL | SKEEKATVEF | STDMSVELPE | NYNQNIKAGE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KHEKENEEFT | GQLKVAKDVE | KLIGQVEIWE | AEAKSVLDQD | DVDTSMEESL | KHLIAKGSMF | DELMARSEDM | LQMDIQNISS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QESFQHVLTT | GLQAKIQEAK | EKVQINVVKL | IAALKNLTDV | SPDLDIRLKM | EESQKELESY | MMRAQQLLGQ | RESPGELISK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| HKEALIISNT | KSLAKYLKAV | EELKNNVTED | IKMSLEEKSR | DVCAKWESLH | HELSLYVQQL | KIDIEKGKLS | DNILKLEKQI |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NKEKKLIRRG | RTKGLIKEHE | ACFSEEGCLY | QLNHHMEVLR | ELCEELPSQK | SQQEVKRLLK | DYEQKIERLL | KCASEIHMTL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QPTAGGTSKN | EGTITTSENR | GGDPHSEAPF | AKSDNQPSTE | KAMEPTMKFS | LASVLRPLQE | ESIMEKDYSA | SINSLLERYD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TYRDILEHHL | QNNKFRITSD | FSSEEDRSSS | CLQAKLTDLQ | VIKNETDARW | KEFEIISLKL | ENHVNDIKKP | FVIKERDTLK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ERERELQMTL | NTRMESLETA | LRLVLPVEKA | SLLLCGSDLP | LHKMAIQGFH | LIDADRIYQH | LRNIQDSIAK | QIEICNRLEE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PGNFVLKELH | PFDLHAMQNI | ILKYKTQFEG | MNHRVQRSED | TLKALEDFLA | SLRTAKLSAE | PVTDLSASDT | QVAQENTLTV |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KNKEGEIHLM | KDKAKHLDKC | LKMLDMSFKD | AERGDDTSCE | NLLDAFSIKL | SETHGYGVQE | EFTEENKLLE | ACIFKNNELL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KNIQDVQSQI | SKIGLKDPTV | PAVKHRKKSL | IRLDKVLDEY | EEEKRHLQEM | ANSLPHFKDG | REKTVNQQCQ | NTVVLWENTK |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ALVTECLEQC | GRVLELLKQY | QNFKSILTTL | IQKEESVISL | QASYMGKENL | KKRIAEIEIV | KEEFNEHLEV | VDKINQVCKN |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LQFYLNKMKT | FEEPPFEKEA | NIIVDRWLDI | NEKTEDYYEN | LGRALALWDK | LFNLKNVIDE | WTEKALQKME | LHQLTEEDRE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| RLKEELQVHE | QKTSEFSRRV | AEIQFLLQSS | EIPLELQVME | SSILNKMEHV | QKCLTGESNC | HALSGSTAEL | REDLDQAKTQ |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| IGMTESLLKA | LSPSDSLEIF | TKLEEIQQQI | LQQKHSMILL | ENQIGCLTPE | LSELKKQYES | VSDLFNTKKS | VLQDHFSKLL |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| NDQCKNFNDW | FSNIKVNLKE | CFESSETKKS | VEQKLQKLSD | FLTLEGRNSK | IKQVDSVLKH | VKKHLPKAHV | KELISWLVGQ |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| EFELEKMESI | CQARAKELED | SLQQLLRLQD | DHRNLRKWLT | NQEEKWKGME | EPGEKTELFC | QALARKREQF | ESVAQLNNSL |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| KEYGFTEEEE | IIMEATCLMD | RYQTLLRQLS | EIEEEDKLLP | TEDQSFNDLA | HDVIHWIKEI | KESLMVLNSS | EGKMPLEERI |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| QKIKEIILLK | PEGDARIETI | MKQAESSEAP | LVQKTLTDIS | NQWDNTLHLA | STYLSHQEKL | LLEGEKYLQS | KEDLRLMLIE |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2639 | 1 | 686.8883 | 34.43 | 2 | 63.0 | 14.6 | 0 | 451-462 | K.DENHLPLVPPNK.L | | |
| 2757 | 1 | 849.0563 | -8.59 | 3 | 65.6 | 10.4 | 0 | 696-717 | K.ATVEFSTDMSVELPENYNQNIK.A | Oxidation: 9 | |
| 2961 | 1 | 927.4882 | -20.92 | 2 | 65.8 | 15.8 | 1 | 864-880 | R.AQQLLGQRESPGELISK.H | | |
| 133 | 1 | 679.8336 | -94.89 | 2 | 31.4 | 13.6 | 1 | 2192-2203 | K.AQDLTSLLKELK.S | | WUP:QUP 6.20<br>QU:MU 0.75 |
| 1892 | 1 | 628.2831 | -31.74 | 2 | 54.0 | 13.1 | 0 | 2204-2214 | K.SQGNYLLECTK.N | | |
| 1662 | 1 | 882.4096 | -80.38 | 2 | 51.0 | 13.3 | 2 | 3618-3632 | K.SEQFEELQSILKKGK.L | | |
| 1911 | 1 | 568.7711 | -62.35 | 2 | 52.2 | 11.0 | 1 | 4627-4636 | K.SLKAGLDYNR.S | | |

## Protein 33: alpha-enolase isoform 1 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|4503571 | **Score:** | 85.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 47.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.7 |
|  |  | **Sequence Coverage [%]:** | 6.9 |
|  |  | **No. of unique Peptides:** | 2 |

### Quantitation

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.82 | **CV:** | 24.50 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 1.59 | **CV:** | 16.64 % | **No. of Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MSILKIHARE IFDSRGNPTV EVDLFTSKGL FRAAVPSGAS TGIYEALELR DNDKTRYMGK GVSKAVEHIN KTIAPALVSK
        90        100        110        120        130        140        150        160
KLNVTEQEKI DKLMIEMDGT ENKSKFGANA ILGVSLAVCK AGAVEKGVPL YRHIADLAGN SEVILPVPAF NVINGGSHAG
       170        180        190        200        210        220        230        240
NKLAMQEFMI LPVGAANFRE AMRIGAEVYH NLKNVIKEKY GKDATNVGDE GGFAPNILEN KEGLELLKTA IGKAGYTDKV
       250        260        270        280        290        300        310        320
VIGMDVAASE FFRSGKYDLD FKSPDDPSRY ISPDQLADLY KSFIKDYPVV SIEDPFDQDD WGAWQKFTAS AGIQVVGDDL
       330        340        350        360        370        380        390        400
TVTNPKRIAK AVNEKSCNCL LLKVNQIGSV TESLQACKLA QANGWGVMVS HRSGETEDTF IADLVVGLCT GQIKTGAPCR
       410        420        430        440
SERLAKYNQL LRIEEELGSK AKFAGRNFRN PLAK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1942 | 1 | 902.8469 | -142.55 | 2 | 54.2 | 18.2 | 0 | 33-50 | R.AAVPSGASTGIYEALELR.D |  | WUP:QUP 1.35<br>QU:MU 1.04 |
| 1618 | 5 | 713.3563 | -14.47 | 2 | 50.5 | 67.0 | 0 | 270-281 | R.YISPDQLADLYK.S |  | WUP:QUP 1.87<br>QU:MU 0.64 |

# Detailed Protein Report

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## Protein 34: usherin isoform B [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|219842266 | **Score:** | 84.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 575.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 6 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.49 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.15 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNCPVLSLGS | GFLFQVIEML | IFAYFASISL | TESRGLFPRL | ENVGAFKKVS | IVPTQAVCGL | PDRSTFCHSS | AAAESIQFCT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QRFCIQDCPY | RSSHPTYTAL | FSAGLSSCIT | PDKNDLHPNA | HSNSASFIFG | NHKSCFSSPP | SPKLMASFTL | AVWLKPEQQG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VMCVIEKTVD | GQIVFKLTIS | EKETMFYYRT | VNGLQPPIKV | MTLGRILVKK | WIHLSVQVHQ | TKISFFINGV | EKDHTPFNAR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TLSGSITDFA | SGTVQIGQSL | NGLEQFVGRM | QDFRLYQVAL | TNREILEVFS | GDLLRLHAQS | HCRCPGSHPR | VHPLAQRYCI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PNDAGDTADN | RVSRLNPEAH | PLSFVNDNDV | GTSWVSNVFT | NITQLNQGVT | ISVDLENGQY | QVFYIIIQFF | SPQPTEIRIQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RKKENSLDWE | DWQYFARNCG | AFGMKNNGDL | EKPDSVNCLQ | LSNFTPYSRG | NVTFSILTPG | PNYRPGYNNF | YNTPSLQEFV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KATQIRFHFH | GQYYTTETAV | NLRHRYYAVD | EITISGRCQC | HGHADNCDTT | SQPYRCLCSQ | ESFTEGLHCD | RCLPLYNDKP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FRQGDQVYAF | NCKPCQCNSH | SKSCHYNISV | DPFPFEHFRG | GGGVCDDCEH | NTTGRNCELC | KDYFFRQVGA | DPSAIDVCKP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CDCDTVGTRN | GSILCDQIGG | QCNCKRHVSG | RQCNQCQNGF | YNLQELDPDG | CSPCNCNTSG | TVDGDITCHQ | NSGQCKCKAN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VIGLRCDHCN | FGFKFLRSFN | DVGCEPCQCN | LHGSVNKFCN | PHSGQCECKK | EAKGLQCDTC | RENFYGLDVT | NCKACDCDTA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GSLPGTVCNA | KTGQCICKPN | VEGRQCNKCL | EGNFYLRQNN | SFLCLPCNCD | KTGTINGSLL | CNKSTGQCPC | KLGVTGLRCN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QCEPHRYNLT | IDNFQHCQMC | ECDSLGTLPG | TICDPISGQC | LCVPNRQGRR | CNQCQPGFYI | SPGNATGCLP | CSCHTTGAVN |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| HICNSLTGQC | VCQDASIAGQ | RCDQCKDHYF | GFDPQTGRCQ | PCNCHLSGAL | NETCHLVTGQ | CFCKQFVTGS | KCDACVPSAS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| HLDVNNLLGC | SKTPFQQPPP | RGQVQSSSAI | NLSWSPPDSP | NAHWLTYSLL | RDGFEIYTTE | DQYPYSIQYF | LDTDLLPYTK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| YSYYIETTNV | HGSTRSVAVT | YKTKPGVPEG | NLTLSYIIPI | GSDSVTLTWT | TLSNQSGPIE | KYILSCAPLA | GGQPCVSYEG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| HETSATIWNL | VPFAKYDFSV | QACTSGGCLH | SLPITVTTAQ | APPQRLSPPK | MQKISSTELH | VEWSPPAELN | GIIIRYELYM |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| RRLRSTKETT | SEESRVFQSS | GWLSPHSFVE | SANENALKPP | QTMTTITGLE | PYTKYEFRVL | AVNMAGSVSS | AWVSERTGES |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| APVFMIPPSV | FPLSSYSLNI | SWEKPADNVT | RGKVVGYDIN | MLSEQSPQQS | IPMAFSQLLH | TAKSQELSYT | VEGLKPYRIY |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EFTITLCNSV | GCVTSASGAG | QTLAAAPAQL | RPPLVKGINS | TTIHLKWFPP | EELNGPSPIY | QLERRESSLP | ALMTTMMKGI |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| RFIGNGYCKF | PSSTHPVNTD | FTGIKASFRT | KVPEGLIVFA | ASPGNQEEYF | ALQLKKGRLY | FLFDPQGSPV | EVTTTNDHGK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QYSDGKWHEI | IAIRHQAFGQ | ITLDGIYTGS | SAILNGSTVI | GDNTGVFLGG | LPRSYTILRK | DPEIIQKGFV | GCLKDVHFMK |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| NYNPSAIWEP | LDWQSSEEQI | NVYNSWEGCP | ASLNEGAQFL | GAGFLELHPY | MFHGGMNFEI | SFKFRTDQLN | GLLLFVYNKD |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| GPDFLAMELK | SGILTFRLNT | SLAFTQVDLL | LGLSYCNGKW | NKVIIKKEGS | FISASVNGLM | KHASESGDQP | LVVNSPVYVG |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| GIPQELLNSY | QHLCLEQGFG | GCMKDVKFTR | GAVVNLASVS | SGAVRVNLDG | CLSTDSAVNC | RGNDSILVYQ | GKEQSVYEGG |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LQPFTEYLYR | VIASHEGGSV | YSDWSRGRTT | GAAPQSVPTP | SRVRSLNGYS | IEVTWDEPVV | RGVIEKYILK | AYSEDSTRPP |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| RMPSASAEFV | NTSNLTGILT | GLLPFKNYAV | TLTACTLAGC | TESSHALNIS | TPQEAPQEVQ | PPVAKSLPSS | LLLSWNPPKK |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| ANGIITQYCL | YMDGRLIYSG | SEENYTVTDL | AVFTPHQFLL | SACTHVGCTN | SSWVLLYTAQ | LPPEHVDSPV | LTVLDSRTIH |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 449 | 1 | 565.3223 | -66.47 | 2 | 35.3 | 13.2 | 1 | 200-209 | K.VMTLGRILVK.K | | |
| 2191 | 1 | 863.3484 | -20.01 | 2 | 55.8 | 14.2 | 0 | 794-811 | K.ACDCDTAGSLPGTVCNAK.T | | |
| 2688 | 2 | 885.4613 | 98.77 | 2 | 63.8 | 13.3 | 0 | 838-851 | R.QNNSFLCLPCNCDK.T | Carbamidomethyl: 7, 10, 12 | |
| 1593 | 1 | 1172.1148 | 23.38 | 2 | 50.1 | 15.7 | 0 | 3098-3119 | K.SNGTQITTVEDTPSDIPTPTIR.G | | |
| 864 | 1 | 471.1407 | -194.52 | 2 | 39.2 | 18.2 | 0 | 3546-3554 | R.GTSLSFSDK.E | | |
| 206 | 1 | 898.4111 | -54.24 | 3 | 32.3 | 10.4 | 2 | 5085-5108 | K.RMSPLNVYPPGENHMGLADTKIPI S | | WUP:QUP 1.15<br>QU:MU 1.49 |

# Detailed Protein Report

**Protein 35:** **PREDICTED: keratin, type I cytoskeletal 10 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530412176 | **Score:** | 84.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 63.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| | | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSVRYSSSKH | YSSSRSGGGG | GGGGCGGGGG | VSSLRISSSK | GSLGGGFSSG | GFSGGSFSRG | SSGGGCFGGS | SGGYGGLGGF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GGGSFRGSYG | SSSFGGSYGG | IFGGGSFGGG | SFGGGSFGGG | GFGGGGFGGG | FGGGFGGDGG | LLSGNEKVTM | QNLNDRLASY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LDKVRALEES | NYELEGKIKE | WYEKHGNSHQ | GEPRDYSKYY | KTIDDLKNQI | LNLTTDNANI | LLQIDNARLA | ADDFRLKYEN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EVALRQSVEA | DINGLRRVLD | ELTLTKADLE | MQIESLTEEL | AYLKKNHEEE | MKDLRNVSTG | DVNVEMNAAP | GVDLTQLLNN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MRSQYEQLAE | QNRKDAEAWF | NEKSKELTTE | IDNNIEQISS | YKSEITELRR | NVQALEIELQ | SQLALKQSLE | ASLAETEGRY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CVQLSQIQAQ | ISALEEQLQQ | IRAETECQNT | EYQQLLDIKI | RLENEIQTYR | SLLEGEGSSG | GGGRGGGSFG | GGYGGGSSGG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GSSGGGHGGG | HGGSSGGGYG | GGSSGGGSSG | GGYGGGSSSG | GHGGSSSGGY | GGGSSGGGGG | GYGGGSSGGG | SSSGGGYGGG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| SSSGGHKSSS | SGSVGESSSK | GPRSAETSWD | TNKTRVIKTI | IEEVAPDGRV | LSSMVESETK | KHYY | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 348 | 1 | 806.4041 | 46.58 | 2 | 34.3 | 11.3 | 1 | 185-198 | K.HGNSHQGEPRDYSK.Y | |

# Detailed Protein Report

## Protein 36: trinucleotide repeat-containing gene 18 protein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|169658378 | **Score:** | 83.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 314.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 4 |

### Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.13 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.90 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578813684 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: trinucleotide repeat-containing gene 18 protein isoform X1 [Homo sapiens] |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDGRDFGPQR | SVHGPPPPLL | SGLAMDSHRV | GAATAGRLPA | SGLPGPLPPG | KYMAGLNLHP | HPGEAFLGSF | VASGMGPSAS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SHGSPVPLPS | DLSFRSPTPS | NLPMVQLWAA | HAHEGFSHLP | SGLYPSYLHL | NHLEPPSSGS | PLLSQLGQPS | IFDTQKGQGP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GGDGFYLPTA | GAPGSLHSHA | PSARTPGGGH | SSGAPAKGSS | SRDGPAKERA | GRGGEPPPLF | GKKDPRARGE | EASGPRGVVD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LTQEARAEGR | QDRGPPRLAE | RLSPFLAESK | TKNAALQPSV | LTMCNGGAGD | VGLPALVAEA | GRGGAKEAAR | QDEGARLLRR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TETLLPGPRP | CPSPLPPPPA | PPKGPPAPPA | ATPAGVYTVF | REQGREHRVV | APTFVPSVEA | FDERPGPIQI | ASQARDARAR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EREAGRPGVL | QAPPGSPRPL | DRPEGLREKN | SVIRSLKRPP | PADAPTVRAT | RASPDPRAYV | PAKELLKPEA | DPRPCERAPR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GPAGPAAQQA | AKLFGLEPGR | PPPTGPEHKW | KPFELGNFAA | TQMAVLAAQH | HHSRAEEEAA | VVAASSSKKA | YLDPGAVLPR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SAATCGRPVA | DMHSAAHGSG | EASAMQSLIK | YSGSFARDAV | AVRPGGCGKK | SPFGGLGTMK | PEPAPTSAGA | SRAQARLPHS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GGPAAGGGRQ | LKRDPERPES | AKAFGREGSG | AQGEAEVRHP | PVGIAVAVAR | QKDSGGSGRL | GPGLVDQERS | LSLSNVKGHG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RADEDCVDDR | ARHREERLLG | ARLDRDQEKL | LRESKELADL | ARLHPTSCAP | NGLNPNLMVT | GGPALAGSGR | WSADPAAHLA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| THPWLPRSGN | ASMWLAGHPY | GLGPPSLHQG | MAPAFPPGLG | GSLPSAYQFV | RDPQSGQLVV | IPSDHLPHFA | ELMERATVPP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LWPALYPPGR | SPLHHAQQLQ | LFSQQHFLRQ | QEFLYLQQQA | AQALELQRSA | QLVQERLKAQ | EHRAEMEEKG | SKRGLEAAGK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| AGLATAGPGL | LPRKPPGLAA | GPAGTYGKAV | SPPPSPRASP | VAALKAKVIQ | KLEDVSKPPA | YAYPATPSSH | PTSPPPASPP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PTPGITRKEE | APENVVEKKD | LELEKEAPSP | FQALFSDIPP | RYPFQALPPH | YGRPYPFLLQ | PTAAADADGL | APDVPLPADG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PERLALSPED | KPIRLSPSKI | TEPLREGPEE | EPLAEREVKA | EVEDMDEGPT | ELPPLESPLP | LPAAEAMATP | SPAGGCGGGL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LEAQALSATG | QSCAEPSECP | DFVEGPEPRV | DSPGRTEPCT | AALDLGVQLT | PETLVEAKEE | PVEVPVAVPV | VEAVPEEGLA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| QVAPSESQPT | LEMSDCDVPA | GEGQCPSLEP | QEAVPVLGST | CFLEEASSDQ | FLPSLEDPLA | GMNALAAAAE | LPQARPLPSP |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| GAAGAQALEK | LEAAESLVLE | QSFLHGITLL | SEIAELELER | RSQEMGGAER | ALVARPSLES | LLAAGSHMLR | EVLDGPVVDP |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LKNLRLPREL | KPNKKYSWMR | KKEERMYAMK | SSLEDMDALE | LDFRMRLAEV | QRQYKEKQRE | LVKLQRRRDS | EDRREEPHRS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| LARRGPGRPR | KRTHAPSALS | PPRKRGKSGH | SSGKLSSKSL | LTSDDYELGA | GIRKRHKGSE | EEHDALIGMG | KARGRNQTWD |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| EHEASSDFIS | QLKIKKKKMA | SDQEQLASKL | DKALSLTKQD | KLKSPFKFSD | SAGGKSKTSG | GCGRYLTPYD | SLLGKNRKAL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| AKGLGLSLKS | SREGKHKRAA | KTRKMEVGFK | ARGQPKSAHS | PFASEVSSYS | YNTDSEEDEE | FLKDEWPAQG | PSSSKLTPSL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| LCSMVAKNSK | AAGGPKLTKR | GLAAPRTLKP | KPATSRKQPF | CLLLREAEAR | SSFSDSSEES | FDQDESSEEE | DEEEELEEED |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| EASGGGYRLG | ARERALSPGL | EESGLGLLAR | FAASALPSPT | VGPSLSVVQL | EAKQKARKKE | ERQSLLGTEF | EYTDSESEVK |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| VRKRSPAGLL | RPKKGLGEPG | PSLAAPTPGA | RGPDPSSPDK | AKLAVEKGRK | ARKLRGPKEP | GFEAGPEASD | DDLWTRRRSE |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| RIFLHDASAA | APAPVSTAPA | TKTSRCAKGG | PLSPRKDAGR | AKDRKDPRKK | KKGKEAGPGA | GLPPPRAPAL | PSEARAPHAS |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| SLTAAKRSKA | KAKGKEVKKE | NRGKGGAVSK | LMESMAAEED | FEPNQDSSFS | EDEHLPRGGA | VERPLTPAPR | SCIIDKDELK |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1629 | 1 | 1052.2731 | 65.37 | 3 | 50.1 | 21.1 | 1 | 271-302 | K. TKNAALQPSVLTMCNGGAGDVGL G | Carbamidomethyl: 14; Oxidation: 13 | |
| 2682 | 1 | 734.8888 | -6.21 | 2 | 63.7 | 11.3 | 2 | 1642-1655 | K.LKSPFKFSDSAGGK.S | | |
| 177 | 1 | 613.7776 | -171.05 | 2 | 31.9 | 22.8 | 1 | 1787-1797 | R.TLKPKPATSRK.Q | | WUP:QUP 1.90<br>QU:MU 1.13 |
| 1643 | 1 | 713.3402 | -67.63 | 2 | 50.8 | 15.8 | 2 | 2464-2476 | K.LDHEGVTSPKSKK.A | | |

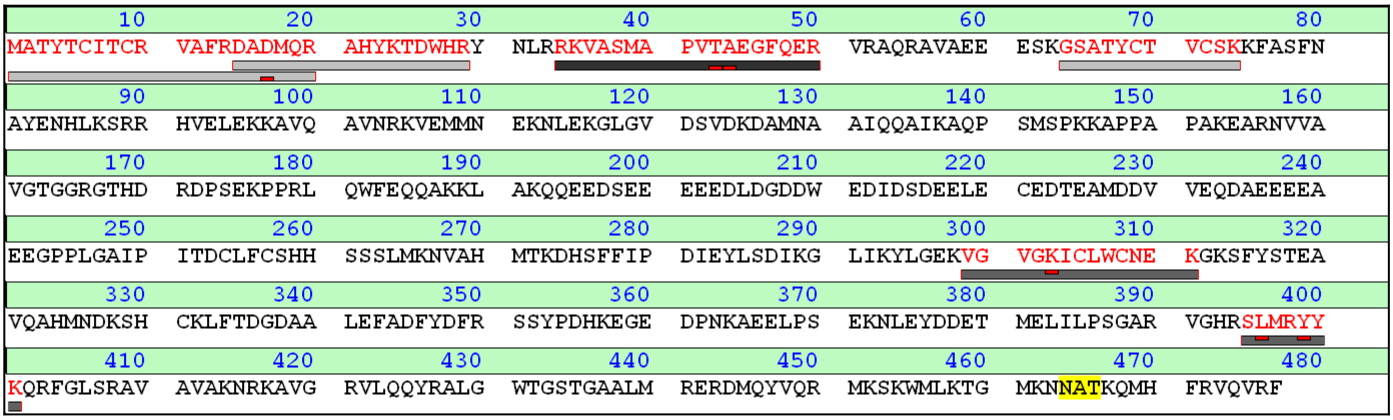
# Detailed Protein Report

## Protein 37: zinc finger protein 622 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|15529978 | **Score:** | 81.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 16.1 |
| | | **No. of unique Peptides:** | 6 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.93 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.47 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |



```
        10         20         30         40         50         60         70         80
MATYTCITCR VAFRDADMQR AHYKTDWHRY NLRRKVASMA PVTAEGFQER VRAQRAVAEE ESKGSATYCT VCSKKFASFN
        90        100        110        120        130        140        150        160
AYENHLKSRR HVELEKKAVQ AVNRKVEMMN EKNLEKGLGV DSVDKDAMNA AIQQAIKAQP SMSPKKAPPA PAKEARNVVA
       170        180        190        200        210        220        230        240
VGTGGRGTHD RDPSEKPPRL QWFEQQAKKL AKQQEEDSEE EEEDLDGDDW EDIDSDEELE CEDTEAMDDV VEQDAEEEEA
       250        260        270        280        290        300        310        320
EEGPPLGAIP ITDCLFCSHH SSSLMKNVAH MTKDHSFFIP DIEYLSDIKG LIKYLGEKVG VGKICLWCNE KGKSFYSTEA
       330        340        350        360        370        380        390        400
VQAHMNDKSH CKLFTDGDAA LEFADFYDFR SSYPDHKEGE DPNKAEELPS EKNLEYDDET MELILPSGAR VGHRSLMRYY
       410        420        430        440        450        460        470        480
KQRFGLSRAV AVAKNRKAVG RVLQQYRALG WTGSTGAALM RERDMQYVQR MKSKWMLKTG MKNNATKQMH FRVQVRF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2592 | 1 | 822.7237 | 16.97 | 3 | 62.4 | 10.6 | 2 | 1-20 | -.MATYTCITCRVAFRDADMQR.A | Carbamidomethyl: 6, 9 | |
| 2687 | 2 | 973.5040 | 65.98 | 2 | 64.7 | 14.9 | 2 | 15-29 | R.DADMQRAHYKTDWHR.Y | Oxidation: 4 | WUP:QUP 1.47<br>QU:MU 0.93 |
| 1830 | 3 | 938.9541 | -36.71 | 2 | 51.2 | 19.3 | 2 | 34-50 | R.RKVASMAPVTAEGFQER.V | | |
| 1757 | 1 | 560.2452 | 1.92 | 2 | 52.3 | 12.6 | 0 | 64-74 | K.GSATYCTVCSK.K | | |
| 2237 | 1 | 753.3462 | -49.90 | 2 | 56.3 | 10.4 | 1 | 299-311 | K.VGVGKICLWCNEK.G | Carbamidomethyl: 7 | |
| 1586 | 1 | 480.6461 | -220.76 | 2 | 49.5 | 14.0 | 1 | 395-401 | R.SLMRYYK.Q | | |

# Detailed Protein Report

## Protein 38: PREDICTED: dynein heavy chain 5, axonemal isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530378724 | **Score:** | 79.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 526.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 4 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDKLQRLKGE | KEAKRALLDA | RHNYLFAIVA | SCLDLNKTEV | EDAILEGNQI | ERIDQLFAVG | GLRHLMFYYQ | DVEEAETGQL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GSLGGVNLVS | GKIKKPKVFV | TEGNDVALTG | VCVFFIRTDP | SKAITPDNIH | QEVSFNMLDA | ADGGLLNSVR | RLLSDIFIPA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LRATSHGWGE | LEGLQDAANI | RQEFLSSLEG | FVNVLSGAQE | SLKEKVNLRK | CDILELKTLK | EPTDYLTLAN | NPETLGKIED |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CMKVWIKQTE | QVLAENNQLL | KEADDVGPRA | ELEHWKKRLS | KFNYLLEQLK | SPDVKAVLAV | LAAAKSKLLK | TWREMDIRIT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DATNEAKDNV | KYLYTLEKCC | DPLYSSDPLS | MMDAIPTLIN | AIKMIYSISH | YYNTSEKITS | LFVKVTNQII | SACKAYITNN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GTASIWNQPQ | DVVEEKILSA | IKLKQEYQLC | FHKTKQKLKQ | NPNAKQFDFS | EMYIFGKFET | FHRRLAKIID | IFTTLKTYSV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LQDSTIEGLE | DMATKYQGIV | ATIKKKEYNF | LDQRKMDFDQ | DYEEFCKQTN | DLHNELRKFM | DVTFAKIQNT | NQALRMLKKF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ERLNIPNLGI | DDKYQLILEN | YGADIDMISK | LYTKQKYDPP | LARNQPPIAG | KILWARQLFH | RIQQPMQLFQ | QHPAVLSTAE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AKPIIRSYNR | MAKVLLEFEV | LFHRAWLRQI | EEIHVGLEAS | LLVKAPGTGE | LFVNFDPQIL | ILFRETECMA | QMGLEVSPLA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TSLFQKRDRY | KRNFSNMKMM | LAEYQRVKSK | IPAAIEQLIV | PHLAKVDEAL | QPGLAALTWT | SLNIEAYLEN | TFAKIKDLEL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LLDRVNDLIE | FRIDAILEEM | SSTPLCQLPQ | EEPLTCEEFL | QMTKDLCVNG | AQILHFKSSL | VEEAVNELVN | MLLDVEVLSE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EESEKISNEN | SVNYKNESSA | KREEGNFDTL | TSSINARANA | LLLTTVTRKK | KETEMLGEEA | RELLSHFNHQ | NMDALLKVTR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NTLEAIRKRI | HSSHTINFRD | SNSASNMKQN | SLPIFRASVT | LAIPNIVMAP | ALEDVQQTLN | KAVECIISVP | KGVRQWSSEL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LSKKKIQERK | MAALQSNEDS | DSDVEMGENE | LQDTLEIASV | NLPIPVQTKN | YYKNVSENKE | IVKLVSVLST | IINSTKKEVI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TSMDCFKRYN | HIWQKGKEEA | IKTFITQSPL | LSEFESQILY | FQNLEQEINA | EPEYVCVGSI | ALYTADLKFA | LTAETKAWMV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VIGRHCNKKY | RSEMENIFML | IEEFNKKLNR | PIKDLDDIRI | AMAALKEIRE | EQISIDFQVG | PIEESYALLN | RYGLLIAREE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| IDKVDTLHYA | WEKLLARAGE | VQNKLVSLQP | SFKKELISAV | EVFLQDCHQF | YLDYDLNGPM | ASGLKPQEAS | DRLIMFQNQF |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| DNIYRKYITY | TGGEELFGLP | ATQYPQLLEI | KKQLNLLQKI | YTLYNSVIET | VNSYYDILWS | EVNIEKINNE | LLEFQNRCRK |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LPRALKDWQA | FLDLKKIIDD | FSECCPLLEY | MASKAMMERH | WERITTLTGH | SLDVGNESFK | LRNIMEAPLL | KYKEEIEDIC |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ISAVKERDIE | QKLKQVINEW | DNKTFTFGSF | KTRGELLLRG | DSTSEIIANM | EDSLMLLGSL | LSNRYNMPFK | AQIQKWVQYL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| SNSTDIIESW | MTVQNLWIYL | EAVFVGGDIA | KQLPKEAKRF | SNIDKSWVKI | MTRAHEVPSV | VQCCVGDETL | GQLLPHLLDQ |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LEICQKSLTG | YLEKKRLCFP | RFFFVSDPAL | LEILGQASDS | HTIQAHLLNV | FDNIKSVKFH | EKIYDRILSI | SSQEGETIEL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| DKPVMAEGNV | EVWLNSLLEE | SQSSLHLVIR | QAAANIQETG | FQLTEFLSSF | PAQVGLLGIQ | MIWTRDSEEA | LRNAKFDKKI |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| MQKTNQAFLE | LLNTLIDVTT | RDLSSTERVK | YETLITIHVH | QRDIFDDLCH | MHIKSPMDFE | WLKQCRFYFN | EDSDKMMIHI |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| TDVAFIYQNE | FLGCTDRLVI | TPLTDRCYIT | LAQALGMSMG | GAPAGPAGTG | KTETTKDMGR | CLGKYVVVFN | CSDQMDFRGL |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| GRIFKGLAQS | GSWGCFDEFN | RIDLPVLSVA | AQQISIILTC | KKEHKKSFIF | TDGDNVTMNP | EFGLFLTMNP | GYAGRQELPE |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| NLKINFRSVA | MMVPDRQIII | RVKLASCGFI | DNVVLARKFF | TLYKLCEEQL | SKQVHYDFGL | RNILSVLRTL | GAAKRANPMD |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1349 | 1 | 991.5669 | 90.75 | 3 | 47.0 | 28.2 | 1 | 1947-1976 | R.CYITLAQALGMSMGGAPAGPAGTGKTETTK.D | Carbamidomethyl: 1; Oxidation: 11, 13 |
| 2802 | 1 | 849.0671 | -21.12 | 3 | 66.2 | 12.2 | 2 | 1999-2021 | R.GLGRIFKGLAQSGSWGCFDEFNR.I | |
| 78 | 1 | 529.5845 | -42.73 | 3 | 29.9 | 11.4 | 2 | 3729-3741 | R.THLMEDVTANKRR.M | Oxidation: 4 |
| 2750 | 1 | 905.4797 | -0.39 | 2 | 65.5 | 16.2 | 2 | 3993-4008 | R.TIAQARKYIVDSMGEK.Y | |

# Detailed Protein Report

## Protein 39: coiled-coil domain-containing protein 168 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|226246554 | **Score:** | 79.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 801.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 6 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 3.74 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.50 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSKQYYSFKK | GVGSGLEDNT | FMTLWDFLES | WIIQNDWVAI | FFIILLGIIF | EIILMKACAS | FWKKPTLPEK | GSSDVQETED |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SCPKSRKLAP | ENWSVINSSS | GERVGTFLEK | RITSSLTSEE | KECNFEDRIL | FSREILWSGT | SESEDQVSPS | SESHVPSSNG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ISSSLPLFYS | EVEETCLSHT | EHPDREYETI | QFSSKKLFSM | MKTNKNKNSG | FSSDLSFSAS | RFTVENEDLD | VAPCPLAHLF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LSRDQVRLLE | ENVRNQIPSK | PKTKLGSRTT | YQCSRSQESL | NQNQPSVGMV | ISVQAQDSFP | GQNAFQNQGL | YEVQFTSQAQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YINHNQESIK | SQPESKASNF | AQPEDVMKKP | FSSSTQDSFQ | SQDLDRNQHF | VEVPSIVEAK | YSVKGLESDE | HLGEDQHCVW |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FIDSNKVKYS | IKGQDTIFKN | AEFLVLTLNP | NLVTEDMPQL | RSVKAQGQQQ | IVSSELNQDS | VYSSVPLLST | IKGQKNRRKT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PDSKSKLSLN | VPSLKAKKTP | TSQVFQITVC | HTLKNRNELG | CKNNTEKKEL | HERKDISDIA | LHLISVSKLI | LPYVKNYSRK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QLVKVMPGLI | KCGHFLQKQN | KSPDTEKINY | AGPLEETGIS | DITKKEKEYD | KENKRLKNIS | PKMLPQLEQS | FMVNTVQLKA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PCLLVETNGK | SKESLKDSIT | QAKGIGITEF | HVLNSKKPFD | LHIPKHKTSL | EEAISKPMQK | LVSSPEMESN | NRMKIQEDLQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SSENSHLQLS | NGEELPTSTP | KTQRCFPREN | TQKQKDFLEL | VLELSNVGLL | ISPGSKMHKS | SEELEAIKIQ | VNTESVNLKE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SKPLILNVTE | DSDLRESEEL | ECNTGSNITN | MHQDKETSDA | FHSATYTTIS | QLPDTETHSI | SKAKADTLRI | IRLSHSASKQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EKLPDEKETQ | NAEYIDKSCT | FKKPQQCDRK | EQEKEANSEL | TQGFRFSIHL | KQKPKYVKFQ | MEQISSGSSK | APNKEQEVQP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QTLSTQTILE | NSPCPMMDPF | QVEKVKQSTD | RPTDRESAGD | PKNPLTMPEN | LPVGELLIET | TEYSVPFGGN | LQKTTDSHIA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EEKEDVKRYL | PAVALGSFNN | HLLTLPYFKR | QEIKKKLSET | KSVLSVKYVI | MKVKKPAISL | MPYINICGTS | NHRKKMGGNF |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EIIIKQILQD | KIAAGMLLNV | IYPPMSILPN | TRMYSRLNAE | NHSHIKLVQE | ESQIEREEKY | PYFINEGNES | QNTLDAKLQD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EVKGVKETLP | KAVLHDSCNL | GLDAHLEKEI | KTEKEMHQPI | PFTETIIESV | VSPIMELSHA | ENVKSTQKTQ | TDCKCTADSE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TPSPISGKSL | IGDPLNQTRE | SYIPSNGSDT | REMGYCFAEE | KTEIPKDLPA | TSPETFNYCT | PVLSCSKVMK | KRVTFALTTS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| TAKPKCVNTK | AVKPSISETV | SVTSHRKKSE | LDFKTKFKKI | NQTKGLVPEC | LNTLCSPMHS | RLQREFCLPA | SQLKQGETAD |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KTYTDVFAKN | SISHDREEKL | QDGKEEEHKV | LLEAAPQLSQ | HLGSEAGQMK | EIHLESDPVL | NCLTLELHIN | GQRLQHQTGF |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| EQTTLETSLQ | MGPLEAEELQ | KANETENDIK | VLGGPKIPPP | KALQALENSD | GLILNAYQKD | NELVKSDEEL | NQPGSTNIQV |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QPQTHFTQTI | LKSTSCPTLD | QFPFEKVESH | VRFSPLKSGE | AKVDEIIFYA | REGGISSDSS | HQKEQAGGTE | KKETAIFGSC |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| MPALSTPKTT | RNLKQFSDMK | TLVNPKCGII | KAKKPSISYM | LNIRAGAGPK | RRKELSCNLT | TKMKELHQGK | KGVDETYAFL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| TMTPDINKYS | KVETEKDTLR | EKRLSSTQVK | QDTSPHEDSI | TSRDIKETLL | QDEEQEERKQ | EALLKVIPQH | LQHFMFRSGQ |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| GKDLDFHKLE | NQGSRKILFV | TKQDVPQQLQ | PAEPIQREET | KKCLQTQNGT | ICTVNSKLLP | LKSEDSVNGE | VLTGAIKRGV |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| PTDRKCMGEQ | HNSGKGEKAE | FNKDLQATVL | ELQKSPHGGE | AQKANLTDME | SGSSNAMNMN | VQHEREDKNI | QKMLTESVPC |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| YSQHLRFSTH | QMKDPDPCKS | GSEPKSPEGR | SWNLSHIVQK | TKQETHFRET | VLEPISGYMM | KQSPHMQEGI | KCMEGLKTSF |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| PKTGKSKIGS | IPRDTPWDEN | PRRKWDSSIS | EKTAWNQKNL | QTVLKPLDFS | SLMSSEYESR | SYTLEFIGKK | SMSPKCVTLK |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2367 | 1 | 805.3600 | -33.80 | 2 | 60.0 | 10.6 | 0 | 1883-1897 | K.CLQTQNGTICTVNSK.L | | |
| 270 | 1 | 642.3049 | -15.58 | 2 | 33.4 | 11.3 | 0 | 2241-2251 | R.QNLDGHITEEK.E | | QU:MU 3.74<br>WUP:QUP 0.50 |
| 2490 | 1 | 610.2540 | -89.47 | 2 | 61.1 | 10.6 | 2 | 3706-3716 | K.QEGKMQEGKGK.S | | |
| 1634 | 1 | 803.8641 | -92.41 | 2 | 50.2 | 10.9 | 0 | 5427-5440 | K.MCILFSKPLPSNLK.L | Oxidation: 1 | |
| 2371 | 8 | 974.2361 | 79.07 | 3 | 60.1 | 12.7 | 2 | 5658-5682 | R.DEDIYFTGFGTIRSGKRPEWLFTGK | | |
| 1685 | 1 | 916.4063 | -73.78 | 2 | 50.8 | 10.7 | 2 | 6846-6860 | R.ECRKETLIITPPSCK.S | Carbamidomethyl: 2, 14 | |

# Detailed Protein Report

**Protein 40:** **hemoglobin subunit epsilon [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4885393 | **Score:** | 77.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 16.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 15.0 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MVHFTAEEKA | AVTSLWSKMN | VEEAGGEALG | RLLVVYPWTQ | RFFDSFGNLS | SPSAILGNPK | VKAHGKKVLT | SFGDAIKNMD |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | |
| NLKPAFAKLS | ELHCDKLHVD | PENFKLLGNV | MVIILATHFG | KEFTPEVQAA | WQKLVSAVAI | ALAHKYH | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2297 | 6 | 596.8075 | -111.81 | 2 | 57.0 | 16.1 | 0 | 134-145 | K.LVSAVAIALAHK.Y | |

# Detailed Protein Report

## Protein 41: PREDICTED: DNA-directed RNA polymerase, mitochondrial isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530425287 | **Score:** | 77.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 145.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 5.4 |
| | | **No. of unique Peptides:** | 4 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.41 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.07 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPSRLRCILG | VYFRLGFPFA | ASVDHETTTP | GRRRGRMRRR | GPVGWPGAAC | VMSALCWGRG | AAGLKRALRP | CGRPGLPGKE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GTAGGVCGPR | RSSSASPQEQ | DQDRRKDWGH | VELLEVLQAR | VRQLQAESVS | EVVVNRVDVA | RLPECGSGDG | SLQPPRKVQM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GAKDATPVPC | GRWAKILEKD | KRTQQMRMQR | LKAKLQMPFQ | SGEFKALTRR | LQVEPRLLSK | QMAGCLEDCT | RQAPESPWEE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QLARLLQEAP | GKLSLDVEQA | PSGQHSQAQL | SGQQQRLLAF | FKCCLLTDQL | PLAHHLLVVH | HGQRQKRKLL | TLDMYNAVML |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GWARQGAFKE | LVYVLFMVKD | AGLTPDLLSY | AAALQCMGRQ | DQDAGTIERC | LEQMSQEGLK | LQALFTAVLL | SEEDRATVLK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AVHKVKPTFS | LPPQLPPPVN | TSKLLRDVYA | KDGRVSYPKL | HLPLKTLQCL | FEKQLHMELA | SRVCVVSVEK | PTLPSKEVKH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ARKTLKTLRD | QWEKALCRAL | RETKNRLERE | VYEGRFSLYP | FLCLLDEREV | VRMLLQVLQA | LPAQGESFTT | LARELSARTF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SRHVVQRQRV | SGQVQALQNH | YRKYLCLLAS | DAEVPEPCLP | RQYWEELGAP | EALREQPWPL | PVQMELGKLL | AEMLVQATQM |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PCSLDKPHRS | SRLVPVLYHV | YSFRNVQQIG | ILKPHPAYVQ | LLEKAAEPTL | TFEAVDVPML | CPPLPWTSPH | SGAFLLSPTK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LMRTVEGATQ | HQELLETCPP | TALHGALDAL | TQLGNCAWRV | NGRVLDLVLQ | LFQAKGCPQL | GVPAPPSEAP | QPPEAHLPHS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AAPARKAELR | RELAHCQKVA | REMHSLRAEA | LYRLSLAQHL | RDRVFWLPHN | MDFRGRTYPC | PPHFNHLGSD | VARALLEFAQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GRPLGPHGLD | WLKIHLVNLT | GLKKREPLRK | RLAFAEEVMD | DILDSADQPL | TGRKWWMGAE | EPWQTLACCM | EVANAVRASD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PAAYVSHLPV | HQDGSCNGLQ | HYAALGRDSV | GAASVNLEPS | DVPQDVYSGV | AAQVEVFRRQ | DAQRGMRVAQ | VLEGFITRKV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VKQTVMTVVY | GVTRYGGRLQ | IEKRLRELSD | FPQEFVWEAS | HYLVRQVFKS | LQEMFSGTRA | IQHWLTESAR | LISHMGSVVE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| WVTPLGVPVI | QPYRLDSKVK | QIGGGIQSIT | YTHNGDISRK | PNTRKQKNGF | PPNFIHSLDS | SHMMLTALHC | YRSPPLCHRK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| GLTFVSVHDC | YWTHAADVSV | MNQVCREQFV | RLHSEPILQD | LSRFLVKRFC | SEPQKILEAS | QLKETLQAVP | KPGAFDLEQV |
| 1290 | | | | | | | |
| KRSTYFFS | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 3 | 1 | 1244.4602 | -117.14 | 2 | 28.9 | 10.3 | 1 | 41-65 | R.<br>GPVGWPGAACVMSALCWGRGA<br>R | Carbamidomethyl: 10;<br>Oxidation: 12 | |
| 77 | 1 | 793.8731 | -24.51 | 2 | 29.9 | 14.5 | 1 | 158-172 | K.VQMGAKDATPVPCGR.W | Carbamidomethyl: 13 | |
| 2861 | 1 | 682.6750 | 3.46 | 3 | 66.2 | 16.6 | 0 | 584-601 | K.YLCLLASDAEVPEPCLPR.Q | Carbamidomethyl: 3 | |
| 390 | 1 | 685.3636 | 4.04 | 2 | 34.8 | 10.5 | 0 | 1043-1054 | K.QTVMTVVYGVTR.Y | Oxidation: 4 | WUP:QUP 1.07<br>QU:MU 1.41 |

# Detailed Protein Report

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## Protein 42: obscurin isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|403501446 | **Score:** | 77.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 867.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 0.7 |
| | | **No. of unique Peptides:** | 5 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.57 | **CV:** | 58.49 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 1.62 | **CV:** | 48.00 % | **No. of Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MDQPQFSGAP RFLTRPKAFV VSVGKDATLS CQIVGNPTPQ VSWEKDQQPV AAGARFRLAQ DGDLYRLTIL DLALGDSGQY

        90        100        110        120        130        140        150        160
VCRARNAIGE AFAAVGLQVD AEAACAEQAP HFLLRPTSIR VREGSEATFR CRVGGSPRPA VSWSKDGRRL GEPDGPRVRV

       170        180        190        200        210        220        230        240
EELGEASALR IRAARPRDGG TYEVRAENPL GAASAAAALV VDSDAADTAS RPGTSTAALL AHLQRRREAM RAEGAPASPP

       250        260        270        280        290        300        310        320
STGTRTCTVT EGKHARLSCY VTGEPKPETV WKKDGQLVTE GRRHVVYEDA QENFVLKILF CKQSDRGLYT CTASNLVGQT

       330        340        350        360        370        380        390        400
YSSVLVVVRE PAVPFKKRLQ DLEVREKESA TFLCEVPQPS TEAAWFKEET RLWASAKYGI EEEGTERRLT VRNVSADDDA

       410        420        430        440        450        460        470        480
VYICETPEGS RTVAELAVQG NLLRKLPRKT AVRVGDTAMF CVELAVPVGP VHWLRNQEEV VAGGRVAISA EGTRHTLTIS

       490        500        510        520        530        540        550        560
QCCLEDVGQV AFMAGDCQTS TQFCVSAPRK PPLQPPVDPV VKARMESSVI LSWSPPPHGE RPVTIDGYLV EKKKLGTYTW

       570        580        590        600        610        620        630        640
IRCHEAEWVA TPELTVADVA EEGNFQFRVS ALNSFGQSPY LEFPGTVHLA PKLAVRTPLK AVQAVEGGEV TFSVDLTVAS

       650        660        670        680        690        700        710        720
AGEWFLDGQA LKASSVYEIH CDRTRHTLTI REVPASLHGA QLKFVANGIE SSIRMEVRAA PGLTANKPPA AAAREVLARL

       730        740        750        760        770        780        790        800
HEEAQLLAEL SDQAAAVTWL KDGRTLSPGP KYEVQASAGR RVLLVRDVAR DDAGLYECVS RGGRIAYQLS VQGLARFLHK

       810        820        830        840        850        860        870        880
DMAGSCVDAV AGGPAQFECE TSEAHVHVHW YKDGMELGHS GERFLQEDVG TRHRLVAATV TRQDEGTYSC RVGEDSVDFR

       890        900        910        920        930        940        950        960
LRVSEPKVVF AKEQLARRKL QAEAGASATL SCEVAQAQTE VTWYKDGKKL SSSSKVCMEA TGCTRRLVVQ QAGQADAGEY

       970        980        990       1000       1010       1020       1030       1040
SCEAGGQRLS FHLDVKEPKV VFAKDQVAHS EVQAEAGASA TLSCEVAQAQ TEVMWYKDGK KLSSSLKVHV EAKGCRRRLV

      1050       1060       1070       1080       1090       1100       1110       1120
VQQAGKTDAG DYSCEARGQR VSFRLHITEP KMMFAKEQSV HNEVQAEAGA SAMLSCEVAQ AQTEVTWYKD GKKLSSSSKV

      1130       1140       1150       1160       1170       1180       1190       1200
GMEVKGCTRR LVLPQAGKAD AGEYSCEAGG QRVSFHLHIT EPKGVFAKEQ SVHNEVQAEA GTTAMLSCEV AQPQTEVTWY

      1210       1220       1230       1240       1250       1260       1270       1280
KDGKKLSSSS KVRMEVKGCT RRLVVQQVGK ADAGEYSCEA GGQRVSFQLH ITEPKAVFAK EQLVHNEVRT EAGASATLSC

      1290       1300       1310       1320       1330       1340       1350       1360
EVAQAQTEVT WYKDGKKLSS SSKVRIEAAG CMRQLVVQQA GQADAGEYTC EAGGQRLSFH LDVSEPKAVF AKEQLAHRKV

      1370       1380       1390       1400       1410       1420       1430       1440
QAEAGAIATL SCEVAQAQTE VTWYKDGKKL SSSSKVRMEA VGCTRRLVVQ QACQADTGEY SCEAGGQRLS FSLDVAEPKV

      1450       1460       1470       1480       1490       1500       1510       1520
VFAKEQPVHR EVQAQAGAST TLSCEVAQAQ TEVMWYKDGK KLSFSSKVRM EAVGCTRRLV VQQAGQAVAG EYSCEAGSQR

      1530       1540       1550       1560       1570       1580       1590       1600
LSFHLHVAEP KAVFAKEQPA SREVQAEAGT SATLSCEVAQ AQTEVTWYKD GKKLSSSSKV RMEAVGCTRR LVVQEAGQAD

      1610       1620       1630       1640       1650       1660       1670       1680
AGEYSCKAGD QRLSFHLHVA EPKVVFAKEQ PAHREVQAEA GASATLSCEV AQAQTEVTWY KDGKKLSSSS KVRVEAVGCT

      1690       1700       1710       1720       1730       1740       1750       1760
RRLVVQQAGQ AEAGEYSCEA GGQQLSFRLQ VAELEPQISE RPCRREPLVV KEHEDIILTA TLATPSAATV TWLKDGVEIR

      1770       1780       1790       1800       1810       1820       1830       1840
RSKRHETASQ GDTHTLTVHG AQVLDSAIYS CRVGAEGQDF PVQVEEVAAK FCRLLEPVCG ELGGTVTLAC ELSPACAEVV

      1850       1860       1870       1880       1890       1900       1910       1920
WRCGNTQLRV GKRFQMVAEG PVRSLTVLGL RAEDAGEYVC ESRDDHTSAQ LTVSVPRVVK FMSGLSTVVA EEGGEATFQC

      1930       1940       1950       1960       1970       1980       1990       2000
VVSPSDVAVV WFRDGALLQP SEKFAISQSG ASHSLTISDL VLEDAGQITV EAEGASSSAA LRVREAPVLF KKKLEPQTVE

      2010       2020       2030       2040       2050       2060       2070       2080
ERSSVTLEVE LTRPWPELRW TRNATALAPG KNVEIHAEGA RHRLVLHNVG FADRGFFGCE TPDDKTQAKL TVEMRQVRLV

      2090       2100       2110       2120       2130       2140       2150       2160
RGLQAVEARE QGTATMEVQL SHADVDGSWT RDGLRFQQGP TCHLAVRGPM HTLTLSGLRP EDSGLMVFKA EGVHTSARLV

      2170       2180       2190       2200       2210       2220       2230       2240
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1991 | 1 | 643.3110 | -83.65 | 2 | 54.8 | 19.9 | 2 | 338-347 | K.RLQDLEVREK.E |  | WUP:QUP 2.55<br>QU:MU 0.33 |
| 961 | 1 | 512.1292 | -217.77 | 2 | 42.1 | 10.5 | 0 | 872-880 | R.VGEDSVDFR.L |  | WUP:QUP 1.03<br>QU:MU 0.98 |
| 2661 | 2 | 686.8980 | -30.78 | 2 | 63.3 | 13.1 | 2 | 881-892 | R.LRVSEPKVVFAK.E |  |  |
| 2091 | 1 | 709.3658 | -116.08 | 2 | 56.0 | 20.8 | 2 | 5981-5992 | R.KYLLQARTAIIK.S |  |  |
| 2727 | 1 | 846.9286 | -83.14 | 2 | 65.2 | 13.0 | 2 | 7693-7708 | K.ASGRALAAKIIPYHPK.D |  |  |

# Detailed Protein Report

## Protein 43: PREDICTED: ceruloplasmin isoform X3 [Homo sapiens]

**Accession:** gi|578807065
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 75.8
**MW [kDa]:** 122.1
**pI:** 5.4
**Sequence Coverage [%]:** 2.6
**No. of unique Peptides:** 2

```
        10         20         30         40         50         60         70         80
MKILILGIFL FLCSTPAWAK EKHYYIGIIE TTWDYASDHG EKKLISVDTE HSNIYLQNGP DRIGRLYKKA LYLQYTDETF
        90        100        110        120        130        140        150        160
RTTIEKPVWL GFLGPIIKAE TGDKVYVHLK NLASRPYTFH SHGITYYKEH EGAIYPDNTT DFQRADDKVY PGEQYTYMLL
       170        180        190        200        210        220        230        240
ATEEQSPGEG DGNCVTRIYH SHIDAPKDIA SGLIGPLIIC KKDSLDKEKE KHIDREFVVM FSVVDENFSW YLEDNIKTYC
       250        260        270        280        290        300        310        320
SEPEKVDKDN EDFQESNRMY SVNGYTFGSL PGLSMCAEDR VKWYLFGMGN EVDVHAAFFH GQALTNKNYR IDTINLFPAT
       330        340        350        360        370        380        390        400
LFDAYMVAQN PGEWMLSCQN LNHLKAGLQA FFQVQECNKS SSKDNIRGKH VRHYYIAAEE IIWNYAPSGI DIFTKENLTA
       410        420        430        440        450        460        470        480
PGSDSAVFFE QGTTRIGGSY KKLVYREYTD ASFTNRKERG PEEEHLGILG PVIWAEVGDT IRVTFHNKGA YPLSIEPIGV
       490        500        510        520        530        540        550        560
RFNKNNEGTY YSPNYNPQSR SVPPSASHVA PTETFTYEWT VPKEVGPTNA DPVCLAKMYY SAVEPTKDIF TGLIGPMKIC
       570        580        590        600        610        620        630        640
KKGSLHANGR QKDVDKEFYL FPTVFDENES LLLEDNIRMF TTAPDQVDKE DEDFQESNKM HSMNGFMYGN QPGLTMCKGD
       650        660        670        680        690        700        710        720
SVVWYLFSAG NEADVHGIYF SGNTYLWRGE RRDTANLFPQ TSLTLHMWPD TEGTFNVECL TTDHYTGGMK QKYTVNQCRR
       730        740        750        760        770        780        790        800
QSEDSTFYLG ERTYYIAAVE VEWDYSPQRE WEKELHHLQE QNVSNAFLDK GEFYIGSKYK KVVYRQYTDS TFRVPVERKA
       810        820        830        840        850        860        870        880
EEEHLGILGP QLHADVGDKV KIIFKNMATR PYSIHAHGVQ TESSTVTPTL PGETLTYVWK IPERSGAGTE DSACIPWAYY
       890        900        910        920        930        940        950        960
STVDQVKDLY SGLIGPLIVC RRPYLKVFNP RRKLEFALLF LVFDENESWY LDDNIKTYSD HPEKVNKDDE EFIESNKMHA
       970        980        990       1000       1010       1020       1030       1040
INGRMFGNLQ GLTMHVGDEV NWYLMGMGNE IDLHTVHFHG HSFQYKHRGV YSSDVFDIFP GTYQTLEMFP RTPGIWLLHC
      1050       1060       1070
HVTDHIHAGM ETTYTVLQNE GGTSM
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2714 | 5 | 735.4243 | 1.19 | 2 | 65.0 | 45.6 | 0 | 188-201 | K.DIASGLIGPLIICK.K | Carbamidomethyl: 13 |
| 2789 | 2 | 788.4137 | -22.96 | 2 | 65.3 | 30.2 | 0 | 888-901 | K.DLYSGLIGPLIVCR.R | Carbamidomethyl: 13 |

# Detailed Protein Report

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| | | | |
|---|---|---|---|
| **Protein 44:** | **probable helicase senataxin [Homo sapiens]** | | |
| **Accession:** | gi\|113722133 | **Score:** | 74.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 302.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.9 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 5 |

## Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 0.43 | **CV:** 0.00 % | **No. of Peptides:** 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSTCCWCTPG | GASTIDFLKR | YASNTPSGEF | QTADEDLCYC | LECVAEYHKA | RDELPFLHEV | LWELETLRLI | NHFEKSMKAE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IGDDDELYIV | DNNGEMPLFD | ITGQDFENKL | RVPLLEILKY | PYLLLHERVN | ELCVEALCRM | EQANCSFQVF | DKHPGIYLFL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VHPNEMVRRW | AILTARNLGK | VDRDDYYDLQ | EVLLCLFKVI | ELGLLESPDI | YTSSVLEKGK | LILLPSHMYD | TTNYKSYWLG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ICMLLTILEE | QAMDSLLLGS | DKQNDFMQSI | LHTMEREADD | DSVDPFWPAL | HCFMVILDRL | GSKVWGQLMD | PIVAFQTIIN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NASYNREIRH | IRNSSVRTKL | EPESYLDDMV | TCSQIVYNYN | PEKTKKDSGW | RTAICPDYCP | NMYEEMETLA | SVLQSDIGQD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MRVHNSTFLW | FIPFVQSLMD | LKDLGVAYIA | QVVNHLYSEV | KEVLNQTDAV | CDKVTEFFLL | ILVSVIELHR | NKKCLHLLWV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SSQQWVEAVV | KCAKLPTTAF | TRSSEKSSGN | CSKGTAMISS | LSLHSMPSNS | VQLAYVQLIR | SLLKEGYQLG | QQSLCKRFWD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KLNLFLRGNL | SLGWQLTSQE | THELQSCLKQ | IIRNIKFKAP | PCNTFVDLTS | ACKISPASYN | KEESEQMGKT | SRKDMHCLEA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SSPTFSKEPM | KVQDSVLIKA | DNTIEGDNNE | QNYIKDVKLE | DHLLAGSCLK | QSSKNIFTER | AEDQIKISTR | KQKSVKEISS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YTPKDCTSRN | GPERGCDRGI | IVSTRLLTDS | STDALEKVST | SNEDFSLKDD | ALAKTSKRKT | KVQKDEICAK | LSHVIKKQHR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KSTLVDNTIN | LDENLTVSNI | ESFYSRKDTG | VQKGDGFIHN | LSLDPSGVLD | DKNGEQKSQN | NVLPKEKQLK | NEELVIFSFH |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ENNCKIQEFH | VDGKELIPFT | EMTNASEKKS | SPFKDLMTVP | ESRDEEMSNS | TSVIYSNLTR | EQAPDISPKS | DTLTDSQIDR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DLHKLSLLAQ | ASVITFPSDS | PQNSSQLQRK | VKEDKRCFTA | NQNNVGDTSR | GQVIIISDSD | DDDDERILSL | EKLTKQDKIC |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LEREHPEQHV | STVNSKEEKN | PVKEEKTETL | FQFEESDSQC | FEFESSSEVF | SVWQDHPDDN | NSVQDGEKKC | LAPIANTTNG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QGCTDYVSEV | VKKGAEGIEE | HTRPRSISVE | EFCEIEVKKP | KRKRSEKPMA | EDPVRPSSSV | RNEGQSDTNK | RDLVGNDFKS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| IDRRTSTPNS | RIQRATTVSQ | KKSSKLCTCT | EPIRKVPVSK | TPKKTHSDAK | KGQNRSSNYL | SCRTTPAIVP | PKKFRQCPEP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TSTAEKLGLK | KGPRKAYELS | QRSLDYVAQL | RDHGKTVGVV | DTRKKTKLIS | PQNLSVRNNK | KLLTSQELQM | QRQIRPKSQK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| NRRRLSDCES | TDVKRAGSHT | AQNSDIFVPE | SDRSDYNCTG | GTEVLANSNR | KQLIKCMPSE | PETIKAKHGS | PATDDACPLN |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| QCDSVVLNGT | VPTNEVIVST | SEDPLGGGDP | TARHIEMAAL | KEGEPDSSSD | AEEDNLFLTQ | NDPEDMDLCS | QMENDNYKLI |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ELIHGKDTVE | VEEDSVSRPQ | LESLSGTKCK | YKDCLETTKN | QGEYCPKHSE | VKAADEDVFR | KPGLPPPASK | PLRPTTKIFS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| SKSTSRIAGL | SKSLETSSAL | SPSLKNKSKG | IQSILKVPQP | VPLIAQKPVG | EMKNSCNVLH | PQSPNNSNRQ | GCKVPFGESK |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| YFPSSSPVNI | LLSSQSVSDT | FVKEVLKWKY | EMFLNFGQCG | PPASLCQSIS | RPVPVRFHNY | GDYFNVFFPL | MVLNTFETVA |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| QEWLNSPNRE | NFYQLQVRKF | PADYIKYWEF | AVYLEECELA | KQLYPKENDL | VFLAPERINE | EKKDTERNDI | QDLHEYHSGY |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| VHKFRRTSVM | RNGKTECYLS | IQTQENFPAN | LNELVNCIVI | SSLVTTQRKL | KAMSLLGSRN | QLARAVLNPN | PMDFCTKDLL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| TTTSERIIAY | LRDFNEDQKK | AIETAYAMVK | HSPSVAKICL | IHGPPGTGKS | KTIVGLLYRL | LTENQRKGHS | DENSNAKIKQ |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| NRVLVCAPSN | AAVDELMKKI | ILEFKEKCKD | KKNPLGNCGD | INLVRLGPEK | SINSEVLKFS | LDSQVNHRMK | KELPSHVQAM |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| HKRKEFLDYQ | LDELSRQRAL | CRGGREIQRQ | ELDENISKVS | KERQELASKI | KEVQGRPQKT | QSIIILESHI | ICCTLSTSGG |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 896 | 1 | 576.9688 | -1.76 | 3 | 41.3 | 12.0 | 1 | 679-694 | K.LEDHLLAGSCLKQSSK.N | | |
| 2700 | 1 | 856.9282 | -25.41 | 2 | 64.9 | 12.2 | 2 | 853-867 | K.NGEQKSQNNVLPKEK.Q | | QU:MU 0.43 |
| 160 | 1 | 896.7503 | -91.72 | 3 | 31.7 | 17.5 | 1 | 1573-1597 | K. AADEDVFRKPGLPPPASKPLRPTT I | | |
| 1617 | 1 | 781.3954 | -38.20 | 2 | 48.5 | 10.2 | 1 | 1613-1627 | K.SLETSSALSPSLKNK.S | | |
| 2158 | 1 | 682.2802 | -2.49 | 3 | 57.4 | 22.7 | 1 | 2220-2235 | K.AQEYGYDQSMMARFCR.L | Carbamidomethyl: 15; Oxidation: 10, 11 | |

# Detailed Protein Report

## Protein 45: glyceraldehyde-3-phosphate dehydrogenase isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|378404908 | **Score:** | 73.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 10.6 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.52 | **CV:** | 14.71 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 2.83 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MVYMFQYDST HGKFHGTVKA ENGKLVINGN PITIFQERDP SKIKWGDAGA EYVVESTGVF TTMEKAGAHL QGGAKRVIIS
        90        100        110        120        130        140        150        160
APSADAPMFV MGVNHEKYDN SLKIISNASC TTNCLAPLAK VIHDNFGIVE GLMTTVHAIT ATQKTVDGPS GKLWRDGRGA
       170        180        190        200        210        220        230        240
LQNIIPASTG AAKAVGKVIP ELNGKLTGMA FRVPTANVSV VDLTCRLEKP AKYDDIKKVV KQASEGPLKG ILGYTEHQVV
       250        260        270        280        290        300
SSDFNSDTHS STFDAGAGIA LNDHFVKLIS WYDNEFGYSN RVVDLMAHMA SKE
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 676 | 3 | 917.4657 | 2.44 | 2 | 38.0 | 53.0 | 0 | 104-120 | K.IISNASCTTNCLAPLAK.V | Carbamidomethyl: 7, 11 | WUP:QUP 2.83<br>QU:MU 0.45 |
| 1648 | 4 | 882.4064 | 1.76 | 2 | 50.9 | 20.6 | 0 | 268-281 | K.LISWYDNEFGYSNR.V | | QU:MU 0.61 |

# Detailed Protein Report

## Protein 46: dynein heavy chain 9, axonemal isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|114155133 | **Score:** | 73.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 511.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 4 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.47 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.21 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRLAEERAAL | AAENADGEPG | ADRRLRLLGT | YVAMSLRPAA | GAWERCAGSA | EAEQLLQAFL | GRDAAEGPRP | LLVVRPGPRG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LAIRPGLEVG | PESGLAGAKA | LFFLRTGPEP | PGPDSFRGAV | VCGDLPAAPL | EHLAALFSEV | VLPVLANEKN | RLNWPHMICE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DVRRHAHSLQ | CDLSVILEQV | KGKTLLPLPA | GSEKMEFADS | KSETVLDSID | KSVIYAIESA | VIKWSYQVQV | VLKRESSQPL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LQGENPTPKV | ELEFWKSRYE | DLKYIYNQLR | TITVRGMAKL | LDKLQSSYFP | AFKAMYRDVV | AALAEAQDIH | VHLIPLQRHL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EALENAEFPE | VKPQLRPLLH | VVCLIWATCK | SYRSPGRLTV | LLQEICNLLI | QQASNYLSPE | DLLRSEVEES | QRKLQVVSDT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LSFFKQEFQD | RRENLHTYFK | ENQEVKEWDF | QSSLVFVRLD | GFLGQLHVVE | GLLKTALDFH | KLGKVEFSGV | RGNALSQQVQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QMHEEFQEMY | RLLSGSSSDC | LYLQSTDFEN | DVSEFNQKVE | DLDRRLGTIF | IQAFDDAPGL | EHAFKLLDIA | GNLLERPLVA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RDTSDKYLVL | IQMFNKDLDA | VRMIYSQHVQ | EEAELGFSPV | HKNMPTVAGG | LRWAQELRQR | IQGPFSNFGR | ITHPCMESAE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GKRMQQKYED | MLSLLEKYET | RLYEDWCRTV | SEKSQYNLSQ | PLLKRDPETK | EITINFNPQL | ISVLKEMSYL | EPREMKHMPE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TAAAMFSSRD | FYRQLVANLE | LMANWYNKVM | KTLLEVEFPL | VEEELQNIDL | RLRAAEETLN | WKTEGICDYV | TEITSSIHDL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EQRIQKTKDN | VEEIQNIMKT | WVTPIFKTKD | GKRESLLSLD | DRHDRMEKYY | NLIKESGLKI | HALVQENLGL | FSADPTSNIW |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KTYVNSIDNL | LLNGFFLAIE | CSLKYLLENT | ECKAGLTPIF | EAQLSLAIPE | LVFYPSLESG | VKGGFCDIVE | GLITSIFRIP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SLVPRLSPQN | GSPHYQVDLD | GIPDLANMRR | TLMERVQRMM | GLCCGYQSTF | SQYSYLYVED | RKEVLGQFLL | YGHILTPEEI |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EDHVEDGIPE | NPPLLSQFKV | QIDSYETLYE | EVCRLEPIKV | FDGWMKIDIR | PFKASLLNII | KRWSLLFKQH | LVDHVTHSLA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| NLDAFIKKSE | SGLLKKVEKG | DFQGLVEIMG | HLMAVKERQS | NTDEMFEPLK | QTIELLKTYE | QELPETVFKQ | LEELPEKWNN |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| IKKVAITVKQ | QVAPLQANEV | TLLRQRCTAF | DAEQQQFWEQ | FHKEAPFRFD | SIHPHQMLDA | RHIEIQQMES | TMASISESAS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LFEVNVPDYK | QLRQCRKEVC | QLKELWDTIG | MVTSSIHAWE | TTPWRNINVE | AMELECKQFA | RHIRNLDKEV | RAWDAFTGLE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| STVWNTLSSL | RAVAELQNPA | IRERHWRQLM | QATGVSFTMD | QDTTLAHLLQ | LQLHHYEDEV | RGIVDKAAKE | MGMEKTLKEL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| QTTWAGMEFQ | YEPHPRTNVP | LLCSDEDLIE | VLEDNQVQLQ | NLVMSKYVAF | FLEEVSGWQK | KLSTVDAVIS | IWFEVQRTWT |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| HLESIFTGSE | DIRAQLPQDS | KRFEGIDIDF | KELAYDAQKI | PNVVQTTNKP | GLYEKLEDIQ | GRLCLCEKAL | AEYLDTKRLA |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| FPRFYFLSSS | DLLDILSNGT | APQQVQRHLS | KLFDNMAKMR | FQLDASGEPT | KTSLGMYSKE | EEYVAFSEPC | DCSGQVEIWL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| NHVLGHMKAT | VRHEMTEGVT | AYEEKPREQW | LFDHPAQVAL | TCTQIWWTTE | VGMAFARLEE | GYESAMKDYY | KKQVAQLKTL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| ITMLIGQLSK | GDRQKIMTIC | TIDVHARDVV | AKMIAQKVDN | AQAFLWLSQL | RHRWDDEVKH | CFANICDAQF | LYSYEYLGNT |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| PRLVITPLTD | RCYITLTQSL | HLTMSGAPAG | PAGTGKTETT | KDLGRALGIL | VYVFNCSEQM | DYKSCGNIYK | GLAQTGAWGC |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| FDEFNRISVE | VLSVVAVQVK | SIQDAIRDKK | QWFSFLGEEI | SLNPSVGIFI | TMNPGYAGRT | ELPENLKSLF | RPCAMVVPDF |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| ELICEIMLVA | EGFIEAQSLA | RKFITLYQLC | KELLSKQDHY | DWGLRAIKSV | LVVAGSLKRG | DPDRPEDQVL | MRSLRDFNIP |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| KIVTDDMPIF | MGLIGDLFPA | LDVPRRRDPN | FEALVRKAIV | DLKLQAEDNF | VLKVVQLEEL | LAVRHSVFVV | GGAGTGKSQV |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2873 | 2 | 731.8707 | -28.75 | 2 | 66.4 | 25.7 | 1 | 1075-1086 | R.LEPIKVFDGWMK.I | | |
| 1912 | 2 | 634.8166 | -103.44 | 2 | 54.3 | 17.9 | 0 | 2134-2144 | K.VVQLEELLAVR.H | | WUP:QUP 2.21<br>QU:MU 0.47 |
| 54 | 1 | 796.7965 | -120.13 | 2 | 30.4 | 11.9 | 0 | 3448-3461 | R.MSVENATILINCER.W | | |
| 1679 | 4 | 648.2912 | -180.05 | 2 | 51.3 | 17.9 | 0 | 4475-4486 | K.WVLAGVALLLQI.- | | |

# Detailed Protein Report

## Protein 47: PREDICTED: histone-lysine N-methyltransferase 2A isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578822195 | **Score:** | 72.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 323.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 5 |

### Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.24 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.78 | **CV:** | 38.96 % | **No. of Peptides:** | 2 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MLAQADKLPM TDKRVASLLK KAKAQLCKIE KSKSLKQTDQ PKAQGQESDS SETSVRGPRI KHVCRRAAVA LGRKRAVFPD
        90        100        110        120        130        140        150        160
DMPTLSALPW EEREKILSSM GNDDKSSIAG SEDAEPLAPP IKPIKPVTRN KAPQEPPVKK GRRSRRCGQC PGCQVPEDCG
       170        180        190        200        210        220        230        240
VCTNCLDKPK FGGRNIKKQC CKMRKCQNLQ WMPSKAYLQK QAKAVKKKEK KSKTSEKKDS KESSVVKNVV DSSQKPTPSA
       250        260        270        280        290        300        310        320
REDPAPKKSS SEPPPRKPVE EKSEEGNVSA PGPESKQATT PASRKSSKQV SQPALVIPPQ PPTTGPPRKE VPKTTPSEPK
       330        340        350        360        370        380        390        400
KKQPPPPESG PEQSKQKKVA PRPSIPVKQK PKEKEKPPPV NKQENAGTLN ILSTLSNGNS SKQKIPADGV HRIRVDFKED
       410        420        430        440        450        460        470        480
CEAENVWEMG GLGILTSVPI TPRVVCFLCA SSGHVEFVYC QVCCEPFHKF CLEENERPLE DQLENWCCRR CKFCHVCGRQ
       490        500        510        520        530        540        550        560
HQATKQLLEC NKCRNSYHPE CLGPNYPTKP TKKKKVWICT KCVRCKSCGS TTPGKGWDAQ WSHDFSLCHD CAKLFAKGNF
       570        580        590        600        610        620        630        640
CPLCDKCYDD DDYESKMMQC GKCDRWVHSK CENLSGTEDE MYEILSNLPE SVAYTCVNCT ERHPAEWRLA LEKELQISLK
       650        660        670        680        690        700        710        720
QVLTALLNSR TTSHLLRYRQ AAKPPDLNPE TEESIPSRSS PEGPDPPVLT EVSKQDDQQP LDLEGVKRKM DQGNYTSVLE
       730        740        750        760        770        780        790        800
FSDDIVKIIQ AAINSDGGQP EIKKANSMVK SFFIRQMERV FPWFSVKKSR FWEPNKVSSN SGMLPNAVLP PSLDHNYAQW
       810        820        830        840        850        860        870        880
QEREENSHTE QPPLMKKIIP APKPKGPGEP DSPTPLHPPT PPILSTDRSR EDSPELNPPP GIEDNRQCAL CLTYGDDSAN
       890        900        910        920        930        940        950        960
DAGRLLYIGQ NEWTHVNCAL WSAEVFEDDD GSLKNVHMAV IRGKQLRCEF CQKPGATVGC CLTSCTSNYH FMCSRAKNCV
       970        980        990       1000       1010       1020       1030       1040
FLDDKKVYCQ RHRDLIKGEV VPENGFEVFR RVFVDFEGIS LRRKFLNGLE PENIHMMIGS MTIDCLGILN DLSDCEDKLF
      1050       1060       1070       1080       1090       1100       1110       1120
PIGYQCSRVY WSTTDARKRC VYTCKIVECR PPVVEPDINS TVEHDENRTI AHSPTSFTES SSKESQNTAE IISPPSPDRP
      1130       1140       1150       1160       1170       1180       1190       1200
PHSQTSGSCY YHVISKVPRI RTPSYSPTQR SPGCRPLPSA GSPTPTTHEI VTVGDPLLSS GLRSIGSRRH STSSLSPQRS
      1210       1220       1230       1240       1250       1260       1270       1280
KLRIMSPMRT GNTYSRNNVS SVSTTGTATD LESSAKVVDH VLGPLNSSTS LGQNTSTSSN LQRTVVTVGN KNSHLDGSSS
      1290       1300       1310       1320       1330       1340       1350       1360
SEMKQSSASD LVSKSSSLKG EKTKVLSSKS SEGSAHNVAY PGIPKLAPQV HNTTSRELNV SKIGSFAEPS SVSFSSKEAL
      1370       1380       1390       1400       1410       1420       1430       1440
SFPHLHLRGQ RNDRDQHTDS TQSANSSPDE DTEVKTLKLS GMSNRSSIIN EHMGSSSRDR RQKGKKSCKE TFKEKHSSKS
      1450       1460       1470       1480       1490       1500       1510       1520
FLEPGQVTTG EEGNLKPEFM DEVLTPEYMG QRPCNNVSSD KIGDKGLSMP GVPKAPPMQV EGSAKELQAP RKRTVKVTLT
      1530       1540       1550       1560       1570       1580       1590       1600
PLKMENESQS KNALKESSPA SPLQIESTSP TEPISASENP GDGPVAQPSP NNTSCQDSQS NNYQNLPVQD RNLMLPDGPK
      1610       1620       1630       1640       1650       1660       1670       1680
PQEDGSFKRR YPRRSARARS NMFFGLTPLY GVRSYGEEDI PFYSSSTGKK RGKRSAEGQV DGADDLSTSD EDDLYYYNFT
      1690       1700       1710       1720       1730       1740       1750       1760
RTVISSGGEE RLASHNLFRE EEQCDLPKIS QLDGVDDGTE SDTSVTATTR KSSQIPKRNG KENGTENLKI DRPEDAGEKE
      1770       1780       1790       1800       1810       1820       1830       1840
HVTKSSVGHK NEPKMDNCHS VSRVKTQGQD SLEAQLSSLE SSRRVHTSTP SDKNLLDTYN TELLKSDSDN NNSDDCGNIL
      1850       1860       1870       1880       1890       1900       1910       1920
PSDIMDFVLK NTPSMQALGE SPESSSSELL NLGEGLGLDS NREKDMGLFE VFSQQLPTTE PVDSSVSSSI SAEEQFELPL
      1930       1940       1950       1960       1970       1980       1990       2000
ELPSDLSVLT TRSPTVPSQN PSRLAVISDS GEKRVTITEK SVASSESDPA LLSPGVDPTP EGHMTPDHFI QGHMDADHIS
      2010       2020       2030       2040       2050       2060       2070       2080
SPPCGSVEQG HGNNQDLTRN SSTPGLQVPV SPTVPIQNQK YVPNSTDSPG PSQISNAAVQ TTPPHLKPAT EKLIVVNQNM
      2090       2100       2110       2120       2130       2140       2150       2160
QPLYVLQTLP NGVTQKIQLT SSVSSTPSVM ETNTSVLGPM GGGLTLTTGL NPSLPTSQSL FPSASKGLLP MSHHQHLHSF
      2170       2180       2190       2200       2210       2220       2230       2240
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1751 | 1 | 1061.1573 | 33.03 | 3 | 51.7 | 15.9 | 2 | 144-170 | R.<br>SRRCGQCPGCQVPEDCGVCTNC<br>F | Carbamidomethyl: 4, 10, 16, 19, 22 | |
| 908 | 1 | 541.3264 | 90.29 | 3 | 41.4 | 12.3 | 2 | 242-256 | R.EDPAPKKSSSEPPPR.K | | WUP:QUP 0.54<br>QU:MU 2.24 |
| 1836 | 13 | 682.2601 | 12.95 | 3 | 52.8 | 16.3 | 1 | 567-582 | K.CYDDDDYESKMMQCGK.C | Carbamidomethyl: 1, 14 | |
| 53 | 1 | 1096.9888 | -34.10 | 2 | 30.4 | 17.5 | 1 | 1264-1284 | R.<br>TVVTVGNKNSHLDGSSSSEMK.<br>Q | Oxidation: 20 | |
| 395 | 1 | 625.3909 | 142.58 | 2 | 34.6 | 10.9 | 2 | 2950-2960 | K.LPCNCGAKKCR.K | Carbamidomethyl: 5 | WUP:QUP 1.14 |

# Detailed Protein Report

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## Protein 48: PREDICTED: ankyrin repeat domain-containing protein 11 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578828959 | **Score:** | 72.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 286.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 6 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.14 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MGLSGIRAGY PLSERQQVAL LMQMTAEESA NSPVDTTPKH PSQSTVCQKG TPNSASKTKD KVNKRNERGE TRLHRAAIRG
        90        100        110        120        130        140        150        160
DARRIKELIS EGADVNVKDF AGWTALHEAC NRGYYDVAKQ LLAAGAEVNT KGLDDDTPLH DAANNGHYKV VKLLLRYGGN
       170        180        190        200        210        220        230        240
PQQSNRKGET PLKVANSPTM VNLLLGKGTY TSSEESSTES SEEEDAPSFA PSSSVDGNNT DSEFEKGLKH KAKNPEPQKA
       250        260        270        280        290        300        310        320
TAPVKDEYEF DEDDEQDRVP PVDDKHLLKK DYRKETKSNS FISIPKMEVK SYTKNNTIAP KKASHRILSD TSDEEDASVT
       330        340        350        360        370        380        390        400
VGTGEKLRLS AHTILPGSKT REPSNAKQQK EKNKVKKKRK KETKGREVRF GKRSDKFCSS ESESESSESG EDDRDSLGSS
       410        420        430        440        450        460        470        480
GCLKGSPLVL KDPSLFSSLS ASSTSSHGSS AAQKQNPSHT DQHTKHWRTD NWKTISSPAW SEVSSLSDST RTRLTSESDY
       490        500        510        520        530        540        550        560
SSEGSSVESL KPVRKRQEHR KRASLSEKKS PFLSSAEGAV PKLDKEGKVV KKHKTKHKHK NKEKGQCSIS QELKLKSFTY
       570        580        590        600        610        620        630        640
EYEDSKQKSD KAILLENDLS TENKLKVLKH DRDHFKKEEK LSKMKLEEKE WLFKDEKSLK RIKDTNKDIS RSFREEKDRS
       650        660        670        680        690        700        710        720
NKAEKERSLK EKSPKEEKLR LYKEERKKKS KDRPSKLEKK NDLKEDKISK EKEKIFKEDK EKLKKEKVYR EDSAFDEYCN
       730        740        750        760        770        780        790        800
KNQFLENEDT KFSLSDDQRD RWFSDLSDSS FDFKGEDSWD SPVTDYRDMK SDSVAKLILE TVKEDSKERR RDSRAREKRD
       810        820        830        840        850        860        870        880
YREPFFRKKD RDYLDKNSEK RKEQTEKHKS VPGYLSEKDK KRRESAEAGR DRKDALESCK ERRDGRAKPE EAHREELKEC
       890        900        910        920        930        940        950        960
GCESGFKDKS DGDFGKGLEP WERHHPAREK EKKDGPDKER KEKTKPERYK EKSSDKDKSE KSILEKCQKD KEFDKCFKEK
       970        980        990       1000       1010       1020       1030       1040
KDTKEKHKDT HGKDKERKAS LDQGKEKKEK AFPGIISEDF SEKKDDKKGK EKSWYIADIF TDESEDDRDS CMGSGFKMGE
      1050       1060       1070       1080       1090       1100       1110       1120
ASDLPRTDGL QEKEEGREAY ASDRHRKSSD KQHPERQKDK EPRDRRKDRG AADAGRDKKE KVFEKHKEKK DKESTEKYKD
      1130       1140       1150       1160       1170       1180       1190       1200
RKDRASVDST QDKKNKQKLP EKAEKKHAAE DKAKSKHKEK SDKEHSKERK SSRSADAEKS LLEKLEEEAL HEYREDSNDK
      1210       1220       1230       1240       1250       1260       1270       1280
ISEVSSDSFT DRGQEPGLTA FLEVSFTEPP GDDKPRESAC LPEKLKEKER HRHSSSSSKK SHDRERAKKE KAEKKEKGED
      1290       1300       1310       1320       1330       1340       1350       1360
YKEGGSRKDS GQYEKDFLEA DAYGVSYNMK ADIEDELDKT IELFSTEKKD KNDSEREPSK KIEKELKPYG SSAINILKEK
      1370       1380       1390       1400       1410       1420       1430       1440
KKREKHREKW RDEKERHRDR HADGLLRHHR DELLRHHRDE QKPATRDKDS PPRVLKDKSR DEGPRLGDAK LKEKFKDGAE
      1450       1460       1470       1480       1490       1500       1510       1520
KEKGDPVKMS NGNDKVAPSK DPGKKDARPR EKLLGDGDLM MTSFERMLSQ KDLEIEERHK RHKERMKQME KLRHRSGDPK
      1530       1540       1550       1560       1570       1580       1590       1600
LKEKAKPADD GRKKGLDIPA KKPPGLDPPF KDKKLKESTP IPPAAENKLH PASGADSKDW LAGPHMKEVL PASPRPDQSR
      1610       1620       1630       1640       1650       1660       1670       1680
PTGVPTPTSV LSCPSYEEVM HTPRTPSCSA DDYADLVFDC ADSQHSTPVP TAPTSACSPS FFDRFSVASS GLSENASQAP
      1690       1700       1710       1720       1730       1740       1750       1760
ARPLSTNLYR SVSVDIRRTP EEEFSVGDKL FRQQSVPAAS SYDSPMPPSM EDRAPLPPVP AEKFACLSPG YYSPDYGLPS
      1770       1780       1790       1800       1810       1820       1830       1840
PKVDALHCPP AAVVTVTPSP EGVFSSLQAK PSPSPRAELL VPSLEGALPP DLDTSEDQQA TAAIIPPEPS YLEPLDEGPF
      1850       1860       1870       1880       1890       1900       1910       1920
SAVITEEPVE WAHPSEQALA SSLIGGTSEN PVSWPVGSDL LLKSPQRFPE SPKRFCPADP LHSAAPGPFS ASEAPYPAPP
      1930       1940       1950       1960       1970       1980       1990       2000
ASPAPYALPV AEPGLEDVKD GVDAVPAAIS TSEAAPYAPP SGLESFFSNC KSLPEAPLDV APEPACVAAV AQVEALGPLE
      2010       2020       2030       2040       2050       2060       2070       2080
NSFLDGSRGL SHLGQVEPVP WADAFAGPED DLDLGPFSLP ELPLQTKDAA DGEAEPVEES LAPPEEMPPG APGVINGGDV
      2090       2100       2110       2120       2130       2140       2150       2160
STVVAEEPPA LPPDQASTRL PAELEPEPSG EPKLDVALEA AVEAETVPEE RARGDPDSSV EPAPVPPEQR PLGSGDQGAE
      2170       2180       2190       2200       2210       2220       2230       2240
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 793 | 1 | 1105.5255 | -96.76 | 2 | 39.9 | 11.9 | 2 | 167-187 | R.KGETPLKVANSPTMVNLLLGK.G | | |
| 462 | 1 | 475.6124 | -248.29 | 2 | 34.3 | 11.4 | 1 | 1171-1179 | K.SSRSADAEK.S | | QU:MU 1.14 |
| 2600 | 1 | 741.8765 | -22.04 | 2 | 62.5 | 14.8 | 2 | 1379-1390 | R.DRHADGLLRHHR.D | | |
| 255 | 1 | 501.2790 | -48.16 | 2 | 31.9 | 12.8 | 2 | 1426-1434 | R.LGDAKLKEK.F | | |
| 2267 | 1 | 937.3359 | -108.02 | 2 | 56.7 | 10.6 | 1 | 1471-1486 | R.EKLLGDGDLMMTSFER.M | Oxidation: 10, 11 | |
| 1507 | 1 | 619.9684 | 9.93 | 3 | 48.5 | 11.3 | 1 | 1471-1486 | R.EKLLGDGDLMMTSFER.M | Oxidation: 11 | |

# Detailed Protein Report

## Protein 49: dynein heavy chain 1, axonemal [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|197927452 | **Score:** | 71.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 487.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 4 |

### Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.67 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.04 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578805960 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: dynein heavy chain 1, axonemal isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEQPNSKGYS | LGRTPQGPEC | SSAPAVQVGT | HRGLEYNPGK | ILPGSDYGLG | NPPALDPKLP | HLPLPPAPPT | LSDLGQPRKS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PLTGTDKKYP | LMKQRGFYSD | ILSPGTLDQL | GEVCRGPRMS | QNLLRQADLD | KFTPRVGSFE | VPEDFQERME | QQCIGSTTRL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LAQTDFPLQA | YEPKMQVPFQ | VLPGQHPRKI | EIERRKQQYL | SLDIEQLLFS | QGIDSNKLMP | RHLDHQHPQT | IEQGHDPIFP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IYLPLKVFDN | EDFDCRTPRE | WINMGLEPGS | LDRKPVPGKA | LLPTDDFLGH | EDPKSQKLKY | KWCEVGVLDY | DEEKKLYLVH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KTDEKGLVRD | EMGRPILNAG | VTTEGRPPLQ | VCQYWVPRIQ | LLFCAEDPCM | FAQRVVQANA | LRKNTEALLL | YNLYVDCMPS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DGQHVISEQS | LSKIKQWALS | TPRMRKGPSV | LEHLSSLARE | VSLDYERSMN | KINFDHVVSS | KPETFSYVTL | PKKEEEQVPE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RGLVSVPKYH | FWEQKEDFTF | VSLLTRPEVI | TALSKVRAEC | NKVTAMSLFH | SSLSKYSHLE | EFEQIQSQTF | SQVQMFLKDS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| WISSLKVAMR | SSLRDMSKGW | YNLYETNWEV | YLMSKLRKLM | ELVKYMLQDT | LRFLVQDSLA | SFSQFISDTC | CSVLNCTDDM |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VWGDDLINSP | YRPRKNPLFI | MDLVLDSSGV | HYSTPLEQFE | ASLLNLFDKG | ILATHAVPQL | EKLVMEDIFI | SGDPLLESVG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LHEPLVEELR | ATIASAVSKA | MIPLQAYAKE | YRKYLELNNN | DIASFLKTYQ | TQGLLAQEVR | EVVLTHLREK | EILDSSLPSS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IIIGPFYINT | DNVKQSLSKK | RKALATSVLD | ILAKNLHKEV | DSICEEFRSI | SRKIYEKPNS | IEELAELREW | MKGIPERLVG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LEERIVKVMD | DYQVMDEFLY | NLSSDDFNDK | WIASNWPSKI | LGQIELVQQQ | HVEDEEKFRK | IQIMDQNNFQ | EKLEGLQLVV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| AGFSIHVEIS | RAHEIANEVR | RVKKQLKDCQ | QLAMLYNNRE | RIFSLPITNY | DKLSRMVKEF | QPYLDLWTTA | SDWLRWSESW |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| MNDPLSAIDA | EQLEKNVVEA | FKTMHKCVKQ | FKDMPACQEV | ALDIRARIEE | FKPYIPLIQG | LRNPGMRIRH | WETLSNQINI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| NVRPKANLTF | ARCLEMNLQD | HIESISKVAE | VAGKEYAIEQ | ALDKMEKEWS | TILFNVLPYK | ATDTYILKSP | DEASQLLDDH |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| IVMTQNMSFS | PYKKPFEQRI | NSWENKLKLT | QEVLEEWLNC | QRSWLYLEPI | FSSEDINQQL | PVESKRYQTM | ERIWKKIMKN |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| AYENREVINV | CSDLRMLDSL | RDCNKILDLV | QKGLSEYLET | KRSAFPRFYF | LSDDELLEIL | SQTKDPTAVQ | PHLRKCFENI |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ARLLFQEDLE | ITHMYSAEGE | EVQLCFSIYP | SSNVEDWLRE | VERSMKASVH | DIIEKAIRAY | PTMPRTQWVL | NWPGQVTIAG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| CQTYWTMEVA | EALEAGNLRS | QLFPQLCQQL | SDLVALVRGK | LSRMQRAVLS | ALIVIEVHAK | DVVSKLIQEN | VVSVNDFQWI |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| SQLRYYWTNN | DLYIRAVNAE | FIYGYEYLGN | SGRLVITPLT | DRCYLTLTGA | LHLKFGGAPA | GPAGTGKTET | TKDLGKALAI |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QTVVFNCSDQ | LDFMAMGKFF | KGLASAGAWA | CFDEFNRIDI | EVLSVVAQQI | TTIQKAQQQR | VERFMFEGVE | IPLVPSCAVF |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| ITMNPGYAGR | TELPDNLKAL | FRPVAMMVPD | YAMITEISLY | SFGFNEASVL | AKKITTTFKL | SSEQLSSQDH | YDFGMRAVKT |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| VISAAGNLKR | ENPSMNEELI | CLRAIRDVNV | PKFLQEDLKL | FSGIVSDLFP | TIKEEDTDYG | ILDEAIREAC | RNSNLKDVEG |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| FLTKCIQLYE | TTVVRHGLML | VGPTGSGKST | CYRVLAAAMT | SLKGQPSISG | GMYEAVNYYV | LNPKSITMGQ | LYGEFDLLTH |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| EWTDGIFSSF | IRAGAITSDT | NKKWYMFDGP | VDAIWIENMN | TVLDDNKKLC | LSSGEIIKLT | EAMTMMFEVQ | DLAVASPATV |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| SRCGMVYLEP | SILGLMPFIE | CWLRKLPPLL | KPYEEHFKAL | FVSFLEESIS | FVRSSVKEVI | ASTNCNLTMS | LLKLLDCFFK |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| PFLPREGLKK | IPSEKLSRIV | ELIEPWFIFS | LIWSVGATGD | SSGRTSFSHW | LRLKMENEQL | TLLFPEEGLV | FDYRLEDAGI |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1891 | 2 | 918.3580 | -147.46 | 2 | 53.5 | 15.4 | 2 | 559-574 | K.DSWISSLKVAMRSSLR.D |  | WUP:QUP 1.04 |
| 178 | 1 | 715.8622 | 76.35 | 2 | 31.9 | 12.3 | 0 | 2496-2506 | R.CMEQWEVTFNK.V | Oxidation: 2 | QU:MU 1.67 |
| 2816 | 1 | 788.8905 | -16.60 | 2 | 65.6 | 10.2 | 1 | 3081-3094 | R.LREVEDGIATMQAK.Y | Oxidation: 11 |  |
| 51 | 1 | 706.3163 | -75.95 | 3 | 30.3 | 15.4 | 2 | 3699-3718 | K.KLSAISLGQGQGPRAEAMMR.S | Oxidation: 18 |  |

# Detailed Protein Report

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## Protein 50: protocadherin Fat 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|13787217 | **Score:** | 71.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 479.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| | | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 3 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578810809 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protocadherin Fat 2 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTIALLGFAI | FLLHCATCEK | PLEGILSSSA | WHFTHSHYNA | TIYENSSPKT | YVESFEKMGI | YLAEPQWAVR | YRIISGDVAN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VFKTEEYVVG | NFCFLRIRTK | SSNTALLNRE | VRDSYTLIIQ | ATEKTLELEA | LTRVVVHILD | QNDLKPLFSP | PSYRVTISED |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MPLKSPICKV | TATDADLGQN | AEFYYAFNTR | SEMFAIHPTS | GVVTVAGKLN | VTWRGKHELQ | VLAVDRMRKI | SEGNGFGSLA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ALVVHVEPAL | RKPPAIASVV | VTPPDSNDGT | TYATVLVDAN | SSGAEVESVE | VVGGDPGKHF | KAIKSYARSN | EFSLVSVKDI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NWMEYLHGFN | LSLQARSGSG | PYFYSQIRGF | HLPPSKLSSL | KFEKAVYRVQ | LSEFSPPGSR | VVMVRVTPAF | PNLQYVLKPS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SENVGFKLNA | RTGLITTTKL | MDFHDRAHYQ | LHIRTSPGQA | STVVVIDIVD | CNNHAPLFNR | SSYDGTLDEN | IPPGTSVLAV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TATDRDHGEN | GYVTYSIAGP | KALPFSIDPY | LGIISTSKPM | DYELMKRIYT | FRVRASDWGS | PFRREKEVSI | FLQLRNLNDN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QPMFEEVNCT | GSIRQDWPVG | KSIMTMSAID | VDELQNLKYE | IVSGNELEYF | DLNHFSGVIS | LKRPFINLTA | GQPTSYSLKI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TASDGKNYAS | PTTLNITVVK | DPHFEVPVTC | DKTGVLTQFT | KTILHFIGLQ | NQESSDEEFT | SLSTYQINHY | TPQFEDHFPQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SIDVLESVPI | NTPLARLAAT | DPDAGFNGKL | VYVIADGNEE | GCFDIELETG | LLTVAAPLDY | EATNFYILNV | TVYDLGTPQK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SSWKLLTVNV | KDWNDNAPRF | PPGGYQLTIS | EDTEVGTTIA | ELTTKDADSE | DNGRVRYTLL | SPTEKFSLHP | LTGELVVTGH |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LDRESEPRYI | LKVEARDQPS | KGHQLFSVTD | LIITLEDVND | NSPQCITEHN | RLKVPEDLPP | GTVLTFLDAS | DPDLGPAGEV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RYVLMDGAHG | TFRVDLMTGA | LILERELDFE | RRAGYNLSLW | ASDGGRPLAR | RTLCHVEVIV | LDVNENLHPP | HFASFVHQGQ |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VQENSPSGTQ | VIVVAAQDDD | SGLDGELQYF | LRAGTGLAAF | SINQDTGMIQ | TLAPLDREFA | SYYWLTVLAV | DRGSVPLSSV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TEVYIEVTDA | NDNPPQMSQA | VFYPSIQEDA | PVGTSVLQLD | AWDPDSSSKG | KLTFNITSGN | YMGFFMIHPV | TGLLSTAQQL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DRENKDEHIL | EVTVLDNGEP | SLKSTSRVVV | GILDVNDNPP | IFSHKLFNVR | LPERLSPVSP | GPVYRLVASD | LDEGLNGRVT |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| YSIEDSDEEA | FSIDLVTGVV | SSSSTFTAGE | YNILTIKATD | SGQPPLSASV | RLHIEWIPWP | RPSSIPLAFD | ETYYSFTVME |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| TDPVNHMVGV | ISVEGRPGLF | WFNISGGDKD | MDFDIEKTTG | SIVIARPLDT | RRRSNYNLTV | EVTDGSRTIA | TQVHIFMIAN |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| INHHRPQFLE | TRYEVRVPQD | TVPGVELLRV | QAIDQDKGKS | LIYTIHGSQD | PGSASLFQLD | PSSGVLVTVG | KLDLGSGPSQ |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| HTLTVMVRDQ | EIPIKRNFVW | VTIHVEDGNL | HPPRFTQLHY | EASVPDTIAP | GTELLQVRAM | DADRGVNAEV | HYSLLKGNSE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| GFFNINALLG | IITLAQKLDQ | ANHAPHTLTV | KAEDQGSPQW | HDLATVIIHV | YPSDRSAPIF | SKSEYFVEIP | ESIPVGSPIL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LVSAMSPSEV | TYELREGNKD | GVFSMNSYSG | LISTQKKLDH | EKISSYQLKI | RGSNMAGAFT | DVMVVVDIID | ENDNAPMFLK |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| STFVGQISEA | APLYSMIMDK | NNNPFVIHAS | DSDKEANSLL | VYKILEPEAL | KFFKIDPSMG | TLTIVSEMDY | ESMPSFQFCV |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| YVHDQGSPVL | FAPRPAQVII | HVRDVNDSPP | RFSEQIYEVA | IVGPIHPGME | LLMVRASDED | SEVNYSIKTG | NADEAVTIHP |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| VTGSISVLNP | AFLGLSRKLT | IRASDGLYQD | TALVKISLTQ | VLDKSLQFDQ | DVYWAAVKEN | LQDRKALVIL | GAQGNHLNDT |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| LSYFLLNGTD | MFHMVQSAGV | LQTRGVAFDR | EQQDTHELAV | EVRDNRTPQR | VAQGLVRVSI | EDVNDNPPKF | KHLPYYTIIQ |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| DGTEPGDVLF | QVSATDEDLG | TNGAVTYEFA | EDYTYFRIDP | YLGDISLKKP | FDYQALNKYH | LKVIARDGGT | PSLQSEEEVL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| VTVRNKSNPL | FQSPYYKVRV | PENITLYTPI | LHTQARSPEG | LRLIYNIVEE | EPLMLFTTDF | KTGVLTVTGP | LDYESKTKHV |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| FTVRATDTAL | GSFSEATVEV | LVEDVNDNPP | TFSQLVYTTS | ISEGLPAQTP | VIQLLASDQD | SGRNRDVSYQ | IVEDGSDVSK |
| 2330 | 2340 | 2350 | 2360 | 2370 | 2380 | 2390 | 2400 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2633 | 1 | 741.3552 | -72.85 | 2 | 63.0 | 15.7 | 1 | 71-83 | R.YRIISGDVANVFK.T | |
| 1721 | 1 | 1030.6326 | 87.08 | 2 | 51.3 | 16.6 | 1 | 993-1011 | R.AGYNLSLWASDGGRPLARR.T | |
| 65 | 2 | 1096.9820 | -88.55 | 2 | 30.5 | 12.9 | 2 | 3376-3395 | K.GELQVAKALDREQASSYSLK.L | |

# Detailed Protein Report

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| | | | |
|---|---|---|---|
| **Protein 51:** | **PREDICTED: protein AHNAK2 isoform X1 [Homo sapiens]** | | |
| **Accession:** | gi\|530403029 | **Score:** | 69.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 605.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 5 |

## Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 1.02 | **CV:** 0.00 % | **No. of Peptides:** 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSRPEAVQEA | TEVTLKTEVE | AGASGYSVTG | GGDQGIFVKQ | VLKDSSAAKL | FNLREGDQLL | STTVFFENIK | YEDALKILQY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SEPYKVQFKI | RRQLPAPQDE | EWASSDAQHG | PQGKEKEDTD | VADGCRETPT | KTLEGDGDQE | RLISKPRVGR | GRQSQRERLS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WPKFQSIKSK | RGPGPQRSHS | SSEAYEPRDA | HDVSPTSTDT | EAQLTVERQE | QKAGPGSQRR | RKFLNLRFRT | GSGQGPSSTG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QPGRGFQSGV | GRAGVLEELG | PWGDSLEETG | AATGSRREER | AEQDREVMPA | QSMPLPTELG | DPRLCEGTPQ | EGGLRAARLH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GKTLEGQAQE | TAVAQRKPRA | QPTPGMSREG | EGEGLQSLEI | GIARLSLRDT | TEGGTQIGPP | EIRVRVHDLK | TPKFAFSTEK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EPERERRLST | PQRGKRQDAS | SKAGTGLKGE | EVEGAGWMPG | REPTTHAEAQ | GDEGDGEEGL | QRTRITEEQD | KGREDTEGQI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RMPKFKIPSL | GWSPSKHTKT | GREKATEDTE | QGREGEATAT | ADRREQRRTE | EGLKDKEDSD | SMTNTTKIQL | IHDEKRLKKE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QILTEKEVAT | KDSKFKMPKF | KMPLFGASAP | GKSMEASVDV | SAPKVEADVS | LLSMQGDLKT | TDLSVQTPSA | DLEVQDGQVD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VKLPEGPLPE | GASLKGHLPK | VQRPSLKMPK | VDLKGPKLDL | KGPKAEVTAP | DVKMSLSSME | VDVQAPRAKL | DGARLEGDLS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LADKEVTAKD | SKFKMPKFKM | PSFGVSAPGK | SMEDSVDVSA | PKVEADVSLS | SMQGDLKATD | LSIQPPSADL | EVQAGQVDVK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LPEGPVPEGA | GPKVHLPKVE | MPSFKMPKVD | LKGPQIDVKG | PKLDLKGPKA | EVTAPDGEVS | LPSMEVDVQA | QKAKLDGAWL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EGDLSLADKD | VTAKDSKFKM | PKFKMPSFGV | SAPGKSIKAL | VDVSAPKVEA | DLSLPSMQGD | LKTTDLSIQP | ASTDLKVQAD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QVDVKLPEGH | LPEGAGLKGH | LPKVEMPSFK | MPKVALKGPQ | VDVKGPKLDL | KSPKAEVTAP | DVEVSLPSVE | VDVEAPGAKL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| DSARLEGELS | LADKDVTAKD | SRFKMPKFKM | PSFGASAPGK | SIEASVDVSA | PKVEADVSLP | SMQGDLKTTD | LSIQPPSADL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EVHAGQVDVK | LLEGHVPEGA | GFKGHLPKVQ | MPSLKMPKVD | LKGPQVEVRG | PKLDLKGHKA | EVTAHEVAVS | LPSVEVDMQA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PGAKLDGAQL | DGDLSLADKD | VTAKDSKFKM | PKFKMPSFGV | SAPGKSIEAS | VDLSAPKVEA | DMSLPSMQGD | LKTTDLSIQP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PSTDLELQAG | QLDVKLPEGP | VPEGAGLKGH | LPKLQMPSFK | VPKVDLKGPE | IDIKGPKLDL | KDPKVEVTAP | DVEVSLPSVE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VDVEAPGAKL | DGGRLEEDMS | LADKDLTTKD | SKFKMPKFKM | PSFGVSAPGK | SIEASVDVSA | PKVEADVSLP | SMQGDLKATD |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LSIQPPSADL | EVQAGQVDVK | LPEGPVSEGA | GLKGHLPKVQ | MPSFKMPKVD | LKGPQIDVKG | PKLDLKGPKV | EVTAPDVKMS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| LSSMEVDVQA | PRAKLDGAQL | EGDLSLADKA | VTAKDSKFKM | PKFKMPSFGV | SAPGKSIEAS | VDVSEPKVEA | DVSLPSMQGD |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LKTTDLSIQS | PSADLEVQAG | QVNVKLPEGP | LPEGAGFKGH | LPKVQMPSLK | MPKVALKGPQ | MDVKGPKLDL | KGPKAEVMAP |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| DVEVSLPSVE | VDVEAPGAKL | DSVRLEGDLS | LADKDVTAKD | SKFKMPKFKM | PSFGVSAPGK | SIEASVDVSA | PKVEAEVSLP |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SMQGDLKTTD | LCIPLPSADL | VVQAGQVDMK | LPEGQVPEGA | GLKGHLPKVD | MPSFKMPKVD | LKGPQTDVKG | AKLDLKGPKA |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| EVTAPDVEVS | LPSMEVDVQA | QKAKLDGARL | EGDLSLADKD | MTAKDSKFKM | PKFKMPSFGV | SAPGRSIEAS | VDVPAPKVEA |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| DVSLPSMQGD | LKTTDLSIQP | PSADLKVQTG | QVDVKLPEGH | VPEGAGLKGH | LPKVEMPSLK | MPKVDLKGPQ | VDIKGPKLDL |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| KDPKVEMRVP | DVEVSLPSME | VDVQAPRAKL | DSAHLQGDLT | LANKDLTTKD | SKFKMPKFKM | PSFGVSAPGK | SIEASVDVSP |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| PKVEADMSLP | SMQGDLKTTD | LSIQPLSADV | KVQAGQVDVK | LLEGPVPEEV | GLKGHLPKLQ | MPSFKVPKVD | LKGPEIDIKG |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2046 | 1 | 596.7306 | -219.53 | 2 | 56.0 | 16.0 | 2 | 384-393 | R.VRVHDLKTPK.F | | QU:MU 1.02 |
| 267 | 1 | 862.8828 | -39.08 | 2 | 33.3 | 11.9 | 1 | 1375-1389 | R.LEEDMSLADKDLTTK.D | Oxidation: 5 | |
| 738 | 1 | 769.3703 | -105.01 | 2 | 39.2 | 11.2 | 2 | 3308-3321 | K.SPQVDIKGPKLDLK.V | | |
| 1307 | 2 | 926.0984 | -40.13 | 3 | 46.5 | 19.2 | 1 | 3391-3417 | R. SIEASLDVSAPKVEADVSLSSMQG A | | |
| 1329 | 1 | 1023.0254 | -12.68 | 2 | 46.8 | 11.6 | 1 | 5662-5679 | R.VMVTSAARTELILPEQDR.K | Oxidation: 2 | |

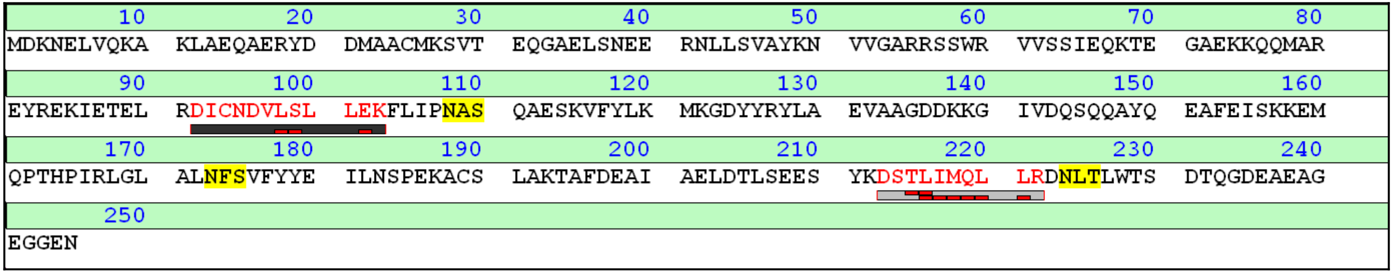
# Detailed Protein Report

## Protein 52: 14-3-3 protein zeta/delta [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4507953 | **Score:** | 69.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 9.0 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530389321 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: 14-3-3 protein zeta/delta isoform X4 [Homo sapiens] |
| gi\|530389319 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: 14-3-3 protein zeta/delta isoform X3 [Homo sapiens] |
| gi\|530389317 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: 14-3-3 protein zeta/delta isoform X2 [Homo sapiens] |
| gi\|208973244 | refseq_human (refseq_human_20140103.fasta) | 14-3-3 protein zeta/delta [Homo sapiens] |
| gi\|208973242 | refseq_human (refseq_human_20140103.fasta) | 14-3-3 protein zeta/delta [Homo sapiens] |
| gi\|208973240 | refseq_human (refseq_human_20140103.fasta) | 14-3-3 protein zeta/delta [Homo sapiens] |
| gi\|208973238 | refseq_human (refseq_human_20140103.fasta) | 14-3-3 protein zeta/delta [Homo sapiens] |
| gi\|21735625 | refseq_human (refseq_human_20140103.fasta) | 14-3-3 protein zeta/delta [Homo sapiens] |



```
        10         20         30         40         50         60         70         80
MDKNELVQKA KLAEQAERYD DMAACMKSVT EQGAELSNEE RNLLSVAYKN VVGARRSSWR VVSSIEQKTE GAEKKQQMAR
        90        100        110        120        130        140        150        160
EYREKIETEL RDICNDVLSL LEKFLIPNAS QAESKVFYLK MKGDYYRYLA EVAAGDDKKG IVDQSQQAYQ EAFEISKKEM
       170        180        190        200        210        220        230        240
QPTHPIRLGL ALNFSVFYYE ILNSPEKACS LAKTAFDEAI AELDTLSEES YKDSTLIMQL LRDNLTLWTS DTQGDEAEAG
       250
EGGEN
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2739 | 1 | 709.8489 | -20.41 | 2 | 64.6 | 22.3 | 0 | 92-103 | R.DICNDVLSLLEK.F | Carbamidomethyl: 3 |
| 2725 | 2 | 595.3333 | -1.39 | 2 | 65.2 | 47.3 | 0 | 213-222 | K.DSTLIMQLLR.D | |

# Detailed Protein Report

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**Protein 53:** **voltage-dependent P/Q-type calcium channel subunit alpha-1A isoform 3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|187828880 | **Score:** | 69.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 256.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 5 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MARFGDEMPA | RYGGGGSGAA | AGVVVGSGGG | RGAGGSRQGG | QPGAQRMYKQ | SMAQRARTMA | LYNPIPVRQN | CLTVNRSLFL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FSEDNVVRKY | AKKITEWPPF | EYMILATIIA | NCIVLALEQH | LPDDDKTPMS | ERLDDTEPYF | IGIFCFEAGI | KIIALGFAFH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KGSYLRNGWN | VMDFVVVLTG | ILATVGTEFD | LRTLRAVRVL | RPLKLVSGIP | SLQVVLKSIM | KAMIPLLQIG | LLLFFAILIF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AIIGLEFYMG | KFHTTCFEEG | TDDIQGESPA | PCGTEEPART | CPNGTKCQPY | WEGPNNGITQ | FDNILFAVLT | VFQCITMEGW |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TDLLYNSNDA | SGNTWNWLYF | IPLIIIGSFF | MLNLVLGVLS | GEFAKERERV | ENRRAFLKLR | RQQQIERELN | GYMEWISKAE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EVILAEDETD | GEQRHPFDGA | LRRTTIKKSK | TDLLNPEEAE | DQLADIASVG | SPFARASIKS | AKLENSTFFH | KKERRMRFYI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RRMVKTQAFY | WTVLSLVALN | TLCVAIVHYN | QPEWLSDFLY | YAEFIFLGLF | MSEMFIKMYG | LGTRPYFHSS | FNCFDCGVII |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GSIFEVIWAV | IKPGTSFGIS | VLRALRLLRI | FKVTKYWASL | RNLVVSLLNS | MKSIISLLFL | LFLFIVVFAL | LGMQLFGGQF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NFDEGTPPTN | FDTFPAAIMT | VFQILTGEDW | NEVMYDGIKS | QGGVQGGMVF | SIYFIVLTLF | GNYTLLNVFL | AIAVDNLANA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QELTKDEQEE | EEAANQKLAL | QKAKEVAEVS | PLSAANMSIA | VKEQQKNQKP | AKSVWEQRTS | EMRKQNLLAS | REALYNEMDP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DERWKAAYTR | HLRPDMKTHL | DRPLVVDPQE | NRNNNTNKSR | AAEPTVDQRL | GQQRAEDFLR | KQARYHDRAR | DPSGSAGLDA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RRPWAGSQEA | ELSREGPYGR | ESDHHAREGS | LEQPGFWEGE | AERGKAGDPH | RRHVHRQGGS | RESRSGSPRT | GADGEHRRHR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| AHRRPGEEGP | EDKAERRARH | REGSRPARGG | EGEGEGPDGG | ERRRRHRHGA | PATYEGDARR | EDKERRHRRR | KENQGSGVPV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SGPNLSTTRP | IQQDLGRQDP | PLAEDIDNMK | NNKLATAESA | APHGSLGHAG | LPQSPAKMGN | STDPGPMLAI | PAMATNPQNA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ASRRTPNNPG | NPSNPGPPKT | PENSLIVTNP | SGTQTNSAKT | ARKPDHTTVD | IPPACPPPLN | HTVVQVNKNA | NPDPLPKKEE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EKKEEEEDDR | GEDGPKPMPP | YSSMFILSTT | NPLRRLCHYI | LNLRYFEMCI | LMVIAMSSIA | LAAEDPVQPN | APRNNVLRYF |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DYVFTGVFTF | EMVIKMIDLG | LVLHQGAYFR | DLWNILDFIV | VSGALVAFAF | TGNSKGKDIN | TIKSLRVLRV | LRPLKTIKRL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PKLKAVFDCV | VNSLKNVFNI | LIVYMLFMFI | FAVVAVQLFK | GKFFHCTDES | KEFEKDCRGK | YLLYEKNEVK | ARDREWKKYE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| FHYDNVLWAL | LTLFTVSTGE | GWPQVLKHSV | DATFENQGPS | PGYRMEMSIF | YVVYFVVFPF | FFVNIFVALI | IITFQEQGDK |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| MMEEYSLEKN | ERACIDFAIS | AKPLTRHMPQ | NKQSFQYRMW | QFVVSPPFEY | TIMAMIALNT | IVLMMKFYGA | SVAYENALRV |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| FNIVFTSLFS | LECVLKVMAF | GILNYFRDAW | NIFDFVTVLG | SITDILVTEF | GNNFINLSFL | RLFRAARLIK | LLRQGYTIRI |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LLWTFVQSFK | ALPYVCLLIA | MLFFIYAIIG | MQVFGNIGID | VEDEDSDEDE | FQITEHNNFR | TFFQALMLLF | RSATGEAWHN |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| IMLSCLSGKP | CDKNSGILTR | ECGNEFAYFY | FVSFIFLCSF | LMLNLFVAVI | MDNFEYLTRD | SSILGPHHLD | EYVRVWAEYD |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| PAACGRIHYK | DMYSLLRVIS | PPLGLGKKCP | HRVACKRLLR | MDLPVADDNT | VHFNSTLMAL | IRTALDIKIA | KGGADKQQMD |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| AELRKEMMAI | WPNLSQKTLD | LLVTPHKSTD | LTVGKIYAAM | MIMEYYRQSK | AKKLQAMREE | QDRTPLMFQR | MEPPSPTQEG |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| GPGQNALPST | QLDPGGALMA | HESGLKESPS | WVTQRAQEMF | QKTGTWSPEQ | GPPTDMPNSQ | PNSQSVEMRE | MGRDGYSDSE |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| HYLPMEGQGR | AASMPRLPAE | NQRRRGRPRG | NNLSTISDTS | PMKRSASVLG | PKARRLDDYS | LERVPPEENQ | RHHQRRRDRS |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 35 | 2 | 796.7935 | -124.10 | 2 | 29.4 | 12.9 | 0 | 12-31 | R.YGGGGSGAAAGVVVGSGGGR.G | |
| 2300 | 2 | 822.4329 | 20.49 | 2 | 57.1 | 15.3 | 1 | 1124-1139 | R.RTPNNPGNPSNPGPPK.T | |
| 118 | 1 | 753.3697 | -54.70 | 2 | 31.4 | 13.4 | 0 | 1533-1546 | R.ACIDFAISAKPLTR.H | |
| 2664 | 1 | 701.8434 | -53.81 | 2 | 63.4 | 12.1 | 0 | 1741-1751 | R.TFFQALMLLFR.S | Oxidation: 7 |
| 2837 | 1 | 913.4693 | 21.67 | 1 | 64.1 | 15.5 | 1 | 1869-1876 | K.CPHRVACK.R | |

# Detailed Protein Report

**Protein 54:** **PREDICTED: striated muscle preferentially expressed protein kinase isoform X4 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530369685 | **Score:** | 68.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 339.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.69 | **CV:** | 86.96 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 1.26 | **CV:** | 205.34 % | **No. of Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKKLWVKKRF | QKTGHSRRAF | GRLTHVFRSC | RKQSYDSETA | EDDISDVQGT | QRLELRDDGA | FSTPTGGSDT | LVGTSLDTPP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TSVTGTSEEQ | VSWWGSGQTV | LEQEAGSGGG | TRRLPGSPSS | VPQSGLRREE | PDLQPQLASE | APRRPAQPPP | SKSALLPPPS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PRVGKRSPPG | PPAQPAATPT | SPHRRTQEPV | LPEDTTTEEK | RGKKSKSSGP | SLAGTAESRP | QTPLSEASGR | LSALGRSPRL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VRAGSRILDK | LQFFEERRRS | LERSDSPPAP | LRPWVPLRKA | RSLEQPKSER | GAPWGTPGAS | QEELRAPGSV | AERRRLFQQK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AASLDERTRQ | RSPASDLELR | FAQELGRIRR | STSREELVRS | HESLRATLQR | APSPREPGEP | PLFSRPSTPK | TSRAVSPAAA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QPPSPSSAEK | PGDEPGRPRS | RGPAGRTEPG | EGPQQEVRRR | DQFPLTRSRA | IQECRSPVPP | PAADPPEART | KAPPGRKREP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PAQAVRFLPW | ATPGLEGAAV | PQTLEKNRAG | PEAEKRLRRG | PEEDGPWGPW | DRRGARSQGK | GRRARPTSPE | LESSDDSYVS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AGEEPLEAPV | FEIPLQNVVV | APGADVLLKC | IITANPPPQV | SWHKDGSALR | SEGRLLLRAE | GERHTLLLRE | ARAADAGSYM |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ATATNELGQA | TCAASLTVRP | GGSTSPFSSP | ITSDEEYLSP | PEEFPEPGET | WPRTPTMKPS | PSQNRRSSDT | GSKAPPTFKV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SLMDQSVREG | QDVIMSIRVQ | GEPKPVVSWL | RNRQPVRPDQ | RRFAEEAEGG | LCRLRILAAE | RGDAGFYTCK | AVNEYGARQC |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EARLEVRAHP | ESRSLAVLAP | LQDVDVGAGE | MALFECLVAG | PTDVEVDWLC | RGRLLQPALL | KCKMHFDGRK | CKLLLTSVHE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DDSGVYTCKL | STAKDELTCS | ARLTVRPSLA | PLFTRLLEDV | EVLEGRAARF | DCKISGTPPP | VVTWTHFGCP | MEESENLRLR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QDGGLHSLHI | AHVGSEDEGL | YAVSAVNTHG | QAHCSAQLYV | EEPRTAASGP | SSKLEKMPSI | PEEPEQGELE | RLSIPDFLRP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LQDLEVGLAK | EAMLECQVTG | LPYPTISWFH | NGHRIQSSDD | RRMTQYRDVH | RLVFPAVGPQ | HAGVYKSVIA | NKLGKAACYA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| HLYVTDVVPG | PPDGAPQVVA | VTGRMVTLTW | NPPRSLDMAI | DPDSLTYTVQ | HQVLGSDQWT | ALVTGLREPG | WAATGLRKGV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| QHIFRVLSTT | VKSSSKPSPP | SEPVQLLEHG | PTLEEAPAML | DKPDIVYVVE | GQPASVTVTF | NHVEAQVVWR | SCRGALLEAR |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| AGVYELSQPD | DDQYCLRICR | VSRRDMGALT | CTARNRHGTQ | TCSVTLELAE | APRFESIMED | VEVGAGETAR | FAVVVEGKPL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PDIMWYKDEV | LLTESSHVSF | VYEENECSLV | VLSTGAQDGG | VYTCTAQNLA | GEVSCKAELA | VHSAQTAMEV | EGVGEDEDHR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GRRLSDFYDI | HQEIGRGAFS | YLRRIVERSS | GLEFAAKFIP | SQAKPKASAR | REARLLARLQ | HDCVLYFHEA | FERRRGLVIV |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| TELCTEELLE | RIARKPTVCE | SEIRAYMRQV | LEGIHYLHQS | HVLHLDVKPE | NLLVWDGAAG | EQQVRICDFG | NAQELTPGEP |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QYCQYGTPEF | VAPEIVNQSP | VSGVTDIWPV | GVVAFLCLTG | ISPFVGENDR | TTLMNIRNYN | VAFEETTFLS | LSREARGFLI |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| KVLVQDRLRP | TAEETLEHPW | FKTQAKGAEV | STDHLKLFLS | RRRWQRSQIS | YKCHLVLRPI | PELLRAPPER | VWVTMPRRPP |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| PSGGLSSSSD | SEEEELEELP | SVPRPLQPEF | SGSRVSLTDI | PTEDEALGTP | ETGAATPMDW | QEQGRAPSQD | QEAPSPEALP |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| SPGQEPAAGA | SPRRGELRRG | SSAESALPRA | GPRELGRGLH | KAASVELPQR | RSPSPGATRL | ARGGLGEGEY | AQRLQALRQR |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LLRGGPEDGK | VSGLRGPLLE | SLGGRARDPR | MARAASSEAA | PHHQPPLENR | GLQKSSSFSQ | GEAEPRGRHR | RAGAPLEIPV |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| ARLGARRLQE | SPSLSALSEA | QPSSPARPSA | PKPSTPKSAE | PSATTPSDAP | QPPAPQPAQD | KAPEPRPEPV | RASKPAPPPQ |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| ALQTLALPLT | PYAQIIQSLQ | LSGHAQGPSQ | GPAAPPSEPK | PHAAVFARVA | SPPPGAPEKR | VPSAGGPPVL | AEKARVPTVP |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 661 | 2 | 480.6345 | -248.82 | 2 | 37.8 | 10.5 | 1 | 10-17 | R.FQKTGHSR.R | | QU:MU 1.46<br>WUP:QUP 0.35 |
| 146 | 1 | 531.9457 | -37.14 | 3 | 31.8 | 25.5 | 2 | 1936-1950 | R.GPLLESLGGRARDPR.M | | WUP:QUP 4.55<br>QU:MU 0.33 |
| 43 | 1 | 796.8047 | -128.81 | 2 | 30.2 | 14.7 | 2 | 2824-2837 | R.FGVVRACRENATGR.T | Carbamidomethyl: 7 | |

# Detailed Protein Report

## Protein 55: PREDICTED: collagen alpha-1(XIV) chain isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530389313 | **Score:** | 67.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 191.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.4 |
| | | **No. of unique Peptides:** | 4 |

### Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.11 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.41 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MKIFQRKMRY WLLPPFLAIV YFCTIVQGQV APPTRLRYNV ISHDSIQISW KAPRGKFGGY KLLVTPTSGG KTNQLNLQNT
        90        100        110        120        130        140        150        160
ATKAIIQGLM PDQNYTVQII AYNKDKESKP AQGQFRIKDL EKRKDPKPRV KVVDRGNGSR PSSPEEVKFV CQTPAIADIV
       170        180        190        200        210        220        230        240
ILVDGSWSIG RFNFRLVRHF LENLVTAFDV GSEKTRIGLA QYSGDPRIEW HLNAFSTKDE VIEAVRNLPY KGGNTLTGLA
       250        260        270        280        290        300        310        320
LNYIFENSFK PEAGSRTGVS KIGILITDGK SQDDIIPPSR NLRESGVELF AIGVKNADVN ELQEIASEPD STHVYNVAEF
       330        340        350        360        370        380        390        400
DLMHTVVESL TRTLCSRVEE QDREIKASAH AITGPPTELI TSEVTARSFM VNWTHAPGNV EKYRVVYYPT RGGKPDEVVV
       410        420        430        440        450        460        470        480
DGTVSSTVLK NLMSLTEYQI AVFAIYAHTA SEGLRGTETT LALPMASDLL LYDVTENSMR VKWDAVPGAS GYLILYAPLT
       490        500        510        520        530        540        550        560
EGLAGDEKEM KIGETHTDIE LSGLLPNTEY TVTVYAMFGE EASDPVTGQE TTLALSPPRN LRISNVGSNS ARLTWDPTSR
       570        580        590        600        610        620        630        640
QINGYRIVYN NADGTEINEV EVDPITTFPL KGLTPLTEYT IAIFSIYDEG QSEPLTGVFT TEEVPAQQYL EIDEVTTDSF
       650        660        670        680        690        700        710        720
RVTWHPLSAD EGLHKLMWIP VYGGKTEEVV LKEEQDSHVI EGLEPGTEYE VSLLAVLDDG SESEVVTAVG TTLDSFWTEP
       730        740        750        760        770        780        790        800
ATTIVPTTSV TSVFQTGIRN LVVGDETTSS LRVKWDISDS DVQQFRVTYM TAQGDPEEEV IGTVMVPGSQ NNLLLKPLLP
       810        820        830        840        850        860        870        880
DTEYKVTVTP IYTDGEGVSV SAPGKTLPSS GPQNLRVSEE WYNRLRITWD PPSSPVKGYR IVYKPVSVPG PTLETFVGAD
       890        900        910        920        930        940        950        960
INTILITNLL SGMDYNVKIF ASQASGFSDA LTGMVKTLFL GVTNLQAKHV EMTSLCAHWQ VHRHATAYRV VIESLQDRQK
       970        980        990       1000       1010       1020       1030       1040
QESTVGGGTT RHCFYGLQPD SEYKISVYTK LQEIEGPSVS IMEKTQSLPT RPPTFPPTIP PAKEVCKAAK ADLVFMVDGS
      1050       1060       1070       1080       1090       1100       1110       1120
WSIGDENFNK IISFLYSTVG ALNKIGTDGT QVAMVQFTDD PRTEFKLNAY KTKETLLDAI KHISYKGGNT KTGKAIKYVR
      1130       1140       1150       1160       1170       1180       1190       1200
DTLFTAESGT RRGIPKVIVV ITDGRSQDDV NKISREMQLD GYSIFAIGVA DADYSELVSI GSKPSARHVF FVDDFDAFKK
      1210       1220       1230       1240       1250       1260       1270       1280
IEDELITFVC ETASATCPVV HKDGIDLAGF KMMEMFGLVE KDFSSVEGVS MEPGTFNVFP CYQLHKDALV SQPTRYLHPE
      1290       1300       1310       1320       1330       1340       1350       1360
GLPSDYTISF LFRILPDTPQ EPFALWEILN KNSDPLVGVI LDNGGKTLTY FNYDQSGDFQ TVTFEGPEIR KIFYGSFHKL
      1370       1380       1390       1400       1410       1420       1430       1440
HIVVSETLVK VVIDCKQVGE KAMNASANIT SDGVEVLGKM VRSRGPGGNS APFQLQMFDI VCSTSWANTD KCCELPGLRD
      1450       1460       1470       1480       1490       1500       1510       1520
DESCPDLPHS CSCSETNEVA LGPAGPPGGP GLRGPKGQQG EPGPKGPDGP RGEIGLPGPQ GPPGPQGPSG LSIQGMPGMP
      1530       1540       1550       1560       1570       1580       1590       1600
GEKGEKGDTG LPGPQGIPGG VGSPGRDGSP GQRGLPGKDG SSGPPGPPGP IGIPGTPGVP GITGSMGPQG ALGPPGVPGA
      1610       1620       1630       1640       1650       1660       1670       1680
KGERGERGDL QSQAMVRSVA RQVCEQLIQS HMARYTAILN QIPSHSSSIR TVQGPPGEPG RPGSPGAPGE QGPPGTPGFP
      1690       1700       1710       1720       1730       1740       1750       1760
GNAGVPGTPG ERGLTGIKGE KGNPGVGTQG PRGPPGPAGP SGESRPGSPG PPGSPGPRGP PGHLGVPGPQ GPSGQPGYCD
      1770       1780       1790
PSSCSAYGVR DLIPYNDYQH
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2684 | 5 | 673.3700 | 31.83 | 2 | 63.7 | 19.1 | 0 | 208-218 | R.IEWHLNAFSTK.D | | |
| 74 | 1 | 809.3972 | -57.78 | 2 | 30.6 | 10.2 | 1 | 740-754 | R.NLVVGDETTSSLRVK.W | | WUP:QUP 0.41<br>QU:MU 2.11 |
| 834 | 1 | 683.9031 | -31.20 | 2 | 40.0 | 13.1 | 1 | 1133-1145 | R.GIPKVIVVITDGR.S | | |
| 2428 | 2 | 637.7139 | -201.25 | 2 | 58.6 | 10.6 | 1 | 1371-1381 | K.VVIDCKQVGEK.A | Carbamidomethyl: 5 | |

# Detailed Protein Report

## Protein 56: DNA-dependent protein kinase catalytic subunit isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|126032350 | **Score:** | 66.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 465.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.9 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 5 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.97 | **CV:** | 59.76 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 2.35 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAGSGAGVRC | SLLRLQETLS | AADRCGAALA | GHQLIRGLGQ | ECVLSSSPAV | LALQTSLVFS | RDFGLLVFVR | KSLNSIEFRE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CREEILKFLC | IFLEKMGQKI | APYSVEIKNT | CTSVYTKDRA | AKCKIPALDL | LIKLLQTFRS | SRLMDEFKIG | ELFSKFYGEL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ALKKKIPDTV | LEKVYELLGL | LGEVHPSEMI | NNAENLFRAF | LGELKTQMTS | AVREPKLPVL | AGCLKGLSSL | LCNFTKSMEE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DPQTSREIFN | FVLKAIRPQI | DLKRYAVPSA | GLRLFALHAS | QFSTCLLDNY | VSLFEVLLKW | CAHTNVELKK | AALSALESFL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KQVSNMVAKN | AEMHKNKLQY | FMEQFYGIIR | NVDSNNKELS | IAIRGYGLFA | GPCKVINAKD | VDFMYVELIQ | RCKQMFLTQT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DTGDDRVYQM | PSFLQSVASV | LLYLDTVPEV | YTPVLEHLVV | MQIDSFPQYS | PKMQLVCCRA | IVKVFLALAA | KGPVLRNCIS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TVVHQGLIRI | CSKPVVLPKG | PESESEDHRA | SGEVRTGKWK | VPTYKDYVDL | FRHLLSSDQM | MDSILADEAF | FSVNSSSESL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NHLLYDEFVK | SVLKIVEKLD | LTLEIQTVGE | QENGDEAPGV | WMIPTSDPAA | NLHPAKPKDF | SAFINLVEFC | REILPEKQAE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FFEPWVYSFS | YELILQSTRL | PLISGFYKLL | SITVRNAKKI | KYFEGVSPKS | LKHSPEDPEK | YSCFALFVKF | GKEVAVKMKQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YKDELLASCL | TFLLSLPHNI | IELDVRAYVP | ALQMAFKLGL | SYTPLAEVGL | NALEEWSIYI | DRHVMQPYYK | DILPCLDGYL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KTSALSDETK | NNWEVSALSR | AAQKGFNKVV | LKHLKKTKNL | SSNEAISLEE | IRIRVVQMLG | SLGGQINKNL | LTVTSSDEMM |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KSYVAWDREK | RLSFAVPFRE | MKPVIFLDVF | LPRVTELALT | ASDRQTKVAA | CELLHSMVMF | MLGKATQMPE | GGQGAPPMYQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LYKRTFPVLL | RLACDVDQVT | RQLYEPLVMQ | LIHWFTNNKK | FESQDTVALL | EAILDGIVDP | VDSTLRDFCG | RCIREFLKWS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| IKQITPQQQE | KSPVNTKSLF | KRLYSLALHP | NAFKRLGASL | AFNNIYREFR | EEESLVEQFV | FEALVIYMES | LALAHADEKS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LGTIQQCCDA | IDHLCRIIEK | KHVSLNKAKK | RRLPRGFPPS | ASLCLLDLVK | WLLAHCGRPQ | TECRHKSIEL | FYKFVPLLPG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| NRSPNLWLKD | VLKEEGVSFL | INTFEGGGCG | QPSGILAQPT | LLYLRGPFSL | QATLCWLDLL | LAALECYNTF | IGERTVGALQ |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VLGTEAQSSL | LKAVAFFLES | IAMHDIIAAE | KCFGTGAAGN | RTSPQEGERY | NYSKCTVVVR | IMEFTTTLLN | TSPEGWKLLK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KDLCNTHLMR | VLVQTLCEPA | SIGFNIGDVQ | VMAHLPDVCV | NLMKALKMSP | YKDILETHLR | EKITAQSIEE | LCAVNLYGPD |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| AQVDRSRLAA | VVSACKQLHR | AGLLHNILPS | QSTDLHHSVG | TELLSLVYKG | IAPGDERQCL | PSLDLSCKQL | ASGLLELAFA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| FGGLCERLVS | LLLNPAVLST | ASLGSSQGSV | IHFSHGEYFY | SLFSETINTE | LLKNLDLAVL | ELMQSSVDNT | KMVSAVLNGM |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LDQSFRERAN | QKHQGLKLAT | TILQHWKKCD | SWWAKDSPLE | TKMAVLALLA | KILQIDSSVS | FNTSHGSFPE | VFTTYISLLA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| DTKLDLHLKG | QAVTLLPFFT | SLTGGSLEEL | RRVLEQLIVA | HFPMQSREFP | PGTPRFNNYV | DCMKKFLDAL | ELSQSPMLLE |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| LMTEVLCREQ | QHVMEELFQS | SFRRIARRGS | CVTQVGLLES | VYEMFRKDDP | RLSFTRQSFV | DRSLLTLLWH | CSLDALREFF |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| STIVVDAIDV | LKSRFTKLNE | STFDTQITKK | MGYYKILDVM | YSRLPKDDVH | AKESKINQVF | HGSCITEGNE | LTKTLIKLCY |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| DAFTENMAGE | NQLLERRRLY | HCAAYNCAIS | VICCVFNELK | FYQGFLFSEK | PEKNLLIFEN | LIDLKRRYNF | PVEVEVPMER |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| KKKYIEIRKE | AREAANGDSD | GPSYMSSLSY | LADSTLSEEM | SQFDFSTGVQ | SYSYSSQDPR | PATGRFRRRE | QRDPTVHDDV |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| LELEMDELNR | HECMAPLTAL | VKHMHRSLGP | PQGEEDSVPR | DLPSWMKFLH | GKLGNPIVPL | NIRLFLAKLV | INTEEVFRPY |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1135 | 1 | 473.1745 | -251.80 | 2 | 44.3 | 15.1 | 0 | 1643-1651 | K.MAVLALLAK.I | Oxidation: 1 | QU:MU 0.56 |
| 9 | 1 | 798.7834 | 5.94 | 3 | 29.1 | 17.8 | 2 | 2314-2334 | K.EVYAAAAEVLGLILRYVMERK.N | | |
| 935 | 1 | 512.1405 | -273.82 | 2 | 41.8 | 10.3 | 0 | 2434-2441 | K.VCLDIIYK.M | Carbamidomethyl: 2 | WUP:QUP 2.35<br>QU:MU 1.68 |
| 272 | 1 | 898.1750 | 46.75 | 3 | 33.4 | 12.1 | 2 | 3030-3050 | K.IWSEPFYQETYLPYMIRSKLK.L | | |
| 2214 | 1 | 722.7106 | -205.39 | 2 | 56.0 | 11.5 | 2 | 3236-3247 | K.FSMKMKMIDSAR.K | | |

# Detailed Protein Report

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**Protein 57:** **semaphorin-5B isoform 3 precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|373432662 | **Score:** | 65.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 116.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.1 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVLAGPLAVS | LLLPSLTLLV | SHLSSSQDVS | SEPSSEQQLC | ALSKHPTVAF | EDLQPWVSNF | TYPGARDFSQ | LALDPSGNQL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IVGARNYLFR | LSLANVSLLQ | ATEWASSEDT | RRSCQSKGKT | EEECQNYVRV | LIVAGRKVFM | CGTNAFSPMC | TSRQVGNLSR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TIEKINGVAR | CPYDPRHNST | AVISSQGELY | AATVIDFSGR | DPAIYRSLGS | GPPLRTAQYN | SKWLNEPNFV | AAYDIGLFAY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FFLRENAVEH | DCGRTVYSRV | ARVCKNDVGG | RFLLEDTWTT | FMKARLNCSR | PGEVPFYYNE | LQSAFHLPEQ | DLIYGVFTTN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VNSIAASAVC | AFNLSAISQA | FNGPFRYQEN | PRAAWLPIAN | PIPNFQCGTL | PETGPNENLT | ERSLQDAQRL | FLMSEAVQPV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TPEPCVTQDS | VRFSHLVVDL | VQAKDTLYHV | LYIGTESGTI | LKALSTASRS | LHGCYLEELH | VLPPGRREPL | RSLRILHSAR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ALFVGLRDGV | LRVPLERCAA | YRSQGACLGA | RDPYCGWDGK | QQRCSTLEDS | SNMSLWTQNI | TACPVRNVTR | DGGFGPWSPW |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QPCEHLDGDN | SGSCLCRARS | CDSPRPRCGG | LDCLGPAIHI | ANCSRNGAWT | PWSSWALCST | SCGIGFQVRQ | RSCSNPAPRH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GGRICVGKSR | EERFCNENTP | CPVPIFWASW | GSWSKCSSNC | GGGMQSRRRA | CENGNSCLGC | GVEFKTCNPE | GCPEVRRNTP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| WTPWLPVNVT | QGGARQEQRF | RFTCRAPLAD | PHGLQFGRRR | TETRTCPADG | SGSCDTDALV | EVLLRSGSTS | PHTVSGGWAA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| WGPWSSCSRD | CELGFRVRKR | TCTNPEPRNG | GLPCVGDAAE | YQDCNPQACP | GEDICLGLHT | EEALCATQAC | PEGWSPWSEW |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SKCTDDGAQS | RSRHCEELLP | GSSACAGNSS | QSRPCPYSEI | PVILPASSME | EATDCAGFNL | IHLVATGISC | FLGSGLLTLA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VYLSCQHCQR | QSQESTLVHP | ATPNHLHYKG | GGTPKNEKYT | PMEFKTLNKN | NLIPDDRANF | YPLQQTNVYT | TTYYPSPLNK |
| 1050 | 1060 | | | | | | |
| HSFRPEASPG | QRCFPNS | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2242 | 7 | 682.6902 | 75.49 | 3 | 58.4 | 22.5 | 2 | 113-129 | R.SCQSKGKTEEECQNYVR.V | Carbamidomethyl: 2 |
| 1478 | 1 | 1061.4566 | -34.44 | 2 | 48.1 | 20.8 | 0 | 765-785 | R.TCPADGSGSCDTDALVEVLLR.S | |

# Detailed Protein Report

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## Protein 58: chromodomain-helicase-DNA-binding protein 2 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|118421089 | **Score:** | 65.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 211.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 5 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.42 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.05 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMRNKDKSQE | EDSSLHSNAS | SHSASEEASG | SDSGSQSESE | QGSDPGSGHG | SESNSSSESS | ESQSESESES | AGSKSQPVLP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EAKEKPASKK | ERIADVKKMW | EEYPDVYGVR | RSNRSRQEPS | RFNIKEEASS | GSESGSPKRR | GQRQLKKQEK | WKQEPSEDEQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EQGTSAESEP | EQKKVKARRP | VPRRTVPKPR | VKKQPKTQRG | KRKKQDSSDE | DDDDDEAPKR | QTRRRAAKNV | SYKEDDDFET |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DSDDLIEMTG | EGVDEQQDNS | ETIEKVLDSR | LGKKGATGAS | TTVYAIEANG | DPSGDFDTEK | DEGEIQYLIK | WKGWSYIHST |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WESEESLQQQ | KVKGLKKLEN | FKKKEDEIKQ | WLGKVSPEDV | EYFNCQQELA | SELNKQYQIV | ERVIAVKTSK | STLGQTDFPA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HSRKPAPSNE | PEYLCKWMGL | PYSECSWEDE | ALIGKKFQNC | IDSFHSRNNS | KTIPTRECKA | LKQRPRFVAL | KKQPAYLGGE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NLELRDYQLE | GLNWLAHSWC | KNNSVILADE | MGLGKTIQTI | SFLSYLFHQH | QLYGPFLIVV | PLSTLTSWQR | EFEIWAPEIN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VVVYIGDLMS | RNTIREYEWI | HSQTKRLKFN | ALITTYEILL | KDKTVLGSIN | WAFLGVDEAH | RLKNDDSLLY | KTLIDFKSNH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RLLITGTPLQ | NSLKELWSLL | HFIMPEKFEF | WEDFEEDHGK | GRENGYQSLH | KVLEPFLLRR | VKKDVEKSLP | AKVEQILRVE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| MSALQKQYYK | WILTRNYKAL | AKGTRGSTSG | FLNIVMELKK | CCNHCYLIKP | PEENERENGQ | EILLSLIRSS | GKLILLDKLL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TRLRERGNRV | LIFSQMVRML | DILAEYLTIK | HYPFQRLDGS | IKGEIRKQAL | DHFNADGSED | FCFLLSTRAG | GLGINLASAD |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TVVIFDSDWN | PQNDLQAQAR | AHRIGQKKQV | NIYRLVTKGT | VEEEIIERAK | KKMVLDHLVI | QRMDTTGRTI | LENNSGRSNS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NPFNKEELTA | ILKFGAEDLF | KELEGEESEP | QEMDIDEILR | LAETRENEVS | TSATDELLSQ | FKVANFATME | DEEELEERPH |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KDWDEIIPEE | QRKKVEEEER | QKELEEIYML | PRIRSSTKKA | QTNDSDSDTE | SKRQAQRSSA | SESETEDSDD | DKKPKRRGRP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RSVRKDLVEG | FTDAEIRRFI | KAYKKFGLPL | ERLECIARDA | ELVDKSVADL | KRLGELIHNS | CVSAMQEYEE | QLKENASEGK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| GPGKRRGPTI | KISGVQVNVK | SIIQHEEEFE | MLHKSIPVDP | EEKKKYCLTC | RVKAAHFDVE | WGVEDDSRLL | LGIYEHGYGN |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| WELIKTDPEL | KLTDKILPVE | TDKKPQGKQL | QTRADYLLKL | LRKGLEKKGA | VTGGEEAKLK | KRKPRVKKEN | KVPRLKEEHG |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| IELSSPRHSD | NPSEEGEVKD | DGLEKSPMKK | KQKKKENKEN | KEKQMSSRKD | KEGDKERKKS | KDKKEKPKSG | DAKSSSKSKR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SQGPVHITAG | SEPVPIGEDE | DDDLDQETFS | ICKERMRPVK | KALKQLDKPD | KGLNVQEQLE | HTRNCLLKIG | DRIAECLKAY |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| SDQEHIKLWR | RNLWIFVSKF | TEFDARKLHK | LYKMAHKKRS | QEEEEQKKKD | DVTGGKKPFR | PEASGSSRDS | LISQSHTSHN |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LHPQKPHLPA | SHGPQMHGHP | RDNYNHPNKR | HFSNADRGDW | QRERKFNYGG | GNNNPPWGSD | RHHQYEQHWY | KDHHYGDRRH |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| MDAHRSGSYR | PNNMSRKRPY | DQYSSDRDHR | GHRDYYDRHH | HDSKRRRSDE | FRPQNYHQQD | FRRMSDHRPA | MGYHGQGPSD |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | |
| HYRSFHTDKL | GEYKQPLPPL | HPAVSDPRSP | PSQKSPHDSK | SPLDHRSPLE | RSLEQKNNPD | YNWNVRKT | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2644 | 1 | 913.4624 | -16.46 | 2 | 63.1 | 14.1 | 1 | 743-759 | K.GTRGSTSGFLNIVMELK.K | Oxidation: 14 | |
| 1777 | 2 | 1022.8922 | -139.78 | 2 | 52.6 | 14.7 | 2 | 932-948 | K.KMVLDHLVIQRMDTTGR.T | Oxidation: 2, 12 | |
| 1792 | 1 | 898.7912 | -12.20 | 3 | 52.2 | 11.6 | 1 | 1212-1234 | K.ISGVQVNVKSIIQHEEEFEMLHK.S | | |
| 2192 | 1 | 885.2814 | -167.85 | 2 | 57.8 | 12.6 | 0 | 1221-1234 | K.SIIQHEEEFEMLHK.S | | |
| 1619 | 1 | 1015.0002 | -35.61 | 2 | 50.0 | 12.7 | 2 | 1531- | R.RNLWIFVSKFTEFDAR.K | | WUP:QUP 1.05 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | 1546 | | | QU:MU 1.42 |

# Detailed Protein Report

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| | | | |
|---|---|---|---|
| **Protein 59:** | **voltage-dependent P/Q-type calcium channel subunit alpha-1A isoform 4 [Homo sapiens]** | | |
| **Accession:** | gi\|187828892 | **Score:** | 65.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 282.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MARFGDEMPA | RYGGGGSGAA | AGVVVGSGGG | RGAGGSRQGG | QPGAQRMYKQ | SMAQRARTMA | LYNPIPVRQN | CLTVNRSLFL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FSEDNVVRKY | AKKITEWPPF | EYMILATIIA | NCIVLALEQH | LPDDDKTPMS | ERLDDTEPYF | IGIFCFEAGI | KIIALGFAFH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KGSYLRNGWN | VMDFVVVLTG | ILATVGTEFD | LRTLRAVRVL | RPLKLVSGIP | SLQVVLKSIM | KAMIPLLQIG | LLLFFAILIF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AIIGLEFYMG | KFHTTCFEEG | TDDIQGESPA | PCGTEEPART | CPNGTKCQPY | WEGPNNGITQ | FDNILFAVLT | VFQCITMEGW |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TDLLYNSNDA | SGNTWNWLYF | IPLIIIGSFF | MLNLVLGVLS | GEFAKERERV | ENRRAFLKLR | RQQQIERELN | GYMEWISKAE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EVILAEDETD | GEQRHPFDAL | RRTTIKKSKT | DLLNPEEAED | QLADIASVGS | PFARASIKSA | KLENSTFFHK | KERRMRFYIR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RMVKTQAFYW | TVLSLVALNT | LCVAIVHYNQ | PEWLSDFLYY | AEFIFLGLFM | SEMFIKMYGL | GTRPYFHSSF | NCFDCGVIIG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SIFEVIWAVI | KPGTSFGISV | LRALRLLRIF | KVTKYWASLR | NLVVSLLNSM | KSIISLLFLL | FLFIVVFALL | GMQLFGGQFN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FDEGTPPTNF | DTFPAAIMTV | FQILTGEDWN | EVMYDGIKSQ | GGVQGGMVFS | IYFIVLTLFG | NYTLLNVFLA | IAVDNLANAQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ELTKDEQEEE | EAANQKLALQ | KAKEVAEVSP | LSAANMSIAV | KEQQKNQKPA | KSVWEQRTSE | MRKQNLLASR | EALYNEMDPD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ERWKAAYTRH | LRPDMKTHLD | RPLVVDPQEN | RNNNTNKSRA | AEPTVDQRLG | QQRAEDFLRK | QARYHDRARD | PSGSAGLDAR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RPWAGSQEAE | LSREGPYGRE | SDHHAREGSL | EQPGFWEGEA | ERGKAGDPHR | RHVHRQGGSR | ESRSGSPRTG | ADGEHRRHRA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| HRRPGEEGPE | DKAERRARHR | EGSRPARGGE | GEGEGPDGGE | RRRRHRHGAP | ATYEGDARRE | DKERRHRRRK | ENQGSGVPVS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GPNLSTTRPI | QQDLGRQDPP | LAEDIDNMKN | NKLATAESAA | PHGSLGHAGL | PQSPAKMGNS | TDPGPMLAIP | AMATNPQNAA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SRRTPNNPGN | PSNPGPPKTP | ENSLIVTNPS | GTQTNSAKTA | RKPDHTTVDI | PPACPPPLNH | TVVQVNKNAN | PDPLPKKEEE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KKEEEEDDRG | EDGPKPMPPY | SSMFILSTTN | PLRRLCHYIL | NLRYFEMCIL | MVIAMSSIAL | AAEDPVQPNA | PRNNVLRYFD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| YVFTGVFTFE | MVIKMIDLGL | VLHQGAYFRD | LWNILDFIVV | SGALVAFAFT | GNSKGKDINT | IKSLRVLRVL | RPLKTIKRLP |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KLKAVFDCVV | NSLKNVFNIL | IVYMLFMFIF | AVVAVQLFKG | KFFHCTDESK | EFEKDCRGKY | LLYEKNEVKA | RDREWKKYEF |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| HYDNVLWALL | TLFTVSTGEG | WPQVLKHSVD | ATFENQGPSP | GYRMEMSIFY | VVYFVVFPFF | FVNIFVALII | ITFQEQGDKM |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| MEEYSLEKNE | RACIDFAISA | KPLTRHMPQN | KQSFQYRMWQ | FVVSPPFEYT | IMAMIALNTI | VLMMKFYGAS | VAYENALRVF |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| NIVFTSLFSL | ECVLKVMAFG | ILNYFRDAWN | IFDFVTVLGS | ITDILVTEFG | NNFINLSFLR | LFRAARLIKL | LRQGYTIRIL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LWTFVQSFKA | LPYVCLLIAM | LFFIYAIIGM | QVFGNIGIDV | EDEDSDEDEF | QITEHNNFRT | FFQALMLLFR | SATGEAWHNI |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| MLSCLSGKPC | DKNSGILTRE | CGNEFAYFYF | VSFIFLCSFL | MLNLFVAVIM | DNFEYLTRDS | SILGPHHLDE | YVRVWAEYDP |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| AAWGRMPYLD | MYQMLRHMSP | PLGLGKKCPA | RVAYKRLLRM | DLPVADDNTV | HFNSTLMALI | RTALDIKIAK | GGADKQQMDA |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| ELRKEMMAIW | PNLSQKTLDL | LVTPHKSTDL | TVGKIYAAMM | IMEYYRQSKA | KKLQAMREEQ | DRTPLMFQRM | EPPSPTQEGG |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| PGQNALPSTQ | LDPGGALMAH | ESGLKESPSW | VTQRAQEMFQ | KTGTWSPEQG | PPTDMPNSQP | NSQSVEMREM | GRDGYSDSEH |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| YLPMEGQGRA | ASMPRLPAEN | QRRRGRPRGN | NLSTISDTSP | MKRSASVLGP | KARRLDDYSL | ERVPPEENQR | HHQRRRDRSH |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| RASERSLGRY | TDVDTGLGTD | LSMTTQSGDL | PSKERDQERG | RPKDRKHRQH | HHHHHHHHHP | PPPDKDRYAQ | ERPDHGRARA |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| RDQRWSRSPS | EGREHMAHRQ | GSSSVSGSPA | PSTSGTSTPR | RGRRQLPQTP | STPRPHVSYS | PVIRKAGGSG | PPQQQQQQQQ |
| 2330 | 2340 | 2350 | 2360 | 2370 | 2380 | 2390 | 2400 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2706 | 1 | 741.8621 | -28.64 | 2 | 64.1 | 11.6 | 2 | 2371-<br>2384 | R.VPGPARSESPRACR.H | |

# Detailed Protein Report

## Protein 60: PREDICTED: CDK5 regulatory subunit-associated protein 2 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578817652 | **Score:** | 64.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 211.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 4 |

### Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.34 | **CV:** | 15.04 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 0.32 | **CV:** | 8.26 % | **No. of Peptides:** | 2 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MMDLVLEEDV TVPGTLSGCS GLVPSVPDDL DGINPNAGLG NGLLPNVSEE TVSPTRARNM KDFENQITEL KKENFNLKLR

        90        100        110        120        130        140        150        160
IYFLEERMQQ EFHGPTEHIY KTNIELKVEV ESLKRELQER EQLLIKASKA VESLAEAGGS EIQRVKEDAR KKVQQVEDLL

       170        180        190        200        210        220        230        240
TKRILLLEKD VTAAQAELEK AFAGTETEKA LRLRLESKLS EMKKMHEGDL AMALVLDEKD RLIEELKLSL KSKEALIQCL

       250        260        270        280        290        300        310        320
KEEKSQMACP DENVSSGELR GLCAAPREEK ERETEAAQME HQKERNSFEE RIQALEEDLR EKEREIATEK KNSLKRDKAI

       330        340        350        360        370        380        390        400
QGLTMALKSK EKKVEELNSE IEKLSAAFAK AREALQKAQT QEFQGSEDYE TALSGKEALS AALRSQNLTK STENHRLRRS

       410        420        430        440        450        460        470        480
IKKITQELSD LQQERERLEK DLEEAHREKS KGDCTIRDLR NEVEKLRNEV NEREKAMENR YKSLLSESNK KLHNQEQVIK

       490        500        510        520        530        540        550        560
HLTESTNQKD VLLQKFNEKD LEVIQQNCYL MAAEDLELRS EGLITEKCSS QQPPGSKTIF SKEKKQSSDY EELIQVLKKE

       570        580        590        600        610        620        630        640
QDIYTHLVKS LQESDSINNL QAELNKIFAL RKQLEQDVLS YQNLRKTLEE QISEIRRREE ESFSLYSDQT SYLSICLEEN

       650        660        670        680        690        700        710        720
NRFQVEHFSQ EELKKKVSDL IQLVKELYTD NQHLKKTIFD LSCMGFQGNG FPDRLASTEQ TEIMKDLSKG GCKNGYLRHT

       730        740        750        760        770        780        790        800
ESKISDCDGA HAPGCLEEGA FINLLAPLFN EKATLLLESR PDLLKVVREL LLGQLFLTEQ EVSGEHLDGK TEKTPKQKGE

       810        820        830        840        850        860        870        880
LVHFVQTNSF SKPHDELKLS CEAQLVKAGE VPKVGLKDAS VQTVATEGDL LRFKHEATRE AWEEKPINTA LSAEHRPENL

       890        900        910        920        930        940        950        960
HGVPGWQAAL LSLPGITNRE AKKSRLPILI KPSRSLGNMY RLPATQEVVT QLQSQILELQ GELKEFKTCN KQLHQKLILA

       970        980        990       1000       1010       1020       1030       1040
EAVMEGRPTP DKTLLNAQPP VGAAYQDSPG EQKGIKTTSS VWRDKEMDSD QQRSYEIDSE ICPPDDLASL PSCKENPEDV

      1050       1060       1070       1080       1090       1100       1110       1120
LSPTSVATYL SSKSQPSAKV SVMGTDQSES INTSNETEYL KQKIHDLETE LEGYQNFIFQ LQKHSQCSEA IITVLCGTEG

      1130       1140       1150       1160       1170       1180       1190       1200
AQDGLSKPKN GSDGEEMTFS SLHQVRYVKH VKILGPLAPE MIDSRVLENL KQQLEEQEYK LQKEQNLNMQ LFSEIHNLQN

      1210       1220       1230       1240       1250       1260       1270       1280
KFRDLSPPRY DSLVQSQARE LSLQRQQIKD GHGICVISRQ HMNTMIKAFE ELLQASDVDY CVAEGFQEQL NQCAELLEKL

      1290       1300       1310       1320       1330       1340       1350       1360
EKLFLNGKSV GVEMNTQNEL MERIEEDNLT YQHLLPESPE PSASHALSDY ETSEKSFFSR DQKQDNETEK TSVMVNSFSQ

      1370       1380       1390       1400       1410       1420       1430       1440
DLLMEHIQEI RTLRKRLEES IKTNEKLRKQ LERQGSEFVQ GSTSIFASGS ELHSSLTSEI HFLRKQNQAL NAMLIKGSRD

      1450       1460       1470       1480       1490       1500       1510       1520
KQKENDKLRE SLSRKTVSLE HLQREYASVK EENERLQKEG SEKERHNQQL IQEVRCSGQE LSRVQEEVKL RQQLLSQNDK

      1530       1540       1550       1560       1570       1580       1590       1600
LLQSLRVELK AYEKLDEEHR RLREASGEGW KGQDPFRDLH SLLMEIQALR LQLERSIETS STLQSRLKEQ LARGAEKAQE

      1610       1620       1630       1640       1650       1660       1670       1680
GALTLAVQAV SIPEVPLQPD KHDGDKYPME SDNSFDLFDS SQAVTPKSVS ETPPLSGNDT DSLSCDSGSS ATSTPCVSRL

      1690       1700       1710       1720       1730       1740       1750       1760
VTGHHLWASK NGRHVLGLIE DYEALLKQIS QGQRLLAEMD IQTQEAPSST SQELGTKGPH PAPLSKFVSS VSTAKLTLEE

      1770       1780       1790       1800       1810       1820       1830       1840
AYRRLKLLWR VSLPEDGQCP LHCEQIGEMK AEVTKLHKKL FEQEKKLQNT MKLLQLSKRQ EKVIFDQLVV THKILRKARG

      1850       1860       1870
NLELRPGGAH PGTCSPSRPG S
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 93 | 1 | 529.5810 | 3.65 | 3 | 30.1 | 13.6 | 1 | 271-283 | K.ERETEAAQMEHQK.E | | WUP:QUP 0.30<br>QU:MU 1.55 |
| 2305 | 1 | 937.4652 | -77.24 | 2 | 57.1 | 11.9 | 1 | 906-921 | R.LPILIKPSRSLGNMYR.L | Oxidation: 14 | |
| 268 | 2 | 501.1673 | -209.52 | 2 | 32.1 | 13.8 | 1 | 1589-1597 | K.EQLARGAEK.A | | WUP:QUP 0.35<br>QU:MU 1.15 |
| 667 | 1 | 575.7990 | -26.64 | 2 | 38.3 | 15.2 | 1 | 1756- | K.LTLEEAYRR.L | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
|  |  |  |  |  |  |  |  | 1764 |  |  |  |

# Detailed Protein Report

## Protein 61: PREDICTED: E3 ubiquitin-protein ligase UBR4 isoform X11 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578798772 | **Score:** | 64.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 574.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 4 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MATSGGEEAA | AAAPAPGTPA | TGADTTPGWE | VAVRPLLSAS | YSAFEMKELP | QLVASVIESE | SEILHHEKQY | EPFYSSFVAL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| STHYITTVCS | LIPRNQLQSV | AAACKVLIEF | SLLRLENPDE | ACAVSQKHLI | LLIKGLCTGC | SRLDRTEIIT | FTAMMKSAKL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PQTVKTLSDV | EDQKELASPV | SPELRQKEVQ | MNFLNQLTSV | FNPRTVASQP | ISTQTLVEGE | NDEQSSTDQA | SAIKTKNVFI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AQNVASLQEL | GGSEKLLRVC | LNLPYFLRYI | NRFQDAVLAN | SFFIMPATVA | DATAVRNGFH | SLVIDVTMAL | DTLSLPVLEP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LNPSRLQDVT | VLSLSCLYAG | VSVATCMAIL | HVGSAQQVRT | GSTSSKEDDY | ESDAATIVQK | CLEIYDMIGQ | AISSSRRAGG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EHYQNFQLLG | AWCLLNSLFL | ILNLSPTALA | DKGKEKDPLA | ALRVRDILSR | TKEGVGSPKL | GPGKGHQGFG | VLSVILANHA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IKLLTSLFQD | LQVEALHKGW | ETDGPPAALS | IMAQSTSIQR | IQRLIDSVPL | MNLLLTLLST | SYRKACVLQR | QRKGSMSSDA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SASTDSNTYY | EDDFSSTEED | SSQDDDSEPI | LGQWFEETIS | PSKEKAAPPP | PPPPPPLESS | PRVKSPSKQA | PGEKGNILAS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RKDPELFLGL | ASNILNFITS | SMLNSRNNFI | RNYLSVSLSE | HHMATLASII | KEVDKDGLKG | SSDEEFAAAL | YHFNHSLVTS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DLQSPNLQNT | LLQQLGVAPF | SEGPWPLYIH | PQSLSVLSRL | LLIWQHKASA | QGDPDVPECL | KVWDRFLSTM | KQNALQGVVP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SETEDLNVEH | LQMLLLIFHN | FTETGRRAIL | SLFVQIIQEL | SVNMDAQMRF | VPLILARLLL | IFDYLLHQYS | KAPVYLFEQV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QHNLLSPPFG | WASGSQDSNS | RRATTPLYHG | FKEVEENWSK | HFSSDAVPHP | RFYCVLSPEA | SEDDLNRLDS | VACDVLFSKL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VKYDELYAAL | TALLAAGSQL | DTVRRKENKN | VTALEACALQ | YYFLILWRIL | GILPPSKTYI | NQLSMNSPEM | SECDILHTLR |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| WSSRLRISSY | VNWIKDHLIK | QGMKAEHASS | LLELASTTKC | SSVKYDVEIV | EEYFARQISS | FCSIDCTTIL | QLHEIPSLQS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| IYTLDAAISK | VQVSLDEHFS | KMAAETDPHK | SSEITKNLLP | ATLQLIDTYA | SFTRAYLLQN | FNEEGTTEKP | SKEKLQGFAA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VLAIGSSRCK | ANTLGPTLVQ | NLPSSVQTVC | ESWNNINTNE | FPNIGSWRNA | FANDTIPSES | YISAVQAAHL | GTLCSQSLPL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| AASLKHTLLS | LVRLTGDLIV | WSDEMNPPQV | IRTLLPLLLE | SSTESVAEIS | SNSLERILGP | AESDEFLARV | YEKLITGCYN |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ILANHADPNS | GLDESILEEC | LQYLEKQLES | SQARKAMEEF | FSDSGELVQI | MMATANENLS | AKFCNRVLKF | FTKLFQLTEK |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SPNPSLLHLC | GSLAQLACVE | PVRLQAWLTR | MTTSPPKDSD | QLDVIQENRQ | LLQLLTTYIV | RENSQVGEGV | CAVLLGTLTP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| MATEMLANGD | GTGFPELMVV | MATLASAGQG | AGHLQLHNAA | VDWLSRCKKY | LSQKNVVEKL | NANVMHGKHV | MILECTCHIM |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| SYLADVTNAL | SQSNGQGPSH | LSVDGEERAI | EVDSDWVEEL | AVEEEDSQAE | DSDEDSLCNK | LCTFTITQKE | FMNQHWYHCH |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| TCKMVDGVGV | CTVCAKVCHK | DHEISYAKYG | SFFCDCGAKE | DGSCLALVKR | TPSSGMSSTM | KESAFQSEPR | ISESLVRHAS |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| TSSPADKAKV | TISDGKVADE | EKPKKSSLCR | TVEGCREELQ | NQANFSFAPL | VLDMLNFLMD | AIQTNFQQAS | AVGSSSRAQQ |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| ALSELHTVEK | AVEMTDQLMV | PTLGSQEGAF | ENVRMNYSGD | QGQTIRQLIS | AHVLRRVAMC | VLSSPHGRRQ | HLAVSHEKGK |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| ITVLQLSALL | KQADSSKRKL | TLTRLASAPV | PFTVLSLTGN | PCKEDYLAVC | GLKDCHVLTF | SSSGSVSDHL | VLHPQLATGN |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| FIIKAVWLPG | SQTELAIVTA | DFVKIYDLCV | DALSPTFYFL | LPSSKIRDVT | FLFNEEGKNI | IVIMSSAGYI | YTQLMEEASS |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| AQQGPFYVTN | VLEINHEDLK | QDSNSQVAGG | GVSVYYSHVL | QMLFFSYCQG | KSFAATISRT | TLEVLQLFPI | NIKSSNGGSK |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 270 | 1 | 530.5999 | -29.12 | 3 | 33.1 | 13.6 | 2 | 1777-1790 | K.VADEEKPKKSSLCR.T | |
| 1928 | 1 | 917.3279 | -102.08 | 2 | 54.5 | 15.2 | 1 | 2608-2623 | K.LPQMETGMDEGKEPQK.Q | Oxidation: 4 |
| 1934 | 1 | 745.7866 | -161.90 | 2 | 54.6 | 10.5 | 1 | 3240-3252 | R.DLHTLDSHVRGIK.K | |
| 375 | 1 | 878.7841 | 3.73 | 3 | 34.7 | 12.0 | 2 | 4668-4690 | K.VFLDCFCKIAAGIKNNSNGHQLK.D | Carbamidomethyl: 5, 7 |

# Detailed Protein Report

| | | | |
|---|---|---|---|
| **Protein 62:** | **centromere protein F [Homo sapiens]** | | |
| **Accession:** | gi\|55770834 | **Score:** | 64.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 357.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSWALEEWKE | GLPTRALQKI | QELEGQLDKL | KKEKQQRQFQ | LDSLEAALQK | QKQKVENEKT | EGTNLKRENQ | RLMEICESLE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KTKQKISHEL | QVKESQVNFQ | EGQLNSGKKQ | IEKLEQELKR | CKSELERSQQ | AAQSADVSLN | PCNTPQKIFT | TPLTPSQYYS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GSKYEDLKEK | YNKEVEERKR | LEAEVKALQA | KKASQTLPQA | TMNHRDIARH | QASSSVFSWQ | QEKTPSHLSS | NSQRTPIRRD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FSASYFSGEQ | EVTPSRSTLQ | IGKRDANSSF | FDNSSSPHLL | DQLKAQNQEL | RNKINELELR | LQGHEKEMKG | QVNKFQELQL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QLEKAKVELI | EKEKVLNKCR | DELVRTTAQY | DQASTKYTAL | EQKLKKLTED | LSCQRQNAES | ARCSLEQKIK | EKEKEFQEEL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SRQQRSFQTL | DQECIQMKAR | LTQELQQAKN | MHNVLQAELD | KLTSVKQQLE | NNLEEFKQKL | CRAEQAFQAS | QIKENELRRS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| MEEMKKENNL | LKSHSEQKAR | EVCHLEAELK | NIKQCLNQSQ | NFAEEMKAKN | TSQETMLRDL | QEKINQQENS | LTLEKLKLAV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ADLEKQRDCS | QDLLKKREHH | IEQLNDKLSK | TEKESKALLS | ALELKKKEYE | ELKEEKTLFS | CWKSENEKLL | TQMESEKENL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QSKINHLETC | LKTQQIKSHE | YNERVRTLEM | DRENLSVEIR | NLHNVLDSKS | VEVETQKLAY | MELQQKAEFS | DQKHQKEIEN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| MCLKTSQLTG | QVEDLEHKLQ | LLSNEIMDKD | RCYQDLHAEY | ESLRDLLKSK | DASLVTNEDH | QRSLLAFDQQ | PAMHHSFANI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IGEQGSMPSE | RSECRLEADQ | SPKNSAILQN | RVDSLEFSLE | SQKQMNSDLQ | KQCEELVQIK | GEIEENLMKA | EQMHQSFVAE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TSQRISKLQE | DTSAHQNVVA | ETLSALENKE | KELQLLNDKV | ETEQAEIQEL | KKSNHLLEDS | LKELQLLSET | LSLEKKEMSS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| IISLNKREIE | ELTQENGTLK | EINASLNQEK | MNLIQKSESF | ANYIDEREKS | ISELSDQYKQ | EKLILLQRCE | ETGNAYEDLS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QKYKAAQEKN | SKLECLLNEC | TSLCENRKNE | LEQLKEAFAK | EHQEFLTKLA | FAEERNQNLM | LELETVQQAL | RSEMTDNQNN |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SKSEAGGLKQ | EIMTLKEEQN | KMQKEVNDLL | QENEQLMKVM | KTKHECQNLE | SEPIRNSVKE | RESERNQCNF | KPQMDLEVKE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ISLDSYNAQL | VQLEAMLRNK | ELKLQESEKE | KECLQHELQT | IRGDLETSNL | QDMQSQEISG | LKDCEIDAEE | KYISGPHELS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TSQNDNAHLQ | CSLQTTMNKL | NELEKICEIL | QAEKYELVTE | LNDSRSECIT | ATRKMAEEVG | KLLNEVKILN | DDSGLLHGEL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VEDIPGGEFG | EQPNEQHPVS | LAPLDESNSY | EHLTLSDKEV | QMHFAELQEK | FLSLQSEHKI | LHDQHCQMSS | KMSELQTYVD |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SLKAENLVLS | TNLRNFQGDL | VKEMQLGLEE | GLVPSLSSSC | VPDSSSLSSL | GDSSFYRALL | EQTGDMSLLS | NLEGAVSANQ |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| CSVDEVFCSS | LQEENLTRKE | TPSAPAKGVE | ELESLCEVYR | QSLEKLEEKM | ESQGIMKNKE | IQELEQLLSS | ERQELDCLRK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QYLSENEQWQ | QKLTSVTLEM | ESKLAAEKKQ | TEQLSLELEV | ARLQLQGLDL | SSRSLLGIDT | EDAIQGRNES | CDISKEHTSE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| TTERTPKHDV | HQICDKDAQQ | DLNLDIEKIT | ETGAVKPTGE | CSGEQSPDTN | YEPPGEDKTQ | GSSECISELS | FSGPNALVPM |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| DFLGNQEDIH | NLQLRVKETS | NENLRLLHVI | EDRDRKVESL | LNEMKELDSK | LHLQEVQLMT | KIEACIELEK | IVGELKKENS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| DLSEKLEYFS | CDHQELLQRV | ETSEGLNSDL | EMHADKSSRE | DIGDNVAKVN | DSWKERFLDV | ENELSRIRSE | KASIEHEALY |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LEADLEVVQT | EKLCLEKDNE | NKQKVIVCLE | EELSVVTSER | NQLRGELDTM | SKKTTALDQL | SEKMKEKTQE | LESHQSECLH |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| CIQVAEAEVK | EKTELLQTLS | SDVSELLKDK | THLQEKLQSL | EKDSQALSLT | KCELENQIAQ | LNKEKELLVK | ESESLQARLS |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| ESDYEKLNVS | KALEAALVEK | GEFALRLSST | QEEVHQLRRG | IEKLRVRIEA | DEKKQLHIAE | KLKERERENDN | SLKDKVENLE |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2707 | 1 | 821.4735 | 62.12 | 2 | 64.1 | 11.9 | 2 | 301-314 | R.LQGHEKEMKGQVNK.F | Oxidation: 8 |
| 1276 | 1 | 917.4679 | 30.80 | 2 | 46.1 | 11.7 | 0 | 2267-2283 | K.ELNEAVAALCGDQEIMK.A | |
| 552 | 1 | 600.8199 | -67.28 | 2 | 35.3 | 13.6 | 1 | 2316-2325 | K.KQLCVLQQLK.E | |

# Detailed Protein Report

| | | | |
|---|---|---|---|
| **Protein 63:** | **Alstrom syndrome protein 1 [Homo sapiens]** | | |
| **Accession:** | gi\|110349786 | **Score:** | 64.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 460.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.56 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.53 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEPEDLPWPG | ELEEEEEEEE | EEEEEEEEEA | AAAAAANVDD | VVVVEEVEEE | AGRELDSDSH | YGPQHLESID | DEEDEEAKAW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LQAHPGRILP | PLSPPQHRYS | EGERTSLEKI | VPLTCHVWQQ | IVYQGNSRTQ | ISDTNVVCLE | TTAQRGSGDD | QKTESWHCLP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QEMDSSQTLD | TSQTRFNVRT | EDTEVTDFPS | LEEGILTQSE | NQVKEPNRDL | FCSPLLVIQD | SFASPDLPLL | TCLTQDQEFA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PDSLFHQSEL | SFAPLRGIPD | KSEDTEWSSR | PSEVSEALFQ | ATAEVASDLA | SSRFSVSQHP | LIGSTAVGSQ | CPFLPSEQGN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NEETISSVDE | LKIPKDCDRY | DDLCSYMSWK | TRKDTQWPEN | NLADKDQVSV | ATSFDITDEN | IATKRSDHFD | AARSYGQYWT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QEDSSKQAET | YLTKGLQGKV | ESDVITLDGL | NENAVVCSER | VAELQRKPTR | ESEYHSSDLR | MLRMSPDTVP | KAPKHLKAGD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TSKGGIAKVT | QSNLKSGITT | TPVDSDIGSH | LSLSLEDLSQ | LAVSSPLETT | TGQHTDTLNQ | KTLADTHLTE | ETLKVTAIPE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PADQKTATPT | VLSSSHSHRG | KPSIFYQQGL | PDSHLTEEAL | KVSAAPGLAD | QTTGMSTLTS | TSYSHREKPG | TFYQQELPES |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NLTEEPLEVS | AAPGPVEQKT | GIPTVSSTSH | SHVEDLLFFY | RQTLPDGHLT | DQALKVSAVS | GPADQKTGTA | TVLSTPHSHR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EKPGIFYQQE | FADSHQTEET | LTKVSATPGP | ADQKTEIPAV | QSSSYSQREK | PSILYPQDLA | DSHLPEEGLK | VSAVAGPADQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KTGLPTVPSS | AYSHREKLLV | FYQQALLDSH | LPEEALKVSA | VSGPADGKTG | TPAVTSTSSA | SSSLGEKPSA | FYQQTLPNSH |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LTEEALKVSI | VPGPGDQKTG | IPSAPSSFYS | HREKPIIFSQ | QTLPDFLFPE | EALKVSAVSV | LAAQKTGTPT | VSSNSHSHSE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KSSVFYQQEL | PDSDLPRESL | KMSAIPGLTD | QKTVPTPTVP | SGSFSHREKP | SIFYQQEWPD | SYATEKALKV | STGPGPADQK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TEIPAVQSSS | YPQREKPSVL | YPQVLSDSHL | PEESLKVSAF | PGPADQMTDT | PAVPSTFYSQ | REKPGIFYQQ | TLPESHLPKE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ALKISVAPGL | ADQKTGTPTV | TSTSYSQHRE | KPSIFHQQAL | PGTHIPEEAQ | KVSAVTGPGN | QKTWIPRVLS | TFYSQREKPG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| IFYQQTLPGS | HIPEEAQKVS | PVLGPADQKT | GTPTPTSASY | SHTEKPGIFY | QQVLPDNHPT | EEALKISVAS | EPVDQTTGTP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| AVTSTSYSQY | REKPSIFYQQ | SLPSSHLTEE | AKNVSAVPGP | ADQKTVIPIL | PSTFYSHTEK | PGVFYQQVLP | HSHPTEEALK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ISVASEPVDQ | TTGTPTVTST | SYSQHTEKPS | IFYQQSLPGS | HLTEEAKNVS | AVPGPGDRKT | GIPTLPSTFY | SHTEKPGSFY |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| QQVLPHSHLP | EEALEVSVAP | GPVDQTIGTP | TVTSPSSSFG | EKPIVIYKQA | FPEGHLPEES | LKVSVAPGPV | GQTTGAPTIT |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| SPSYSQHRAK | SGSFYQLALL | GSQIPEEALR | VSSAPGPADQ | TTGIPTITST | SYSFGEKPIV | NYKQAFPDGH | LPEEALKVSI |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| VSGPTEKKTD | IPAGPLGSSA | LGEKPITFYR | QALLDSPLNK | EVVKVSAAPG | PADQKTETLP | VHSTSYSNRG | KPVIFYQQTL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| SDSHLPEEAL | KVPPVPGPDA | QKTETPSVSS | SLYSYREKPI | VFYQQALPDS | ELTQEALKVS | AVPQPADQKT | GLSTVTSSFY |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SHTEKPNISY | QQELPDSHLT | EEALKVSNVP | GPADQKTGVS | TVTSTSYSHR | EKPIVSYQRE | LPHFTEAGLK | ILRVPGPADQ |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| KTGINILPSN | SYPQREHSVI | SYEQELPDLT | EVTLKAIGVP | GPADQKTGIQ | IASSSSYSNR | EKASIFHQQE | LPDVTEEALN |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| VFVVPGQGDR | KTEIPTVPLS | YYSRREKPSV | ISQQELPDSH | LTEEALKVSP | VSIPAEQKTG | IPIGLSSSYS | HSHKEKLKIS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| TVHIPDDQKT | EFPAATLSSY | SQIEKPKIST | VIGPNDQKTP | SQTAFHSSYS | QTVKPNILFQ | QQLPDRDQSK | GILKISAVPE |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| LTDVNTGKPV | SLSSSYFHRE | KSNIFSPQEL | PGSHVTEDVL | KVSTIPGPAG | QKTVLPTALP | SSFSHREKPD | IFYQKDLPDR |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 881 | 1 | 555.8212 | 17.82 | 2 | 40.6 | 26.2 | 0 | 1219-1229 | K.VSPVLGPADQK.T |  | QU:MU 2.56<br>WUP:QUP 0.53 |
| 1890 | 1 | 1036.8846 | -93.94 | 2 | 54.0 | 16.6 | 2 | 2503-2519 | R.NAEEEESRVRAHAWNMK.F | Oxidation: 16 |  |

# Detailed Protein Report

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**Protein 64:** **PREDICTED: Golgin subfamily A member 4 isoform X7 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530372330 | **Score:** | 64.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 259.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 5 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MFKKLKQKIS EEQQQLQQAL APAQASSNSS TPTRMRSRTS SFTEQLDEGT PNRESGDTQS FAQKLQLRVP SVESLFRSPI
        90        100        110        120        130        140        150        160
KESLFRSSSK ESLVRTSSRE SLNRLDLDSS TASFDPPSDM DSEAEDLVGN SDSLNKEQLI QRLRRMERSL SSYRGKYSEG
       170        180        190        200        210        220        230        240
ILSQSQDKSL RRIAELREEL QMDQQAKKHL QEEFDASLEE KDQYISVLQT QVSLLKQRLR NGPMNVDVLK PLPQLEPQAE
       250        260        270        280        290        300        310        320
VFTKEENPES DGEPVVEDGT SVKTLETLQQ RVKRQENLLK RCKETIQSHK EQCTLLTSEK EALQEQLDER LQELEKIKDL
       330        340        350        360        370        380        390        400
HMAEKTKLIT QLRDAKNLIE QLEQDKGMVI AETKRQMHET LEMKEEEIAQ LRSRIKQMTT QGEELREQKE KSERAAFEEL
       410        420        430        440        450        460        470        480
EKALSTAQKT EEARRKLKAE MDEQIKTIEK TSEEERISLQ QELSRVKQEV VDVMKKSSEE QIAKLQKLHE KELARKEQEL
       490        500        510        520        530        540        550        560
TKKLQTRERE FQEQMKVALE KSQSEYLKIS QEKEQQESLA LEELELQKKA ILTESENKLR DLQQEAETYR TRILELESSL
       570        580        590        600        610        620        630        640
EKSLQENKNQ SKDLAVHLEA EKNKHNKEIT VMVEKHKTEL ESLKHQQDAL WTEKLQVLKQ QYQTEMEKLR EKCEQEKETL
       650        660        670        680        690        700        710        720
LKDKEIIFQA HIEEMNEKTL EKLDVKQTEL ESLSSELSEV LKARHKLEEE LSVLKDQTDK MKQELEAKMD EQKNHHQQQV
       730        740        750        760        770        780        790        800
DSIIKEHEVS IQRTEKALKD QINQLELLLK ERDKHLKEHQ AHVENLEADI KRSEGELQQA SAKLDVFQSY QSATHEQTKA
       810        820        830        840        850        860        870        880
YEEQLAQLQQ KLLDLETERI LLTKQVAEVE AQKKDVCTEL DAHKIQVQDL MQQLEKQNSE MEQKVKSLTQ VYESKLEDGN
       890        900        910        920        930        940        950        960
KEQEQTKQIL VEKENMILQM REGQKKEIEI LTQKLSAKED SIHILNEEYE TKFKNQEKKM EKVKQKAKEM QETLKKKLLD
       970        980        990       1000       1010       1020       1030       1040
QEAKLKKELE NTALELSQKE KQFNAKMLEM AQANSAGISD AVSRLETNQK EQIESLTEVH RRELNDVISI WEKKLNQQAE
      1050       1060       1070       1080       1090       1100       1110       1120
ELQEIHEIQL QEKEQEVAEL KQKILLFGCE KEEMNKEITW LKEEGVKQDT TLNELQEQLK QKSAHVNSLA QDETKLKAHL
      1130       1140       1150       1160       1170       1180       1190       1200
EKLEVDLNKS LKENTFLQEQ LVELKMLAEE DKRKVSELTS KLKTTDEEFQ SLKSSHEKSN KSLEDKSLEF KKLSEELAIQ
      1210       1220       1230       1240       1250       1260       1270       1280
LDICCKKTEA LLEAKTNELI NISSSKTNAI LSRISHCQHR TTKVKEALLI KTCTVSELEA QLRQLTEEQN TLNISFQQAT
      1290       1300       1310       1320       1330       1340       1350       1360
HQLEEKENQI KSMKADIESL VTEKEALQKE GGNQQQAASE KESCITQLKK ELSENINAVT LMKEELKEKK VEISSLSKQL
      1370       1380       1390       1400       1410       1420       1430       1440
TDLNVQLQNS ISLSEKEAAI SSLRKQYDEE KCELLDQVQD LSFKVDTLSK EKISALEQVD DWSNKFSEWK KKAQSRFTQH
      1450       1460       1470       1480       1490       1500       1510       1520
QNTVKELQIQ LELKSKEAYE KDEQINLLKE ELDQQNKRFD CLKGEMEDDK SKMEKKESNL ETELKSQTAR IMELEDHITQ
      1530       1540       1550       1560       1570       1580       1590       1600
KTIEIESLNE VLKNYNQQKD IEHKELVQKL QHFQELGEEK DNRVKEAEEK ILTLENQVYS MKAELETKKK ELEHVNLSVK
      1610       1620       1630       1640       1650       1660       1670       1680
SKEEELKALE DRLESESAAK LAELKRKAEQ KIAAIKKQLL SQMEEKEEQY KKGTESHLSE LNTKLQERER EVHILEEKLK
      1690       1700       1710       1720       1730       1740       1750       1760
SVESSQSETL IVPRSAKNVA AYTEQEEADS QGCVQKTYEE KISVLQRNLT EKEKLLQRVG QEKEETVSSH FEMRCQYQER
      1770       1780       1790       1800       1810       1820       1830       1840
LIKLEHAEAK QHEDQSMIGH LQEELEEKNK KYSLIVAQHV EKEGGKNNIQ AKQNLENVFD DVQKTLQEKE LTCQILEQKI
      1850       1860       1870       1880       1890       1900       1910       1920
KELDSCLVRQ KEVHRVEMEE LTSKYEKLQA LQQMDGRNKP TELLEENTEE KSKSHLVQPK LLSNMEAQHN DLEFKLAGAE
      1930       1940       1950       1960       1970       1980       1990       2000
REKQKLGKEI VRLQKDLRML RKEHQQELEI LKKEYDQERE EKIKQEQEDL ELKHNSTLKQ LMREFNTQLA QKEQELEMTI
      2010       2020       2030       2040       2050       2060       2070       2080
KETINKAQEV EAELLESHQE ETNQLLKKIA EKDDDLKRTA KRYEEILDAR EEEMTAKVRD LQTQLEELQK KYQQKLEQEE
      2090       2100       2110       2120       2130       2140       2150       2160
NPGNDNVTIM ELQTQLAQKT TLISDSKLKE QEFREQIHNL EDRLKKYEKN VYATTVGTPY KGGNLYHTDV SLFGEPTEFE
      2170       2180       2190       2200       2210       2220
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 362 | 2 | 539.2298 | -100.57 | 2 | 33.2 | 13.3 | 1 | 947-955 | K.AKEMQETLK.K | |
| 2557 | 1 | 715.3634 | 85.34 | 2 | 61.9 | 10.2 | 1 | 1479-1490 | R.FDCLKGEMEDDK.S | |
| 2790 | 2 | 683.3645 | 24.15 | 3 | 65.3 | 12.8 | 1 | 1813-1829 | K.QNLENVFDDVQKTLQEK.E | |
| 190 | 1 | 716.5084 | 147.04 | 2 | 32.1 | 12.0 | 2 | 1840-1851 | K.IKELDSCLVRQK.E | |
| 1522 | 1 | 620.4115 | 154.27 | 3 | 48.7 | 15.7 | 2 | 1850-1864 | R.QKEVHRVEMEELTSK.Y | Oxidation: 9 |

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# Detailed Protein Report

## Protein 65: smoothelin isoform e [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|333360860 | **Score:** | 63.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 104.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MGGMGTPGDL HAACPSTTRR DALCLGPEFE FDLRHSAGCP GDLGFFPLDP DTEAGGSGCL PTWLPLRRLA RGRLEVTADL
        90        100        110        120        130        140        150        160
AERRRIRSAI RELQRQELER EEEALASKRF RAERQDNKEN WLHSQQREAE QRAALARLAG QLESMNDVEE LTALLRSAGE
       170        180        190        200        210        220        230        240
YEERKLIRAA IRRVRAQEIE AATLAGRLYS GRPNSGSRED SKGLAAHRLE QCEVPEREEQ EQQAEVSKPT PTPEGTSQDV
       250        260        270        280        290        300        310        320
TTVTLLLRAP PGSTSSSPAS PSSSPTPASP EPPLEPAEAQ CLTAEVPGSP EPPPSPPKTT SPEPQESPTL PSTEGQVVNK
       330        340        350        360        370        380        390        400
LLSGPKETPA AQSPTRGPSD TKRADVAGPR PCQRSLSVLS PRQPAQNRES TPLASGPSSF QRAGSVRDRV HKFTSDSPMA
       410        420        430        440        450        460        470        480
ARLQDGTPQA ALSPLTPARL LGPSLTSTTP ASSSSGSSSR GPSDTSSRFS KEQRGVAQPL AQLRSCPQEE GPRGRGLAAR
       490        500        510        520        530        540        550        560
PLENRAGGPV ARSEEPGAPL PVAVGTAEPG GSMKTTFTIE IKDGRGQAST GRVLLPTGNQ RAELTLGLRA PPTLLSTSSG
       570        580        590        600        610        620        630        640
GKSTITRVNS PGTLARLGSV THVTSFSHAP PSSRGGCSIK MEAEPAEPLA AAVEAANGAE QTRVNKAPEG RSPLSAEELM
       650        660        670        680        690        700        710        720
TIEDEGVLDK MLDQSTDFEE RKLIRAALRE LRQRKRDQRD KERERRLQEA RGRPGEGRGN TATETTTRHS QRAADGSAVS
       730        740        750        760        770        780        790        800
TVTKTERLVH SNDGTRTART TTVESSFVRR SENGSGSTMM QTKTFSSSSS SKKMGSIFDR EDQASPRAGS LAALEKRQAE
       810        820        830        840        850        860        870        880
KKKELMKAQS LPKTSASQAR KAMIEKLEKE GAAGSPGGPR AAVQRSTSFG VPNANSIKQM LLDWCRAKTR GYEHVDIQNF
       890        900        910        920        930        940        950        960
SSSWSDGMAF CALVHNFFPE AFDYGQLSPQ NRRQNFEVAF SSAETHADCP QLLDTEDMVR LREPDWKCVY TYIQEFYRCL
       970        980
VQKGLVKTKK S
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1663 | 1 | 1044.8761 | -92.00 | 2 | 50.6 | 17.6 | 1 | 1-20 | -.MGGMGTPGDLHAACPSTTRR.D | Carbamidomethyl: 14;<br>Oxidation: 1 |

# Detailed Protein Report

## Protein 66: PREDICTED: 14-3-3 protein epsilon isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530410617 | **Score:** | 63.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 11.3 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578840292 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: 14-3-3 protein epsilon isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDDREDLVYQ | AKLAEQAERY | DEMVESMKKV | AGMDVELTVE | ERNLLSVAYK | NVIGARRASW | RIISSIEQKE | ENKGGEDKLK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MIREYRQMVE | TELKLICCDI | LDVLDKHLIP | AANTGESKVF | YYKMKGDYHR | YLAEFATGND | RKEAAENSLV | AYKAASDIAM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TELPPTHPIR | LGLALNFSVF | YYEILNSPDR | ACRLAKAAFD | DAIAELDTLS | EESYKDSTLI | MQLLRDNLTL | WTSDMQGDDS |
| 250 | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2589 | 1 | 1045.0814 | 94.73 | 2 | 62.4 | 16.1 | 2 | 13-29 | K.LAEQAERYDEMVESMKK.V | Oxidation: 11, 15 |

# Detailed Protein Report

**Protein 67:** **PREDICTED: dynein heavy chain 10, axonemal isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530401632 | **Score:** | 63.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 528.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 4 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDDLRVLWMR | DRVYAAFGIT | DPQLFEDLLN | RDDGQGEDLI | LHFLNQASEE | EGPSALFIYR | TMVPEEVEVE | IDEIPVLSEE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GEEEEETYSQ | KVESVDKVRA | KRVSLRTESL | GQPLNREDEE | MDKEISEKLP | SKRTAKHIME | KMHLHMLCTP | LPEEFLDQNV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VFFLRNTKEA | ISEATDMKEA | MEIMPETLEY | GIINANVLHF | LKNIICQVFL | PALSFNQHRT | STTVGVTSGE | VSNSSEHESD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LPPMPGEAVE | YHSIQLIRDE | FLMNVQKFAS | NIQRTMQQLE | GEIKLEMPII | SVEGEVSDLA | ADPETVDILE | QCVINWLNQI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| STAVEAQLKK | TPQGKGPLAE | IEFWRERNAT | LSALHEQTKL | PIVRKVLDVI | KESDSMLVAN | LQPVFTELFK | FHTEASDNVR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FLSTVERYFK | NITHGSGFHV | VLDTIPAMMS | ALRMVWIISR | HYNKDERMIP | LMERIAWEIA | ERVCRVVNLR | TLFKENRASA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QSKTLEARNT | LRLWKKAYFD | TRAKIEASGR | EDRWEFDRKR | LFERTDYMAT | ICQDLSDVLQ | ILEEFYNIFG | PELKAVTGDP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KRIDDVLCRV | DGLVTPMENL | TFDPFSIKSS | QFWKYVMDEF | KIEVLVIEKE | AKHFIDESFK | TLRSAEAAFD | MLLKFKHIRS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| REAVNRQMMM | KFNDILAQYC | KEIDIINKIF | VQNLENPPLY | KNHPPVAGAI | YWERSLFFRI | KHTILRFQEV | QEILDSDRGQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EVKQKYLEVG | RTMKEYEDRK | YEQWMEVTEQ | VLPALMKKSL | LTKSSIATEE | PSTLERGAVF | AINFSPALRE | IINETKYLEQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LGFTVPELAR | NVALQEDKFL | RYTAGIQRML | DHYHMLIGTL | NDAESVLLKD | HSQELLRVFR | SGYKRLNWNS | LGIGDYITGC |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KQAIGKFESL | VHQIHKNADD | ISSRLTLIEA | INLFKYPAAK | SEEELPGVKE | FFEHIERERA | SDVDHMVRWY | LAIGPLLTKV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| EGLVVHTNTG | KAPKLASYYK | YWEKKIYEVL | TKLILKNLQS | FNSLILGNVP | LFHTETILTA | PEIILHPNTN | EIDKMCFHCV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RNCVEITKHF | VRWMNGSCIE | CPPQKGEEEE | VVIINFYNDI | SLNPQIIEQA | VMIPQNVHRI | LINLMKYLQK | WKRYRPLWKL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DKAIVMEKFA | AKKPPCVAYD | EKLQFYSKIA | YEVMRHPLIK | DEHCIRLQLR | HLANTVQENA | KSWVISLGKL | LNESAKEELY |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| NLHEEMEHLA | KNLRKIPNTL | EDLKFVLATI | AEIRSKSLVM | ELRYRDVQER | YRTMAMYNLF | PPDAEKELVD | KIESIWSNLF |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| NDSVNVEHAL | GDIKRTFTEL | TRGEIMNYRV | QIEEFAKRFY | SEGPGSVGDD | LDKGVELLGV | YERELARHEK | SRQELANAEK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LFDLPITMYP | ELLKVQKEMS | GLRMIYELYE | GLKVAKEEWS | QTLWINLNVQ | ILQEGIEGFL | RALRKLPRPV | RGLSVTYYLE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| AKMKAFKDSI | PLLLDLKNEA | LRDRHWKELM | EKTSVFFEMT | ETFTLENMFA | MELHKHTDVL | NEIVTAAIKE | VAIEKAVKEI |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| LDTWENMKFT | VVKYCKGTQE | RGYILGSVDE | IIQSLDDNTF | NLQSISGSRF | VGPFLQTVHK | WEKTLSLIGE | VIEIWMLVQR |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KWMYLESIFI | GGDIRSQLPE | EAKKFDNIDK | VFKRIMGETL | KDPVIKRCCE | APNRLSDLQN | VSEGLEKCQK | SLNDYLDSKR |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| NAFPRFFFIS | DDELLSILGS | SDPLCVQEHM | IKMYDNIASL | RFNDGDSGEK | LVSAMISAEG | EVMEFRKILR | AEGRVEDWMT |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| AVLNEMRRTN | RLITKEAIFR | YCEDRSRVDW | MLLYQGMVVL | AASQVWWTWE | VEDVFHKAQK | GEKQAMKNYG | RKMHRQIDEL |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| VTRITMPLSK | NDRKKYNTVL | IIDVHARDIV | DSFIRGSILE | AREFDWESQL | RFYWDREPDE | LNIRQCTGTF | GYGYEYMGLN |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| GRLVITPLTD | RIYLTLTQAL | SMYLGGAPAG | PAGTGKTETT | KDLAKALGLL | CVVTNCGEGM | DYRAVGKIFS | GLAQCGAWGC |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| FDEFNRIDAS | VLSVISSQIQ | TIRNALIHQL | TTFQFEGQEI | SLDSRMGIFI | TMNPGYAGRT | ELPESVKALF | RPVVVIVPDL |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| QQICEIMLFS | EGFLEAKTLA | KKMTVLYKLA | REQLSKQYHY | DFGLRALKSV | LVMAGELKRG | SSDLREDVVL | MRALRDMNLP |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1643 | 1 | 938.9588 | -53.24 | 2 | 50.3 | 11.9 | 2 | 624-639 | R.SAEAAFDMLLKFKHIR.S | |
| 2459 | 1 | 1045.2266 | -235.83 | 1 | 61.2 | 14.2 | 0 | 940-948 | R.ASDVDHMVR.W | Oxidation: 7 |
| 2662 | 1 | 835.4217 | 30.04 | 2 | 61.6 | 11.7 | 1 | 2634-2646 | K.RLLVFMDDMNMPR.V | Oxidation: 6, 9 |
| 1556 | 1 | 502.7809 | -7.71 | 2 | 49.7 | 11.3 | 1 | 3742-3750 | K.ATEVSEKLK.L | |

# Detailed Protein Report

**Protein 68:** **14-3-3 protein sigma [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5454052 | **Score:** | 62.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.5 |
| | | **Sequence Coverage [%]:** | 11.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MERASLIQKA | KLAEQAERYE | DMAAFMKGAV | EKGEELSCEE | RNLLSVAYKN | VVGGQRAAWR | VLSSIEQKSN | EEGSEEKGPE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VREYREKVET | ELQGVCDTVL | GLLDSHLIKE | AGDAESRVFY | LKMKGDYYRY | LAEVATGDDK | KRIIDSARSA | YQEAMDISKK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EMPPTNPIRL | GLALNFSVFH | YEIANSPEEA | ISLAKTTFDE | AMADLHTLSE | DSYKDSTLIM | QLLRDNLTLW | TADNAGEEGG |
| 250 | | | | | | | |
| EAPQEPQS | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2035 | 3 | 1051.3758 | -123.72 | 2 | 55.8 | 15.4 | 2 | 10-27 | K.AKLAEQAERYEDMAAFMK.G | |

# Detailed Protein Report

## Protein 69: dynein heavy chain 2, axonemal [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|75677365 | **Score:** | 62.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 507.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 5 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530409951 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: dynein heavy chain 2, axonemal isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSKAEKKQR | LSGRGSSQAS | WSGRATRAAV | ATQEQGNAPA | VSEPELQAEL | PKEEPEPRLE | GPQAQSEESV | EPEADVKPLF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LSRAALTGLA | DAVWTQEHDA | ILEHFAQDPT | ESILTIFIDP | CFGLKLELGM | PVQTQNQLVY | FIRQAPVPIT | WENFEATVQF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GTVRGPYIPA | LLRLLGGVFA | PQIFANTGWP | ESIRNHFASH | LHKFLACLTD | TRYKLEGHTV | LYIPAEAMNM | KPEMVIKDKE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LVQRLETSMI | HWTRQIKEML | SAQETVETGE | NLGPLEEIEF | WRNRCMDLSG | ISKQLVKKGV | KHVESILHLA | KSSYLAPFMK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LAQQIQDGSR | QAQSNLTFLS | ILKEPYQELA | FMKPKDISSK | LPKLISLIRI | IWVNSPHYNT | RERLTSLFRK | VCDCQYHFAR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| WEDGKQGPLP | CFFGAQGPQI | TRNLLEIEDI | FHKNLHTLRA | VRGGILDVKN | TCWHEDYNKF | RAGIKDLEVM | TQNLITSAFE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LVRDVPHGVL | LLDTFHRLAS | REAIKRTYDK | KAVDLYMLFN | SELALVNRER | NKKWPDLEPY | VAQYSGKARW | VHILRRRIDR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VMTCLAGAHF | LPRIGTGKES | VHTYQQMVQA | IDELVRKTFQ | EWTSSLDKDC | IRRLDTPLLR | ISQEKAGMLD | VNFDKSLLIL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FAEIDYWERL | LFETPHYVVN | VAERAEDLRI | LRENLLLVAR | DYNRIIAMLS | PDEQALFKER | IRLLDKKIHP | GLKKLHWALK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GASAFFITEC | RIHASKVQMI | VNEFKASTLT | IGWRAQEMSE | KLLVRISGKR | VYRDLEFEED | QREHRAAVQQ | KLMNLHQDVV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TIMTNSYEVF | KNDGPEIQQQ | WMLYMIRLDR | MMEDALRLNV | KWSLLELSKA | INGDGKTSPN | PLFQVLVILK | NDLQGSVAQV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EFSPTLQTLA | GVVNDIGNHL | FSTISVFCHL | PDILTKRKLH | REPIQTVVEQ | DEDIKKIQTQ | ISSGMTNNAS | LLQNYLKTWD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| MYREIWEINK | DSFIHRYQRL | NPPVSSFVAD | IARYTEVANN | VQKEETVTNI | QFVLLDCSHL | KFSLVQHCNE | WQNKFATLLR |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EMAAGRLLEL | HTYLKENAEK | ISRPPQTLEE | LGVSLQLVDA | LKHDLANVET | QIPPIHEQFA | ILEKYEVPVE | DSVLEMLDSL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| NGEWVVFQQT | LLDSKQMLKK | HKEKFKTGLI | HSADDFKKKA | HTLLEDFEFK | GHFTSNVGYM | SALDQITQVR | AMLMAMREEE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| NSLRANLGIF | KIEQPPSKDL | QNLEKELDAL | QQIWEIARDW | EENWNEWKTG | RFLILQTETM | ETTAHGLFRR | LTKLAKEYKD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| RNWEIIETTR | SKIEQFKRTM | PLISDLRNPA | LRERHWDQVR | DEIQREFDQE | SESFTLEQIV | ELGMDQHVEK | IGEISASATK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ELAIEVALQN | IAKTWDVTQL | DIVPYKDKGH | HRLRGTEEVF | QALEDNQVAL | STMKASRFVK | AFEKDVDHWE | RCLSLILEVI |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EMILTVQRQW | MYLENIFLGE | DIRKQLPNES | TLFDQVNSNW | KAIMDRMNKD | NNALRSTHHP | GLLDTLIEMN | TILEDIQKSL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| DMYLETKRHI | FPRFYFLSND | DLLEILGQSR | NPEAVQPHLK | KCFDNIKLLR | IQKVGGPSSK | WEAVGMFSGD | GEYIDFLHSV |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| FLEGPVESWL | GDVEQTMRVT | LRDLLRNCHL | ALRKFLNKRD | KWVKEWAGQV | VITASQIQWT | ADVTKCLLTA | KERADKKILK |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| VMKKNQVSIL | NKYSEAIRGN | LTKIMRLKIV | ALVTIEIHAR | DVLEKLYKSG | LMDVNSFDWL | SQLRFYWEKD | LDDCVIRQTN |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| TQFQYNYEYL | GNSGRLVITP | LTDRCYMTLT | TALHLHRGGS | PKGPAGTGKT | ETVKDLGKAL | GIYVIVVNCS | EGLDYKSMGR |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| MYSGLAQTGA | WGCFDEFNRI | NIEVLSVVAH | QILCILSALA | AGLTHFHFDG | FEINLVWSCG | IFITMNPGYA | GRTELPENLK |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| SMFRPIAMVV | PDSTLIAEII | LFGEGFGNCK | ILAKKVYTLY | SLAVQQLSRQ | DHYDFGLRAL | TSLLRYAGKK | RRLQPDLTDE |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| EVLLLSMRDM | NIAKLTSVDA | PLFNAIVQDL | FPNIELPVID | YGKLRETVEQ | EIRDMGLQST | PFTLTKVFQL | YETKNSRHST |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| MIVGCTGSGK | TASWRILQAS | LSSLCRAGDP | NFNIVREFPL | NPKALSLGEL | YGEYDLSTNE | WTDGILSSVM | RTACADEKPD |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 271 | 1 | 701.3595 | -80.46 | 2 | 33.1 | 11.1 | 2 | 1681-1692 | K.VMKKNQVSILNK.Y | |
| 2974 | 1 | 826.4375 | -16.40 | 2 | 65.9 | 10.8 | 2 | 1693-1706 | K.YSEAIRGNLTKIMR.L | |
| 1377 | 1 | 976.4425 | -17.17 | 2 | 46.8 | 10.3 | 1 | 2078-2095 | R.HSTMIVGCTGSGKTASWR.I | Carbamidomethyl: 8;<br>Oxidation: 4 |
| 2410 | 1 | 1023.8441 | -100.67 | 2 | 60.0 | 14.9 | 2 | 4373-4389 | K.KSAKGMYSCPCYYYPNR.A | Oxidation: 6 |
| 2695 | 1 | 1044.5484 | 84.19 | 2 | 63.9 | 15.3 | 2 | 4373-4389 | K.KSAKGMYSCPCYYYPNR.A | Carbamidomethyl: 9 |

# Detailed Protein Report

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**Protein 70:** **PREDICTED: nebulin isoform X22 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530370465 | **Score:** | 62.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 961.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 3 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MADDEDYEEV | VEYYTEEVVY | EEVPGETITK | IYETTTTRTS | DYEQSETSKP | ALAQPALAQP | ASAKPVERRK | VIRKKVDPSK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FMTPYIAHSQ | KMQDLFSPNK | YKEKFEKTKG | QPYASTTDTP | ELRRIKKVQD | QLSEVKYRMD | GDVAKTICHV | DEKAKDIEHA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KKVSQQVSKV | LYKQNWEDTK | DKYLLPPDAP | ELVQAVKNTA | MFSKKLYTED | WEADKSLFYP | YNDSPELRRV | AQAQKALSDV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AYKKGLAEQQ | AQFTPLADPP | DIEFAKKVTN | QVSKQKYKED | YENKIKGKWS | ETPCFEVANA | RMNADNISTR | KYQEDFENMK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DQIYFMQTET | PEYKMNKKAG | VAASKVKYKE | DYEKNKGKAD | YNVLPASENP | QLRQLKAAGD | ALSDKLYKEN | YEKTKAKSIN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YCETPKFKLD | TVLQNFSSDK | KYKDSYLKDI | LGHYVGSFED | PYHSHCMKVT | AQNSDKNYKA | EYEEDRGKGF | FPQTITQEYE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AIKKLDQCKD | HTYKVHPDKT | KFTQVTDSPV | LLQAQVNSKQ | LSDLNYKAKH | ESEKFKCHIP | PDTPAFIQHK | VNAYNLSDNL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YKQDWEKSKA | KKFDIKVDAI | PLLAAKANTK | NTSDVMYKKD | YEKNKGKMIG | VLSINDDPKM | LHSLKVAKNQ | SDRLYKENYE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KTKAKSMNYC | ETPKYQLDTQ | LKNFSEARYK | DLYVKDVLGH | YVGSMEDPYH | THCMKVAAQN | SDKSYKAEYE | EDKGKCYFPQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TITQEYEAIK | KLDQCKDHTY | KVHPDKTKFT | AVTDSPVLLQ | AQLNTKQLSD | LNYKAKHEGE | KFKCHIPADA | PQFIQHRVNA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| YNLSDNVYKQ | DWEKSKAKKF | DIKVDAIPLL | AAKANTKNTS | DVMYKKDYEK | SKGKMIGALS | INDDPKMLHS | LKTAKNQSDR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EYRKDYEKSK | TIYTAPLDML | QVTQAKKSQA | IASDVDYKHI | LHSYSYPPDS | INVDLAKKAY | ALQSDVEYKA | DYNSWMKGCG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| WVPFGSLEME | KAKRASDILN | EKKYRQHPDT | LKFTSIEDAP | ITVQSKINQA | QRSDIAYKAK | GEEIIHKYNL | PPDLPQFIQA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KVNAYNISEN | MYKADLKDLS | KKGYDLRTDA | IPIRAAKAAR | QAASDVQYKK | DYEKAKGKMV | GFQSLQDDPK | LVHYMNVAKI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QSDREYKKDY | EKTKSKYNTP | HDMFNVVAAK | KAQDVVSNVN | YKHSLHHYTY | LPDAMDLELS | KNMMQIQSDN | VYKEDYNNWM |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KGIGWIPIGS | LDVEKVKKAG | DALNEKKYRQ | HPDTLKFTSI | VDSPVMVQAK | QNTKQVSDIL | YKAKGEDVKH | KYTMSPDLPQ |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| FLQAKCNAYN | ISDVCYKRDW | YDLIAKGNNV | LGDAIPITAA | KASRNIASDY | KYKEAYEKSK | GKHVGFRSLQ | DDPKLVHYMN |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VAKLQSDREY | KKNYENTKTS | YHTPGDMVSI | TAAKMAQDVA | TNVNYKQPLH | HYTYLPDAMS | LEHTRNVNQI | QSDNVYKDEY |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| NSFLKGIGWI | PIGSLEVEKV | KKAGDALNER | KYRQHPDTVK | FTSVPDSMGM | VLAQHNTKQL | SDLNYKVEGE | KLKHKYTIDP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ELPQFIQAKV | NALNMSDAHY | KADWKKTIAK | GYDLRPDAIP | IVAAKSSRNI | ASDCKYKEAY | EKAKGKQVGF | LSLQDDPKLV |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| HYMNVAKIQS | DREYKKGYEA | SKTKYHTPLD | MVSVTAAKKS | QEVATNANYR | QSYHHYTLLP | DALNVEHSRN | AMQIQSDNLY |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| KSDFTNWMKG | IGWVPIESLE | VEKAKKAGEI | LSEKKYRQHP | EKLKFTYAMD | TMEQALNKSN | KLNMDKRLYT | EKWNKDKTTI |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| HVMPDTPDIL | LSRVNQITMS | DKLYKAGWEE | EKKKGYDLRP | DAIAIKAARA | SRDIASDYKY | KKAYEQAKGK | HIGFRSLEDD |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| PKLVHFMQVA | KMQSDREYKK | GYEKSKTSFH | TPVDMLSVVA | AKKSQEVATN | ANYRNVIHTY | NMLPDAMSFE | LAKNMMQIQS |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| DNQYKADYAD | FMKGIGWLPL | GSLEAEKNKK | AMEIISEKKY | RQHPDTLKYS | TLMDSMNMVL | AQNNAKIMNE | HLYKQAWEAD |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| KTKVHIMPDI | PQIILAKANA | INMSDKLYKL | SLEESKKKGY | DLRPDAIPIK | AAKASRDIAS | DYKYKYNYEK | GKGKMVGFRS |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| LEDDPKLVHS | MQVAKMQSDR | EYKKNYENTK | TSYHTPADML | SVTAAKDAQA | NITNTNYKHL | IHKYILLPDA | MNIELTRNMN |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 457 | 2 | 544.7651 | 77.28 | 2 | 35.3 | 13.1 | 0 | 646-654 | K.SMNYCETPK.Y | Oxidation: 2 |
| 2640 | 1 | 701.8709 | 47.97 | 2 | 63.1 | 10.8 | 0 | 6260-6270 | R.CQYILSDLEYR.H | |
| 2657 | 1 | 994.4910 | 10.30 | 2 | 63.3 | 10.6 | 1 | 8000-8015 | K.LNQENFSSVLYKENMR.K | Oxidation: 15 |

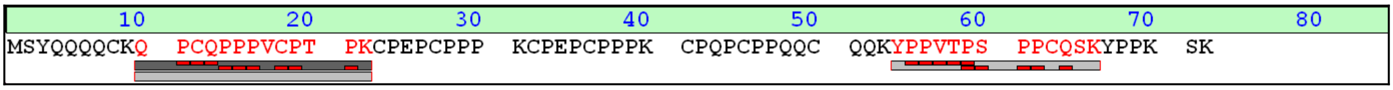
# Detailed Protein Report

## Protein 71: small proline-rich protein 2A [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5174693 | **Score:** | 62.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 8.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 36.1 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.33 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.12 | **CV:** | 29.24 % | **No. of Peptides:** | 2 |



| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2928 | 1 | 724.8814 | 36.56 | 2 | 65.4 | 11.5 | 0 | 10-22 | K.QPCQPPPVCPTPK.C | Carbamidomethyl: 3 | |
| 88 | 3 | 753.3275 | -50.62 | 2 | 30.8 | 36.7 | 0 | 10-22 | K.QPCQPPPVCPTPK.C | Carbamidomethyl: 3, 9 | WUP:QUP 1.49<br>QU:MU 1.33 |
| 171 | 1 | 729.5012 | 195.91 | 2 | 31.9 | 13.8 | 0 | 54-66 | K.YPPVTPSPPCQSK.Y | Carbamidomethyl: 10 | WUP:QUP 0.84 |

# Detailed Protein Report

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**Protein 72:** **PREDICTED: UDP-glucose:glycoprotein glucosyltransferase 1 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578804601 | **Score:** | 60.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 176.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 5.9 |
| | | **No. of unique Peptides:** | 5 |

```
        10         20         30         40         50         60         70         80
MGCKGDASGA CAAGVCYKMG VLVVLTVLWL FSSVKADSKA ITTSLTTKWF STPLLLEASE FLAEDSQEKF WNFVEASQNI
        90        100        110        120        130        140        150        160
GSSDHDGTDY SYYHAILEAA FQFLSPLQQN LFKFCLSLRS YSATIQAFQQ IAADEPPPEG CNSFFSVHGK KTCESDTLEA
       170        180        190        200        210        220        230        240
LLLTASERPK PLLFKGDHRY PSSNPESPVV IFYSEIGSEE FSNFHRQLIS KSNAGKINYV FRHYIFNPRK EPVYLSGYGV
       250        260        270        280        290        300        310        320
ELAIKSTEYK AKDDTQVKGT EVNTTVIGEN DPIDEVQGFL FGKLRDLHPD LEGQLKELRK HLVESTNEMA PLKVWQLQDL
       330        340        350        360        370        380        390        400
SFQTAARILA SPVELALVVM KDLSQNFPTK ARAITKTAVS SELRTEVEEN QKYFKGTLGL QPGDSALFIN GLHMDLDTQD
       410        420        430        440        450        460        470        480
IFSLFDVLRN EARVMEGLHR LGIEGLSLHN VLKLNIQPSE ADYAVDIRSP AISWVNNLEV DSRYNSWPSS LQELLRPTFP
       490        500        510        520        530        540        550        560
GVIRQIRKNL HNMVFIVDPA HETTAELMNT AEMFLSNHIP LRIGFIFVVN DSEDVDGMQD AGVAVLRAYN YVAQEVDDYH
       570        580        590        600        610        620        630        640
AFQTLTHIYN KVRTGEKVKV EHVVSVLEKK YPYVEVNSIL GIDSAYDRNR KEARGYYEQT GVGPLPVVLF NGMPFEREQL
       650        660        670        680        690        700        710        720
DPDELETITM HKILETTTFF QRAVYLGELP HDQDVVEYIM NQPNVVPRIN SRILTAERDY LDLTASNNFF VDDYARFTIL
       730        740        750        760        770        780        790        800
DSQGKTAAVA NSMNYLTKKG MSSKEIYDDS FIRPVTFWIV GDFDSPSGRQ LLYDAIKHQK SSNNVRISMI NNPAKEISYE
       810        820        830        840        850        860        870        880
NTQISRAIWA ALQTQTSNAA KNFITKMAKE GAAEALAAGA DIAEFSVGGM DFSLFKEVFE SSKMDFILSH AVYCRDVLKL
       890        900        910        920        930        940        950        960
KKGQRAVISN GRIIGPLEDS ELFNQDDFHL LENIILKTSG QKIKSHIQQL RVEEDVASDL VMKVDALLSA QPKGDPRIEY
       970        980        990       1000       1010       1020       1030       1040
QFFEDRHSAI KLRPKEGETY FDVVAVVDPV TREAQRLAPL LLVLAQLINM NLRVFMNCQS KLSDMPLKSF YRYVLEPEIS
      1050       1060       1070       1080       1090       1100       1110       1120
FTSDNSFAKG PIAKFLDMPQ SPLFTLNLNT PESWMVESVR TPYDLDNIYL EEVDSVVAAE YELEYLLLEG HCYDITTGQP
      1130       1140       1150       1160       1170       1180       1190       1200
PRGLQFTLGT SANPVIVDTI VMANLGYFQL KANPGAWILR LRKGRSEDIY RIYSHDGTDS PPDADEVVIV LNNFKSKIIK
      1210       1220       1230       1240       1250       1260       1270       1280
VKVQKKADMV NEDLLSDGTS ENESGFWDSF KWGFTGQKTE EVKQDKDDII NIFSVASGHL YERFLRIMML SVLKNTKTPV
      1290       1300       1310       1320       1330       1340       1350       1360
KFWFLKNYLS PTFKEFIPYM ANEYNFQYEL VQYKWPRWLH QQTEKQRIIW GYKILFLDVL FPLVVDKFLF VDADQIVRTD
      1370       1380       1390       1400       1410       1420       1430       1440
LKELRDFNLD GAPYGYTPFC DSRREMDGYR FWKSGYWASH LAGRKYHISA LYVVDLKKFR KIAAGDRLRG QYQGLSQDPN
      1450       1460       1470       1480       1490       1500       1510       1520
SLSNLDQDLP NNMIHQVPIK SLPQEWLWCE TWCDDASKKR AKTIDLCNNP MTKEPKLEAA VRIVPEWQDY DQEIKQLQIR
      1530       1540       1550
FQKEKETGAL YKEKTKEPSR EGPQKREEL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1283 | 1 | 882.7587 | -117.26 | 2 | 45.6 | 10.6 | 1 | 1-18 | -.MGCKGDASGACAAGVCYK.M | Carbamidomethyl: 11;<br>Oxidation: 1 |
| 1565 | 1 | 1018.8365 | -18.21 | 3 | 49.3 | 12.6 | 2 | 611-637 | R.KEARGYYEQTGVGPLPVVLFNGMPFER.E | |
| 1888 | 1 | 600.2525 | -61.03 | 3 | 53.5 | 13.2 | 0 | 638-652 | R.EQLDPDELETITMHK.I | |
| 2009 | 1 | 599.9210 | -67.30 | 3 | 53.5 | 11.7 | 1 | 1014-1028 | R.VFMNCQSKLSDMPLK.S | Carbamidomethyl: 5 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2056 | 1 | 973.8963 | -78.49 | 2 | 54.1 | 12.8 | 0 | 1033-1049 | R.YVLEPEISFTSDNSFAK.G | |

# Detailed Protein Report

**Protein 73:** **PREDICTED: biorientation of chromosomes in cell division protein 1-like 1 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530376284 | **Score:** | 60.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 335.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.83 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.83 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MATNPQPQPP | PPAPPPPPPQ | PQPQPPPPPP | GPGAGPGAGG | AGGAGAGAGD | PQLVAMIVNH | LKSQGLFDQF | RRDCLADVDT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KPAYQNLRQR | VDNFVANHLA | THTWSPHLNK | NQLRNNIRQQ | VLKSGMLESG | IDRIISQVVD | PKINHTFRPQ | VEKAVHEFLA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TLNHKEEGSG | NTAPDDEKPD | TSLITQGVPT | PGPSANVAND | AMSILETITS | LNQEASAARA | STETSNAKTS | ERASKKLPSQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PTTDTSTDKE | RTSEDMADKE | KSTADSGGEG | LETAPKSEEF | SDLPCPVEEI | KNYTKEHNNL | ILLNKDVQQE | SSEQKNKSTD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KGEKKPDSNE | KGERKKEKKE | KTEKKFDHSK | KSEDTQKVKD | EKQAKEKEVE | SLKLPSEKNS | NKAKTVEGTK | EDFSLIDSDV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DGLTDITVSS | VHTSDLSSFE | EDTEEEVVTS | DSMEEGEITS | DDEEKNKQNK | TKTQTSDSSE | GKTKSVRHAY | VHKPYLYSKY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YSDSDDELTV | EQRRQSIAKE | KEERLLRRQI | NREKLEEKRK | QKAEKTKSSK | TKGQGRSSVD | LEESSTKSLE | PKAARIKEVL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KERKVLEKKV | ALSKKRKKDS | RNVEENSKKK | QQYEEDSKET | LKTSEHCEKE | KISSSKELKH | VHAKSEPSKP | ARRLSESLHV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VDENKNESKL | EREHKRRTST | PVIMEGVQEE | TDTRDVKRQV | ERSEICTEEP | QKQKSTLKNE | KHLKKDDSET | PHLKSLLKKE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VKSSKEKPER | EKTPSEDKLS | VKHKYKGDCM | HKTGDETELH | SSEKGLKVEE | NIQKQSQQTK | LSSDDKTERK | SKHRNERKLS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VLGKDGKPVS | EYIIKTDENV | RKENNKKERR | LSAEKTKAEH | KSRRSSDSKI | QKDSLGSKQH | GITLQRRSES | YSEDKCDMDS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TNMDSNLKPE | EVVHKEKRRT | KSLLEEKLVL | KSKSKTQGKQ | VKVVETELQE | GATKQATTPK | PDKEKNTEEN | DSEKQRKSKV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| EDKPFEETGV | EPVLETASSS | AHSTQKDSSH | RAKLPLAKEK | YKSDKDSTST | RLERKLSDGH | KSRSLKHSSK | DIKKKDENKS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| DDKDGKEVDS | SHEKARGNSS | LMEKKLSRRL | CENRRGSLSQ | EMAKGEEKLA | ANTLSTPSGS | SLQRPKKSGD | MTLIPEQEPM |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EIDSEPGVEN | VFEVSKTQDN | RNNNSQQDID | SENMKQKTSA | TVQKDELRTC | TADSKATAPA | YKPGRGTGVN | SNSEKHADHR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| STLTKKMHIQ | SAVSKMNPGE | KEPIHRGTTE | VNIDSETVHR | MLLSAPSEND | RVQKNLKNTA | AEEHVAQGDA | TLEHSTNLDS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SPSLSSVTVV | PLRESYDPDV | IPLFDKRTVL | EGSTASTSPA | DHSALPNQSL | TVRESEVLKT | SDSKEGGEGF | TVDTPAKASI |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| TSKRHIPEAH | QATLLDGKQG | KVIMPLGSKL | TGVIVENENI | TKEGGLVDMA | KKENDLNAEP | NLKQTIKATV | ENGKKDGIAV |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DHVVGLNTEK | YAETVKLKHK | RSPGKVKDIS | IDVERRNENS | EVDTSAGSGS | APSVLHQRNG | QTEDVATGPR | RAEKTSVATS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| TEGKDKDVTL | SPVKAGPATT | TSSETRQSEV | ALPCTSIEAD | EGLIIGTHSR | NNPLHVGAEA | SECTVFAAAE | EGGAVVTEGF |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| AESETFLTST | KEGESGECAV | AESEDRAADL | LAVHAVKIEA | NVNSVVTEEK | DDAVTSAGSE | EKCDGSLSRD | SEIVEGTITF |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| ISEVESDGAV | TSAGTEIRAG | SISSEEVDGS | QGNMMRMGPK | KETEGTVTCT | GAEGRSDNFV | ICSVTGAGPR | EERMVTGAGV |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| VLGDNDAPPG | TSASQEGDGS | VNDGTEGESA | VTSTGITEDG | EGPASCTGSE | DSSEGFAISS | ESEENGESAM | DSTVAKEGTN |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| VPLVAAGPCD | DEGIVTSTGA | KEEDEEGEDV | VTSTGRGNEI | GHASTCTGLG | EESEGVLICE | SAEGDSQIGT | VVEHVEAEAG |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| AAIMNANENN | VDSMSGTEKG | SKDTDICSSA | KGIVESSVTS | AVSGKDEVTP | VPGGCEGPMT | SAASDQSDSQ | LEKVEDTTIS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| TGLVGGSYDV | LVSGEVPECE | VAHTSPSEKE | DEDIITSVEN | EECDGLMATT | ASGDITNQNS | LAGGKNQGKV | LIISTSTTND |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| YTPQVSAITD | VEGGLSDALR | TEENMEGTRV | TTEEFEAPMP | SAVSGDDSQL | TASRSEEKDE | CAMISTSIGE | EFELPISSAT |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1228 | 1 | 954.9820 | 37.30 | 2 | 45.5 | 23.8 | 0 | 658-674 | R.TSTPVIMEGVQEETDTR.D | Oxidation: 7 | QU:MU 0.83<br>WUP:QUP 1.83 |
| 2965 | 1 | 557.6376 | 40.39 | 3 | 65.8 | 10.0 | 2 | 2881-2894 | K.YPVETTLKMKDDSK.T | Oxidation: 9 | |

# Detailed Protein Report

| | | | |
|---|---|---|---|
| **Protein 74:** | **PREDICTED: striated muscle preferentially expressed protein kinase isoform X14 [Homo sapiens]** | | |
| **Accession:** | gi\|578803490 | **Score:** | 59.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 283.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | |
|---|---|---|---|
| ***WUP:QUP*** | **Median:** 0.74 | **CV:** 0.00 % | **No. of Peptides:** 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQKARGTRGE | DAGTRAPPSP | GVPPKRAKVG | AGGGAPVAVA | GAPVFLRPLK | NAAVCAGSDV | RLRVVVSGTP | QPSLRWFRDG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QLLPAPAPEP | SCLWLRRCGA | QDAGVYSCMA | QNERGRASCE | AVLTVLEVGD | SETAEDDISD | VQGTQRLELR | DDGAFSTPTG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GSDTLVGTSL | DTPPTSVTGT | SEEQVSWWGS | GQTVLEQEAG | SGGGTRRLPG | SPRQAQATGA | GPRHLGVEPL | VRASRANLVG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ASWGSEDSLS | VASDLYGSAF | SLYRGRALSI | HVSVPQSGLR | REEPDLQPQL | ASEAPRRPAQ | PPPSKSALLP | PPSPRVGKRS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PPGPPAQPAA | TPTSPHRRTQ | EPVLPEDTTT | EEKRGKKSKS | SGPSLAGTAE | SRPQTPLSEA | SGRLSALGRS | PRLVRAGSRI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LDKLQFFEER | RRSLERSDSP | PAPLRPWVPL | RKARSLEQPK | SERGAPWGTP | GASQEELRAP | GSVAERRRLF | QQKAASLDER |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TRQRSPASDL | ELRFAQELGR | IRRSTSREEL | VRSHESLRAT | LQRAPSPREP | GEPPLFSRPS | TPKTSRAVSP | AAAQPPSPSS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AEKPGDEPGR | PRSRGPAGRT | EPGEGPQQEV | RRRDQFPLTR | SRAIQECRSP | VPPPAADPPE | ARTKAPPGRK | REPPAQAVRF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LPWATPGLEG | AAVPQTLEKN | RAGPEAEKRL | RRGPEEDGPW | GPWDRRGARS | QGKGRRARPT | SPELESSDDS | YVSAGEEPLE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| APVFEIPLQN | VVVAPGADVL | LKCIITANPP | PQVSWHKDGS | ALRSEGRLLL | RAEGERHTLL | LREARAADAG | SYMATATNEL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GQATCAASLT | VRPGGSTSPF | SSPITSDEEY | LSPPEEFPEP | GETWPRTPTM | KPSPSQNRRS | SDTGSKAPPT | FKVSLMDQSV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| REGQDVIMSI | RVQGEPKPVV | SWLRNRQPVR | PDQRRFAEEA | EGGLCRLRIL | AAERGDAGFY | TCKAVNEYGA | RQCEARLEVR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| AHPESRSLAV | LAPLQDVDVG | AGEMALFECL | VAGPTDVEVD | WLCRGRLLQP | ALLKCKMHFD | GRKCKLLLTS | VHEDDSGVYT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| CKLSTAKDEL | TCSARLTVRP | SLAPLFTRLL | EDVEVLEGRA | ARFDCKISGT | PPPVVTWTHF | GCPMEESENL | RLRQDGGLHS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LHIAHVGSED | EGLYAVSAVN | THGQAHCSAQ | LYVEEPRTAA | SGPSSKLEKM | PSIPEEPEQG | ELERLSIPDF | LRPLQDLEVG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LAKEAMLECQ | VTGLPYPTIS | WFHNGHRIQS | SDDRRMTQYR | DVHRLVFPAV | GPQHAGVYKS | VIANKLGKAA | CYAHLYVTDV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VPGPPDGAPQ | VVAVTGRMVT | LTWNPPRSLD | MAIDPDSLTY | TVQHQVLGSD | QWTALVTGLR | EPGWAATGLR | KGVQHIFRVL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| STTVKSSSKP | SPPSEPVQLL | EHGPTLEEAP | AMLDKPDIVY | VVEGQPASVT | VTFNHVEAQV | VWRSCRGALL | EARAGVYELS |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| QPDDDQYCLR | ICRVSRRDMG | ALTCTARNRH | GTQTCSVTLE | LAEAPRFESI | MEDVEVGAGE | TARFAVVVEG | KPLPDIMWYK |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| DEVLLTESSH | VSFVYEENEC | SLVVLSTGAQ | DGGVYTCTAQ | NLAGEVSCKA | ELAVHSAQTA | MEVEGVGEDE | DHRGRRLSDF |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| YDIHQEIGRG | AFSYLRRIVE | RSSGLEFAAK | FIPSQAKPKA | SARREARLLA | RLQHDCVLYF | HEAFERRRGL | VIVTELCTEE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LLERIARKPT | VCESEIRAYM | RQVLEGIHYL | HQSHVLHLDV | KPENLLVWDG | AAGEQQVRIC | DFGNAQELTP | GEPQYCQYGT |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| PEFVAPEIVN | QSPVSGVTDI | WPVGVVAFLC | LTGISPFVGE | NDRTTLMNIR | NYNVAFEETT | FLSLSREARG | FLIKVLVQDR |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| LRPTAEETLE | HPWFKTQAKG | AEVSTDHLKL | FLSRRRWQRS | QISYKCHLVL | RPIPELLRAP | PERVWVTMPR | RPPPSGGLSS |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| SSDSEEEELE | ELPSVPRPLQ | PEFSGSRVSL | TDIPTEDEAL | GTPETGAATP | MDWQEQGRAP | SQDQEAPSPE | ALPSPGQEPA |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| AGASPRRGEL | RRGSSAESAL | PRAGPRELGR | GLHKAASVEL | PQRRSPSPGA | TRLARGGLGE | GEYAQRLQAL | RQRLLRGGPE |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| DGKVSGLRGP | LLESLGGRAR | DPRMARAASS | EAAPHHQPPL | ENRGLQKSSS | FSQGEAEPRG | RHRRAGAPLE | IPVARLGARR |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 257 | 1 | 765.3459 | -79.23 | 2 | 33.2 | 16.1 | 0 | 2578-2592 | R.SESVPSLGLEAAIEK.L | | WUP:QUP 0.74 |

# Detailed Protein Report

## Protein 75: myosin-9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|12667788 | **Score:** | 59.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 226.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 3 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAQQAADKYL | YVDKNFINNP | LAQADWAAKK | LVWVPSDKSG | FEPASLKEEV | GEEAIVELVE | NGKKVKVNKD | DIQKMNPPKF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SKVEDMAELT | CLNEASVLHN | LKERYYSGLI | YTYSGLFCVV | INPYKNLPIY | SEEIVEMYKG | KKRHEMPPHI | YAITDTAYRS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MMQDREDQSI | LCTGESGAGK | TENTKKVIQY | LAYVASSHKS | KKDQGELERQ | LLQANPILEA | FGNAKTVKND | NSSRFGKFIR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| INFDVNGYIV | GANIETYLLE | KSRAIRQAKE | ERTFHIFYYL | LSGAGEHLKT | DLLLEPYNKY | RFLSNGHVTI | PGQQDKDMFQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ETMEAMRIMG | IPEEEQMGLL | RVISGVLQLG | NIVFKKERNT | DQASMPDNTA | AQKVSHLLGI | NVTDFTRGIL | TPRIKVGRDY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VQKAQTKEQA | DFAIEALAKA | TYERMFRWLV | LRINKALDKT | KRQGASFIGI | LDIAGFEIFD | LNSFEQLCIN | YTNEKLQQLF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NHTMFILEQE | EYQREGIEWN | FIDFGLDLQP | CIDLIEKPAG | PPGILALLDE | ECWFPKATDK | SFVEKVMQEQ | GTHPKFQKPK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QLKDKADFCI | IHYAGKVDYK | ADEWLMKNMD | PLNDNIATLL | HQSSDKFVSE | LWKDVDRIIG | LDQVAGMSET | ALPGAFKTRK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GMFRTVGQLY | KEQLAKLMAT | LRNTNPNFVR | CIIPNHEKKA | GKLDPHLVLD | QLRCNGVLEG | IRICRQGFPN | RVVFQEFRQR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YEILTPNSIP | KGFMDGKQAC | VLMIKALELD | SNLYRIGQSK | VFFRAGVLAH | LEEERDLKIT | DVIIGFQACC | RGYLARKAFA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KRQQQLTAMK | VLQRNCAAYL | KLRNWQWWRL | FTKVKPLLQV | SRQEEEMMAK | EEELVKVREK | QLAAENRLTE | METLQSQLMA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EKLQLQEQLQ | AETELCAEAE | ELRARLTAKK | QELEEICHDL | EARVEEEEER | CQHLQAEKKK | MQQNIQELEE | QLEEEESARQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KLQLEKVTTE | AKLKKLEEEQ | IILEDQNCKL | AKEKKLLEDR | IAEFTTNLTE | EEEKSKSLAK | LKNKHEAMIT | DLEERLRREE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KQRQELEKTR | RKLEGDSTDL | SDQIAELQAQ | IAELKMQLAK | KEEELQAALA | RVEEEAAQKN | MALKKIRELE | SQISELQEDL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ESERASRNKA | EKQKRDLGEE | LEALKTELED | TLDSTAAQQE | LRSKREQEVN | ILKKTLEEEA | KTHEAQIQEM | RQKHSQAVEE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LAEQLEQTKR | VKANLEKAKQ | TLENERGELA | NEVKVLLQGK | GDSEHKRKKV | EAQLQELQVK | FNEGERVRTE | LADKVTKLQV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| ELDNVTGLLS | QSDSKSSKLT | KDFSALESQL | QDTQELLQEE | NRQKLSLSTK | LKQVEDEKNS | FREQLEEEEE | AKHNLEKQIA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| TLHAQVADMK | KKMEDSVGCL | ETAEEVKRKL | QKDLEGLSQR | HEEKVAAYDK | LEKTKTRLQQ | ELDDLLVDLD | HQRQSACNLE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KKQKKFDQLL | AEEKTISAKY | AEERDRAEAE | AREKETKALS | LARALEEAME | QKAELERLNK | QFRTEMEDLM | SSKDDVGKSV |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| HELEKSKRAL | EQQVEEMKTQ | LEELEDELQA | TEDAKLRLEV | NLQAMKAQFE | RDLQGRDEQS | EEKKKQLVRQ | VREMEAELED |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| ERKQRSMAVA | ARKKLEMDLK | DLEAHIDSAN | KNRDEAIKQL | RKLQAQMKDC | MRELDDTRAS | REEILAQAKE | NEKKLKSMEA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| EMIQLQEELA | AAERAKRQAQ | QERDELADEI | ANSSGKGALA | LEEKRRLEAR | IAQLEEELEE | EQGNTELIND | RLKKANLQID |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| QINTDLNLER | SHAQKNENAR | QQLERQNKEL | KVKLQEMEGT | VKSKYKASIT | ALEAKIAQLE | EQLDNETKER | QAACKQVRRT |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| EKKLKDVLLQ | VDDERRNAEQ | YKDQADKAST | RLKQLKRQLE | EAEEEAQRAN | ASRRKLQREL | EDATETADAM | NREVSSLKNK |
| 1930 | 1940 | 1950 | 1960 | 1970 | | | |
| LRRGDLPFVV | PRRMARKGAG | DGSDEEVDGK | ADGAEAKPAE | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2655 | 1 | 822.4643 | 30.49 | 2 | 64.2 | 12.9 | 2 | 1213-1226 | K.ANLEKAKQTLENER.G | |
| 187 | 1 | 849.4195 | -61.73 | 2 | 32.3 | 21.9 | 2 | 1358- | K.QIATLHAQVADMKKK.M | Oxidation: 12 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | 1372 | | |
| 2426 | 1 | 625.6164 | -235.71 | 2 | 60.8 | 13.5 | 0 | 1593-1602 | R.EMEAELEDER.K | |

# Detailed Protein Report

## Protein 76: 14-3-3 protein eta [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4507951 | **Score:** | 59.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 28.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 11.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGDREQLLQR | ARLAEQAERY | DDMASAMKAV | TELNEPLSNE | DRNLLSVAYK | NVVGARRSSW | RVISSIEQKT | MADGNEKKLE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KVKAYREKIE | KELETVCNDV | LSLLDKFLIK | NCNDFQYESK | VFYLKMKGDY | YRYLAEVASG | EKKNSVVEAS | EAAYKEAFEI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SKEQMQPTHP | IRLGLALNFS | VFYYEIQNAP | EQACLLAKQA | FDDAIAELDT | LNEDSYKDST | LIMQLLRDNL | TLWTSDQQDE |
| 250 | | | | | | | |
| EAGEGN | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2722 | 1 | 1044.5326 | 52.39 | 2 | 65.2 | 11.7 | 2 | 11-28 | R.ARLAEQAERYDDMASAMK.A | Oxidation: 13, 17 |

# Detailed Protein Report

## Protein 77: fibronectin isoform 6 preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|47132549 | **Score:** | 59.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 239.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 3 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLRGPGPGLL | LLAVQCLGTA | VPSTGASKSK | RQAQQMVQPQ | SPVAVSQSKP | GCYDNGKHYQ | INQQWERTYL | GNALVCTCYG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GSRGFNCESK | PEAEETCFDK | YTGNTYRVGD | TYERPKDSMI | WDCTCIGAGR | GRISCTIANR | CHEGGQSYKI | GDTWRRPHET |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GGYMLECVCL | GNGKGEWTCK | PIAEKCFDHA | AGTSYVVGET | WEKPYQGWMM | VDCTCLGEGS | GRITCTSRNR | CNDQDTRTSY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RIGDTWSKKD | NRGNLLQCIC | TGNGRGEWKC | ERHTSVQTTS | SGSGPFTDVR | AAVYQPQPHP | QPPPYGHCVT | DSGVVYSVGM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QWLKTQGNKQ | MLCTCLGNGV | SCQETAVTQT | YGGNSNGEPC | VLPFTYNGRT | FYSCTTEGRQ | DGHLWCSTTS | NYEQDQKYSF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CTDHTVLVQT | RGGNSNGALC | HFPFLYNNHN | YTDCTSEGRR | DNMKWCGTTQ | NYDADQKFGF | CPMAAHEEIC | TTNEGVMYRI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GDQWDKQHDM | GHMMRCTCVG | NGRGEWTCIA | YSQLRDQCIV | DDITYNVNDT | FHKRHEEGHM | LNCTCFGQGR | GRWKCDPVDQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| CQDSETGTFY | QIGDSWEKYV | HGVRYQCYCY | GRGIGEWHCQ | PLQTYPSSSG | PVEVFITETP | SQPNSHPIQW | NAPQPSHISK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| YILRWRPKNS | VGRWKEATIP | GHLNSYTIKG | LKPGVVYEGQ | LISIQQYGHQ | EVTRFDFTTT | STSTPVTSNT | VTGETTPFSP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LVATSESVTE | ITASSFVVSW | VSASDTVSGF | RVEYELSEEG | DEPQYLDLPS | TATSVNIPDL | LPGRKYIVNV | YQISEDGEQS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LILSTSQTTA | PDAPPDPTVD | QVDDTSIVVR | WSRPQAPITG | YRIVYSPSVE | GSSTELNLPE | TANSVTLSDL | QPGVQYNITI |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| YAVEENQEST | PVVIQQETTG | TPRSDTVPSP | RDLQFVEVTD | VKVTIMWTPP | ESAVTGYRVD | VIPVNLPGEH | GQRLPISRNT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FAEVTGLSPG | VTYYFKVFAV | SHGRESKPLT | AQQTTKLDAP | TNLQFVNETD | STVLVRWTPP | RAQITGYRLT | VGLTRRGQPR |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QYNVGPSVSK | YPLRNLQPAS | EYTVSLVAIK | GNQESPKATG | VFTTLQPGSS | IPPYNTEVTE | TTIVITWTPA | PRIGFKLGVR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PSQGGEAPRE | VTSDSGSIVV | SGLTPGVEYV | YTIQVLRDGQ | ERDAPIVNKV | VTPLSPPTNL | HLEANPDTGV | LTVSWERSTT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PDITGYRITT | TPTNGQQGNS | LEEVVHADQS | SCTFDNLSPG | LEYNVSVYTV | KDDKESVPIS | DTIIPAVPPP | TDLRFTNIGP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DTMRVTWAPP | PSIDLTNFLV | RYSPVKNEED | VAELSISPSD | NAVVLTNLLP | GTEYVVSVSS | VYEQHESTPL | RGRQKTGLDS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PTGIDFSDIT | ANSFTVHWIA | PRATITGYRI | RHHPEHFSGR | PREDRVPHSR | NSITLTNLTP | GTEYVVSIVA | LNGREESPLL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| IGQQSTVSDV | PRDLEVVAAT | PTSLLISWDA | PAVTVRYYRI | TYGETGGNSP | VQEFTVPGSK | STATISGLKP | GVDYTITVYA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| VTGRGDSPAS | SKPISINYRT | EIDKPSQMQV | TDVQDNSISV | KWLPSSSPVT | GYRVTTTPKN | GPGPTKTKTA | GPDQTEMTIE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| GLQPTVEYVV | SVYAQNPSGE | SQPLVQTAVT | TIPAPTDLKF | TQVTPTSLSA | QWTPPNVQLT | GYRVRVTPKE | KTGPMKEINL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| APDSSSVVVS | GLMVATKYEV | SVYALKDTLT | SRPAQGVVTT | LENVSPPRRA | RVTDATETTI | TISWRTKTET | ITGFQVDAVP |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| ANGQTPIQRT | IKPDVRSYTI | TGLQPGTDYK | IYLYTLNDNA | RSSPVVIDAS | TAIDAPSNLR | FLATTPNSLL | VSWQPPRARI |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| TGYIIKYEKP | GSPPREVVPR | PRPGVTEATI | TGLEPGTEYT | IYVIALKNNQ | KSEPLIGRKK | TGQEALSQTT | ISWAPFQDTS |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| EYIISCHPVG | TDEEPLQFRV | PGTSTSATLT | GLTRGATYNI | IVEALKDQQR | HKVREEVVTV | GNSVNEGLNQ | PTDDSCFDPY |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| TVSHYAVGDE | WERMSESGFK | LLCQCLGFGS | GHFRCDSSRW | CHDNGVNYKI | GEKWDRQGEN | GQMMSCTCLG | NGKGEFKCDP |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| HEATCYDDGK | TYHVGEQWQK | EYLGAICSCT | CFGGQRGWRC | DNCRRPGGEP | SPEGTTGQSY | NQYSQRYHQR | TNTNVNCPIE |
| 2170 | 2180 |  |  |  |  |  |  |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1763 | 1 | 1044.9953 | 44.20 | 2 | 51.9 | 16.6 | 1 | 534-550 | K.RHEEGHMLNCTCFGQGR.G | Carbamidomethyl: 10, 12 |
| 2765 | 1 | 904.4689 | 14.28 | 2 | 65.7 | 16.9 | 0 | 923-938 | K.VTIMWTPPESAVTGYR.V | |
| 1706 | 1 | 796.3662 | -51.72 | 2 | 51.1 | 15.3 | 0 | 1525-1539 | R.GDSPASSKPISINYR.T | |

# Detailed Protein Report

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## Protein 78: polyribonucleotide nucleotidyltransferase 1, mitochondrial precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|188528628 | **Score:** | 58.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 85.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.8 |
| | | **Sequence Coverage [%]:** | 5.5 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

***WUP:QUP*** **Median:** 0.72 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MAACRYCCSC LRLRPLSDGP FLLPRRDRAL TQLQVRALWS SAGSRAVAVD LGNRKLEISS GKLARFADGS AVVQSGDTAV
        90        100        110        120        130        140        150        160
MVTAVSKTKP SPSQFMPLVV DYRQKAAAAG RIPTNYLRRE IGTSDKEILT SRIIDRSIRP LFPAGYFYDT QVLCNLLAVD
       170        180        190        200        210        220        230        240
GVNEPDVLAI NGASVALSLS DIPWNGPVGA VRIGIIDGEY VVNPTRKEMS SSTLNLVVAG APKSQIVMLE ASAENILQQD
       250        260        270        280        290        300        310        320
FCHAIKVGVK YTQQIIQGIQ QLVKETGVTK RTPQKLFTPS PEIVKYTHKL AMERLYAVFT DYEHDKVSRD EAVNKIRLDT
       330        340        350        360        370        380        390        400
EEQLKEKFPE ADPYEIIESF NVVAKEVFRS IVLNEYKRCD GRDLTSLRNV SCEVDMFKTL HGSALFQRGQ TQVLCTVTFD
       410        420        430        440        450        460        470        480
SLESGIKSDQ VITAINGIKD KNFMLHYEFP PYATNEIGKV TGLNRRELGH GALAEKALYP VIPRDFPFTI RVTSEVLESN
       490        500        510        520        530        540        550        560
GSSSMASACG GSLALMDSGV PISSAVAGVA IGLVTKTDPE KGEIEDYRLL TDILGIEDYN GDMDFKIAGT NKGITALQAD
       570        580        590        600        610        620        630        640
IKLPGIPIKI VMEAIQQASV AKKEILQIMN KTISKPRASR KENGPVVETV QVPLSKRAKF VGPGGYNLKK LQAETGVTIS
       650        660        670        680        690        700        710        720
QVDEETFSVF APTPSAMHEA RDFITEICKD DQEQQLEFGA VYTATITEIR DTGVMVKLYP NMTAVLLHNT QLDQRKIKHP
       730        740        750        760        770        780        790
TALGLEVGQE IQVKYFGRDP ADGRMRLSRK VLQSPATTVV RTLNDRSSIV MGEPISQSSS NSQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2849 | 8 | 973.4915 | -40.84 | 2 | 64.3 | 15.3 | 2 | 120-136 | R.EIGTSDKEILTSRIIDR.S | | |
| 80 | 1 | 586.3280 | 116.43 | 2 | 30.9 | 28.4 | 0 | 369-378 | R.NVSCEVDMFK.T | | WUP:QUP 0.72 |
| 2737 | 1 | 885.4690 | -31.70 | 2 | 64.6 | 15.2 | 1 | 751-766 | K.VLQSPATTVVRTLNDR.S | | |

# Detailed Protein Report

## Protein 79: ATP-binding cassette sub-family A member 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|116734710 | **Score:** | 58.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 191.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.87 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.16 | **CV:** | 176.78 % | **No. of Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAVLRQLALL | LWKNYTLQKR | KVLVTVLELF | LPLLFSGILI | WLRLKIQSEN | VPNATIYPGQ | SIQELPLFFT | FPPPGDTWEL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AYIPSHSDAA | KTVTETVRRA | LVINMRVRGF | PSEKDFEDYI | RYDNCSSSVL | AAVVFEHPFN | HSKEPLPLAV | KYHLRFSYTR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RNYMWTQTGS | FFLKETEGWH | TTSLFPLFPN | PGPREPTSPD | GGEPGYIREG | FLAVQHAVDR | AIMEYHADAA | TRQLFQRLTV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TIKRFPYPPF | IADPFLVAIQ | YQLPLLLLLS | FTYTALTIAR | AVVQEKERRL | KEYMRMMGLS | SWLHWSAWFL | LFFLFLLIAA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SFMTLLFCVK | VKPNVAVLSR | SDPSLVLAFL | LCFAISTISF | SFMVSTFFSK | ANMAAAFGGF | LYFFTYIPYF | FVAPRYNWMT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LSQKLCSCLL | SNVAMAMGAQ | LIGKFEAKGM | GIQWRDLLSP | VNVDDDFCFG | QVLGMLLLDS | VLYGLVTWYM | EAVFPGQFGV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PQPWYFFIMP | SYWCGKPRAV | AGKEEEDSDP | EKALRNEYFE | AEPEDLVAGI | KIKHLSKVFR | VGNKDRAAVR | DLNLNLYEGQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ITVLLGHNGA | GKTTTLSMLT | GLFPPTSGRA | YISGYEISQD | MVQIRKSLGL | CPQHDILFDN | LTVAEHLYFY | AQLKGLSRQK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CPEEVKQMLH | IIGLEDKWNS | RSRFLSGGMR | RKLSIGIALI | AGSKVLILDE | PTSGMDAISR | RAIWDLLQRQ | KSDRTIVLTT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HFMDEADLLG | DRIAIMAKGE | LQCCGSSLFL | KQKYGAGYHM | TLVKEPHCNP | EDISQLVHHH | VPNATLESSA | GAELSFILPR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ESTHRFEGLF | AKLEKKQKEL | GIASFGASIT | TMEEVFLRVG | KLVDSSMDIQ | AIQLPALQYQ | HERRASDWAV | DSNLCGAMDP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SDGIGALIEE | ERTAVKLNTG | LALHCQQFWA | MFLKKAAYSW | REWKMVAAQV | LVPLTCVTLA | LLAINYSSEL | FDDPMLRLTL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GEYGRTVVPF | SVPGTSQLGQ | QLSEHLKDAL | QAEGQEPREV | LGDLEEFLIF | RASVEGGGFN | ERCLVAASFR | DVGERTVVNA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LFNNQAYHSP | ATALAVVDNL | LFKLLCGPHA | SIVVSNFPQP | RSALQAAKDQ | FNEGRKGFDI | ALNLLFAMAF | LASTFSILAV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SERAVQAKHV | QFVSGVHVAS | FWLSALLWDL | ISFLIPSLLL | LVVFKAFDVR | AFTRDGHMAD | TLLLLLLYGW | AIIPLMYLMN |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| FFFLGAATAY | TRLTIFNILS | GIATFLMVTI | MRIPAVKLEE | LSKTLDHVFL | VLPNHCLGMA | VSSFYENYET | RRYCTSSEVA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| AHYCKKYNIQ | YQENFYAWSA | PGVGRFVASM | AASGCAYLIL | LFLIETNLLQ | RLRGILCALR | RRRTLTELYT | RMPVLPEDQD |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VADERTRILA | PSPDSLLHTP | LIIKELSKVY | EQRVPLLAVD | RLSLAVQKGE | CFGLLGFNGA | GKTTTFKMLT | GEESLTSGDA |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| FVGGHRISSD | VGKVRQRIGY | CPQFDALLDH | MTGREMLVMY | ARLRGIPERH | IGACVENTLR | GLLLEPHANK | LVRTYSGGNK |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| RKLSTGIALI | GEPAVIFLDE | PSTGMDPVAR | RLLWDTVARA | RESGKAIIIT | SHSMEECEAL | CTRLAIMVQG | QFKCLGSPQH |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LKSKFGSGYS | LRAKVQSEGQ | QEALEEFKAF | VDLTFPGSVL | EDEHQGMVHY | HLPGRDLSWA | KVFGILEKAK | EKYGVDDYSV |
| 1690 | 1700 | 1710 | | | | | |
| SQISLEQVFL | SFAHLQPPTA | EEGR | | | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 198 | 1 | 424.2139 | -143.01 | 3 | 32.2 | 15.7 | 1 | 672-684 | R.KLSIGIALIAGSK.V | | |
| 32 | 1 | 877.8644 | -76.86 | 2 | 29.3 | 10.4 | 1 | 739-753 | K.GELQCCGSSLFLKQK.Y | Carbamidomethyl: 5, 6 | WUP:QUP 0.35 |
| 535 | 3 | 607.3148 | 34.29 | 2 | 36.7 | 32.6 | 0 | 988-998 | K.DALQAEGQEPR.E | | QU:MU 0.87<br>WUP:QUP 3.82 |

# Detailed Protein Report

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**Protein 80:** **sp110 nuclear body protein isoform a [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|190343010 | **Score:** | 58.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 78.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 10.2 |
| | | **No. of unique Peptides:** | 4 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFTMTRAMEE | ALFQHFMHQK | LGIAYAIHKP | FPFFEGLLDN | SIITKRMYME | SLEACRNLIP | VSRVVHNILT | QLERTFNLSL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LVTLFSQINL | REYPNLVTIY | RSFKRVGASY | ERQSRDTPIL | LEAPTGLAEG | SSLHTPLALP | PPQPPQPSCS | PCAPRVSEPG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TSSQQSDEIL | SESPSPSDPV | LPLPALIQEG | RSTSVTNDKL | TSKMNAEEDS | EEMPSLLTST | VQVASDNLIP | QIRDKEDPQE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MPHSPLGSMP | EIRDNSPEPN | DPEEPQEVSS | TPSDKKGKKR | KRCIWSTPKR | RHKKKSLPGG | TASSRHGIQK | KLKRVDQVPQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KKDDSTCNST | VETRAQKART | ECARKSRSEE | IIDGTSEMNE | GKRSQKTPST | PRRVTQGAAS | PGHGIQEKLQ | VVDKVTQRKD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DSTWNSEVMM | RVQKARTKCA | RKSRSKEKKK | EKDICSSSKR | RFQKNIHRRG | KPKSDTVDFH | CSKLPVTCGE | AKGILYKKKM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KHGSSVKCIR | NEDGTWLTPN | EFEVEGKGRN | AKNWKRNIRC | EGMTLGELLK | RKNSDECEVC | CQGGQLLCCG | TCPRVFHEDC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HIPPVEAKRM | LWSCTFCRMK | RSSGSQQCHH | VSKTLERQMQ | PQDQLIRDYG | EPFQEAMWLD | LVKERLITEM | YTVAWFVRDM |
| 650 | 660 | 670 | 680 | 690 | | | |
| RLMFRNHKTF | YKASDFGQVG | LDLEAEFEKD | LKDVLGFHEA | NDGGFWTLP | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1618 | 1 | 882.8999 | 95.52 | 3 | 48.5 | 11.3 | 2 | 374-398 | R.VTQGAASPGHGIQEKLQVVDKVTQR.K | |
| 220 | 1 | 978.1311 | -3.65 | 3 | 32.7 | 10.8 | 2 | 482-507 | K.HGSSVKCIRNEDGTWLTPNEFEVEGK.G | |
| 1829 | 1 | 781.3008 | -84.17 | 2 | 53.2 | 11.5 | 2 | 569-580 | K.RMLWSCTFCRMK.R | |
| 2660 | 1 | 484.7692 | 52.33 | 2 | 61.6 | 14.6 | 1 | 639-645 | R.DMRLMFR.N | |

# Detailed Protein Report

## Protein 81: filaggrin [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|60097902 | **Score:** | 58.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 434.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 3 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSTLLENIFA | IINLFKQYSK | KDKNTDTLSK | KELKELLEKE | FRQILKNPDD | PDMVDVFMDH | LDIDHNKKID | FTEFLLMVFK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LAQAYYESTR | KENLPISGHK | HRKHSHHDKH | EDNKQEENKE | NRKRPSSLER | RNNRKGNKGR | SKSPRETGGK | RHESSSEKKE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RKGYSPTHRE | EEYGKNHHNS | SKKEKNKTEN | TRLGDNRKRL | SERLEEKEDN | EEGVYDYENT | GRMTQKWIQS | GHIATYYTIQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DEAYDTTDSL | LEENKIYERS | RSSDGKSSSQ | VNRSRHENTS | QVPLQESRTR | KRRGSRVSQD | RDSEGHSEDS | ERHSGSASRN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HHGSAWEQSR | DGSRHPRSHD | EDRASHGHSA | DSSRQSGTRH | AETSSRGQTA | SSHEQARSSP | GERHGSGHQQ | SADSSRHSAT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GRGQASSAVS | DRGHRGSSGS | QASDSEGHSE | NSDTQSVSGH | GKAGLRQQSH | QESTRGRSGE | RSGRSGSSLY | QVSTHEQPDS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AHGRTGTSTG | GRQGSHHEQA | RDSSRHSASQ | EGQDTIRGHP | GSSRGGRQGS | HHEQSVNRSG | HSGSHHSHTT | SQGRSDASHG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QSGSRSASRQ | TRNEEQSGDG | TRHSGSRHHE | ASSQADSSRH | SQVGQGQSSG | PRTSRNQGSS | VSQDSDSQGH | SEDSERWSGS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ASRNHHGSAQ | EQSRDGSRHP | RSHHEDRAGH | GHSADSSRKS | GTRHTQNSSS | GQAASSHEQA | RSSAGERHGS | RHQLQSADSS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RHSGTGHGQA | SSAVRDSGHR | GSSGSQATDS | EGHSEDSDTQ | SVSGHGQAGH | HQQSHQESAR | DRSGERSRRS | GSFLYQVSTH |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KQSESSHGWT | GPSTGVRQGS | HHEQARDNSR | HSASQDGQDT | IRGHPGSSRR | GRQGSHHEQS | VDRSGHSGSH | HSHTTSQGRS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DASRGQSGSR | SASRTTRNEE | QSRDGSRHSG | SRHHEASSHA | DISRHSQAGQ | GQSEGSRTSR | RQGSSVSQDS | DSEGHSEDSE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RWSGSASRNH | RGSAQEQSRH | GSRHPRSHHE | DRAGHGHSAD | SSRQSGTPHA | ETSSGGQAAS | SHEQARSSPG | ERHGSRHQQS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ADSSRHSGIP | RRQASSAVRD | SGHWGSSGSQ | ASDSEGHSEE | SDTQSVSGHG | QDGPHQQSHQ | ESARDWSGGR | SGRSGSFIYQ |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| VSTHEQSESA | HGRTRTSTGR | RQGSHHEQAR | DSSRHSASQE | GQDTIRAHPG | SRRGGRQGSH | HEQSVDRSGH | SGSHHSHTTS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| QGRSDASHGQ | SGSRSASRQT | RKDKQSGDGS | RHSGSRHHEA | ASWADSSRHS | QVGQEQSSGS | RTSRHQGSSV | SQDSDSERHS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DDSERLSGSA | SRNHHGSSRE | QSRDGSRHPG | FHQEDRASHG | HSADSSRQSG | THHTESSSHG | QAVSSHEQAR | SSPGERHGSR |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| HQQSADSSRH | SGIGHRQASS | AVRDSGHRGS | SGSQVTNSEG | HSEDSDTQSV | SAHGQAGPHQ | QSHKESARGQ | SGESSGRSRS |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| FLYQVSSHEQ | SESTHGQTAP | STGGRQGSRH | EQARNSSRHS | ASQDGQDTIR | GHPGSSRGGR | QGSYHEQSVD | RSGHSGYHHS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| HTTPQGRSDA | SHGQSGPRSA | SRQTRNEEQS | GDGSRHSGSR | HHEPSTRAGS | SRHSQVGQGE | SAGSKTSRRQ | GSSVSQDRDS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| EGHSEDSERR | SESASRNHYG | SAREQSRHGS | RNPRSHQEDR | ASHGHSAESS | RQSGTRHAET | SSGGQAASSQ | EQARSSPGER |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| HGSRHQQSAD | SSTDSGTGRR | QDSSVVGDSG | NRGSSGSQAS | DSEGHSEESD | TQSVSAHGQA | GPHQQSHQES | TRGQSGERSG |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| RSGSFLYQVS | THEQSESAHG | RTGPSTGGRQ | RSRHEQARDS | SRHSASQEGQ | DTIRGHPGSS | RGGRQGSHYE | QSVDSSGHSG |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| SHHSHTTSQE | RSDVSRGQSG | SRSVSRQTRN | EKQSGDGSRH | SGSRHHEASS | RADSSRHSQV | GQGQSSGPRT | SRNQGSSVSQ |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| DSDSQGHSED | SERWSGSASR | NHLGSAWEQS | RDGSRHPGSH | HEDRAGHGHS | ADSSRQSGTR | HTESSSRGQA | ASSHEQARSS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| AGERHGSHHQ | LQSADSSRHS | GIGHGQASSA | VRDSGHRGYS | GSQASDSEGH | SEDSDTQSVS | AQGKAGPHQQ | SHKESARGQS |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| GESSGRSGSF | LYQVSTHEQS | ESTHGQSAPS | TGGRQGSHYD | QAQDSSRHSA | SQEGQDTIRG | HPGPSRGGRQ | GSHQEQSVDR |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2478 | 1 | 589.2111 | -88.51 | 2 | 60.9 | 15.3 | 1 | 898-907 | R.NEEQSRDGSR.H | |
| 46 | 1 | 731.3139 | -20.71 | 3 | 30.3 | 16.4 | 1 | 3577-3596 | R.HPTSHHEDRAGHGHSAESSR.Q | |
| 371 | 1 | 938.4376 | 1.41 | 2 | 34.6 | 15.1 | 2 | 3797-3814 | R.SDASHGQSGSRSASRETR.N | |

# Detailed Protein Report

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## Protein 82: desmoplakin isoform I [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|58530840 | **Score:** | 58.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 331.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 4 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.24 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSCNGGSHPR | INTLGRMIRA | ESGPDLRYEV | TSGGGGTSRM | YYSRRGVITD | QNSDGYCQTG | TMSRHQNQNT | IQELLQNCSD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CLMRAELIVQ | PELKYGDGIQ | LTRSRELDEC | FAQANDQMEI | LDSLIREMRQ | MGQPCDAYQK | RLLQLQEQMR | ALYKAISVPR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VRRASSKGGG | GYTCQSGSGW | DEFTKHVTSE | CLGWMRQQRA | EMDMVAWGVD | LASVEQHINS | HRGIHNSIGD | YRWQLDKIKA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DLREKSAIYQ | LEEEYENLLK | ASFERMDHLR | QLQNIIQATS | REIMWINDCE | EEELLYDWSD | KNTNIAQKQE | AFSIRMSQLE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VKEKELNKLK | QESDQLVLNQ | HPASDKIEAY | MDTLQTQWSW | ILQITKCIDV | HLKENAAYFQ | FFEEAQSTEA | YLKGLQDSIR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KKYPCDKNMP | LQHLLEQIKE | LEKEREKILE | YKRQVQNLVN | KSKKIVQLKP | RNPDYRSNKP | IILRALCDYK | QDQKIVHKGD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ECILKDNNER | SKWYVTGPGG | VDMLVPSVGL | IIPPPNPLAV | DLSCKIEQYY | EAILALWNQL | YINMKSLVSW | HYCMIDIEKI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RAMTIAKLKT | MRQEDYMKTI | ADLELHYQEF | IRNSQGSEMF | GDDDKRKIQS | QFTDAQKHYQ | TLVIQLPGYP | QHQTVTTTEI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| THHGTCQDVN | HNKVIETNRE | NDKQETWMLM | ELQKIRRQIE | HCEGRMTLKN | LPLADQGSSH | HITVKINELK | SVQNDSQAIA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EVLNQLKDML | ANFRGSEKYC | YLQNEVFGLF | QKLENINGVT | DGYLNSLCTV | RALLQAILQT | EDMLKVYEAR | LTEEETVCLD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LDKVEAYRCG | LKKIKNDLNL | KKSLLATMKT | ELQKAQQIHS | QTSQQYPLYD | LDLGKFGEKV | TQLTDRWQRI | DKQIDFRLWD |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LEKQIKQLRN | YRDNYQAFCK | WLYDAKRRQD | SLESMKFGDS | NTVMRFLNEQ | KNLHSEISGK | RDKSEEVQKI | AELCANSIKD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| YELQLASYTS | GLETLLNIPI | KRTMIQSPSG | VILQEAADVH | ARYIELLTRS | GDYYRFLSEM | LKSLEDLKLK | NTKIEVLEEE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LRLARDANSE | NCNKNKFLDQ | NLQKYQAECS | QFKAKLASLE | ELKRQAELDG | KSAKQNLDKC | YGQIKELNEK | ITRLTYEIED |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EKRRRKSVED | RFDQQKNDYD | QLQKARQCEK | ENLGWQKLES | EKAIKEKEYE | IERLRVLLQE | EGTRKREYEN | ELAKVRNHYN |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EEMSNLRNKY | ETEINITKTT | IKEISMQKED | DSKNLRNQLD | RLSRENRDLK | DEIVRLNDSI | LQATEQRRRA | EENALQQKAC |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| GSEIMQKKQH | LEIELKQVMQ | QRSEDNARHK | QSLEEAAKTI | QDKNKEIERL | KAEFQEEAKR | RWEYENELSK | VRNNYDEEII |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| SLKNQFETEI | NITKTTIHQL | TMQKEEDTSG | YRAQIDNLTR | ENRSLSEEIK | RLKNTLTQTT | ENLRRVEEDI | QQQKATGSEV |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SQRKQQLEVE | LRQVTQMRTE | ESVRYKQSLD | DAAKTIQDKN | KEIERLKQLI | DKETNDRKCL | EDENARLQRV | QYDLQKANSS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ATETINKLKV | QEQELTRLRI | DYERVSQERT | VKDQDITRFQ | NSLKELQLQK | QKVEEELNRL | KRTASEDSCK | RKKLEEELEG |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| MRRSLKEQAI | KITNLTQQLE | QASIVKKRSE | DDLRQQRDVL | DGHLREKQRT | QEELRRLSSE | VEALRRQLLQ | EQESVKQAHL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| RNEHFQKAIE | DKSRSLNESK | IEIERLQSLT | ENLTKEHLML | EEELRNLRLE | YDDLRRGRSE | ADSDKNATIL | ELRSQLQISN |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| NRTLELQGLI | NDLQRERENL | RQEIEKFQKQ | ALEASNRIQE | SKNQCTQVVQ | ERESLLVKIK | VLEQDKARLQ | RLEDELNRAK |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| STLEAETRVK | QRLECEKQQI | QNDLNQWKTQ | YSRKEEAIRK | IESEREKSER | EKNSLRSEIE | RLQAEIKRIE | ERCRRKLEDS |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| TRETQSQLET | ERSRYQREID | KLRQRPYGSH | RETQTECEWT | VDTSKLVFDG | LRKKVTAMQL | YECQLIDKTT | LDKLLKGKKS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| VEEVASEIQP | FLRGAGSIAG | ASASPKEKYS | LVEAKRKKLI | SPESTVMLLE | AQAATGGIID | PHRNEKLTVD | SAIARDLIDF |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| DDRQQIYAAE | KAITGFDDPF | SGKTVSVSEA | IKKNLIDRET | GMRLLEAQIA | SGGVVDPVNS | VFLPKDVALA | RGLIDRDLYR |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2092 | 1 | 1045.4569 | 7.22 | 2 | 56.0 | 12.2 | 0 | 46-64 | R.GVITDQNSDGYCQTGTMSR.H | Carbamidomethyl: 12 | |
| 2178 | 4 | 596.7430 | -119.04 | 2 | 57.6 | 11.1 | 1 | 1330-1339 | R.LKAEFQEEAK.R | | QU:MU 2.24 |
| 1858 | 1 | 616.2551 | -101.28 | 2 | 53.1 | 10.2 | 1 | 1488-1497 | K.QLIDKETNDR.K | | |
| 2393 | 1 | 1176.1976 | 83.64 | 2 | 59.8 | 12.7 | 2 | 2465-2484 | R.RVVIVDPETNKEMSVQEAYK.K | Oxidation: 13 | |

# Detailed Protein Report

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**Protein 83:** **PREDICTED: glutamine-rich protein 2 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578831523 | **Score:** | 57.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 72.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 8.1 |
| | | **No. of unique Peptides:** | 4 |

## Quantitation

***WUP:QUP*** **Median:** 1.84 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MRSRPAKPTW RRSSSCWHRW VERLQRILEG EGNQEAGKEL KAGELRLQLG VLRVTVADIE KELAELRESQ DRGKAAMENS
        90        100        110        120        130        140        150        160
VSEASLYLQD QLDKLRMIIE SMLTSSSTLL SMSMAPHKAH TLAPGQIDPE ATCPACSLDV SHQVSTLVRR YEQLQDMVNS
       170        180        190        200        210        220        230        240
LAVSRPSKKA KLQRQDEELL GRVQSAILQV QGDCEKLNIT TSNLIEDHRQ KQKDIAMLYQ GLEKLEKEKA NREHLEMEID
       250        260        270        280        290        300        310        320
VKADKSALAT KVSRVQFDAT TEQLNHMMQE LVAKMSGQEQ DWQKMLDRLL TEMDNKLDRL ELDPVKQLLE DRWKSLRQQL
       330        340        350        360        370        380        390        400
RERPPLYQAD EAAAMRRQLL AHFHCLSCDR PLETPVTGHA IPVTPAGPGL PGHHSIRPYT VFELEQVRQH SRNLKLGSAF
       410        420        430        440        450        460        470        480
PRGDLAQMEQ SVGRLRSMHS KMLMNIEKVQ IHFGGSTKAS SQIIRELLHA QCLGSPCYKR VTDMADYTYS TVPRRCGGSH
       490        500        510        520        530        540        550        560
TLTYPYHRSR PQHLPRGLYP TEEIQIAMKH DEVDILGLDG HIYKGRMDTR LPGILRKDSS GTSKRKSQQP RPHVHRPPSL
       570        580        590        600        610        620        630        640
SSNGQLPSRP QSAQISAGNT SVSSRQQKDR PSSEGRLSQP NTAHPPSSAA VANRGLERHV DMPPGEGLEE PTRGPRSSTA
       650
Q
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2513 | 1 | 410.0863 | -280.49 | 2 | 61.4 | 19.3 | 1 | 68-74 | R.ESQDRGK.A | | |
| 592 | 1 | 1105.2058 | 124.92 | 2 | 35.8 | 10.7 | 1 | 151-169 | R.YEQLQDMVNSLAVSRPSKK.A | Oxidation: 7 | |
| 2139 | 1 | 937.3370 | -142.40 | 2 | 56.6 | 10.9 | 1 | 322-337 | R.ERPPLYQADEAAAMRR.Q | | WUP:QUP 1.84 |
| 16 | 1 | 537.2110 | -148.15 | 2 | 29.8 | 16.9 | 0 | 429-438 | K.VQIHFGGSTK.A | | |

# Detailed Protein Report

## Protein 84: complement C3 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|115298678 | **Score:** | 57.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 187.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGPTSGPSLL | LLLLTHLPLA | LGSPMYSIIT | PNILRLESEE | TMVLEAHDAQ | GDVPVTVTVH | DFPGKKLVLS | SEKTVLTPAT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NHMGNVTFTI | PANREFKSEK | GRNKFVTVQA | TFGTQVVEKV | VLVSLQSGYL | FIQTDKTIYT | PGSTVLYRIF | TVNHKLLPVG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RTVMVNIENP | EGIPVKQDSL | SSQNQLGVLP | LSWDIPELVN | MGQWKIRAYY | ENSPQQVFST | EFEVKEYVLP | SFEVIVEPTE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KFYYIYNEKG | LEVTITARFL | YGKKVEGTAF | VIFGIQDGEQ | RISLPESLKR | IPIEDGSGEV | VLSRKVLLDG | VQNPRAEDLV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GKSLYVSATV | ILHSGSDMVQ | AERSGIPIVT | SPYQIHFTKT | PKYFKPGMPF | DLMVFVTNPD | GSPAYRVPVA | VQGEDTVQSL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TQGDGVAKLS | INTHPSQKPL | SITVRTKKQE | LSEAEQATRT | MQALPYSTVG | NSNNYLHLSV | LRTELRPGET | LNVNFLLRMD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RAHEAKIRYY | TYLIMNKGRL | LKAGRQVREP | GQDLVVLPLS | ITTDFIPSFR | LVAYYTLIGA | SGQREVVADS | VWVDVKDSCV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GSLVVKSGQS | EDRQPVPGQQ | MTLKIEGDHG | ARVVLVAVDK | GVFVLNKKNK | LTQSKIWDVV | EKADIGCTPG | SGKDYAGVFS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DAGLTFTSSS | GQQTAQRAEL | QCPQPAARRR | RSVQLTEKRM | DKVGKYPKEL | RKCCEDGMRE | NPMRFSCQRR | TRFISLGEAC |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KKVFLDCCNY | ITELRRQHAR | ASHLGLARSN | LDEDIIAEEN | IVSRSEFPES | WLWNVEDLKE | PPKNGISTKL | MNIFLKDSIT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TWEILAVSMS | DKKGICVADP | FEVTVMQDFF | IDLRLPYSVV | RNEQVEIRAV | LYNYRQNQEL | KVRVELLHNP | AFCSLATTKR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RHQQTVTIPP | KSSLSVPYVI | VPLKTGLQEV | EVKAAVYHHF | ISDGVRKSLK | VVPEGIRMNK | TVAVRTLDPE | RLGREGVQKE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DIPPADLSDQ | VPDTESETRI | LLQGTPVAQM | TEDAVDAERL | KHLIVTPSGC | GEQNMIGMTP | TVIAVHYLDE | TEQWEKFGLE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KRQGALELIK | KGYTQQLAFR | QPSSAFAAFV | KRAPSTWLTA | YVVKVFSLAV | NLIAIDSQVL | CGAVKWLILE | KQKPDGVFQE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DAPVIHQEMI | GGLRNNNEKD | MALTAFVLIS | LQEAKDICEE | QVNSLPGSIT | KAGDFLEANY | MNLQRSYTVA | IAGYALAQMG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| RLKGPLLNKF | LTTAKDKNRW | EDPGKQLYNV | EATSYALLAL | LQLKDFDFVP | PVVRWLNEQR | YYGGGYGSTQ | ATFMVFQALA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| QYQKDAPDHQ | ELNLDVSLQL | PSRSSKITHR | IHWESASLLR | SEETKENEGF | TVTAEGKGQG | TLSVVTMYHA | KAKDQLTCNK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| FDLKVTIKPA | PETEKRPQDA | KNTMILEICT | RYRGDQDATM | SILDISMMTG | FAPDTDDLKQ | LANGVDRYIS | KYELDKAFSD |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| RNTLIIYLDK | VSHSEDDCLA | FKVHQYFNVE | LIQPGAVKVY | AYYNLEESCT | RFYHPEKEDG | KLNKLCRDEL | CRCAEENCFI |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| QKSDDKVTLE | ERLDKACEPG | VDYVYKTRLV | KVQLSNDFDE | YIMAIEQTIK | SGSDEVQVGQ | QRTFISPIKC | REALKLEEKK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | |
| HYLMWGLSSD | FWGEKPNLSY | IIGKDTWVEH | WPEEDECQDE | ENQKQCQDLG | AFTESMVVFG | CPN | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2396 | 4 | 701.3860 | -50.24 | 2 | 59.8 | 21.6 | 0 | 892-904 | K.SSLSVPYVIVPLK.T | |
| 1824 | 2 | 1087.0109 | 22.47 | 2 | 51.1 | 15.7 | 2 | 1505-1522 | K.LCRDELCRCAEENCFIQK.S | |
| 192 | 1 | 650.8121 | 22.36 | 2 | 31.2 | 19.9 | 0 | 1536-1546 | K.ACEPGVDYVYK.T | Carbamidomethyl: 2 |

# Detailed Protein Report

## Protein 85: fatty acid-binding protein, epidermal [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4557581 | **Score:** | 57.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 15.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 10.4 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MATVQQLEGR WRLVDSKGFD EYMKELGVGI ALRKMGAMAK PDCIITCDGK NLTIKTESTL KTTQFSCTLG EKFEETTADG
        90        100        110        120        130        140
RKTQTVCNFT DGALVQHQEW DGKESTITRK LKDGKLVVEC VMNNVTCTRI YEKVE
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1139 | 2 | 847.8676 | -43.89 | 2 | 44.4 | 57.2 | 0 | 116-129 | K.LVVECVMNNVTCTR.I | Carbamidomethyl: 5, 12 |

# Detailed Protein Report

## Protein 86: uncharacterized protein C4orf21 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|254826809 | **Score:** | 57.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 236.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| | | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530377937 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: uncharacterized protein C4orf21 isoform X1 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MESQEFIVLY THQKMKKSKV WQDGILKITH LGNKAILYDD KGACLESLFL KCLEVKPGDD LESDRYLITV EEVKVAGAIG
        90        100        110        120        130        140        150        160
IVKQNVNKEA PELNSRTFIS SGRSLGCQPS GLKRKFTGFQ GPRQVPKKMV IMESGESAAS HEAKKTGPTI FSPFCSMPPL
       170        180        190        200        210        220        230        240
FPTVGKKDVN NILADPENIV TYKNRERNAM DFSSVFSPSF QINPEVLCEE NYFCSPVNSG NKLSDSLLTN EPVKRDSLAS
       250        260        270        280        290        300        310        320
HYSGVSQNIR SKAQILALLK SESSSSCEEL NSEMTEHFPQ KQPQGSLKIA TKPKYLIQQE ECAEMKSTEN LYYQHQSENT
       330        340        350        360        370        380        390        400
MRNKSRWAMY LSSQSSPIHS STVDGNDTER KPKAQEDDVN SNLKDLSLQK IIQFVETYAE ERKKYNVDQS VGNNDPSWNQ
       410        420        430        440        450        460        470        480
EVKLEIPSFN ESSSLQVTCS SAENDGILSE SDIQEDNKIP FNQNDKGCIK GSVLIKENAQ EVNTCGTLEK EYEQSESSLP
       490        500        510        520        530        540        550        560
ELKHLQIESS NNSRISDDIT DMISESKMDN ESLNSIHESL SNVTQPFLEV TFNLNNFETS DTEEESQESN KISQDSESWV
       570        580        590        600        610        620        630        640
KDILVNDGNS CFQKRSENTN CEEIEGEHLP FLTSVSDKPT VTFPVKETLP SQFCDKTYVG FDMGICKTEN TGKEIEEYSD
       650        660        670        680        690        700        710        720
TLSNFESFKW TDAVYGDNKE DANKPIQEVR INYDFALPPN KSKGINMNLH IPHIQNQIAE NSNLFSEDAQ PQPFILGSDL
       730        740        750        760        770        780        790        800
DKNDEHVLPS TSSSDNSVQL LNTNQNHYEC IALDKSNTHI SNSLFYPLGK KHLISKDTEA HISEPEDLGK IRSPPPDHVE
       810        820        830        840        850        860        870        880
VETAREGKQY WNPRNSSELS GLVNTISILK SLCEHSTALD SLEILKKKNT VFQQGTQQTY EPDSPPEVRK PFITVVSPKS
       890        900        910        920        930        940        950        960
PHLHKDSQQI LKEDEVELSE PLQSVQFSSS GSKEETAFQA VIPKQIERKT CDPKPVEFQG HQVKGSATSG VMVRGHSSQL
       970        980        990       1000       1010       1020       1030       1040
GCSQFPDSTE YENFMTETPE LPSTCMQIDF LQVTSPEENI STLSPVSTFS LNSRDEDFMV EFSETSLKAR TLPDDLHFLN
      1050       1060       1070       1080       1090       1100       1110       1120
LEGMKKSRSL ENENLQRLSL LSRTQVPLIT LPRTDGPPDL DSHSYMINSN TYESSGSPML NLCEKSAVLS FSIEPEDQNE
      1130       1140       1150       1160       1170       1180       1190       1200
TFFSEESREV NPGDVSLNNI STQSKWLKYQ NTSQCNVATP NRVDKRITDG FFAEAVSGMH FRDTSERQSD AVNESSLDSV
      1210       1220       1230       1240       1250       1260       1270       1280
HLQMIKGMLY QQRQDFSSQD SVSRKKVLSL NLKQTSKTEE IKNVLGGSTC YNYSVKDLQE ISGSELCFPS GQKIKSAYLP
      1290       1300       1310       1320       1330       1340       1350       1360
QRQIHIPAVF QSPAHYKQTF TSCLIEHLNI LLFGLAQNLQ KALSKVDISF YTSLKGEKLK NAENNVPSCH HSQPAKLVMV
      1370       1380       1390       1400       1410       1420       1430       1440
KKEGPNKGRL FYTCDGPKAD RCKFFKWLED VTPGYSTQEG ARPGMVLSDI KSIGLYLRSQ KIPLYEECQL LVRKGFDFQR
      1450       1460       1470       1480       1490       1500       1510       1520
KQYGKLKKFT TVNPEFYNEP KTKLYLKLSR KERSSAYSKN DLWVVSKTLD FELDTFIACS AFFGPSSINE IEILPLKGYF
      1530       1540       1550       1560       1570       1580       1590       1600
PSNWPTNMVV HALLVCNAST ELTTLKNIQD YFNPATLPLT QYLLTTSSPT IVSNKRVSKR KFIPPAFTNV STKFELLSLG
      1610       1620       1630       1640       1650       1660       1670       1680
ATLKLASELI QVHKLNKDQA TALIQIAQMM ASHESIEEVK ELQTHTFPIT IIHGVFGAGK SYLLAVVILF FVQLFEKSEA
      1690       1700       1710       1720       1730       1740       1750       1760
PTIGNARPWK LLISSSTNVA VDRVLLGLLS LGFENFIRVG SVRKIAKPIL PYSLHAGSEN ESEQLKELHA LMKEDLTPTE
      1770       1780       1790       1800       1810       1820       1830       1840
RVYVRKSIEQ HKLGTNRTLL KQVRVVGVTC AACPFPCMND LKFPVVVLDE CSQITEPASL LPIARFECEK LILVGDPKQL
      1850       1860       1870       1880       1890       1900       1910       1920
PPTIQGSDAA HENGLEQTLF DRLCLMGHKP ILLRTQYRCH PAISAIANDL FYKGALMNGV TEIERSPLLE WLPTLCFYNV
      1930       1940       1950       1960       1970       1980       1990       2000
KGLEQIERDN SFHNVAEATF TLKLIQSLIA SGIAGSMIGV ITLYKSQMYK LCHLLSAVDF HHPDIKTVQV STVDAFQGAE
      2010       2020       2030       2040       2050       2060       2070       2080
KEIIILSCVR TRQVGFIDSE KRMNVALTRG KRHLLIVGNL ACLRKNQLWG RVIQHCEGRE DGLQHANQYE PQLNHLLKDY
      2090       2100       2110
FEKQVEEKQK KKSEKEKSKD KSHS
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1998 | 1 | 902.8620 | -77.52 | 2 | 55.4 | 13.3 | 1 | 128-144 | K.KMVIMESGESAASHEAK.K | |
| 2085 | 1 | 698.2938 | -180.04 | 2 | 56.0 | 10.9 | 1 | 282-294 | K.QPQGSLKIATKPK.Y | |

# Detailed Protein Report

| | | | |
|---|---|---|---|
| **Protein 87:** | **PREDICTED: beta/gamma crystallin domain-containing protein 3 isoform X1 [Homo sapiens]** | | |
| **Accession:** | gi\|530373918 | **Score:** | 57.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 298.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***WUP:QUP*** | **Median:** | 1.04 | **CV:** | 0.00 % | **No. of Peptides:** | 1 | |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKGNLLEGPL | EDSDCSKTSF | NKENSLTNNP | ELQNIASSNN | LLNKNAWGSI | ERNRSSPSSV | TNSSYDGESD | SQHHLSCEPV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SQTNRNLVCS | ALLTGSNHRK | VPCSPDFQRV | TTTENTIKEN | STVMSNRTLV | QREELVEPQG | PAISDFSCSK | SDGSDTTEQE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| STNLPSPNKS | IRHEHLQLPE | SECSDKQTID | SSSKQAATHT | NIIALQRHAV | TDTEFVNEGK | RLSAQDSQKN | VAVREIRRET |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ESASAGESIA | SSHVKAPEDK | IESLPKDTDQ | YFETKAKKLD | FRSHDKIPHI | RMNKKDLASL | NYISESAVVA | SLGNENAPEL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KFELNRSHIS | ETPLDSESPQ | QAEVSPDAKT | SLSLDCKKLN | FSISPPTFVS | GVGMLSKLDI | PDLMNEGSPV | PIETGNVNIV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GISYQPRKCK | EENVKNHVEA | AGRKSPPPSF | CLEYTSAIFE | FKEVLSNSEK | CQVLPGSEAS | GPHLTGLELL | SFDSGNLSKD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CSSILSQDPN | RVELVSSNTK | ANMSIIEKSD | SLSLEAKTAN | IVSKAEIDGQ | NNVLVESHSG | RGKTISLSKV | SLSKVEPRNI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SQDKMSSFPL | KITHVPEKPI | LSELTFLEVE | QGKRFQSINH | NEIGEKCSDA | GLKENCQAEL | SPAASKYEDK | PEPEVDALGS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PPALLKSNIS | WILPPIHDEK | ISRQMAQNCE | AHTCVFHQSL | DICGTKKISG | HSEMAELSLT | NISPKFQETG | SMKVNSPFLD |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SDSSLEKNSS | ASEDSSFLKV | PSVLKLEKKS | SSYRKKENIH | FLNGGIDSVS | SSSSYPEEVS | MIVNSHKPQN | NLDSIQVTKD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LTHEGTSVTN | LLYPTTSYLE | FETSVSIGTE | VTPFQEHFGI | YTGKISIDFP | TAAQFDNLVE | AETGAVAGPA | ASVNSSGQQC |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SEASAEHIEA | RRRAHDQLLD | LKSSLLKKAD | TLIGEIFNSV | REELKFKHTV | STCQEHIAIE | GIMNLGTLKE | DISEKNPSEV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TLTEIQQTEG | LEEQGMENMS | EVKEKPCVSP | TVGEKNLLVD | PNSMNVSCLL | EDKARELVNE | IIYVAQEKLR | NDTFEDTEDT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| WDSELQANTS | KILNSDSVKP | HDVVREFLVS | EQPVNQSTQI | SENKVLNEFF | SLSNLASGTE | SIKGGEIVLY | QKSLFSGNGS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GLSDSINLQE | SDTVLLAEDM | SHKRLDDRVK | THLFRSEDCN | ETMEIENVDN | NKTETEDRRT | LVLNFKWPPL | VNDDIHAPGT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SKSSLSDSLV | CISEKNLPGH | SKNTPLAMSD | VGKVHKKDNE | INIGKIELIP | SMLETGKTNK | KDAELNILKY | EAVPPMIEMG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| RIHKMDAELN | VTKTEPKANV | FKMGEVYQMD | AESCIEKTEG | SAVILGMEKA | YKMKDTEGDI | GKIEVIPMMP | EVKNIHQKDA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| EGDIVKTEMT | PVTVDMENIY | QTHAEGDIGK | TGTIALSEVE | NIHQKGGEGI | SEKAEVIPVT | LAMENTYQKD | AEGDIGKAEV |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| MPVRLEMENT | YPKDTERDGG | KTEVMPLALE | VVNTYQKNAK | GFTGNTEGSV | LKMEATYRKT | AEEVIKNTEI | VPCVLKVKEA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| HETAPAPLEM | EKACKRDVKE | TIGATVSTPS | VIEMEKISPE | DRGENIGKHK | VLPAVVDIEK | IHGTGLELTT | KQGEAMLPAF |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| ESKTPQEYAE | GSVEETKEEP | TEIKEGLIAH | ENRLPTYFRG | YESPTLSKDY | EGYPAPAMPD | FQPGDTTVRL | DKRMSLTAIY |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| DKRRETDYSD | KGYNLAFVSQ | DEQENSSFTI | LYEEPLQEED | KYASAEARQT | QSVLFHDTSA | DSMPVLACER | SESRTDLVHH |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| FEKGTKLGET | FDSDSSEMFL | SVEAKRYKIY | PLALSPIYED | DSSQEDILSS | EVSPGHHGPR | KSRDSENQSS | SVLSLLQSVS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| ERLKMNFDED | DREAADEEEE | EEEAAVLHKG | DLRAGSGERV | TFQLPDPSIT | FYPDDQESVG | ISKNSYVMPN | EPTTSNLQVG |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LWPEKTSFLQ | KSDLTSKLHS | SLKSAYHQYL | QTSQSHSSEK | GARFGGIFQE | PVSKYFRVQD | SPGRLSPFIE | NVDKQTLRCN |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| PRPGKMVIYD | LHESTYKQEV | YCNIPDATSW | SFPNGVLIKV | VRGCWILYEK | PHFRGQKCVL | EEGEKVLNRD | WILQNRRHPQ |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| RNFILGSLKR | VLKDCSIPEI | ELFPQSDPAC | CPVYIQRAVP | NLEELNISKS | VSFTVKSGVW | LAYPDINFKG | QATVLEEDHG |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1963 | 1 | 918.3504 | -135.25 | 2 | 54.9 | 12.1 | 1 | 501-517 | K.ANMSIIEKSDSLSLEAK.T | | WUP:QUP 1.04 |
| 137 | 1 | 793.8712 | -30.92 | 2 | 31.4 | 10.2 | 1 | 1430-1444 | K.DAEGDIGKAEVMPVR.L | | |
| 1726 | 1 | 900.4572 | 47.30 | 3 | 49.9 | 14.8 | 1 | 1649-1672 | K.DYEGYPAPAMPDFQPGDTTVRLDR | Oxidation: 10 | |

# Detailed Protein Report

**Protein 88:** **PREDICTED: protein KIAA1199 isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578827243 | **Score:** | 56.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 90.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 5.8 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MYSHGNLEIP | WSLPVLITPC | TRQKSSRCFP | ADPAPPTRSK | WQIKDVVGYN | SLGHCFFTED | GPEERNTFDH | CLGLLVKSGT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LLPSDRDSKM | CKMITEDSYP | GYIPKPRQDC | NAVSTFWMAN | PNNNLINCAA | AGSEETGFWF | IFHHVPTGPS | VGMYSPGYSE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HIPLGKFYNN | RAHSNYRAGM | IIDNGVKTTE | ASAKDKRPFL | SIISARYSPH | QDADPLKPRE | PAIIRHFIAY | KNQDHGAWLR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GGDVWLDSCR | FADNGIGLTL | ASGGTFPYDD | GSKQEIKNSL | FVGESGNVGT | EMMDNRIWGP | GGLDHSGRTL | PIGQNFPIRG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IQLYDGPINI | QNCTFRKFVA | LEGRHTSALA | FRLNNAWQSC | PHNNVTGIAF | EDVPITSRVF | FGEPGPWFNQ | LDMDGDKTSV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FHDVDGSVSE | YPGSYLTKND | NWLVRHPDCI | NVPDWRGAIC | SGCYAQMYIQ | AYKTSNLRMK | IIKNDFPSHP | LYLEGALTRS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| THYQQYQPVV | TLQKGYTIHW | DQTAPAELAI | WLINFNKGDW | IRVGLCYPRG | TTFSILSDVH | NRLLKQTSKT | GVFVRTLQMD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KVEQSYPGRS | HYYWDEDSGL | LFLKLKAQNE | REKFAFCSMK | GCERIKIKAL | IPKNAGVSDC | TATAYPKFTE | RAVVDVPMPK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KLFGSQLKTK | DHFLEVKMES | SKQHFFHLWN | DFAYIEVDGK | KYPSSEDGIQ | VVVIDGNQGR | VVSHTSFRNS | ILQGIPWQLF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NYVATIPDNS | IVLMASKGRY | VSRGPWTRVL | EKLGADRGLK | LKEQMAFVGF | KGSFRPIWVT | LDTEDHKAKI | FQVVPIPVVK |
| 810 | | | | | | | |
| KKKL | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1123 | 3 | 473.1123 | -298.74 | 2 | 44.2 | 17.0 | 0 | 78-86 | K.SGTLLPSDR.D | |
| 737 | 1 | 936.9549 | 11.85 | 2 | 39.2 | 10.8 | 0 | 570-584 | R.SHYYWDEDSGLLFLK.L | |
| 143 | 1 | 796.0835 | 178.80 | 2 | 30.7 | 10.0 | 2 | 740-752 | R.YVSRGPWTRVLEK.L | |

# Detailed Protein Report

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**Protein 89:** **PREDICTED: rapamycin-insensitive companion of mTOR isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530378756 | **Score:** | 56.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 159.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.42 | **CV:** | 4.84 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 0.71 | **CV:** | 68.39 % | **No. of Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGIIATFRSW | AGIINLCKPG | NSGIQSLIGV | LCIPNMEIRR | GLLEVLYDIF | RLPLPVVTEE | FIEALLSVDP | GRFQDSWRLS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DGFVAAEAKT | ILPHRARSRP | DLMDNYLALI | LSAFIRNGLL | EGLVEVITNS | DDHISVRATI | LLGELLHMAN | TILPHSHSHH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LHCLPTLMNM | AASFDIPKEK | RLRASAALNC | LKRFHEMKKR | GPKPYSLHLD | HIIQKAIATH | QKRDQYLRVQ | KDIFILKDTE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EALLINLRDS | QVLQHKENLE | WNWNLIGTIL | KWPNVNLRNY | KDEQLHRFVR | RLLYFYKPSS | KLYANLDLDF | AKAKQLTVVG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CQFTEFLLES | EEDGQGYLED | LVKDIVQWLN | ASSGMKPERS | LQNNGLLTTL | SQHYFLFIGT | LSCHPHGVKM | LEKCSVFQCL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LNLCSLKNQD | HLLKLTVSSL | DYSRDGLARV | ILSKILTAAT | DACRLYATKH | LRVLLRANVE | FFNNWGIELL | VTQLHDKNKT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ISSEALDILD | EACEDKANLH | ALIQMKPALS | HLGDKGLLLL | LRFLSIPKGF | SYLNERGYVA | KQLEKWHREY | NSKYVDLIEE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QLNEALTTYR | KPVDGDNYVR | RSNQRLQRPH | VYLPIHLYGQ | LVHHKTGCHL | LEVQNIITEL | CRNVRTPDLD | KWEEIKKLKA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SLWALGNIGS | SNWGLNLLQE | ENVIPDILKL | AKQCEVLSIR | GTCVYVLGLI | AKTKQGCDIL | KCHNWDAVRH | SRKHLWPVVP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DDVEQLCNEL | SSIPSTLSLN | SESTSSRHNS | ESESVPSSMF | ILEDDRFGSS | STSTFFLDIN | EDTEPTFYDR | SGPIKDKNSF |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PFFASSKLVK | NRILNSLTLP | NKKHRSSSDP | KGGKLSSESK | TSNRRIRTLT | EPSVDFNHSD | DFTPISTVQK | TLQLETSFMG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| NKHIEDTGST | PSIGENDLKF | TKNFGTENHR | ENTSRERLVV | ESSTSSHMKI | RSQSFNTDTT | TSGISSMSSS | PSRETVGVDA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TTMDTDCGSM | STVVSTKTIK | TSHYLTPQSN | HLSLSKSNSV | SLVPPGSSHT | LPRRAQSLKA | PSIATIKSLA | DCNFSYTSSR |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| DAFGYATLKR | LQQQRMHPSL | SHSEALASPA | KDVLFTDTIT | MKANSFESRL | TPSRFMKALS | YASLDKEDLL | SPINQNTLQR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SSSVRSMVSS | ATYGGSDDYI | GLALPVDIND | IFQVKDIPYF | QTKNIPPHDD | RGARAFAHDA | GGLPSGTGGL | VKNSFHLLRQ |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| QMSLTEIMNS | IHSDASLFLE | STEDTGLQEH | TDDNCLYCVC | IEILGFQPSN | QLSAICSHSD | FQDIPYSDWC | EQTIHNPLEV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VPSKFSGISG | CSDGVSQEGS | ASSTKSTELL | LGVKTIPDDT | PMCRILLRKE | VLRLVINLSS | SVSTKCHETG | LLTIKEKYPQ |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | |
| TFDDICLYSE | VSHLLSHCTF | RLPCRRFIQE | LFQDVQFLQM | HEEAEAVLAT | PPKQPIVDTS | AES | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2751 | 1 | 805.9143 | -22.12 | 2 | 65.5 | 23.4 | 1 | 435-449 | K.ILTAATDACRLYATK.H | | WUP:QUP<br>QU:MU | 1.32<br>2.54 |
| 275 | 1 | 795.2750 | -158.71 | 2 | 33.1 | 12.4 | 1 | 916-929 | R.ERLVVESSTSSHMK.I | | WUP:QUP<br>QU:MU | 0.38<br>2.31 |

# Detailed Protein Report

## Protein 90: dynein heavy chain 11, axonemal [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|459642365 | **Score:** | 56.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 520.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAQVAAREA | RDFREAPTLR | LTSGAGLEAV | GAVELEEEEE | NEEEAAARRA | RSFAQDARVR | FLGGRLAMML | GFTEEKWSQY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LESEDNRQVL | GEFLESTSPA | CLVFSFAASG | RLAASQEIPR | DANHKLVFIS | KKITESIGVN | DFSQVVLFGE | LPALSLGHVS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AFLDEILVPV | LSNKNNHKSW | SCFTSQDMEY | HIEVMKKKMY | IFRGKMSRRT | LLPIPTVAGK | MDLDQNCSEN | KPPSNERIIL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HAIESVVIEW | SHQIQEIIER | DSVQRLLNGL | HLSPQAELDF | WMMRRENLSC | IYDQLQAPVV | LKMVKILTTK | QSSYFPTLKD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IFLAVENALL | EAQDVELYLR | PLRRHIQCLQ | ETEFPQTRIL | IAPLFHTICL | IWSHSKFYNT | PARVIVLLQE | FCNLFINQAT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AYLSPEDLLR | GEIEESLEKV | QVAVNILKTF | KNSFFNYRKK | LASYFMGRKL | RPWDFQSHLV | FCRFDKFLDR | LIKIEDIFAT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TLEFEKLERL | EFGGTKGAIL | NGQVHEMSEE | LMELCKLFKQ | STYDPSDCTN | MEFESDYVAF | KSKTLEFDRR | LGTIICEAFF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NCNGLEAAFK | LLTIFGNFLE | KPVVMEIFSL | HYSTLVHMFN | TELDVCKQLY | NEHMKQIECG | HVVLNKNMPF | TSGNMKWAQQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VLQRLQMFWS | NFASLRYLFL | GNPDHALVYQ | KYVEMTTLLD | QFESRIYNEW | KSNVDEICEF | NLNQPLVKFS | AINGLLCVNF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DPKLVAVLRE | VKYLLMLKKQ | DIPDSALAIF | KKRNTILKYI | GNLDLLVQGY | NKLKQTLLEV | EYPLIEDELR | AIDEQLTAAT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TWLTWQDDCW | GYIERVRAAT | SELEHRVERT | QKNVKVIQQT | MRGWARCVLP | PRREHRREAA | FTLEDKGDLF | TKKYKLIQGD |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GCKIHNLVEE | NRKLFKANPS | LDTWKIYVEF | IDDIVVEGFF | QAIMHDLDFF | LKNTEKQLKP | APFFQAQMIL | LPPEIVFKPS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LDREAGDGFY | DLVEEMLCNS | FRMSAQMNRI | ATHLEIKNYQ | NDMDNMLGLA | EVRQEIMNRV | VNVINKVLDF | RNTLETHTYL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| WVDDRAEFMK | HFLLYGHAVS | SDEMDAHANE | EIPEQPPTLE | QFKEQIDIYE | ALYVQMSKFE | DFRVFDSWFK | VDMKPFKVSL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LTIIKKWSWM | FQEHLLRFVI | DSLNELQEFI | KETDSGLQRE | LNEGDHDGLV | DIMVHLLAVR | SRQRATDELF | EPLKETITLL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ESYGQKMPEQ | VYIQLEELPE | RWETTKKIAA | TVRHEVSPLH | NAEVTLIRKK | CILFDAKQAE | FRERFRHYAP | LGFNAENPYT |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| ALDKANEELE | ALEEEMLQMQ | ESTRLFEVAL | PEYKQMKQCR | KEIKLLKGLW | DVIIYVRRSI | DNWTKTQWRQ | IHVEQMDVEL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| RRFAKEIWSL | NKEVRVWDAY | TGLEGTVKDM | TASLRAITEL | QSPALRDRHW | HQLMKAIGVK | FLINEATTLA | DLLALRLHRV |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EDDVRRIVDK | AVKELGTEKV | ITEISQTWAT | MKFSYEVHYR | TGIPLLKSDE | QLFETLEHNQ | VQLQTLLQSK | YVEYFIEQVL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| SWQNKLNIAD | LVIFTWMEVQ | RTWSHLESIF | VCSEDIRIQL | VKDARRFDGV | DAEFKELMFK | TAKVENVLEA | TCRPNLYEKL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KDLQSRLSLC | EKALAEYLET | KRIAFPRFYF | VSSADLLDIL | SKGAQPKQVT | CHLAKLFDSI | ADLQFEDNQD | VSAHRAVGMY |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| SKEKEYVPFQ | AECECVGHVE | TWLLQLEQTM | QETVRHSITE | AIVAYEEKPR | ELWIFDFPAQ | VALTSSQIWW | TTDVGIAFSR |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| LEEGYETALK | DFHKKQISQL | NTLITLLLGE | LPPGDRQKIM | TICTIDVHAR | DVVAKLISQK | VVSPQAFTWL | SQLRHRWEDT |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| QKHCFVNICD | AQFQYFYEYL | GNSPRLVITP | LTDRCYITLT | QSLHLTMSGA | PAGPAGTGKT | ETTKDLGRAL | GMMVYVFNCS |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| EQMDYKSIGN | IYKGLVQTGA | WGCFDEFNRI | SVEVLSVVAV | QVKMIHDAIR | NRKKRFVFLG | EAITLKPSVG | IFITMNPGYA |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| GRTELPENLK | ALFRPCAMVA | PDIELICEIL | LVAEGFVDAR | ALARKFITLY | TLCKELLSKQ | DHYDWGLRAI | KSVLVVAGSL |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| KRGDKNRPED | QVLMRALRDF | NMPKIVTDDI | PVFLGLVGDL | FPALDVPRRR | KLHFEQMVRQ | STLELRLQPE | ESFILKVVQL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2496 | 1 | 822.4302 | -68.99 | 2 | 61.8 | 12.6 | 1 | 2977-2990 | R.LQLKIILCFSPVGR.T | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 91: rap guanine nucleotide exchange factor 3 isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|148747859 | **Score:** | 55.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 103.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.98 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.01 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKVGWPGESC | WQVGLAVEDS | PALGAPRVGA | LPDVVPEGTL | LNMVLRRMHR | PRSCSYQLLL | EHQRPSCIQG | LRWTPLTNSE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ESLDFSESLE | QASTERVLRA | GRQLHRHLLA | TCPNLIRDRK | YHLRLYRQCC | SGRELVDGIL | ALGLGVHSRS | QVVGICQVLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DEGALCHVKH | DWAFQDRDAQ | FYRFPGPEPE | PVGTHEMEEE | LAEAVALLSQ | RGPDALLTVA | LRKPPGQRTD | EELDLIFEEL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LHIKAVAHLS | NSVKRELAAV | LLFEPHSKAG | TVLFSQGDKG | TSWYIIWKGS | VNVVTHGKGL | VTTLHEGDDF | GQLALVNDAP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RAATIILRED | NCHFLRVDKQ | DFNRIIKDVE | AKTMRLEEHG | KVVLVLERAS | QGAGPSRPPT | PGRNRYTVMS | GTPEKILELL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LEAMGPDSSA | HDPTETFLSD | FLLTHRVFMP | SAQLCAALLH | HFHVEPAGGS | EQERSTYVCN | KRQQILRLVS | QWVALYGSML |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HTDPVATSFL | QKLSDLVGRD | TRLSNLLREQ | WPERRRCHRL | ENGCGNASPQ | MKARNLPVWL | PNQDEPLPGS | SCAIQVGDKV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PYDICRPDHS | VLTLQLPVTA | SVREVMAALA | QEDGWTKGQV | LVKVNSAGDA | IGLQPDARGV | ATSLGLNERL | FVVNPQEVHE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LIPHPDQLGP | TVGSAEGLDL | VSAKDLAGQL | TDHDWSLFNS | IHQVELIHYV | LGPQHLRDVT | TANLERFMRR | FNELQYWVAT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ELCLCPVPGP | RAQLLRKFIK | LAAHLKEQKN | LNSFFAVMFG | LSNSAISRLA | HTWERLPHKV | RKLYSALERL | LDPSWNHRVY |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RLALAKLSPP | VIPFMPLLLK | DMTFIHEGNH | TLVENLINFE | KMRMMARAAR | MLHHCRSHNP | VPLSPLRSRV | SHLHEDSQVA |
| 890 | 900 | 910 | 920 | 930 | | | |
| RISTCSEQSL | STRSPASTWA | YVQQLKVIDN | QRELSRLSRE | LEP | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1402 | 1 | 727.3976 | -11.71 | 2 | 45.9 | 15.2 | 0 | 256-268 | R.ELAAVLLFEPHSK.A | | QU:MU 1.98<br>WUP:QUP 1.01 |
| 1805 | 1 | 937.7928 | -121.06 | 2 | 52.4 | 13.0 | 1 | 517-532 | R.CHRLENGCGNASPQMK.A | Carbamidomethyl: 1, 8;<br>Oxidation: 15 | |

# Detailed Protein Report

## Protein 92: fanconi-associated nuclease 1 isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|226246523 | **Score:** | 55.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 114.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.7 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.83 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.53 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578840975 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: fanconi-associated nuclease 1 isoform X4 [Homo sapiens] |
| gi\|578840973 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: fanconi-associated nuclease 1 isoform X3 [Homo sapiens] |
| gi\|578840971 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: fanconi-associated nuclease 1 isoform X2 [Homo sapiens] |
| gi\|578840969 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: fanconi-associated nuclease 1 isoform X1 [Homo sapiens] |
| gi\|530405539 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: fanconi-associated nuclease 1 isoform X4 [Homo sapiens] |
| gi\|530405537 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: fanconi-associated nuclease 1 isoform X3 [Homo sapiens] |
| gi\|530405535 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: fanconi-associated nuclease 1 isoform X2 [Homo sapiens] |
| gi\|530405533 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: fanconi-associated nuclease 1 isoform X1 [Homo sapiens] |

# Detailed Protein Report

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MMSEGKPPDK | KRPRRSLSIS | KNKKKASNSI | ISCFNNAPPA | KLACPVCSKM | VPRYDLNRHL | DEMCANNDFV | QVDPGQVGLI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NSNVSMVDLT | SVTLEDVTPK | KSPPPKTNLT | PGQSDSAKRE | VKQKISPYFK | SNDVVCKNQD | ELRNRSVKVI | CLGSLASKLS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RKYVKAKKSI | DKDEEFAGSS | PQSSKSTVVK | SLIDNSSEIE | DEDQILENSS | QKENVFKCDS | LKEECIPEHM | VRGSKIMEAE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SQKATRECEK | SALTPGFSDN | AIMLFSPDFT | LRNTLKSTSE | DSLVKQECIK | EVVEKREACH | CEEVKMTVAS | EAKIQLSDSE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AKSHSSADDA | SAWSNIQEAP | LQDDSCLNND | IPHSIPLEQG | SSCNGPGQTT | GHPYYLRSFL | VVLKTVLENE | DDMLLFDEQE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KGIVTKFYQL | SATGQKLYVR | LFQRKLSWIK | MTKLEYEEIA | LDLTPVIEEL | TNAGFLQTES | ELQELSEVLE | LLSAPELKSL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AKTFHLVNPN | GQKQQLVDAF | LKLAKQRSVC | TWGKNKPGIG | AVILKRAKAL | AGQSVRICKG | PRAVFSRILL | LFSLTDSMED |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EDAACGGQGQ | LSTVLLVNLG | RMEFPSYTIN | RKTHIFQDRD | DLIRYAAATH | MLSDISSAMA | NGNWEEAKEL | AQCAKRDWNR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LKNHPSLRCH | EDLPLFLRCF | TVGWIYTRIL | SRFVEILQRL | HMYEEAVREL | ESLLSQRIYC | PDSRGRWWDR | LALNLHQHLK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RLEPTIKCIT | EGLADPEVRT | GHRLSLYQRA | VRLRESPSCK | KFKHLFQQLP | EMAVQDVKHV | TITGRLCPQR | GMCKSVFVME |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AGEAADPTTV | LCSVEELALA | HYRRSGFDQG | IHGEGSTFST | LYGLLLWDII | FMDGIPDVFR | NACQAFPLDL | CTDSFFTSRR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PALEARLQLI | HDAPEESLRA | WVAATWHEQE | GRVASLVSWD | RFTSLQQAQD | LVSCLGGPVL | SGVCRHLAAD | FRHCRGGLPD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | | |
| LVVWNSQSRH | FKLVEVKGPN | DRLSHKQMIW | LAELQKLGAE | VEVCHVVAVG | AKSQSLS | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 691 | 1 | 765.8997 | 57.54 | 2 | 38.6 | 18.5 | 1 | 223-235 | K.EECIPEHMVRGSK.I | Oxidation: 8 | |
| 60 | 5 | 768.2851 | -144.27 | 2 | 30.4 | 19.5 | 2 | 233-246 | R.GSKIMEAESQKATR.E | | QU:MU 0.83<br>WUP:QUP 1.53 |
| 97 | 2 | 826.6883 | -79.67 | 3 | 31.1 | 17.4 | 0 | 922-945 | R.FTSLQQAQDLVSCLGGPVLSGVCH | | |

# Detailed Protein Report

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**Protein 93:** **replication factor C subunit 1 isoform 1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|32528306 | **Score:** | 55.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 128.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 7.5 |
| | | **No. of unique Peptides:** | 5 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDIRKFFGVI | PSGKKLVSET | VKKNEKTKSD | EETLKAKKGI | KEIKVNSSRK | EDDFKQKQPS | KKKRIIYDSD | SESEETLQVK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NAKKPPEKLP | VSSKPGKISR | QDPVTYISET | DEEDDFMCKK | AASKSKENGR | STNSHLGTSN | MKKNEENTKT | KNKPLSPIKL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TPTSVLDYFG | TGSVQRSNKK | MVASKRKELS | QNTDESGLND | EAIAKQLQLD | EDAELERQLH | EDEEFARTLA | MLDEEPKTKK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ARKDTEAGET | FSSVQANLSK | AEKHKYPHKV | KTAQVSDERK | SYSPRKQSKY | ESSKESQQHS | KSSADKIGEV | SSPKASSKLA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IMKRKEESSY | KEIEPVASKR | KENAIKLKGE | TKTPKKTKSS | PAKKESVSPE | DSEKKRTNYQ | AYRSYLNREG | PKALGSKEIP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KGAENCLEGL | IFVITGVLES | IERDEAKSLI | ERYGGKVTGN | VSKKTNYLVM | GRDSGQSKSD | KAAALGTKII | DEDGLLNLIR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TMPGKKSKYE | IAVETEMKKE | SKLERTPQKN | VQGKRKISPS | KKESESKKSR | PTSKRDSLAK | TIKKETDVFW | KSLDFKEQVA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EETSGDSKAR | NLADDSSENK | VENLLWVDKY | KPTSLKTIIG | QQGDQSCANK | LLRWLRNWQK | SSSEDKKHAK | FGKFSGKDDG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SSFKAALLSG | PPGVGKTTTA | SLVCQELGYS | YVELNASDTR | SKSSLKAIVA | ESLNNTSIKG | FYSNGAASSV | STKHALIMDE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VDGMAGNEDR | GGIQELIGLI | KHTKIPIICM | CNDRNHPKIR | SLVHYCFDLR | FQRPRVEQIK | GAMMSIAFKE | GLKIPPPAMN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EIILGANQDI | RQVLHNLSMW | CARSKALTYD | QAKADSHRAK | KDIKMGPFDV | ARKVFAAGEE | TAHMSLVDKS | DLFFHDYSIA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PLFVQENYIH | VKPVAAGGDM | KKHLMLLSRA | ADSICDGDLV | DSQIRSKQNW | SLLPAQAIYA | SVLPGELMRG | YMTQFPTFPS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| WLGKHSSTGK | HDRIVQDLAL | HMSLRTYSSK | RTVNMDYLSL | LRDALVQPLT | SQGVDGVQDV | VALMDTYYLM | KEDFENIMEI |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SSWGGKPSPF | SKLDPKVKAA | FTRAYNKEAH | LTPYSLQAIK | ASRHSTSPSL | DSEYNEELNE | DDSQSDEKDQ | DAIETDAMIK |
| 1130 | 1140 | 1150 | | | | | |
| KKTKSSKPSK | PEKDKEPRKG | KGKSSKK | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 967 | 1 | 530.7788 | -57.17 | 2 | 40.4 | 11.1 | 2 | 42-50 | K.EIKVNSSRK.E | |
| 1884 | 1 | 974.4729 | 4.34 | 2 | 51.9 | 11.6 | 2 | 125-142 | K.SKENGRSTNSHLGTSNMK.K | |
| 1563 | 1 | 949.5033 | -22.26 | 2 | 49.7 | 10.2 | 1 | 469-485 | K.IIDEDGLLNLIRTMPGK.K | |
| 2929 | 1 | 965.1417 | 7.65 | 3 | 65.4 | 10.9 | 1 | 657-682 | K.TTTASLVCQELGYSYVELNASDTRSK.S | Carbamidomethyl: 8 |
| 1265 | 1 | 990.4490 | -59.66 | 2 | 45.4 | 11.3 | 2 | 745-760 | K.IPIICMCNDRNHPKIR.S | Carbamidomethyl: 5 |

# Detailed Protein Report

## Protein 94: protein S100-A11 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5032057 | **Score:** | 54.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 11.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 10.5 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MAKISSPTET ERCIESLIAV FQKYAGKDGY NYTLSKTEFL SFMNTELAAF TKNQKDPGVL DRMMKKLDTN SDGQLDFSEF
        90        100        110
LNLIGGLAMA CHDSFLKAVP SQKRT
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2752 | 3 | 654.3389 | -24.71 | 2 | 65.5 | 54.9 | 0 | 13-23 | R.CIESLIAVFQK.Y | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 95: collagen alpha-1(XXVIII) chain precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|154759255 | **Score:** | 54.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 116.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.6 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***WUP:QUP*** **Median:** 2.39 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWNRYFVFYL | LLLSAFTSQT | VSGQRKKGPK | SNLLARKSDV | QGSICFIDIV | FIVDSSESSK | IALFDKQKDF | VDSLSDKIFQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LTPGRSLEYD | IKLAALQFSS | SVQIDPPFSS | WKDLQTFKQK | VKSMNLIGQG | TFSYYAISNA | TRLLKREGRK | DGVKVVLLMT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DGIDHPKNPD | VQSISEDARI | SGISFITIAL | STVVNEAKLR | LISGDSSSEP | TLLLSDPTLV | DKIQDRLDIL | FEKKCERKIC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ECEKGDPGDP | GPPGTHGNPG | IKGERGPKGN | PGNAQKGEAG | ERGPGGIPGY | KGDKGERGEC | GKPGIKGDKG | SPGPYGPKGP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RGIQGITGPP | GDPGPKGFQG | NKGEPGPPGP | YGSPGAPGIG | QQGIKGERGQ | EGRPGAPGPI | GVGEPGQPGP | RGPEGVPGER |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GLPGEGFPGP | KGEKGSEGPT | GPQGLQGLSI | KGEKGDIGPV | GPQGPMGIPG | IGSQGEQGIQ | GPIGPPGPQG | PAGQGLPGSK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GEVGQMGPTG | PRGPVGIGVQ | GPKGEPGSIG | LPGQPGVPGE | DGAAGKKGEA | GLPGARGPEG | PPGKGQPGPK | GDEGKKGSKG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NQGQRGLPGP | EGPKGEPGIM | GPFGMPGTSI | PGPPGPKGDR | GGPGIPGFKG | EPGLSIRGPK | GVQGPRGPVG | APGLKGDGYP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GVPGPRGLPG | PPGPMGLRGV | GDTGAKGEPG | VRGPPGPSGP | RGVGTQGPKG | DTGQKGLPGP | PGPPGYGSQG | IKGEQGPQGF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PGPKGTMGHG | LPGQKGEHGE | RGDVGKKGDK | GEIGEPGSPG | KQGLQGPKGD | LGLTKEEIIK | LITEICGCGP | KCKETPLELV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FVIDSSESVG | PENFQIIKNF | VKTMADRVAL | DLATARIGII | NYSHKVEKVA | NLKQFSSKDD | FKLAVDNMQY | LGEGTYTATA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LQAANDMFED | ARPGVKKVAL | VITDGQTDSR | DKEKLTEVVK | NASDTNVEIF | VIGVVKKNDP | NFEIFHKEMN | LIATDPEHVY |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QFDDFFTLQD | TLKQKLFQKI | CEDFDSYLVQ | IFGSSSPQPG | FGMSGEELSE | STPEPQKEIS | ESLSVTRDQD | EDDKAPEPTW |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ADDLPATTSS | EATTTPRPLL | STPVDGAEDP | RCLEALKPGN | CGEYVVRWYY | DKQVNSCARF | WFSGCNGSGN | RFNSEKECQE |
| 1130 | | | | | | | |
| TCIQG | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1277 | 1 | 990.9708 | -72.85 | 2 | 45.6 | 13.8 | 2 | 150-167 | R.KDGVKVVLLMTDGIDHPK.N | Oxidation: 10 | WUP:QUP 2.39 |
| 201 | 1 | 714.3696 | -12.54 | 3 | 32.5 | 18.4 | 2 | 667-689 | K.GEPGVRGPPGPSGPRGVGTQGPG | | |

# Detailed Protein Report

## Protein 96: ATP-binding cassette sub-family A member 12 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|27881501 | **Score:** | 54.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 256.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 4 |

## Quantitation

| | | | |
|---|---|---|---|
| ***WUP:QUP*** | **Median:** 1.33 | **CV:** 0.00 % | **No. of Peptides:** 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFTYIKIITS | GDSDNITHVW | NEDDGQTLSP | SSLAAQLLIL | ENFEDALLNI | SANSPYIPYL | ACVRNVTDSL | ARGSPENLRL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LQSTIRFKKS | FLRNGSYEDY | FPPVPEVLKS | KLSQLRNLTE | LLCESETFSL | IEKSCQLSDM | SFGSLCEESE | FDLQLLEAAE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LGTEIAASLL | YHDNVISKKV | RDLLTGDPSK | INLNMDQFLE | QALQMNYLEN | ITQLIPIIEA | MLHVNNSADA | SEKPGQLLEM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FKNVEELKED | LRRTTGMSNR | TIDKLLAIPI | PDNRAEIISQ | VFWLHSCDTN | ITTPKLEDAM | KEFCNLSLSE | RSRQSYLIGL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TLLHYLNIYN | FTYKVFFPRK | DQKPVEKMME | LFIRLKEILN | QMASGTHPLL | DKMRSLKQMH | LPRSVPLTQA | MYRSNRMNTP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QGSFSTISQA | LCSQGITTEY | LTAMLPSSQR | PKGNHTKDFL | TYKLTKEQIA | SKYGIPINST | PFCFSLYKDI | INMPAGPVIW |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AFLKPMLLGR | ILYAPYNPVT | KAIMEKSNVT | LRQLAELREK | SQEWMDKSPL | FMNSFHLLNQ | AIPMLQNTLR | NPFVQVFVKF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SVGLDAVELL | KQIDELDILR | LKLENNIDII | DQLNTLSSLT | VNISSCVLYD | RIQAAKTIDE | MEREAKRLYK | SNELFGSVIF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KLPSNRSWHR | GYDSGNVFLP | PVIKYTIRMS | LKTAQTTRSL | RTKIWAPGPH | NSPSHNQIYG | RAFIYLQDSI | ERAIIELQTG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RNSQEIAVQV | QAIPYPCFMK | DNFLTSVSYS | LPIVLMVAWV | VFIAAFVKKL | VYEKDLRLHE | YMKMMGVNSC | SHFFAWLIES |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VGFLLVTIVI | LIIILKFGNI | LPKTNGFILF | LYFSDYSFSV | IAMSYLISVF | FNNTNIAALI | GSLIYIIAFF | PFIVLVTVEN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ELSYVLKVFM | SLLSPTAFSY | ASQYIARYEE | QGIGLQWENM | YTSPVQDDTT | SFGWLCCLIL | ADSFIYFLIA | WYVRNVFPGT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| YGMAAPWYFP | ILPSYWKERF | GCAEVKPEKS | NGLMFTNIMM | QNTNPSASPE | YMFSSNIEPE | PKDLTVGVAL | HGVTKIYGSK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VAVDNLNLNF | YEGHITSLLG | PNGAGKTTTI | SMLTGLFGAS | AGTIFVYGKD | IKTDLHTVRK | NMGVCMQHDV | LFSYLTTKEH |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LLLYGSIKVP | HWTKKQLHEE | VKRTLKDTGL | YSHRHKRVGT | LSGGMKRKLS | ISIALIGGSR | VVILDEPSTG | VDPCSRRSIW |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DVISKNKTAR | TIILSTHHLD | EAEVLSDRIA | FLEQGGLRCC | GSPFYLKEAF | GDGYHLTLTK | KKSPNLNANA | VCDTMAVTAM |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| IQSHLPEAYL | KEDIGGELVY | VLPPFSTKVS | GAYLSLLRAL | DNGMGDLNIG | CYGISDTTVE | EVFLNLTKES | QKNSAMSLEH |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LTQKKIGNSN | ANGISTPDDL | SVSSSNFTDR | DDKILTRGER | LDGFGLLLKK | IMAILIKRFH | HTRRNWKGLI | AQVILPIVFV |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| TTAMGLGTLR | NSSNSYPEIQ | ISPSLYGTSE | QTAFYANYHP | STEALVSAMW | DFPGIDNMCL | NTSDLQCLNK | DSLEKWNTSG |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| EPITNFGVCS | CSENVQECPK | FNYSPPHRRT | YSSQVIYNLT | GQRVENYLIS | TANEFVQKRY | GGWSFGLPLT | KDLRFDITGV |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| PANRTLAKVW | YDPEGYHSLP | AYLNSLNNFL | LRVNMSKYDA | ARHGIIMYSH | PYPGVQDQEQ | ATISSLIDIL | VALSILMGYS |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| VTTASFVTYV | VREHQTKAKQ | LQHISGIGVT | CYWVTNFIYD | MVFYLVPVAF | SIGIIAIFKL | PAFYSENNLG | AVSLLLLLFG |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| YATFSWMYLL | AGLFHETGMA | FITYVCVNLF | FGINSIVSLS | VVYFLSKEKP | NDPTLELISE | TLKRIFLIFP | QFCFGYGLIE |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| LSQQQSVLDF | LKAYGVEYPN | ETFEMNKLGA | MFVALVSQGT | MFFSLRLLIN | ESLIKKLRLF | FRKFNSSHVR | ETIDEDEDVR |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| AERLRVESGA | AEFDLVQLYC | LTKTYQLIHK | KIIAVNNISI | GIPAGECFGL | LGVNGAGKTT | IFKMLTGDII | PSSGNILIRN |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| KTGSLGHVDS | HSSLVGYCPQ | EDALDDLVTV | EEHLYFYARV | HGIPEKDIKE | TVHKLLRRLH | LMPFKDRATS | MCSYGTKRKL |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| STALALIGKP | SILLLDEPSS | GMDPKSKRHL | WKIISEEVQN | KCSVILTSHS | MEECEALCTR | LAIMVNGKFQ | CIGSLQHIKS |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1898 | 1 | 890.3676 | -104.02 | 2 | 53.6 | 10.7 | 1 | 341-354 | K.DQKPVEKMMELFIR.L | Oxidation: 8 | WUP:QUP 1.33 |
| 1953 | 1 | 590.7822 | 22.74 | 2 | 52.8 | 13.4 | 1 | 519-527 | R.EKSQEWMDK.S | | |
| 2766 | 1 | 702.8107 | -71.83 | 2 | 65.0 | 19.2 | 1 | 612-623 | R.IQAAKTIDEMER.E | | |
| 2087 | 1 | 753.3822 | -28.39 | 2 | 56.5 | 10.9 | 0 | 651-664 | R.GYDSGNVFLPPVIK.Y | | |

# Detailed Protein Report

## Protein 97: PREDICTED: pericentrin isoform X6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530419254 | **Score:** | 54.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 355.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| | | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 2 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFTVSDHPPE | QHGMFTVGDH | PPEQRGMFTV | SDHPPEQHGM | FTVSDHPPEQ | RGMFTISDHQ | PEQRGMFTVS | DHTPEQRGIF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TISDHPAEQR | GMFTKECEQE | CELAITDLES | GREDEAGLHQ | SQAVHGLELE | ALRLSLSNMH | TAQLELTQAN | LQKEKETALT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ELREMLNSRR | AQELALLQSR | QQHELELLRE | QHAREKEEVV | LRCGQEAAEL | KEKLQSEMEK | NAQIVKTLKE | DWESEKDLCL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ENLRKELSAK | HQSEMEDLQN | QFQKELAEQR | AELEKIFQDK | NQAERALRNL | ESHHQAAIEK | LREDLQSEHG | RCLEDLEFKF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KESEKEKQLE | LENLQASYED | LKAQSQEEIR | RLWSQLDSAR | TSRQELSELH | EQLLARTSRV | EDLEQLKQRE | KTQHESELEQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LRIYFEKKLR | DAEKTYQEDL | TLLQQRLQGA | REDALLDSVE | VGLSCVGLEE | KPEKGRKDHV | DELEPERHKE | SLPRFQAELE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ESHRHQLEAL | ESPLCIQHEG | HVSDRCCVET | SALGHEWRLE | PSEGHSQELP | WVHLQGVQDG | DLEADTERAA | RVLGLETEHK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VQLSLLQTEL | KEEIELLKIE | NRNLYGKLQH | ETRLKDDLEK | VKHNLIEDHQ | KELNNAKQKT | ELMKQEFQRK | ETDWKVMKEE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LQREAEEKLT | LMLLELREKA | ESEKQTIINK | FELREAEMRQ | LQDQQAAQIL | DLERSLTEQQ | GRLQQLEQDL | TSDDALHCSQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CGREPPTAQD | GELAALHVKE | DCALQLMLAR | SRFLEERKEI | TEKFSAEQDA | FLQEAQEQHA | RELQLLQERH | QQQLLSVTAE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LEARHQAALG | ELTASLESKQ | GALLAARVAE | LQTKHAADLG | ALETRHLSSL | DSLESCYLSE | FQTIREEHRQ | ALELLRADFE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EQLWKKDSLH | QTILTQELEK | LKRKHEGELQ | SVRDHLRTEV | STELAGTVAH | ELQGVHQGEF | GSEKKTALHE | KEETLRLQSA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QAQPFHQEEK | ESLSLQLQKK | NHQVQQLKDQ | VLSLSHEIEE | CRSELEVLQQ | RRERENREGA | NLLSMLKADV | NLSHSERGAL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QDALRRLLGL | FGETLRAAVT | LRSRIGERVG | LCLDDAGAGL | ALSTAPALEE | TWSDVALPEL | DRTLSECAEM | SSVAEISSHM |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RESFLMSPES | VRECEQPIRR | VFQSLSLAVD | GLMEMALDSS | RQLEEARQIH | SRFEKEFSFK | NEETAQVVRK | HQELLECLKE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ESAAKAELAL | ELHKTQGTLE | GFKVETADLK | EVLAGKEDSE | HRLVLELESL | RRQLQQAAQE | QAALREECTR | LWSRGEATAT |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DAEAREAALR | KEVEDLTKEQ | SETRKQAEKD | RSALLSQMKI | LESELEEQLS | QHRGCAKQAE | AVTALEQQVA | SLDKHLRNQR |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| QFMDEQAAER | EHEREEFQQE | IQRLEGQLRQ | AAKPQPWGPR | DSQQAPLDGE | VELLQQKLRE | KLDEFNELAI | QKESADRQVL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| MQEEEIKRLE | EMNINIRKKV | AQLQEEVEKQ | KNIVKGLEQD | KEVLKKQQMS | SLLLASTLQS | TLDAGRCPEP | PSGSPPEGPE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| IQLEVTQRAL | LRRESEVLDL | KEQLEKMKGD | LESKNEEILH | LNLKLDMQNS | QTAVSLRELE | EENTSLKVIY | TRSSEIEELK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| ATIENLQENQ | KRLQKEKAEE | IEQLHEVIEK | LQHELSLMGP | VVHEVSDSQA | GSLQSELLCS | QAGGPRGQAL | QGELEAALEA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| KEALSRLLAD | QERRHSQALE | ALQQRLQGAE | EAAELQLAEL | ERNVALREAE | VEDMASRIQE | FEAALKAKEA | TIAERNLEID |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| ALNQRKAAHS | AELEAVLLAL | ARIRRALEQQ | PLAAGAAPPE | LQWLRAQCAR | LSRQLQVLHQ | RFLRCQVELD | RRQARRATAH |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| TRVPGAHPQP | RMDGGAKAQV | TGDVEASHDA | ALEPVVPDPQ | GDLQPVLVTL | KDAPLCKQEG | VMSVLTVCQR | QLQSELLLVK |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| NEMRLSLEDG | GKGKEKVLED | CQLPKVDLVA | QVKQLQEKLN | RLLYSMTFQN | VDAADTKSLW | PMASAHLLES | SWSDDSCDGE |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| EPDISPHIDT | CDANTATGGV | TDVIKNQAID | ACDANTTPGG | VTDVIKNWDS | LIPDEMPDSP | IQEKSECQDM | SLSSPTSVLG |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| GSRHQSHTAE | AGPRKSPVGM | LDLSSWSSPE | VLRKDWTLEP | WPSLPVTPHS | GALSLCSADT | SLGDRADTSL | PQTQGPGLLC |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2710 | 4 | 1044.5270 | 3.44 | 2 | 65.0 | 25.0 | 2 | 1173-1189 | R.FEKEFSFKNEETAQVVR.K | |
| 490 | 2 | 472.1760 | -159.67 | 2 | 34.6 | 13.3 | 1 | 3049-3056 | R.TRESPPTR.D | |

# Detailed Protein Report

## Protein 98: glutathione S-transferase P [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4504183 | **Score:** | 53.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 23.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 7.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.64 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPPYTVVYFP | VRGRCAALRM | LLADQGQSWK | EEVVTVETWQ | EGSLKASCLY | GQLPKFQDGD | LTLYQSNTIL | RHLGRTLGLY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GKDQQEAALV | DMVNDGVEDL | RCKYISLIYT | NYEAGKDDYV | KALPGQLKPF | ETLLSQNQGG | KTFIVGDQIS | FADYNLLDLL |
| 170 | 180 | 190 | 200 | 210 | 220 | | |
| LIHEVLAPGC | LDAFPLLSAY | VGRLSARPKL | KAFLASPEYV | NLPINGNGKQ | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1649 | 4 | 942.4739 | -4.87 | 2 | 50.9 | 53.5 | 0 | 56-71 | K.FQDGDLTLYQSNTILR.H | | QU:MU 0.64 |

# Detailed Protein Report

## Protein 99: PREDICTED: complement receptor type 1 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578800553 | **Score:** | 53.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 224.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.52 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 4.24 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MCLGRMGASS | PRSPEPVGPP | APGLPFCCGG | SLLAVVVLLA | LPVAWGQCNA | PEWLPFARPT | NLTDEFEFPI | GTYLNYECRP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GYSGRPFSII | CLKNSVWTGA | KDRCRRKSCR | NPPDPVNGMV | HVIKGIQFGS | QIKYSCTKGY | RLIGSSSATC | IISGDTVIWD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NETPICDRIP | CGLPPTITNG | DFISTNRENF | HYGSVVTYRC | NPGSGGRKVF | ELVGEPSIYC | TSNDDQVGIW | SGPAPQCIIP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NKCTPPNVEN | GILVSDNRSL | FSLNEVVEFR | CQPGFVMKGP | RRVKCQALNK | WEPELPSCSR | VCQPPPDVLH | AERTQRDKDN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FSPGQEVFYS | CEPGYDLRGA | ASMRCTPQGD | WSPAAPTCEV | KSCDDFMGQL | LNGRVLFPVN | LQLGAKVDFV | CDEGFQLKGS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SASYCVLAGM | ESLWNSSVPV | CEQIFCPSPP | VIPNGRHTGK | PLEVFPFGKT | VNYTCDPHPD | RGTSFDLIGE | STIRCTSDPQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GNGVWSSPAP | RCGILGHCQA | PDHFLFAKLK | TQTNASDFPI | GTSLKYECRP | EYYGRPFSIT | CLDNLVWSSP | KDVCKRKSCK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TPPDPVNGMV | HVITDIQVGS | RINYSCTTGH | RLIGHSSAEC | ILSGNAAHWS | TKPPICQRIP | CGLPPTIANG | DFISTNRENF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HYGSVVTYRC | NPGSGGRKVF | ELVGEPSIYC | TSNDDQVGIW | SGPAPQCIIP | NKCTPPNVEN | GILVSDNRSL | FSLNEVVEFR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CQPGFVMKGP | RRVKCQALNK | WEPELPSCSR | VCQPPPDVLH | AERTQRDKDN | FSPGQEVFYS | CEPGYDLRGA | ASMRCTPQGD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| WSPAAPTCEV | KSCDDFMGQL | LNGRVLFPVN | LQLGAKVDFV | CDEGFQLKGS | SASYCVLAGM | ESLWNSSVPV | CEQIFCPSPP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VIPNGRHTGK | PLEVFPFGKT | VNYTCDPHPD | RGTSFDLIGE | STIRCTSDPQ | GNGVWSSPAP | RCGILGHCQA | PDHFLFAKLK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TQTNASDFPI | GTSLKYECRP | EYYGRPFSIT | CLDNLVWSSP | KDVCKRKSCK | TPPDPVNGMV | HVITDIQVGS | RINYSCTTGH |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RLIGHSSAEC | ILSGNAAHWS | TKPPICQRIP | CGLPPTIANG | DFISTNRENF | HYGSVVTYRC | NPGSGGRKVF | ELVGEPSIYC |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TSNDDQVGIW | SGPAPQCIIP | NKCTPPNVEN | GILVSDNRSL | FSLNEVVEFR | CQPGFVMKGP | RRVKCQALNK | WEPELPSCSR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VCQPPPDVLH | AERTQRDKDN | FSPGQEVFYS | CEPGYDLRGA | ASLHCTPQGD | WSPEAPRCAV | KSCDDFLGQL | PHGRVLFPLN |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LQLGAKVSFV | CDEGFRLKGS | SVSHCVLVGM | RSLWNNSVPV | CEHIFCPNPP | AILNGRHTGT | PSGDIPYGKE | ISYTCDPHPD |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| RGMTFNLIGE | STIRCTSDPH | GNGVWSSPAP | RCELSVRAGH | CKTPEQFPFA | SPTIPINDFE | FPVGTSLNYE | CRPGYFGKMF |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SISCLENLVW | SSVEDNCRRK | SCGPPPEPFN | GMVHINTDTQ | FGSTVNYSCN | EGFRLIGSPS | TTCLVSGNNV | TWDKKAPICE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| IISCEPPPTI | SNGDFYSNNR | TSFHNGTVVT | YQCHTGPDGE | QLFELVGERS | IYCTSKDDQV | GVWSSPPPRC | ISTNKCTAPE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| VENAIRVPGN | RSFFTLTEII | RFRCQPGFVM | VGSHTVQCQT | NGRWGPKLPH | CSRVCQPPPE | ILHGEHTLSH | QDNFSPGQEV |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| FYSCEPSYDL | RGAASLHCTP | QGDWSPEAPR | CTVKSCDDFL | GQLPHGRVLL | PLNLQLGAKV | SFVCDEGFRL | KGRSASHCVL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| AGMKALWNSS | VPVCEQIFCP | NPPAILNGRH | TGTPFGDIPY | GKEISYACDT | HPDRGMTFNL | IGESSIRCTS | DPQGNGVWSS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| PAPRCELSVP | AACPHPPKIQ | NGHYIGGHVS | LYLPGMTISY | ICDPGYLLVG | KGFIFCTDQG | IWSQLDHYCK | EVNCSFPLFM |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| NGISKELEMK | KVYHYGDYVT | LKCEDGYTLE | GSPWSQCQAD | DRWDPPLAKC | TSRTHDALIV | GTLSGTIFFI | LLIIFLSWII |
| 2010 | 2020 | 2030 | 2040 | 2050 | | | |
| LKHRKGNNAH | ENPKEVAIHL | HSQGGSSVHP | RTLQTNEENS | RVLP | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 73 | 2 | 826.3528 | -22.94 | 3 | 30.6 | 30.9 | 1 | 339-361 | R.<br>GAASMRCTPQGDWSPAAPTCEV<br>S | Carbamidomethyl: 7, 20 | WUP:QUP<br>QU:MU | 4.24<br>0.52 |

# Detailed Protein Report

## Protein 100: PREDICTED: sterol regulatory element-binding protein 1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530410590 | **Score:** | 53.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 121.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.3 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.57 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.19 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDEPPFSEAA | LEQALGEPCD | LDAALLTDIE | DMLQLINNQD | SDFPGLFDPP | YAGSGAGGTD | PASPDTSSPG | SLSPPPATLS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SSLEAFLSGP | QAAPSPLSPP | QPAPTPLKMY | PSMPAFSPGP | GIKEESVPLS | ILQTPTPQPL | PGALLPQSFP | APAPPQFSST |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PVLGYPSPPG | GFSTGSPPGN | TQQPLPGLPL | ASPPGVPPVS | LHTQVQSVVP | QQLLTVTAAP | TAAPVTTTVT | SQIQQVLLQP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HFIKADSLLL | TAMKTDGATV | KAAGLSPLVS | GTTVQTGPLP | TLVSGGTILA | TVPLVVDAEK | LPINRLAAGS | KAPASAQSRG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EKRTAHNAIE | KRYRSSINDK | IIELKDLVVG | TEAKLNKSAV | LRKAIDYIRF | LQHSNQKLKQ | ENLSLRTAVH | KSKSLKDLVS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ACGSGGNTDV | LMEGVKTEVE | DTLTPPPSDA | GSPFQSSPLS | LGSRGSGSGG | SGSDSEPDSP | VFEDSKAKPE | QRPSLHSRGM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LDRSRLALCT | LVFLCLSCNP | LASLLGARGL | PSPSDTTSVY | HSPGRNVLGT | ESRDGPGWAQ | WLLPPVVWLL | NGLLVLVSLV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LLFVYGEPVT | RPHSGPAVYF | WRHRKQADLD | LARGDFAQAA | QQLWLALRAL | GRPLPTSHLD | LACSLLWNLI | RHLLQRLWVG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RWLAGRAGGL | QQDCALRVDA | SASARDAALV | YHKLHQLHTM | GKHTGGHLTA | TNLALSALNL | AECAGDAVSV | ATLAEIYVAA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ALRVKTSLPR | ALHFLTRFFL | SSARQACLAQ | SGSVPPAMQW | LCHPVGHRFF | VDGDWSVLST | PWESLYSLAG | NPVDPLAQVT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QLFREHLLER | ALNCVTQPNP | SPGSADGDKE | FSDALGYLQL | LNSCSDAAGA | PAYSFSISSS | MATTTGVDPV | AKWWASLTAV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VIHWLRRDEE | AAERLCPLVE | HLPRVLQESE | RPLPRAALHS | FKAARALLGC | AKAESGPASL | TICEKASGYL | QDSLATTPAS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SSIDKAVQLF | LCDLLLVVRT | SLWRQQQPPA | PAPAAQGTSS | RPQASALELR | GFQRDLSSLR | RLAQSFRPAM | RRVFLHEATA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RLMAGASPTR | THQLLDRSLR | RRAGPGGKGG | AVAELEPRPT | RREHAEALLL | ASCYLPPGFL | SAPGQRVGML | AEAARTLEKL |
| 1130 | 1140 | 1150 | | | | | |
| GDRRLLHDCQ | QMLMRLGGGT | TVTSS | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1578 | 1 | 798.3570 | -33.20 | 2 | 49.4 | 11.7 | 0 | 109-123 | K.MYPSMPAFSPGPGIK.E | Oxidation: 5 | |
| 783 | 1 | 676.8811 | 19.88 | 2 | 39.8 | 12.5 | 0 | 1069-1081 | K.GGAVAELEPRPTR.R | | WUP:QUP 1.19<br>QU:MU 1.57 |

# Detailed Protein Report

## Protein 101: PREDICTED: guanine nucleotide exchange factor VAV3 isoform X4 [Homo sapiens]

**Accession:** gi|530361574
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl, Oxidation

**Score:** 52.8
**MW [kDa]:** 72.1
**pI:** 6.9
**Sequence Coverage [%]:** 6.8
**No. of unique Peptides:** 3

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEPWKQCAQW | LIHCKVLPTN | HRVTWDSAQV | FDLAQTLRDG | VLLCQLLNNL | RAHSINLKEI | NLRPQMSQFL | CLKNIRTFLT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ACCETFGMRK | SELFEAFDLF | DVRDFGKVIE | TLSRLSRTPI | ALATGIRPFP | TEESINDEDI | YKGLPDLIDE | TLVEDEEDLY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DCVYGEDEGG | EVYEDLMKAE | EAHQPKCPEN | DIRSCCLAEI | KQTEEKYTET | LESIEKYFMA | PLKRFLTAAE | FDSVFINIPE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LVKLHRNLMQ | EIHDSIVNKN | DQNLYQVFIN | YKERLVIYGQ | YCSGVESAIS | SLDYISKTKE | DVKLKLEECS | KRANNGKFTL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RDLLVVPMQR | VLKYHLLLQE | LVKHTTDPTE | KANLKLALDA | MKDLAQYVNE | VKRDNETLRE | IKQFQLSIEN | LNQPVLLFGR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PQGDGEIRIT | TLDKHTKQER | HIFLFDLAVI | VCKRKGDNYE | MKEIIDLQQY | KIANNPTTDK | ENKKWSYGFY | LIHTQGQNGL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EFYCKTKDLK | KKWLEQFEMA | LSNIRPDYAD | SNFHDFKMHT | FTRVTSCKVC | QMLLRGTFYQ | GYLCFKCGAR | AHKECLGRVD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| NCGRVNSGEQ | GTLKLPEKRT | NGLRRTPKQV | DPDVPCLLHF | FISMAPATRS | IVKSQKKNKK | F | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 154 | 1 | 968.4666 | 19.86 | 2 | 31.6 | 10.4 | 1 | 74-89 | K.NIRTFLTACCETFGMR.K | Carbamidomethyl: 10;<br>Oxidation: 15 |
| 877 | 1 | 705.9834 | 77.48 | 2 | 41.0 | 16.1 | 1 | 322-333 | R.DLLVVPMQRVLK.Y | |
| 103 | 1 | 807.7358 | -182.29 | 2 | 31.0 | 26.3 | 2 | 551-564 | R.AHKECLGRVDNCGR.V | Carbamidomethyl: 12 |

# Detailed Protein Report

## Protein 102: PREDICTED: extracellular sulfatase Sulf-1 isoform X1 [Homo sapiens]

**Accession:** gi|578815628
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 52.7
**MW [kDa]:** 129.6
**pI:** 9.5
**Sequence Coverage [%]:** 5.7
**No. of unique Peptides:** 3

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578815632 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: extracellular sulfatase Sulf-1 isoform X3 [Homo sapiens] |
| gi\|578815630 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: extracellular sulfatase Sulf-1 isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKYSCCALVL | AVLGTELLGS | LCSTVRSPRF | RGRIQQERKN | IRPNIILVLT | DDQDVELGSL | QVMNKTRKIM | EHGGATFINA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FVTTPMCCPS | RSSMLTGKYV | HNHNVYTNNE | NCSSPSWQAM | HEPRTFAVYL | NNTGYRTAFF | GKYLNEYNGS | YIPPGWREWL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GLIKNSRFYN | YTVCRNGIKE | KHGFDYAKDY | FTDLITNESI | NYFKMSKRMY | PHRPVMMVIS | HAAPHGPEDS | APQFSKLYPN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ASQHITPSYN | YAPNMDKHWI | MQYTGPMLPI | HMEFTNILQR | KRLQTLMSVD | DSVERLYNML | VETGELENTY | IIYTADHGYH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IGQFGLVKGK | SMPYDFDIRV | PFFIRGPSVE | PGSIVPQIVL | NIDLAPTILD | IAGLDTPPDV | DGKSVLKLLD | PEKPGNRFRT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NKKAKIWRDT | FLVERGKFLR | KKEESSKNIQ | QSNHLPKYER | VKELCQQARY | QTACEQPGQK | WQCIEDTSGK | LRIHKCKGPS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DLLTVRQSTR | NLYARGFHDK | DKECSCRESG | YRASRSQRKS | QRQFLRNQGT | PKYKPRFVHT | RQTRSLSVEF | EGEIYDINLE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EEEELQVLQP | RNIAKRHDEG | HKGPRDLQAS | SGGNRGRMLA | DSSNAVGPPT | TVRVTHKCFI | LPNDSIHCER | ELYQSARAWK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DHKAYIDKEI | EALQDKIKNL | REVRGHLKRR | KPEECSCSKQ | SYYNKEKGVK | KQEKLKSHLH | PFKEAAQEVD | SKLQLFKENN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RRRKKERKEK | RRQRKGEECS | LPGLTCFTHD | NNHWQTAPFW | NLGSFCACTS | SNNNTYWCLR | TVNETHNFLF | CEFATGFLEY |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FDMNTDPYQL | TNTVHTVERG | ILNQLHVQLM | ELRSCQGYKQ | CNPRPKNLDV | EDSYGMDGKV | NQPRLTADIN | WQGLEELHSV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| NENIYEYRQN | YRLSLVDWTN | YLKDLDRVFA | LLKSHYEQNK | TNKTQTAQSD | GFLVVSAEHA | VSMEMASADS | DEDPRHKVGK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TPHLTLPADL | QTLHLNRPTL | SPESKLEWNN | DIPEVNHLNS | EHWRKTEKWT | GHEETNHLET | DFSGDGMTEL | ELGPSPRLQP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| IRRHPKELPQ | YGGPGKDIFE | DQLYLPVHSD | GISVHQMFTM | ATAEHRSNSS | IAGKMLTKVE | KNHEKEKSQH | LEGSASSSLS |
| 1130 | | | | | | | |
| SD | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2819 | 1 | 701.9509 | -109.35 | 3 | 65.7 | 16.7 | 2 | 329-345 | K.GKSMPYDFDIRVPFFIR.G | Oxidation: 4 |
| 2524 | 1 | 813.8725 | -59.59 | 2 | 61.5 | 11.6 | 1 | 428-440 | K.NIQQSNHLPKYER.V | |
| 2488 | 1 | 673.3201 | -4.49 | 3 | 61.7 | 13.8 | 2 | 577-595 | R.HDEGHKGPRDLQASSGGNR.G | |

# Detailed Protein Report

## Protein 103: transcription initiation factor TFIID subunit 1-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|24429572 | **Score:** | 52.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 207.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 4 |

### Quantitation

| | | | |
|---|---|---|---|
| ***WUP:QUP*** | **Median:** 0.54 | **CV:** 0.00 % | **No. of Peptides:** 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRPGCDLLLR | AAATVTAAIM | SDSDSEEDSS | GGGPFTLAGI | LFGNISGAGQ | LEGESVLDDE | CKKHLAGLGA | LGLGSLITEL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TANEELTGTG | GALVNDEGWI | RSTEDAVDYS | DINEVAEDES | QRHQQTMGSL | QPLYHSDYDE | DDYDADCEDI | DCKLMPPPPP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PPGPMKKDKD | QDAITCVSES | GEDIILPSII | APSFLASEKV | DFSSYSDSES | EMGPQEATQA | ESEDGKLTLP | LAGIMQHDAT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KLLPSVTELF | PEFRPGKVLR | FLHLFGPGKN | VPSVWRSARR | KRKKHRELIQ | EEQIQEVECS | VESEVSQKSL | WNYDYAPPPP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PEQCLADDEI | TMMVPVESKF | SQSTGDVDKV | TDTKPRVAEW | RYGPARLWYD | MLGVSEDGSG | FDYGFKLRKT | QHEPVIKSRM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MEEFRKLEES | NGTDLLADEN | FLMVTQLHWE | DSIIWDGEDI | KHKGTKPQGA | SLAGWLPSIK | TRNVMAYNVQ | QGFAPTLDDD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KPWYSIFPID | NEDLVYGRWE | DNIIWDAQAM | PRLLEPPVLA | LDPNDENLIL | EIPDEKEEAT | SNSPSKESKK | ESSLKKSRIL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LGKTGVIREE | PQQNMSQPEV | KDPWNLSNDE | YYFPKQQGLR | GTFGGNIIQH | SIPAMELWQP | FFPTHMGPIK | IRQFHRPPLK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KYSFGALSQP | GPHSVQPLLK | HIKKKAKMRE | QERQASGGGE | LFFMRTPQDL | TGKDGDLILA | EYSEENGPLM | MQVGMATKIK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NYYKRKPGKD | PGAPDCKYGE | TVYCHTSPFL | GSLHPGQLLQ | ALENNLFRAP | VYLHKMPETD | FLIIRTRQGY | YIRELVDIFV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VGQQCPLFEV | PGPNSRRANM | HIRDFLQVFI | YRLFWKSKDR | PRRIRMEDIK | KAFPSHSESS | IRKRLKLCAD | FKRTGMDSNW |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| WVLKSDFRLP | TEEEIRAKVS | PEQCCAYYSM | IAAKQRLKDA | GYGEKSFFAP | EEENEEDFQM | KIDDEVHAAP | WNTTRAFIAA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| MKGKCLLEVT | GVADPTGCGE | GFSYVKIPNK | PTQQKDDKEP | QAVKKTVTGT | DADLRRLSLK | NAKQLLRKFG | VPEEEIKKLS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RWEVIDVVRT | MSTEQAHSGE | GPMSKFARGS | RFSVAEHQER | YKEECQRIFD | LQNKVLSSTE | VLSTDTDSIS | AEDSDFEEMG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KNIENMLQNK | KTSSQLSREW | EEQERKELRR | MLLVAGSAAS | GNNHRDDVTA | SMTSLKSSAT | GHCLKIYRTF | RDEEGKEYVR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| CETVRKPAVI | DAYVRIRTTK | DEKFIQKFAL | FDEKHREEMR | KERRRIQEQL | RRLKRNQEKE | KLKGPPEKKP | KKMKERPDLK |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LKCGACGAIG | HMRTNKFCPL | YYQTNVPPSK | PVAMTEEQEE | ELEKTVIHND | NEELIKVEGT | KIVFGKQLIE | NVHEVRRKSL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VLKFPKQQLP | PKKKRRVGTT | VHCDYLNIPH | KSIHRRRTDP | MVTLSSILES | IINDMRDLPN | THPFHTPVNA | KVVKDYYKII |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| TRPMDLQTLR | ENVRKCLYPS | REEFREHLEL | IVKNSATYNG | PKHSLTQISQ | SMLDLCDEKL | KEKEDKLARL | EKAINPLLDD |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| DDQVAFSFIL | DNIVTQKMMA | VPDSWPFHHP | VNKKFVPDYY | KMIVNPVDLE | TIRKNISKHK | YQSRESFLDD | VNLILANSVK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| YNGPESQYTK | TAQEIVNICY | QTITEYDEHL | TQLEKDICTA | KEAALEEAEL | ESLDPMTPGP | YTSQPPDMYD | TNTSLSTSRD |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| ASVFQDESNL | SVLDISTATP | EKQMCQGQGR | LGEEDSDVDV | EGYDDEEEDG | KPKPPAPEGG | DGDLADEEEG | TVQQPEASVL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | |
| YEDLLISEGE | DDEEDAGSDE | EGDNPFSAIQ | LSESGSDSDV | GYGGIRPKQP | FMLQHASGEH | KDGHGK | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2709 | 1 | 813.0615 | 149.49 | 2 | 62.3 | 13.8 | 0 | 227-241 | K.LTLPLAGIMQHDATK.L | Oxidation: 9 | |
| 1183 | 1 | 839.3834 | 23.08 | 2 | 44.9 | 11.4 | 0 | 1050-1065 | R.TMSTEQAHSGEGPMSK.F | | |
| 14 | 1 | 847.2854 | -163.39 | 2 | 29.8 | 15.5 | 2 | 1069-1082 | R.GSRFSVAEHQERYK.E | | |
| 2649 | 1 | 835.4339 | 3.24 | 2 | 61.4 | 11.7 | 1 | 1150-1165 | R.RMLLVAGSAASGNNHR.D | Oxidation: 2 | WUP:QUP 0.54 |

# Detailed Protein Report

## Protein 104: origin recognition complex subunit 6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|7657427 | **Score:** | 52.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 28.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 20.6 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

*QU:MU* **Median:** 0.94 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGSELIGRLA | PRLGLAEPDM | LRKAEEYLRL | SRVKCVGLSA | RTTETSSAVM | CLDLAASWMK | CPLDRAYLIK | LSGLNKETYQ |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| SCLKSFECLL | GLNSNIGIRD | LAVQFSCIEA | VNMASKILKS | YESSLPQTQQ | VDLDLSRPLF | TSAALLSACK | ILKLKVDKNK |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| MVATSGVKKA | IFDRLCKQLE | KIGQQVDREP | GDVATPPRKR | KKIVVEAPAK | EMEKVEEMPH | KPQKDEDLTQ | DYEEWKRKIL |
| **250** | **260** | | | | | | |
| ENAASAQKAT | AE | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2162 | 1 | 701.2632 | -88.04 | 3 | 57.4 | 14.6 | 0 | 42-60 | R.TTETSSAVMCLDLAASWMK.C | Carbamidomethyl: 10 | QU:MU 0.94 |
| 55 | 1 | 930.9009 | -129.85 | 2 | 30.4 | 14.2 | 2 | 61-76 | K.CPLDRAYLIKLSGLNK.E | Carbamidomethyl: 1 | |
| 2540 | 1 | 941.9343 | -22.57 | 2 | 61.7 | 12.6 | 0 | 100-116 | R.DLAVQFSCIEAVNMASK.I | Carbamidomethyl: 8 | |

# Detailed Protein Report

## Protein 105: PREDICTED: zinc finger protein 510 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530390743 | **Score:** | 51.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 72.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 8.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAPVQKNLYR | DVMLENYSNL | VSVGYCCFKP | EVIFKLEQGE | EPWFSEEEFS | NQSHPKDYRG | DDLIKQNKKI | KDKHLEQAIC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| INNKTLTTEE | EKVLGKPFTL | HVAAVASTKM | SCKCNSWEVN | LQSISEFIIN | NRNYSTKKIG | CGNVCENSPF | KINFEKTQTG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EKFYEHNKNM | KALNYNENLP | KHPKFQTLEQ | AFECNKIGKA | FNDKANCVKH | NSSHTGETSS | KDDEFRKNCD | KKTLFDHRRT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GTGKKHLHLN | QCGKSFEKST | VEEYNKLNMG | IKHYELNPSG | NNFNRKAHLT | DPQTAVIEEN | PLVSNDRTQT | WVKSSEYHEN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KKSYQTSVHR | VRRRSHSMMK | PYKCNECGKS | FCQKGHLIQH | QRTHTGEKPF | ECSECGKTFS | QKSHLSTHQR | IHTAEKPYKC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NECGKTFVQK | STLRGHQRIH | TGEKPYECSE | CGKTFVQKST | LRDHHRIHTG | EKSFQCNQCG | KTFGQKSNLR | IHQRTHTGEK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TYQCNECEKS | FWRKDHLIQH | QKTHTGEKPF | KCNECGKTFA | RTSTLRVHQR | IHTGEKPFKC | NECGKKFVRK | AILSDHQRIH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| TGEKPFQCNK | CGKTFGQKSN | LRIHQRTHSG | EKSYECNEYG | KLCKKSTLSL | YQKIQGEGNP | Y | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 282 | 1 | 627.0085 | 98.28 | 3 | 33.2 | 10.2 | 2 | 481-494 | K.TYQCNECEKSFWRK.D | Carbamidomethyl: 7 |

# Detailed Protein Report

**Protein 106:** **PREDICTED: protein odd-skipped-related 2 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530388731 | **Score:** | 51.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 43.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 4.54 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGLRAEEGKR | KPPRSVRGEV | SPSQGPLAQE | DEARRLRSCT | PACHPGKRGK | GGHRARRQRS | AWDLTTHPLT | HRSQELRGAA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ATEGFLYVLL | SHWVFVGAPR | PPASDSWKKG | LVPSAPPASR | KMGSKALPAP | IPLHPSLQLT | NYSFLQAVNT | FPATVDHLQG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LYGLSAVQTM | HMNHWTLGYP | NVHEITRSTI | TEMAAAQGLV | DARFPFPALP | FTTHLFHPKQ | GAIAHVLPAL | HKDRPRFDFA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NLAVAATQED | PPKMGDLSKL | SPGLGSPISG | LSKLTPDRKP | SRGRLPSKTK | KEFICKFCGR | HFTKSYNLLI | HERTHTDERP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YTCDICHKAF | RRQDHLRDHR | YIHSKEKPFK | CQECGKGFCQ | SRTLAVHKTL | HMQTSSPTAA | SSAAKCSGET | VICGGTA |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 857 | 2 | 663.6905 | -200.92 | 2 | 40.8 | 13.1 | 1 | 36-47 | R.LRSCTPACHPGK.R | Carbamidomethyl: 8 | WUP:QUP 4.54 |

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# Detailed Protein Report

## Protein 107: protein SOGA1 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|257467639 | **Score:** | 51.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 183.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEAPAAEPPV | RGCGPQPAPA | PAPAPERKKS | HRAPSPARPK | DVAGWSLAKG | RRGPGPGSAV | ACSAAFSSRP | DKKGRAVAPG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ARGAGVRVAG | VRTGVRAKGR | PRSGAGPRPP | PPPPSLTDSS | SEVSDCASEE | ARLLGLELAL | SSDAESAAGG | PAGVRTGQPA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QPAPSAQQPP | RPPASPDEPS | VAASSVGSSR | LPLSASLAFS | DLTEEMLDCG | PSGLVRELEE | LRSENDYLKD | EIEELRAEML |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EMRDVYMEED | VYQLQELRQQ | LDQASKTCRI | LQYRLRKAER | RSLRAAQTGQ | VDGELIRGLE | QDVKVSKDIS | MRLHKELEVV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EKKRARLEEE | NEELRQRLIE | TELAKQVLQT | ELERPREHSL | KKRGTRSLGK | ADKKTLVQED | SADLKCQLHF | AKEESALMCK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KLTKLAKEND | SMKEELLKYR | SLYGDLDSAL | SAEELADAPH | SRETELKVHL | KLVEEEANLL | SRRIVELEVE | NRGLRAEMDD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| MKDHGGGCGG | PEARLAFSAL | GGGECGESLA | ELRRHLQFVE | EEAELLRRSS | AELEDQNKLL | LNELAKFRSE | HELDVALSED |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SCSVLSEPSQ | EELAAAKLQI | GELSGKVKKL | QYENRVLLSN | LQRCDLASCQ | STRPMLETDA | EAGDSAQCVP | APLGETHESH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AVRLCRAREA | EVLPGLREQA | ALVSKAIDVL | VADANGFTAG | LRLCLDNECA | DFRLHEAPDN | SEGPRDTKLI | HAILVRLSVL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QQELNAFTRK | ADAVLGCSVK | EQQESFSSLP | PLGSQGLSKE | ILLAKDLGSD | FQPPDFRDLP | EWEPRIREAF | RTGDLDSKPD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PSRSFRPYRA | EDNDSYASEI | KELQLVLAEA | HDSLRGLQEQ | LSQERQLRKE | EADNFNQKMV | QLKEDQQRAL | LRREFELQSL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SLQRRLEQKF | WSQEKNMLVQ | ESQQFKHNFL | LLFMKLRWFL | KRWRQGKVLP | SEGDDFLEVN | SMKELYLLME | EEEINAQHSD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NKACTGDSWT | QNTPNEYIKT | LADMKVTLKE | LCWLLRDERR | GLTELQQQFA | KAKATWETER | AELKGHTSQM | ELKTGKGAGE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RAGPDWKAAL | QREREEQQHL | LAESYSAVME | LTRQLQISER | NWSQEKLQLV | ERLQGEKQQV | EQQVKELQNR | LSQLQKAADP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| WVLKHSELEK | QDNSWKETRS | EKIHDKEAVS | EVELGGNGLK | RTKSVSSMSE | FESLLDCSPY | LAGGDARGKK | LPNNPAFGFV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SSEPGDPEKD | TKEKPGLSSR | DCNHLGALAC | QDPPGRQMQR | SYTAPDKTGI | RVYYSPPVAR | RLGVPVVHDK | EGKIIIEPGF |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LFTTAKPKES | AEADGLAESS | YGRWLCNFSR | QRLDGGSAGS | PSAAGPGFPA | ALHDFEMSGN | MSDDMKEITN | CVRQAMRSGS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LERKVKSTSS | QTVGLASVGT | QTIRTVSVGL | QTDPPRSSLH | GKAWSPRSSS | LVSVRSKQIS | SSLDKVHSRI | ERPCCSPKYG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SPKLQRRSVS | KLDSSKDRSL | WNLHQGKQNG | SAWARSTTTR | DSPVLRNIND | GLSSLFSVVE | HSGSTESVWK | LGMSETRAKP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| EPPKYGIVQE | FFRNVCGRAP | SPTSSAGEEG | TKKPEPLSPA | SYHQPEGVAR | ILNKKAAKLG | SSEEVRLTML | PQVGKDGVLR |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | |
| DGDGAVVLPN | EDAVCDCSTQ | SLTSCFARSS | RSAIRHSPSK | CRLHPSESSW | GGEERALPPS | E | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 63 | 1 | 1097.5505 | -104.35 | 1 | 30.7 | 13.5 | 2 | 93-102 | R.TGVRAKGRPR.S | |
| 2190 | 1 | 701.1048 | 122.16 | 3 | 57.8 | 13.2 | 2 | 1426-1443 | K.VHSRIERPCCSPKYGSPK.L | Carbamidomethyl: 9 |
| 2282 | 1 | 701.1125 | 133.17 | 3 | 58.4 | 14.5 | 2 | 1426-1443 | K.VHSRIERPCCSPKYGSPK.L | Carbamidomethyl: 10 |

# Detailed Protein Report

## Protein 108: PAS domain-containing protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|157785548 | **Score:** | 51.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 87.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.3 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKMRGEKRRD | KVNPKSSQRK | LNWIPSFPTY | DYFNQVTLQL | LDGFMITLST | DGVIICVAEN | ISSLLGHLPA | EIVGKKLLSL |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| LPDEEKDEVY | QKIILKFPLL | NSETHIEFCC | HLKRGNVEHG | DSSAYENVKF | IVNVRDICNE | FPVVFSGLFS | SHLCADFAAC |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| VPQEDRLYLV | GNVCILRTQL | LQQLYTSKAV | SDEAVLTQDS | DEEPFVGELS | SSQGQRGHTS | MKAVYVEPAA | AAAAAAISDD |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| QIDIAEVEQY | GPQENVHMFV | DSDSTYCSST | VFLDTMPESP | ALSLQDFRGE | PEVNPLYRAD | PVDLEFSVDQ | VDSVDQEGPM |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| DQQDPENPVA | PLDQAGLMDP | VDPEDSVDLG | AAGASAQPLQ | PSSPVAYDII | SQELELMKKL | KEQLEERTWL | LHDAIQNQQN |
| **410** | **420** | **430** | **440** | **450** | **460** | **470** | **480** |
| ALELMMDHLQ | KQPNTLRHVV | IPDLQSSEAV | PKKQQKQHAG | QVKRPLPHPK | DVKCFCGLSL | SNSLKNTGEL | QEPCVAFNQQ |
| **490** | **500** | **510** | **520** | **530** | **540** | **550** | **560** |
| QLVQQEQHLK | EQQRQLREQL | QQLREQRKVQ | KQKKMQEKKK | LQEQKMQEKK | KLQEQRRQKK | KKLQERKKWQ | GQMLQKEPEE |
| **570** | **580** | **590** | **600** | **610** | **620** | **630** | **640** |
| EQQKQQLQEQ | PLKHNVIVGN | ERVQICLQNP | RDVSVPLCNH | PVRFLQAQPI | VPVQRAAEQQ | PSGFYQDENC | GQQEDESQSF |
| **650** | **660** | **670** | **680** | **690** | **700** | **710** | **720** |
| YPEAYQGPPV | NQLPLIDTSN | SEAISSSSIP | QFPITSDSTI | STLETPQDYI | RLWQELSDSL | GPVVQVNTWS | CDEQGTLHGQ |
| **730** | **740** | **750** | **760** | **770** | **780** | | |
| PTYHQVQVSE | VGVEGPPDPQ | AFQGPAAYQP | DQMRSAEQTR | LMPAEQRDSN | KPC | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2772 | 2 | 557.6353 | 40.20 | 3 | 65.8 | 22.5 | 1 | 451-465 | K.DVKCFCGLSLSNSLK.N | Carbamidomethyl: 4 |
| 2612 | 1 | 1045.0458 | -11.45 | 2 | 62.7 | 10.6 | 1 | 574-591 | K.HNVIVGNERVQICLQNPR.D | |

# Detailed Protein Report

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## Protein 109: zinc finger protein 92 isoform 1 [Homo sapiens]

**Accession:** gi|37537684
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl, Oxidation

**Score:** 51.5
**MW [kDa]:** 60.2
**pI:** 10.3
**Sequence Coverage [%]:** 8.9
**No. of unique Peptides:** 3

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVDKTPVMCS | HFAQDVWPEH | SIKDSFQKVI | LRTYGKYGHE | NLQLRKDHKS | VDACKVYKGG | YNGLNQCLTT | TDSKIFQCDK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YVKVFHKFPN | VNRNKIRHTG | KKPFKCKNRG | KSFCMLSQLT | QHKKIHTREY | SYKCEECGKA | FNWSSTLTKH | KIIHTGEKPY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KCEECGKAFN | RSSNLTKHKI | IHTGEKPYKC | EECGKAFNRS | STLTKHKRIH | TEEKPYKCEE | CGKAFNQFSI | LNKHKRIHME |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DKPYKCEECG | KAFRVFSILK | KHKIIHTGEK | PYKCEECGKA | FNQFSNLTKH | KIIHTGEKPY | KCDECGKAFN | QSSTLTKHKR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IHTGEKPYKC | EECGKAFKQS | STLTEHKIIH | TGEKPYKCEK | CGKAFSWSSA | FTKHKRNHME | DKPYKCEECG | KAFSVFSTLT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KHKIIHTREK | PYKCEECGKA | FNQSSIFTKH | KIIHTEGKSY | KCEKCGNAFN | QSSNLTARKI | IYTGEKPYKY | EECDKAFNKF |
| 490 | 500 | 510 | 520 | | | | |
| STLITHQIIY | TGEKPCKHEC | GRAFNKSSNY | TKEKLQT | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2753 | 1 | 920.1206 | 24.93 | 3 | 65.6 | 10.2 | 1 | 1-23 | -.MVDKTPVMCSHFAQDVWPEHSIK.D | Carbamidomethyl: 9;<br>Oxidation: 8 |
| 1095 | 1 | 540.7909 | -75.68 | 2 | 41.9 | 25.1 | 1 | 252-260 | K.AFRVFSILK.K | |
| 2728 | 6 | 741.8636 | 30.01 | 2 | 64.4 | 16.2 | 0 | 445-458 | K.CGNAFNQSSNLTAR.K | |

# Detailed Protein Report

## Protein 110: PREDICTED: supervillin isoform X13 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578818553 | **Score:** | 51.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 217.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.4 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | |
|---|---|---|---|
| ***WUP:QUP*** | **Median:** 0.55 | **CV:** 0.00 % | **No. of Peptides:** 1 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MKPNVFGREK SDFNKKNLSF LGFPRQRKVS SFQKEFSLED KEQLANHERG IDAQLLVALP KVAELRQIFE PKKKEFLEMK
        90        100        110        120        130        140        150        160
RKERIARRLE GIENDTQPIL LQSCTGLVTH RLLEEDTPRY MRASDPASPH IGRSNEEEET SDSSLEKQTR SKYCTETSGV
       170        180        190        200        210        220        230        240
HGDSPYGSGT MDTHSLESKA ERIARYKAER RRQLAEKYGL TLDPEADSEY LSRYTKSRKE PDAVEKRGGK SDKQEESSRD
       250        260        270        280        290        300        310        320
ASSLYPGTET MGLRTCAGES KDYALHVGDG SSDPEVLLNI ENQRRGQELS ATRQAHDLSP AAESSSTFSF SGRDSSFTEV
       330        340        350        360        370        380        390        400
PRSPKHAHSS SLQQAASRSP SFGDPQLSPE ARPRCTSHSE TPTVDDEEKV DERAKLSVAA KRLLFREMEK SFDEQNVPKR
       410        420        430        440        450        460        470        480
RSRNTAVEQR LRRLQDRSLT QPITTEEVVI AATEPIPASC SGGTHPVMAR LPSPTVARSA VQPARLQASA HQKALAKDQT
       490        500        510        520        530        540        550        560
NEGKELAEQG EPDSSTLSLA EKLALFNKLS QPVSKAISTR NRIDTRQRRM NARYQTQPVT LGEVEQVQSG KLIPFSPAVN
       570        580        590        600        610        620        630        640
TSVSTVASTV APMYAGDLRT KPPLDHNASA TDYKFSSSIE NSDSPVRSIL KSQAWQPLVE GSENKGMLRE YGETESKRAL
       650        660        670        680        690        700        710        720
TGRDSGMEKY GSFEEAEASY PILNRAREGD SHKESKYAVP RRGSLERANP PITHLGDEPK EFSMAKMNAQ GNLDLRDRLP
       730        740        750        760        770        780        790        800
FEEKVEVENV MKRKFSLRAA EFGEPTSEQT GTAAGKTIAQ TTAPVSWKPQ DSSEQPQEKL CKNPCAMFAA GEIKTPTGEG
       810        820        830        840        850        860        870        880
LLDSPSKTMS IKERLALLKK SGEEDWRNRL SRRQEGGKAP ASSLHTQEAG RSLIKKEEGG VADDSAISNL LWEPVYASTY
       890        900        910        920        930        940        950        960
SPAIPAAHKY LSFVSINQRV TESRESQMTI EERKQLITVR EEAWKTRGRG AANDSTQFTV AGRMVKKGLA SPTAITPVAS
       970        980        990       1000       1010       1020       1030       1040
PICGKTRGTT PVSKPLEDIE ARPDMQLESD LKLDRLETFL RRLNNKVGGM HETVLTVTGK SVKEVMKPDD DETFAKFYRS
      1050       1060       1070       1080       1090       1100       1110       1120
VDYNMPRSPV EMDEDFDVIF DPYAPKLTSS VAEHKRAVRP KRRVQASKNP LKMLAAREDL LQEYTEQRLN VAFMESKRMK
      1130       1140       1150       1160       1170       1180       1190       1200
VEKMSSNSNF SEVTLAGLAS KENFSNVSLR SVNLTEQNSN NSAVPYKRLM LLQIKGRRHV QTRLVEPRAS ALNSGDCFLL
      1210       1220       1230       1240       1250       1260       1270       1280
LSPHCCFLWV GEFANVIEKA KASELATLIQ TKRELGCRAT YIQTIEEGIN THTHAAKDFW KLLGGQTSYQ SAGDPKEDEL
      1290       1300       1310       1320       1330       1340       1350       1360
YEAAIIETNC IYRLMDDKLV PDDDYWGKIP KCSLLQPKEV LVFDFGSEVY VWHGKEVTLA QRKIAFQLAK HLWNGTFDYE
      1370       1380       1390       1400       1410       1420       1430       1440
NCDINPLDPG ECNPLIPRKG QGRPDWAIFG RLTEHNETIL FKEKFLDWTE LKRSNEKNPG ELAQHKEDPR TDVKAYDVTR
      1450       1460       1470       1480       1490       1500       1510       1520
MVSMPQTTAG TILDGVNVGR GYGLVEGHDR RQFEITSVSV DVWHILEFDY SRLPKQSIGQ FHEGDAYVVK WKFMVSTAVG
      1530       1540       1550       1560       1570       1580       1590       1600
SRQKGEHSVR AAGKEKCVYF FWQGRHSTVS EKGTSALMTV ELDEERGAQV QVLQGKEPPC FLQCFQGGMV VHSGRREEEE
      1610       1620       1630       1640       1650       1660       1670       1680
ENVQSEWRLY CVRGEVPVEG NLLEVACHCS SLRSRTSMVV LNVNKALIYL WHGCKAQAHT KEVGRTAANK IKEQCPLEAG
      1690       1700       1710       1720       1730       1740       1750       1760
LHSSSKVTIH ECDEGSEPLG FWDALGRRDR KAYDCMLQDP GSFNFAPRLF ILSSSSGDFA ATEFVYPARA PSVVSSMPFL
      1770       1780       1790       1800       1810       1820       1830       1840
QEDLYSAPQP ALFLVDNHHE VYLWQGWWPI ENKITGSARI RWASDRKSAM ETVLQYCKGK NLKKPAPKSY LIHAGLEPLT
      1850       1860       1870       1880       1890       1900       1910       1920
FTNMFPSWEH REDIAEITEM DTEVSNQITL VEDVLAKLCK TIYPLADLLA RPLPEGVDPL KLEIYLTDED FEFALDMTRD
      1930       1940       1950
EYNALPAWKQ VNLKKAKGLF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 874 | 1 | 903.4160 | -143.87 | 2 | 40.5 | 11.0 | 1 | 50-66 | R.GIDAQLLVALPKVAELR.Q | | |
| 2793 | 1 | 846.4331 | 0.98 | 2 | 66.1 | 19.3 | 1 | 323-338 | R.SPKHAHSSSLQQAASR.S | | WUP:QUP 0.55 |
| 2904 | 1 | 974.3155 | -109.14 | 2 | 65.1 | 10.9 | 0 | 1712- | K.AYDCMLQDPGSFNFAPR.L | Oxidation: 5 | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | 1728 | | | |

# Detailed Protein Report

## Protein 111: testis-specific serine/threonine-protein kinase 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|194294513 | **Score:** | 51.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.3 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 3.74 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.50 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDDATVLRKK | GYIVGINLGK | GSYAKVKSAY | SERLKFNVAV | KIIDRKKTPT | DFVERFLPRE | MDILATVNHG | SIIKTYEIFE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TSDGRIYIIM | ELGVQGDLLE | FIKCQGALHE | DVARKMFRQL | SSAVKYCHDL | DIVHRDLKCE | NLLLDKDFNI | KLSDFGFSKR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CLRDSNGRII | LSKTFCGSAA | YAAPEVLQSI | PYQPKVYDIW | SLGVILYIMV | CGSMPYDDSD | IRKMLRIQKE | HRVDFPRSKN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LTCECKDLIY | RMLQPDVSQR | LHIDEILSHS | WLQPPKPKAT | SSASFKREGE | GKYRAECKLD | TKTGLRPDHR | PDHKLGAKTQ |
| 330 | 340 | 350 | 360 | | | | |
| HRLLVVPENE | NRMEDRLAET | SRAKDHHISG | AEVGKAST | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1388 | 1 | 570.1598 | -180.58 | 2 | 45.7 | 10.7 | 1 | 238-246 | R.SKNLTCECK.D | Carbamidomethyl: 6, 8 | |
| 136 | 2 | 642.2923 | -49.74 | 2 | 30.6 | 19.6 | 2 | 293-302 | K.YRAECKLDTK.T | Carbamidomethyl: 5 | QU:MU 3.74<br>WUP:QUP 0.50 |

# Detailed Protein Report

## Protein 112: PREDICTED: ankyrin repeat domain-containing protein 12 isoform X6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578832112 | **Score:** | 51.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 202.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.4 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.51 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 4.73 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVNVPELLLG | QSPSRNDTKI | INSEEAQSVN | PSSVDENIDS | ETEKDSLICE | SKQILPSKTP | LPSALDEYEF | KDDDDEEINK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MIDDRHILRK | EQRKENEPEA | EKTHLFAKQE | KAFYPKSFKS | KKQKPSRVLY | SSTESSDEEA | LQNKKISTSC | SVIPETSNSD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MQTKKEYVVS | GEHKQKGKVK | RKLKNQNKNK | ENQELKQEKE | GKENTRITNL | TVNTGLDCSE | KTREEGNFRK | SFSPKDDTSL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HLFHISTGKS | PKHSCGLSEK | QSTPLKQEHT | KTCLSPGSSE | MSLQPDLVRY | DNTESEFLPE | SSSVKSCKHK | EKSKHQKDFH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LEFGEKSNAK | IKDEDHSPTF | ENSDCTLKKM | DKEGKTLKKH | KLKHKEREKE | KHKKEIEGEK | EKYKTKDSAK | ELQRSVEFDR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EFWKENFFKS | DETEDLFLNM | EHESLTLEKK | SKLEKNIKDD | KSTKEKHVSK | ERNFKEERDK | IKKESEKSFR | EEKIKDLKEE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RENIPTDKDS | EFTSLGMSAI | EESIGLHLVE | KEIDIEKQEK | HIKESKEKPE | KRSQIKEKDI | EKMERKTFEK | EKKIKHEHKS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EKDKLDLSEC | VDKIKEKDKL | YSHHTEKCHK | EGEKSKNTAA | IKKTDDREKS | REKMDRKHDK | EKPEKERHLA | ESKEKHLMEK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KNKQSDNSEY | SKSEKGKNKE | KDRELDKKEK | SRDKESINIT | NSKHIQEEKK | SSIVDGNKAQ | HEKPLSLKEK | TKDEPLKTPD |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GKEKDKKDKD | IDRYKERDKH | KDKIQINSLL | KLKSEADKPK | PKSSPASKDT | RPKEKRLVND | DLMQTSFERM | LSLKDLEIEQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| WHKKHKEKIK | QKEKERLRNR | NCLELKIKDK | EKTKHTPTES | KNKELTRSKS | SEVTDAYTKE | KQPKDAVSNR | SQSVDTKNVM |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TLGKSSFVSD | NSLNRSPRSE | NEKPGLSSRS | VSMISVASSE | DSCHTTVTTP | RPPVEYDSDF | MLESSESQMS | FSQSPFLSIA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KSPALHEREL | DSLADLPERI | KPPYANRLST | SHLRSSSVED | VKLIISEGRP | TIEVRRCSMP | SVICEHTKQF | QTISEESNQG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SLLTVPGDTS | PSPKPEVFSN | VPERDLSNVS | NIHSSFATSP | TGASNSKYVS | ADRNLIKNTA | PVNTVMDSPV | HLEPSSQVGV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| IQNKSWEMPV | DRLETLSTRD | FICPNSNIPD | QESSLQSFCN | SENKVLKENA | DFLSLRQTEL | PGNSCAQDPA | SFMPPQQPCS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| FPSQSLSDAE | SISKHMSLSY | VANQEPGILQ | QKNAVQIISS | ALDTDNESTK | DTENTFVLGD | VQKTDAFVPV | YSDSTIQEAS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PNFEKAYTLP | VLPSEKDFNG | SDASTQLNTH | YAFSKLTYKS | SSGHEVENST | TDTQVISHEK | ENKLESLVLT | HLSRCDSDLC |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| EMNAGMPKGN | LNEQDPKHCP | ESEKCLLSIE | DEESQQSILS | SLENHSQQST | QPEMHKYGQL | VKVELEENAE | DDKTENQIPQ |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| RMTRNKANTM | ANQSKQILAS | CTLLSEKDSE | SSSPRGRIRL | TEDDDPQIHH | PRKRKVSRVP | QPVQVSPSLL | QAKEKTQQSL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| AAIVDSLKLD | EIQPYSSERA | NPYFEYLHIR | KKIEEKRKLL | CSVIPQAPQY | YDEYVTFNGS | YLLDGNPLSK | ICIPTITPPP |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| SLSDPLKELF | RQQEVVRMKL | RLQHSIEREK | LIVSNEQEVL | RVHYRAARTL | ANQTLPFSAC | TVLLDAEVYN | VPLDSQSDDS |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| KTSVRDRFNA | RQFMSWLQDV | DDKFDKLKTC | LLMRQQHEAA | ALNAVQRLEW | QLKLQELDPA | TYKSISIYEI | QEFYVPLVDV |
| 1770 | | | | | | | |
| NDDFELTPI | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 468 | 1 | 572.6830 | -230.04 | 2 | 34.3 | 15.5 | 2 | 447-455 | K.HVSKERNFK.E | | WUP:QUP 4.73<br>QU:MU 0.51 |
| 110 | 1 | 1083.4576 | -80.32 | 2 | 31.3 | 13.6 | 2 | 865-884 | K.DAVSNRSQSVDTKNVMTLGK.S | Oxidation: 16 | |
| 623 | 1 | 824.1088 | -20.46 | 3 | 37.4 | 10.9 | 2 | 995-1016 | R.SSSVEDVKLIISEGRPTIEVRR.C | | |

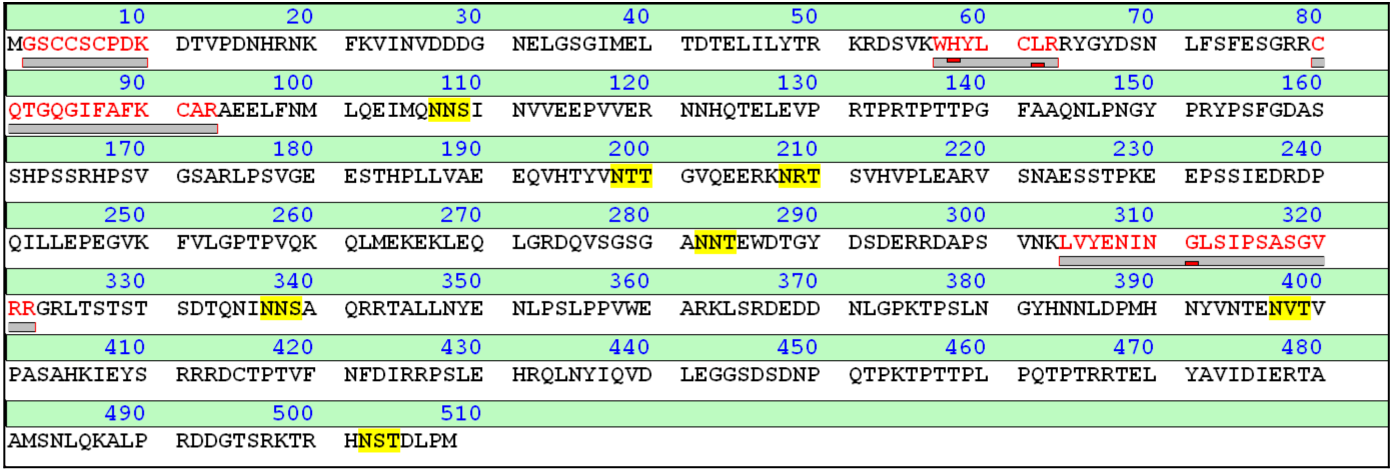
# Detailed Protein Report

## Protein 113: fibroblast growth factor receptor substrate 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|110347408 | **Score:** | 51.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 9.6 |
| | | **No. of unique Peptides:** | 4 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|507834075 | refseq_huma (refseq_human_20140103.fasta) | fibroblast growth factor receptor substrate 2 [Homo sapiens] |
| gi\|507834073 | refseq_huma (refseq_human_20140103.fasta) | fibroblast growth factor receptor substrate 2 [Homo sapiens] |
| gi\|507834071 | refseq_huma (refseq_human_20140103.fasta) | fibroblast growth factor receptor substrate 2 [Homo sapiens] |
| gi\|507834069 | refseq_huma (refseq_human_20140103.fasta) | fibroblast growth factor receptor substrate 2 [Homo sapiens] |
| gi\|507834066 | refseq_huma (refseq_human_20140103.fasta) | fibroblast growth factor receptor substrate 2 [Homo sapiens] |
| gi\|507834061 | refseq_huma (refseq_human_20140103.fasta) | fibroblast growth factor receptor substrate 2 [Homo sapiens] |
| gi\|110347414 | refseq_huma (refseq_human_20140103.fasta) | fibroblast growth factor receptor substrate 2 [Homo sapiens] |



```
        10         20         30         40         50         60         70         80
MGSCCSCPDK DTVPDNHRNK FKVINVDDDG NELGSGIMEL TDTELILYTR KRDSVKWHYL CLRRYGYDSN LFSFESGRRC
        90        100        110        120        130        140        150        160
QTGQGIFAFK CARAEELFNM LQEIMQNNSI NVVEEPVVER NNHQTELEVP RTPRTPTTPG FAAQNLPNGY PRYPSFGDAS
       170        180        190        200        210        220        230        240
SHPSSRHPSV GSARLPSVGE ESTHPLLVAE EQVHTYVNTT GVQEERKNRT SVHVPLEARV SNAESSTPKE EPSSIEDRDP
       250        260        270        280        290        300        310        320
QILLEPEGVK FVLGPTPVQK QLMEKEKLEQ LGRDQVSGSG ANNTEWDTGY DSDERRDAPS VNKLVYENIN GLSIPSASGV
       330        340        350        360        370        380        390        400
RRGRLTSTST SDTQNINNSA QRRTALLNYE NLPSLPPVWE ARKLSRDEDD NLGPKTPSLN GYHNNLDPMH NYVNTENVTV
       410        420        430        440        450        460        470        480
PASAHKIEYS RRRDCTPTVF NFDIRRPSLE HRQLNYIQVD LEGGSDSDNP QTPKTPTTPL PQTPTRRTEL YAVIDIERTA
       490        500        510
AMSNLQKALP RDDGTSRKTR HNSTDLPM
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1454 | 1 | 450.0854 | -157.84 | 2 | 48.4 | 13.2 | 0 | 2-10 | M.GSCCSCPDK.D | |
| 390 | 1 | 524.3566 | 177.97 | 2 | 33.5 | 14.0 | 0 | 57-63 | K.WHYLCLR.R | Carbamidomethyl: 5 |
| 2420 | 1 | 822.3542 | -46.73 | 2 | 60.7 | 12.7 | 1 | 80-93 | R.CQTGQGIFAFKCAR.A | Carbamidomethyl: 1, 12 |
| 1513 | 1 | 1023.0018 | -57.43 | 2 | 49.1 | 11.1 | 1 | 304-322 | K.LVYENINGLSIPSASGVRR.G | |

# Detailed Protein Report

**Protein 114:** **PREDICTED: ral GTPase-activating protein subunit alpha-2 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530425829 | **Score:** | 50.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 216.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 3 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFSRRSHGDV | KKSTQKVLDP | KKDVLTRLKH | LRALLDNVDA | NDLKQFFETN | YSQIYFIFYE | NFIALENSLK | LKGNNKSQRE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ELDSILFLFE | KILQFLPERI | FFRWHYQSIG | STLKKLLHTG | NSIKIRCEGI | RLFLLWLQAL | QTNCAEEQVL | IFACLVPGFP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AVMSSRGPCT | LETLINPSPS | VADVKIYPEE | ITPLLPAISG | EKIAEDQTCF | FLQILLKYMV | IQAASLEWKN | KENQDTGFKF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LFTLFRKYYL | PHLFPSFTKL | TNIYKPVLDI | PHLRPKPVYI | TTTRDNENIY | STKIPYMAAR | VVFIKWIVTF | FLEKKYLTAT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QNTKNGVDVL | PKIIQTVGGG | AVQERAPELD | GGGPTEQDKS | HSNSSTLSDR | RLSNSSLCSI | EEEHRMVYEM | VQRILLSTRG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YVNFVNEVFH | QAFLLPSCEI | AVTRKVVQVY | RKWILQDKPV | FMEEPDRKDV | AQEDAEKLGF | SETDSKEASS | ESSGHKRSSS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| WGRTYSFTSA | MSRGCVTEEE | NTNVKAGVQA | LLQVFLTNSA | NIFLLEPCAE | VPVLLKEQVD | ACKAVLIIFR | RMIMELTMNK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KTWEQMLQIL | LRITEAVMQK | PKDKQIKDLF | AQSLAGLLFR | TLMVAWIRAN | LCVYISRELW | DDFLGVLSSL | TEWEELINEW |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ANIMDSLTAV | LARTVYGVEM | TNLPLDKLSE | QKEKKQRGKG | CVLDPQKGTT | VGRSFSLSWR | SHPDVTEPMR | FRSATTSGAP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GVEKARNIVR | QKATEVEECQ | QSENAPAAGS | GHLTVGQQQQ | VLRSSSTSDI | PEPLCSDSSQ | GQKAENTQNS | SSSEPQPIQE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NKGHVKREHE | GITILVRRSS | SPAELDLKDD | LQQTQGKCRE | RQKSESTNSD | TTLGCTNEAE | LSMGPWQTCE | EDPELNTPTD |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VVADADARHW | LQLSPTDASN | LTDSSECLTD | DCSIIAGGSL | TGWHPDSAAV | LWRRVLGILG | DVNNIQSPKI | HARVFCYLYE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LWYKLAKIRD | NLAISLDNQS | SPSPPVLIPP | LRMFASWLFK | AATLPNEYKE | GKLQAYRLIC | AMMTRRQDVL | PNSDFLVHFY |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LVMHLGLTSE | DQDILNTIIR | HCPPRFFSLG | FPGFSMLVGD | FITAAARVLS | TDILTAPRSE | AVTVLGSLVC | FPNTYQEIPL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LQSVPEVNEA | ITGTEDVKHY | LINILLKNAT | EEPNEYARCI | AVCSLGVWIC | EELAQCTSHP | QVKEAINVIG | VTLKFPNKIV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| AQVACDVLQL | LVSYWEKLQM | FETSLPRKMA | EILVATVAFL | LPSAEYSSVE | TDKKFIVSLL | LCLLDWCMAL | PVSVLLHPVS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TAVLEEQHSA | RAPLLDYIYR | VLHCCVCGSS | TYTQQSHYIL | TLADLSSTDY | DPFLPLANVK | SSEPVQYHSS | AELGNLLTVE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| EEKKRRSLEL | IPLTARMVMA | HLVNHLGHYP | LSGGPAILHS | LVSENHDNAH | VEGSELSFEV | FRSPNLQLFV | FNDSTLISYL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| QTPTEGPVGG | SPVGSLSDVR | VIVRDISGKY | SWDGKVLYGP | LEGCLAPNGR | NPSFLISSWH | RDTFGPQKDS | SQVEEGDDVL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| DKLLENIGHT | SPECLLPSQL | NLNEPSLTPC | GMNYDQEKEI | IEVILRQNAQ | EDEYIQSHNF | DSAMKVTSQG | QPSPVEPRGP |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| FYFCRLLLDD | LGMNSWDRRK | NFHLLKKNSK | LLRELKNLDS | RQCRETHKIA | VFYIAEGQED | KCSILSNERG | SQAYEDFVAG |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LGWEVDLSTH | CGFMGGLQRN | GSTGQTAPYY | ATSTVEVIFH | VSTRMPSDSD | DSLTKKLRHL | GNDEVHIVWS | EHSRDYRRGI |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| IPTAFGDVSI | IIYPMKNHMF | FIAITKKPEV | PFFGPLFDGA | IVSGKLLPSL | VCATCINASR | AVKCLIPLYQ | SFYEERALYL |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| EAIIQNHREV | MTFEDFAAQV | FSPSPSYSLS | GTGALASSLS | ADLEEPLSEE | ETEHPLLPLP | RATKPRISRK | FRCCTSALSR |
| 1930 | | | | | | | |
| SSH | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1746 | 2 | 1023.9594 | -58.70 | 2 | 51.6 | 16.7 | 1 | 433-448 | K.WILQDKPVFMEEPDRK.D | Oxidation: 10 |
| 584 | 1 | 666.3548 | 8.18 | 2 | 37.3 | 10.6 | 1 | 713-726 | R.SATTSGAPGVEKAR.N | |
| 1736 | 1 | 1273.5367 | -62.63 | 2 | 51.5 | 13.3 | 0 | 1341- | K.SSEPVQYHSSAELGNLLTVEEEK.K | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | 1363 | | |

# Detailed Protein Report

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## Protein 115: zinc finger protein 281 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|6912752 | **Score:** | 50.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 96.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 5.3 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.61 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.43 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|526253064 | refseq_huma<br>(refseq_human_20140103.fasta) | zinc finger protein 281 isoform 1 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MKIGSGFLSG GGGTGSSGGS GSGGGGSGGG GGGGSSGRRA EMEPTFPQGM VMFNHRLPPV TSFTRPAGSA APPPQCVLSS
        90        100        110        120        130        140        150        160
STSAAPAAEP PPPPAPDMTF KKEPAASAAA FPSQRTSWGF LQSLVSIKQE KPADPEEQQS HHHHHHHHYG GLFAGAEERS
       170        180        190        200        210        220        230        240
PGLGGGEGGS HGVIQDLSIL HQHVQQQPAQ HHRDVLLSSS SRTDDHHGTE EPKQDTNVKK AKRPKPESQG IKAKRKPSAS
       250        260        270        280        290        300        310        320
SKPSLVGDGE GAILSPSQKP HICDHCSAAF RSSYHLRRHV LIHTGERPFQ CSQCSMGFIQ KYLLQRHEKI HSREKPFGCD
       330        340        350        360        370        380        390        400
QCSMKFIQKY HMERHKRTHS GEKPYKCDTC QQYFSRTDRL LKHRRTCGEV IVKGATSAEP GSSNHTNMGN LAVLSQGNTS
       410        420        430        440        450        460        470        480
SSRRKTKSKS IAIENKEQKT GKTNESQISN NINMQSYSVE MPTVSSSGGI IGTGIDELQK RVPKLIFKKG SRKNTDKNYL
       490        500        510        520        530        540        550        560
NFVSPLPDIV GQKSLSGKPS GSLGIVSNNS VETIGLLQST SGKQGQISSN YDDAMQFSKK RRYLPTASSN SAFSINVGHM
       570        580        590        600        610        620        630        640
VSQQSVIQSA GVSVLDNEAP LSLIDSSALN AEIKSCHDKS GIPDEVLQSI LDQYSNKSES QKEDPFNIAE PRVDLHTSGE
       650        660        670        680        690        700        710        720
HSELVQEENL SPGTQTPSND KASMLQEYSK YLQQAFEKST NASFTLGHGF QFVSLSSPLH NHTLFPEKQI YTTSPLECGF
       730        740        750        760        770        780        790        800
GQSVTSVLPS SLPKPPFGML FGSQPGLYLS ALDATHQQLT PSQELDDLID SQKNLETSSA FQSSSQKLTS QKEQKNLESS
       810        820        830        840        850        860        870        880
TGFQIPSQEL ASQIDPQKDI EPRTTYQIEN FAQAFGSQFK SGSRVPMTFI TNSNGEVDHR VRTSVSDFSG YTNMMSDVSE
       890        900
PCSTRVKTPT SQSYR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2793 | 1 | 840.4111 | 74.23 | 2 | 65.3 | 14.1 | 1 | 347-359 | K.CDTCQQYFSRTDR.L | Carbamidomethyl: 4 | |
| 698 | 2 | 495.2768 | -16.50 | 2 | 37.2 | 25.1 | 1 | 408-416 | K.SKSIAIENK.E | | QU:MU 0.61<br>WUP:QUP 0.43 |
| 2862 | 1 | 693.8668 | 91.67 | 4 | 66.2 | 11.6 | 1 | 861-885 | R.<br>VRTSVSDFSGYTNMMSDVSEPCS<br>V | Oxidation: 14 | |

# Detailed Protein Report

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**Protein 116:** **PREDICTED: midasin isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578812559 | **Score:** | 50.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 627.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEHFLLEVAA | APLRLIAAKN | EKSRSELGRF | LAKQVWTPQD | RQCVLSTLAQ | LLLDKDCTVL | VGRQLRPLLL | DLLERNAEAI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KAGGQINHDL | HERLCVSMSK | LIGNHPDVLP | FALRYFKDTS | PVFQRLFLES | SDANPVRYGR | RRMKLRDLME | AAFKFLQQEQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SVFRELWDWS | VCVPLLRSHD | TLVRWYTANC | LALVTCMNEE | HKLSFLKKIF | NSDELIHFRL | RLLEEAQLQD | LEKALVLANP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EVSLWRKQKE | LQYLQGHLVS | SDLSPRVTAV | CGVVLPGQLP | APGELGGNRS | SSREQELALR | SYVLVESVCK | SLQTLAMAVA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SQNAVLLEGP | IGCGKTSLVE | YLAAVTGRTK | PPQLLKVQLG | DQTDSKMLLG | MYRCTDVPGE | FVWQPGTLTQ | AATMGHWILL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EDIDYAPLDV | VSVLIPLLEN | GELLIPGRGD | CLKVAPGFQF | FATRRLLSCG | GNWYRPLNSH | ATLLDKYWTK | IHLDNLDKRE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LNEVLQSRYP | SLLAVVDHLL | DIYIQLTGEK | HHSWSDSSVG | CEQAPEEVSE | ARRENKRPTL | EGRELSLRDL | LNWCNRIAHS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FDSSSLSASL | NIFQEALDCF | TAMLSEHTSK | LKMAEVIGSK | LNISRKKAEF | FCQLYKPEIV | INELDLQVGR | VRLLRKQSEA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VHLQREKFTF | AATRPSSVLI | EQLAVCVSKG | EPVLLVGETG | TGKTSTIQYL | AHITGHRLRV | VNMNQQSDTA | DLLGGYKPVD |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HKLIWLPLRE | AFEELFAQTF | SKKQNFTFLG | HIQTCYRQKR | WHDLLRLMQH | VHKSAVNKDG | KDSETGLLIK | EKWEAFGLRL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NHAQQQMKMT | ENTLLFAFVE | GTLAQAVKKG | EWILLDEINL | AAPEILECLS | GLLEGSSGSL | VLLDRGDTEP | LVRHPDFRLF |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ACMNPATDVG | KRNLPPGIRN | RFTELYVEEL | ESKEDLQVLI | VDYLKGLSVN | KNTVQGIINF | YTALRKESGT | KLVDGTGHRP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| HYSLRTLCRA | LRFAASNPCG | NIQRSLYEGF | CLGFLTQLDR | ASHPIVQKLI | CQHIVPGNVK | SLLKQPIPEP | KGGRLIQVEG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| YWIAVGDKEP | TIDETYILTS | SVKLNLRDIV | RVVSAGTYPV | LIQGETSVGK | TSLIQWLAAA | TGNHCVRINN | HEHTDIQEYI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GCYTSDSSGK | LVFKEGVLID | AMRKGYWIIL | DELNLAPTDV | LEALNRLLDD | NRELLVTETQ | EVVKAHPRFM | LFATQNPPGL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| YGGRKVLSRA | FRNRFVELHF | DELPSSELET | ILHKRCSLPP | SYCSKLVKVM | LDLQSYRRSS | SVFAGKQGFI | TLRDLFRWAE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| RYRLAEPTEK | EYDWLQHLAN | DGYMLLAGRV | RKQEEIDVIQ | EVLEKHFKKK | LCPQSLFSKE | NVLKLLGKLS | TQISTLECNF |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| GHIVWTEGMR | RLAMLVGRAL | EFGEPVLLVG | DTGCGKTTIC | QVFAALANQK | LYSVSCHLHM | ETSDFLGGLR | PVRQKPNDKE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EIDTSRLFEW | HDGPLVQAMK | EDGFFLLDEI | SLADDSVLER | LNSVLEVEKS | LVLAEKGSPE | DKDSEIELLT | AGKKFRILAT |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| MNPGGDFGKK | ELSPALRNRF | TEIWCPQSTS | REDLIQIISH | NLRPGLCLGR | IDPKGSDIPE | VMLDFIDWLT | HQEFGRKCVV |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| SIRDILSWVN | FMNKMGEEAA | LKRPEIISTV | TSFVHAACLV | YIDGIGSGVT | SSGFGTALLA | RKECLKFLIK | RLAKIVRLTE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| YQKNELKIYD | RMKAKEFTGI | DNLWGIHPFF | IPRGPVLHRN | NIADYALSAG | TTAMNAQRLL | RATKLKKPIL | LEGSPGVGKT |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SLVGALAKAS | GNTLVRINLS | EQTDITDLFG | ADLPVEGGKG | GEFAWRDGPL | LAALKAGHWV | VLDELNLASQ | SVLEGLNACF |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| DHRGEIYVPE | LGMSFQVQHE | KTKIFGCQNP | FRQGGGRKGL | PRSFLNRFTQ | VFVDPLTVID | MEFIASTLFP | AIEKNIVKKM |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| VAFNNQIDHE | VTVEKKWGQK | GGPWEFNLRD | LFRWCQLMLV | DQSPGCYDPG | QHVFLVYGER | MRTEEDKKKV | IAVFKDVFGS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| NSNPYMGTRL | FRITPYDVQL | GYSVLSRGSC | VPHPSRHPLL | LLHQSFQPLE | SIMKCVQMSW | MVILVGPASV | GKTSLVQLLA |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| HLTGHTLKIM | AMNSAMDTTE | LLGGFEQVDL | IRPWRRLLEK | VEGTVRALLR | DSLLISADDA | EVVLRAWSHF | LLTYKPKCLG |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 558 | 1 | 512.6910 | -181.41 | 2 | 35.4 | 13.3 | 2 | 1688-1695 | K.IYDRMKAK.E | |
| 1915 | 1 | 918.3456 | -31.31 | 2 | 53.8 | 12.2 | 1 | 4832-4848 | K.EEKEEAEADDGGQGEDK.I | |

## Protein 117: PREDICTED: integrin beta-4 isoform X9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578830859 | **Score:** | 50.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 198.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVVAVRNRAG | SEGLESPSWG | LREGQQEGQE | GRRKRMAGPR | PSPWARLLLA | ALISVSLSGT | LANRCKKAPV | KSCTECVRVD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KDCAYCTDEM | FRDRRCNTQA | ELLAAGCQRE | SIVVMESSFQ | ITEETQIDTT | LRRSQMSPQG | LRVRLRPGEE | RHFELEVFEP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LESPVDLYIL | MDFSNSMSDD | LDNLKKMGQN | LARVLSQLTS | DYTIGFGKFV | DKVSVPQTDM | RPEKLKEPWP | NSDPPFSFKN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VISLTEDVDE | FRNKLQGERI | SGNLDAPEGG | FDAILQTAVC | TRDIGWRPDS | THLLVFSTES | AFHYEADGAN | VLAGIMSRND |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ERCHLDTTGT | YTQYRTQDYP | SVPTLVRLLA | KHNIIPIFAV | TNYSYSYYEK | LHTYFPVSSL | GVLQEDSSNI | VELLEEAFNR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IRSNLDIRAL | DSPRGLRTEV | TSKMFQKTRT | GSFHIRRGEV | GIYQVQLRAL | EHVDGTHVCQ | LPEDQKGNIH | LKPSFSDGLK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| MDAGIICDVC | TCELQKEVRS | ARCSFNGDFV | CGQCVCSEGW | SGQTCNCSTG | SLSDIQPCLR | EGEDKPCSGR | GECQCGHCVC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YGEGRYEGQF | CEYDNFQCPR | TSGFLCNDRG | RCSMGQCVCE | PGWTGPSCDC | PLSNATCIDS | NGGICNGRGH | CECGRCHCHQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QSLYTDTICE | INYSAIHPGL | CEDLRSCVQC | QAWGTGEKKG | RTCEECNFKV | KMVDELKRAE | EVVVRCSFRD | EDDDCTYSYT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| MEGDGAPGPN | STVLVHKKKD | CPPGSFWWLI | PLLLLLLPLL | ALLLLLCWKY | CACCKACLAL | LPCCNRGHMV | GFKEDHYMLR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ENLMASDHLD | TPMLRSGNLK | GRDVVRWKVT | NNMQRPGFAT | HAASINPTEL | VPYGLSLRLA | RLCTENLLKP | DTRECAQLRQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EVEENLNEVY | RQISGVHKLQ | QTKFRQQPNA | GKKQDHTIVD | TVLMAPRSAK | PALLKLTEKQ | VEQRAFHDLK | VAPGYYTLTA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DQDARGMVEF | QEGVELVDVR | VPLFIRPEDD | DEKQLLVEAI | DVPAGTATLG | RRLVNITIIK | EQARDVVSFE | QPEFSVSRGD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QVARIPVIRR | VLDGGKSQVS | YRTQDGTAQG | NRDYIPVEGE | LLFQPGEAWK | ELQVKLLELQ | EVDSLLRGRQ | VRRFHVQLSN |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PKFGAHLGQP | HSTTIIIRDP | DELDRSFTSQ | MLSSQPPPHG | DLGAPQNPNA | KAAGSRKIHF | NWLPPSGKPM | GYRVKYWIQG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DSESEAHLLD | SKVPSVELTN | LYPYCDYEMK | VCAYGAQGEG | PYSSLVSCRT | HQEVPSEPGR | LAFNVVSSTV | TQLSWAEPAE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TNGEITAYEV | CYGLVNDDNR | PIGPMKKVLV | DNPKNRMLLI | ENLRESQPYR | YTVKARNGAG | WGPEREAIIN | LATQPKRPMS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| IPIIPDIPIV | DAQSGEDYDS | FLMYSDDVLR | SPSGSQRPSV | SDDTEHLVNG | RMDFAFPGST | NSLHRMTTTS | AAAYGTHLSP |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| HVPHRVLSTS | STLTRDYNSL | TRSEHSHSTT | LPRDYSTLTS | VSSHDSRLTA | GVPDTPTRLV | FSALGPTSLR | VSWQEPRCER |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PLQGYSVEYQ | LLNGGELHRL | NIPNPAQTSV | VVEDLLPNHS | YVFRVRAQSQ | EGWGREREGV | ITIESQVHPQ | SPLCPLPGSA |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| FTLSTPSAPG | PLVFTALSPD | SLQLSWERPR | RPNGDIVGYL | VTCEMAQGGG | PATAFRVDGD | SPESRLTVPG | LSENVPYKFK |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| VQARTTEGFG | PEREGIITIE | SQDGGPFPQL | GSRAGLFQHP | LQSEYSSITT | THTSATEPFL | VDGLTLGAQH | LEAGGSLTRH |
| 1770 | 1780 | 1790 | | | | | |
| VTQEFVSRTL | TTSGTLSTHM | DQQFFQT | | | | | |

| Cmpd. | No. of | m/z meas. | Δ m/z | z | Rt | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

| | Cmpds. | | [ppm] | | [min] | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 1596 | 1 | 480.7905 | 34.21 | 2 | 49.7 | 13.2 | 1 | 1-8 | -.MVVAVRNR.A | Oxidation: 1 |
| 522 | 1 | 678.9701 | 154.68 | 2 | 36.5 | 13.0 | 1 | 403-414 | R.SNLDIRALDSPR.G | |

# Detailed Protein Report

**Protein 118:** **PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X10 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578799003 | **Score:** | 50.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 433.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 4 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGWRAAGALL | LALLLHGRLL | AVTHGLRAYD | GLSLPEDIET | VTASQMRWTH | SYLSDDEDML | ADSISGDDLG | SGDLGSGDFQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MVYFRALVNF | TRSIEYSPQL | EDAGSREFRE | VSEAVVDTLE | SEYLKIPGDQ | VVSVVFIKEL | DGWVFVELDV | GSEGNADGAQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IQEMLLRVIS | SGSVASYVTS | PQGFQFRRLG | TAQTPPPPPA | AVAVAVTPVP | QFPRACTEAE | FACHSYNECV | ALEYRCDRRP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DCRDMSDELN | CEEPVLGISP | TFSLLVETTS | LPPRPETTIM | RQPPVTHAPQ | PLLPGSVRPL | PCGPQEAACR | NGHCIPRDYL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CDGQEDCEDG | SDELDCGPPP | PCEPNEFPCG | NGHCALKLWR | CDGDFDCEDR | TDEANCPTKR | PEEVCGPTQF | RCVSTNMCIP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ASFHCDEESD | CPDRSDEFGC | MPPQVVTPPR | ESIQASRGQT | VTFTCVAIGV | PTPIINWRLN | WGHIPSHPRV | TVTSEGGRGT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LIIRDVKESD | QGAYTCEAMN | ARGMVFGIPD | GVLELVPQRA | GPCPDGHFYL | EHSAACLPCF | CFGITSVCQS | TRRFRDQIRL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RFDQPDDFKG | VNVTMPAQPG | TPPLSSTQLQ | IDPSLHEFQL | VDLSRRFLVH | DSFWALPEQF | LGNKVDSYGG | SLRYNVRYEL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ARGMLEPVQR | PDVVLMGAGY | RLLSRGHTPT | QPGALNQRQV | QFSEEHWVHE | SGRPVQRAEL | LQVLQSLEAV | LIQTVYNTKM |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ASVGLSDIAM | DTTVTHATSH | GRAHSVEECR | CPIGYSGLSC | ESCDAHFTRV | PGGPYLGTCS | GCNCNGHASS | CDPVYGHCLN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| CQHNTEGPQC | NKCKAGFFGD | AMKATATSCR | PCPCPYIDAS | RRFSDTCFLD | TDGQATCDAC | APGYTGRRCE | SCAPGYEGNP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| IQPGGKCRPV | NQEIVRCDER | GSMGTSGEAC | RCKNNVVGRL | CNECADGSFH | LSTRNPDGCL | KCFCMGVSRH | CTSSSWSRAQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LHGASEEPGH | FSLTNAASTH | TTNEGIFSPT | PGELGFSSFH | RLLSGPYFWS | LPSRFLGDKV | TSYGGELRFT | VTQRSQPGST |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PLHGQPLVVL | QGNNIILEHH | VAQEPSPGQP | STFIVPFREQ | AWQRPDGQPA | TREHLLMALA | GIDTLLIRAS | YAQQPAESRV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SGISMDVAVP | EETGQDPALE | VEQCSCPPGY | RGPSCQDCDT | GYTRTPSGLY | LGTCERCSCH | GHSEACEPET | GACQGCQHHT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EGPRCEQCQP | GYYGDAQRGT | PQDCQLCPCY | GDPAAGQAAH | TCFLDTDGHP | TCDACSPGHS | GRHCERCAPG | YYGNPSQGQP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| CQRDSQVPGP | IGCNCDPQGS | VSSQCDAAGQ | CQCKAQVEGL | TCSHCRPHHF | HLSASNPDGC | LPCFCMGITQ | QCASSAYTRH |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LISTHFAPGD | FQGFALVNPQ | RNSRLTGEFT | VEPVPEGAQL | SFGNFAQLGH | ESFYWQLPET | YQGDKGEAYF | ARMRRAHQRT |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LPMALAPGLW | EVLARLLPPF | HQNRTSLSEE | QLRAAVTAGR | IPEPPEGRDW | AQRASQVDEA | QRRMDAEIWQ | LLSSFAAQPQ |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PPPQGLSPHP | QPAAALRAAP | PPSSSSSSSS | SSASLSFSPG | SQFSLSYEGF | SLLPGSLYYW | QLPRAFLGDK | VAAYGGKLRY |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| TLSYTAGPQG | SPLSDPDVQI | TGNNIMLVAS | QPALQGPERR | SYEIMFREEF | WRRPDGQPAT | REHLLMALAD | LDELLIRATF |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| SSVPLAASIS | AVSLEVAQPG | PSNRPRALEV | EECRCPPGYI | GLSCQDCAPG | YTRTGSGLYL | GHCELCECNG | HSDLCHPETG |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| ACSQCQHNAA | GEFCELCAPG | YYGDATAGTP | EDCQPCACPL | TNPENMFSRT | CESLGAGGYR | CTACEPGYTG | QYCEQCGPGY |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| VGNPSVQGGQ | CLPETNQAPL | VVEVHPARSI | VPQGGSHSLR | CQVSGSPPHY | FYWSREDGRP | VPSGTQQRHQ | GSELHFPSVQ |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| PSDAGVYICT | CRNLHQSNTS | RAELLVTEAP | SKPITVTVEE | QRSQSVRPGA | DVTFICTAKS | KSPAYTLVWT | RLHNGKLPTR |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| AMDFNGILTI | RNVQLSDAGT | YVCTGSNMFA | MDQGTATLHV | QASGTLSAPV | VSIHPPQLTV | QPGQLAEFRC | SATGSPTPTL |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| EWTGGPGGQL | PAKAQIHGGI | LRLPAVEPTD | QAQYLCRAHS | SAGQQVARAV | LHVHGGGGPR | VQVSPERTQV | HAGRTVRLYC |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2417 | 1 | 1175.2100 | -20.32 | 2 | 60.1 | 10.2 | 1 | 5-27 | R.AAGALLLALLLHGRLLAVTHGLR.A | |
| 2083 | 1 | 1052.3950 | -135.43 | 2 | 56.4 | 13.6 | 0 | 643-661 | R.GMLEPVQRPDVVLMGAGYR.L | Oxidation: 2 |
| 85 | 1 | 827.0046 | 173.12 | 2 | 31.0 | 13.9 | 0 | 920-934 | R.LCNECADGSFHLSTR.N | |
| 1714 | 1 | 1011.6020 | 66.80 | 3 | 51.7 | 12.9 | 1 | 3926-3953 | R.FDAGSGMATIRHPTPLALGHFHTVTLLR.S | Oxidation: 7 |

# Detailed Protein Report

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## Protein 119: fibrillin-1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|281485550 | **Score:** | 50.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 312.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 3 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MRRGRLLEIA LGFTVLLASY TSHGADANLE AGNVKETRAS RAKRRGGGGH DALKGPNVCG SRYNAYCCPG WKTLPGGNQC

        90        100        110        120        130        140        150        160
IVPICRHSCG DGFCSRPNMC TCPSGQIAPS CGSRSIQHCN IRCMNGGSCS DDHCLCQKGY IGTHCGQPVC ESGCLNGGRC

       170        180        190        200        210        220        230        240
VAPNRCACTY GFTGPQCERD YRTGPCFTVI SNQMCQGQLS GIVCTKTLCC ATVGRAWGHP CEMCPAQPHP CRRGFIPNIR

       250        260        270        280        290        300        310        320
TGACQDVDEC QAIPGLCQGG NCINTVGSFE CKCPAGHKLN EVSQKCEDID ECSTIPGICE GGECTNTVSS YFCKCPPGFY

       330        340        350        360        370        380        390        400
TSPDGTRCID VRPGYCYTAL TNGRCSNQLP QSITKMQCCC DAGRCWSPGV TVAPEMCPIR ATEDFNKLCS VPMVIPGRPE

       410        420        430        440        450        460        470        480
YPPPPLGPIP PVLPVPPGFP PGPQIPVPRP PVEYLYPSRE PPRVLPVNVT DYCQLVRYLC QNGRCIPTPG SYRCECNKGF

       490        500        510        520        530        540        550        560
QLDLRGECID VDECEKNPCA GGECINNQGS YTCQCRAGYQ STLTRTECRD IDECLQNGRI CNNGRCINTD GSFHCVCNAG

       570        580        590        600        610        620        630        640
FHVTRDGKNC EDMDECSIRN MCLNGMCINE DGSFKCICKP GFQLASDGRY CKDINECETP GICMNGRCVN TDGSYRCECF

       650        660        670        680        690        700        710        720
PGLAVGLDGR VCVDTHMRST CYGGYKRGQC IKPLFGAVTK SECCCASTEY AFGEPCQPCP AQNSAEYQAL CSSGPGMTSA

       730        740        750        760        770        780        790        800
GSDINECALD PDICPNGICE NLRGTYKCIC NSGYEVDSTG KNCVDINECV LNSLLCDNGQ CRNTPGSFVC TCPKGFIYKP

       810        820        830        840        850        860        870        880
DLKTCEDIDE CESSPCINGV CKNSPGSFIC ECSSESTLDP TKTICIETIK GTCWQTVIDG RCEININGAT LKSQCCSSLG

       890        900        910        920        930        940        950        960
AAWGSPCTLC QVDPICGKGY SRIKGTQCED IDECEVFPGV CKNGLCVNTR GSFKCQCPSG MTLDATGRIC LDIRLETCFL

       970        980        990       1000       1010       1020       1030       1040
RYEDEECTLP IAGRHRMDAC CCSVGAAWGT EECEECPMRN TPEYEELCPR GPGFATKEIT NGKPFFKDIN ECKMIPSLCT

      1050       1060       1070       1080       1090       1100       1110       1120
HGKCRNTIGS FKCRCDSGFA LDSEERNCTD IDECRISPDL CGRGQCVNTP GDFECKCDEG YESGFMMMKN CMDIDECQRD

      1130       1140       1150       1160       1170       1180       1190       1200
PLLCRGGVCH NTEGSYRCEC PPGHQLSPNI SACIDINECE LSAHLCPNGR CVNLIGKYQC ACNPGYHSTP DRLFCVDIDE

      1210       1220       1230       1240       1250       1260       1270       1280
CSIMNGGCET FCTNSEGSYE CSCQPGFALM PDQRSCTDID ECEDNPNICD GGQCTNIPGE YRCLCYDGFM ASEDMKTCVD

      1290       1300       1310       1320       1330       1340       1350       1360
VNECDLNPNI CLSGTCENTK GSFICHCDMG YSGKKGKTGC TDINECEIGA HNCGKHAVCT NTAGSFKCSC SPGWIGDGIK

      1370       1380       1390       1400       1410       1420       1430       1440
CTDLDECSNG THMCSQHADC KNTMGSYRCL CKEGYTGDGF TCTDLDECSE NLNLCGNGQC LNAPGGYRCE CDMGFVPSAD

      1450       1460       1470       1480       1490       1500       1510       1520
GKACEDIDEC SLPNICVFGT CHNLPGLFRC ECEIGYELDR SGGNCTDVNE CLDPTTCISG NCVNTPGSYI CDCPPDFELN

      1530       1540       1550       1560       1570       1580       1590       1600
PTRVGCVDTR SGNCYLDIRP RGDNGDTACS NEIGVGVSKA SCCCSLGKAW GTPCEMCPAV NTSEYKILCP GGEGFRPNPI

      1610       1620       1630       1640       1650       1660       1670       1680
TVILEDIDEC QELPGLCQGG KCINTFGSFQ CRCPTGYYLN EDTRVCDDVN ECETPGICGP GTCYNTVGNY TCICPPDYMQ

      1690       1700       1710       1720       1730       1740       1750       1760
VNGGNNCMDM RRSLCYRNYY ADNQTCDGEL LFNMTKKMCC CSYNIGRAWN KPCEQCPIPS TDEFATLCGS QRPGFVIDIY

      1770       1780       1790       1800       1810       1820       1830       1840
TGLPVDIDEC REIPGVCENG VCINMVGSFR CECPVGFFYN DKLLVCEDID ECQNGPVCQR NAECINTAGS YRCDCKPGYR

      1850       1860       1870       1880       1890       1900       1910       1920
FTSTGQCNDR NECQEIPNIC SHGQCIDTVG SFYCLCHTGF KTNDDQTMCL DINECERDAC GNGTCRNTIG SFNCRCNHGF

      1930       1940       1950       1960       1970       1980       1990       2000
ILSHNNDCID VDECASGNGN LCRNGQCINT VGSFQCQCNE GYEVAPDGRT CVDINECLLE PRKCAPGTCQ NLDGSYRCIC

      2010       2020       2030       2040       2050       2060       2070       2080
PPGYSLQNEK CEDIDECVEE PEICALGTCS NTEGSFKCLC PEGFSLSSSG RRCQDLRMSY CYAKFEGGKC SSPKSRNHSK

      2090       2100       2110       2120       2130       2140       2150       2160
QECCCALKGE GWGDPCELCP TEPDEAFRQI CPYGSGIIVG PDDSAVDMDE CKEPDVCKHG QCINTDGSYR CECPFGYILA

      2170       2180       2190       2200       2210       2220       2230       2240
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1872 | 1 | 1057.6895 | -79.32 | 3 | 53.8 | 11.0 | 2 | 610-636 | R.YCKDINECETPGICMNGRCVNTDGSYR.C | Carbamidomethyl: 2, 19; Oxidation: 15 |
| 748 | 8 | 635.3242 | 75.75 | 2 | 37.8 | 23.9 | 1 | 2482-2492 | R.SCKDLDECATK.Q | Carbamidomethyl: 8 |
| 2864 | 1 | 703.3686 | 82.89 | 2 | 66.3 | 15.8 | 0 | 2681-2694 | R.IGQGHCVSGMGMGR.G | Oxidation: 12 |

# Detailed Protein Report

## Protein 120: PREDICTED: nuclear receptor corepressor 1 isoform X13 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578830118 | **Score:** | 50.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 277.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 3 |

### Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.77 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.67 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MSSSGYPPNQ GAFSTEQSRY PPHSVQYTFP NTRHQQEFAV PDYRSSHLEV SQASQLLQQQ QQQQLRRRPS LLSEFHPGSD
        90        100        110        120        130        140        150        160
RPQERRTSYE PFHPGPSPVD HDSLESKRPR LEQVSDSHFQ RVSAAVLPLV HPLPEGLRAS ADAKKDPAFG GKHEAPSSPI
       170        180        190        200        210        220        230        240
SGQPCGDDQN ASPSKLSKEE LIQSMDRVDR EIAKVEQQIL KLKKKQQQLE EEAAKPPEPE KPVSPPPVEQ KHRSIVQIIY
       250        260        270        280        290        300        310        320
DENRKKAEEA HKIFEGLGPK VELPLYNQPS DTKVYHENIK TGVPARRMMK NQVMRKKLIL FFKRRNHARK QREQKICQRY
       330        340        350        360        370        380        390        400
DQLMEAWEKK VDRIENNPRR KAKESKTREY YEKQFPEIRK QREQQERFQR VGQRGAGLSA TIARSEHEIS EIIDGLSEQE
       410        420        430        440        450        460        470        480
NNEKQMRQLS VIPPMMFDAE QRRVKFINMN GLMEDPMKVY KDRQFMNVWT DHEKEIFKDK FIQHPKNFGL IASYLERKSV
       490        500        510        520        530        540        550        560
PDCVLYYYLT KKNENYKALV RRNYGKRRGR NQQQIARPSQ EEKVEEKEED KAEKTEKKEE EKKDEEEKDE KEDSKENTKE
       570        580        590        600        610        620        630        640
KDKIDGTAEE TEEREQATPR GRKTANSQGR RKGRITRSMT NEAAAASAAA AAATEEPPPP LPPPPEPIST EPVETSRWTE
       650        660        670        680        690        700        710        720
EEMEVAKKGL VEHGRNWAAI AKMVGTKSEA QCKNFYFNYK RRHNLDNLLQ QHKQKTSRKP REERDVSQCE SVASTVSAQE
       730        740        750        760        770        780        790        800
DEDIEASNEE ENPEDSEGAE NSSDTESAPS PSPVEAVKPS EDSPENATSR GNTEPAVELE PTTETAPSTS PSLAVPSTKP
       810        820        830        840        850        860        870        880
AEDESVETQV NDSISAETAE QMDVDQQEHS AEEGSVCDPP PATKADSVDV EVRVPENHAS KVEGDNTKER DLDRASEKVE
       890        900        910        920        930        940        950        960
PRDEDLVVAQ QINAQRPEPQ SDNDSSATCS ADEDVDGEPE RQRMFPMDSK PSLLNPTGSI LVSSPLKPNP LDLPQLQHRA
       970        980        990       1000       1010       1020       1030       1040
AVIPPMVSCT PCNIPIGTPV SGYALYQRHI KAMHESALLE EQRQRQEQID LECRSSTSPC GTSKSPNREW EGKSVAYMPY
      1050       1060       1070       1080       1090       1100       1110       1120
AEVKRALEQE AQMHNTAARS ASPCRLSPRE VSKAAPQPDM SAARYSVPPV LQPAPHQVIT NLPEGVRLPT TRPTRPPPPL
      1130       1140       1150       1160       1170       1180       1190       1200
IPSSKTTVAS EKPSFIMGGS ISQGTPGTYL TSHNQASYTQ ETPKPSVGSI SLGLPRQQES AKSATLPYIK QEEFSPRSQN
      1210       1220       1230       1240       1250       1260       1270       1280
SQPEGLLVRA QHEGVVRGTA GAIQEGSITR GTPTSKISVE SIPSLRGSIT QGTPALPQTG IPTEALVKGS ISRMPIEDSS
      1290       1300       1310       1320       1330       1340       1350       1360
PEKGREEAAS KGHVIYEGKS GHILSYDNIK NAREGTRSPR TAHEISLKRS YESVEGNIKQ GMSMRESPVS APLEGLICRA
      1370       1380       1390       1400       1410       1420       1430       1440
LPRGSPHSDL KERTVLSGSI MQGTPRATTE SFEDGLKYPK QIKRESPPIR AFEGAITKGK PYDGITTIKE MGRSIHEIPR
      1450       1460       1470       1480       1490       1500       1510       1520
QDILTQESRK TPEVVQSTRP IIEGSISQGT PIKFDNNSGQ SAIKHNVKSL ITGPSKLSRG MPPLEIVPEN IKVVERGKYE
      1530       1540       1550       1560       1570       1580       1590       1600
DVKAGETVRS RHTSVVSSGP SVLRSTLHEA PKAQLSPGIY DDTSARRTPV SYQNTMSRGS PMMNRTSDVT ISSNKSTNHE
      1610       1620       1630       1640       1650       1660       1670       1680
RKSTLTPTQR ESIPAKSPVP GVDPVVSHSP FDPHHRGSTA GEVYRSHLPT HLDPAMPFHR ALDPAAAAYL FQRQLSPTPG
      1690       1700       1710       1720       1730       1740       1750       1760
YPSQYQLYAM ENTRQTILND YITSQQMQVN LRPDVARGLS PREQPLGLPY PATRGIIDLT NMPPTILVPH PGGTSTPPMD
      1770       1780       1790       1800       1810       1820       1830       1840
RITYIPGTQI TFPPRPYNSA SMSPGHPTHL AAAASAERER EREREKERER ERIAAASSDL YLRPGSEQPG RPGSHGYVRS
      1850       1860       1870       1880       1890       1900       1910       1920
PSPSVRTQET MLQQRPSVFQ GTNGTSVITP LDPTAQLRIM PLPAGGPSIS QGLPASRYNT AADALAALVD AAASAPQMDV
      1930       1940       1950       1960       1970       1980       1990       2000
SKTKESKHEA ARLEENLRSR SAAVSEQQQL EQKTLEVEKR SVQCLYTSSA FPSGKPQPHS SVVYSEAGKD KGPPPKSRYE
      2010       2020       2030       2040       2050       2060       2070       2080
EELRTRGKTT ITAANFIDVI ITRQIASDKD ARERGSQSSD SSSSLSSHRY ETPSDAIEVI SPASSPAPPQ EKLQTYQPEV
      2090       2100       2110       2120       2130       2140       2150       2160
VKANQAENDP TRQYEGPLHH YRPQQESPSP QQQLPPSSQA EGMGQVPRTH RLITLADHIC QIITQDFARN QVSSQTPQQP
      2170       2180       2190       2200       2210       2220       2230       2240
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2870 | 1 | 973.5098 | 46.41 | 2 | 64.6 | 11.5 | 1 | 426-441 | K.FINMNGLMEDPMKVYK.D | Oxidation: 8 | |
| 47 | 3 | 1068.4733 | -12.48 | 2 | 30.3 | 15.3 | 2 | 2030-2049 | K.DARERGSQSSDSSSSLSSHR.Y | | QU:MU 1.77<br>WUP:QUP 0.67 |
| 911 | 1 | 492.2027 | -52.98 | 2 | 40.9 | 10.7 | 0 | 2341-2349 | K.ALMGSFDDK.V | | |

# Detailed Protein Report

**Protein 121:** **tenascin-X isoform 1 precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|188528648 | **Score:** | 50.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 457.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 4 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MMPAQYALTS SLVLLVLLST ARAGPFSSRS NVTLPAPRPP PQPGGHTVGA GVGSPSSQLY EHTVEGGEKQ VVFTHRINLP
        90        100        110        120        130        140        150        160
PSTGCGCPPG TEPPVLASEV QALRVRLEIL EELVKGLKEQ CTGGCCPASA QAGTGQTDVR TLCSLHGVFD LSRCTCSCEP
       170        180        190        200        210        220        230        240
GWGGPTCSDP TDAEIPPSSP PSASGSCPDD CNDQGRCVRG RCVCFPGYTG PSCGWPSCPG DCQGRGRCVQ GVCVCRAGFS
       250        260        270        280        290        300        310        320
GPDCSQRSCP RGCSQRGRCE GGRCVCDPGY TGDDCGMRSC PRGCSQRGRC ENGRCVCNPG YTGEDCGVRS CPRGCSQRGR
       330        340        350        360        370        380        390        400
CKDGRCVCDP GYTGEDCGTR SCPWDCGEGG RCVDGRCVCW PGYTGEDCST RTCPRDCRGR GRCEDGECIC DTGYSGDDCG
       410        420        430        440        450        460        470        480
VRSCPGDCNQ RGRCEDGRCV CWPGYTGTDC GSRACPRDCR GRGRCENGVC VCNAGYSGED CGVRSCPGDC RGRGRCESGR
       490        500        510        520        530        540        550        560
CMCWPGYTGR DCGTRACPGD CRGRGRCVDG RCVCNPGFTG EDCGSRRCPG DCRGHGLCED GVCVCDAGYS GEDCSTRSCP
       570        580        590        600        610        620        630        640
GGCRGRGQCL DGRCVCEDGY SGEDCGVRQC PNDCSQHGVC QDGVCICWEG YVSEDCSIRT CPSNCHGRGR CEEGRCLCDP
       650        660        670        680        690        700        710        720
GYTGPTCATR MCPADCRGRG RCVQGVCLCH VGYGGEDCGQ EEPPASACPG GCGPRELCRA GQCVCVEGFR GPDCAIQTCP
       730        740        750        760        770        780        790        800
GDCRGRGECH DGSCVCKDGY AGEDCGEEVP TIEGMRMHLL EETTVRTEWT PAPGPVDAYE IQFIPTTEGA SPPFTARVPS
       810        820        830        840        850        860        870        880
SASAYDQRGL APGQEYQVTV RALRGTSWGL PASKTITTMI DGPQDLRVVA VTPTTLELGW LRPQAEVDRF VVSYVSAGNQ
       890        900        910        920        930        940        950        960
RVRLEVPPEA DGTLLTDLMP GVEYVVTVTA ERGRAVSYPA SVRANTGSSP LGLLGTTDEP PPSGPSTTQG AQAPLLQQRP
       970        980        990       1000       1010       1020       1030       1040
QELGELRVLG RDETGRLRVV WTAQPDTFAY FQLRMRVPEG PGAHEEVLPG DVRQALVPPP PPGTPYELSL HGVPPGGKPS
      1050       1060       1070       1080       1090       1100       1110       1120
DPIIYQGIMD KDEEKPGKSS GPPRLGELTV TDRTSDSLLL RWTVPEGEFD SFVIQYKDRD GQPQVVPVEG PQRSAVITSL
      1130       1140       1150       1160       1170       1180       1190       1200
DPGRKYKFVL YGFVGKKRHG PLVAEAKILP QSDPSPGTPP HLGNLWVTDP TPDSLHLSWT VPEGQFDTFM VQYRDRDGRP
      1210       1220       1230       1240       1250       1260       1270       1280
QVVPVEGPER SFVVSSLDPD HKYRFTLFGI ANKKRYGPLT ADGTTAPERK EEPPRPEFLE QPLLGELTVT GVTPDSLRLS
      1290       1300       1310       1320       1330       1340       1350       1360
WTVAQGPFDS FMVQYKDAQG QPQAVPVAGD ENEVTVPGLD PDRKYKMNLY GLRGRQRVGP ESVVAKTAPQ EDVDETPSPT
      1370       1380       1390       1400       1410       1420       1430       1440
ELGTEAPESP EEPLLGELTV TGSSPDSLSL FWTVPQGSFD SFTVQYKDRD GRPRAVRVGG KESEVTVGGL EPGHKYKMHL
      1450       1460       1470       1480       1490       1500       1510       1520
YGLHEGQRVG PVSAVGVTAP QQEETPPATE SPLEPRLGEL TVTDVTPNSV GLSWTVPEGQ FDSFIVQYKD KDGQPQVVPV
      1530       1540       1550       1560       1570       1580       1590       1600
AADQREVTVY NLEPERKYKM NMYGLHDGQR MGPLSVVIVT APLPPAPATE ASKPPLEPRL GELTVTDITP DSVGLSWTVP
      1610       1620       1630       1640       1650       1660       1670       1680
EGEFDSFVVQ YKDRDGQPQV VPVAADQREV TIPDLEPSRK YKFLLFGIQD GKRRSPVSVE AKTVARGDAS PGAPPRLGEL
      1690       1700       1710       1720       1730       1740       1750       1760
WVTDPTPDSL RLSWTVPEGQ FDSFVVQFKD KDGPQVVPVE GHERSVTVTP LDAGRKYRFL LYGLLGKKRH GPLTADGTTE
      1770       1780       1790       1800       1810       1820       1830       1840
ARSAMDDTGT KRPPKPRLGE ELQVTTVTQN SVGLSWTVPE GQFDSFVVQY KDRDGQPQVV PVEGSLREVS VPGLDPAHRY
      1850       1860       1870       1880       1890       1900       1910       1920
KLLLYGLHHG KRVGPISAVA ITAGREETET ETTAPTPPAP EPHLGELTVE EATSHTLHLS WMVTEGEFDS FEIQYTDRDG
      1930       1940       1950       1960       1970       1980       1990       2000
QLQMVRIGGD RNDITLSGLE SDHRYLVTLY GFSDGKHVGP VHVEALTVPE EEKPSEPPTA TPEPPIKPRL GELTVTDATP
      2010       2020       2030       2040       2050       2060       2070       2080
DSLSLSWTVP EGQFDHFLVQ YRNGDGQPKA VRVPGHEEGV TISGLEPDHK YKMNLYGFHG GQRMGPVSVV GVTAAEEETP
      2090       2100       2110       2120       2130       2140       2150       2160
SPTEPSMEAP EPAEEPLLGE LTVTGSSPDS LSLSWTVPQG RFDSFTVQYK DRDGRPQVVR VGGEESEVTV GGLEPGRKYK
      2170       2180       2190       2200       2210       2220       2230       2240
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2748 | 1 | 1085.5225 | -113.03 | 1 | 65.5 | 14.6 | 0 | 107-115 | R.LEILEELVK.G | |
| 15 | 1 | 1103.5160 | 91.05 | 2 | 29.8 | 14.6 | 1 | 264-282 | R.CVCDPGYTGDDCGMRSCPR.G | Carbamidomethyl: 1, 3, 12 |
| 29 | 1 | 1103.5152 | 82.27 | 2 | 30.1 | 10.9 | 0 | 445-464 | R.CENGVCVCNAGYSGEDCGVR.S | Carbamidomethyl: 6, 8, 17 |
| 2993 | 1 | 557.9657 | 38.29 | 3 | 66.2 | 10.2 | 0 | 2141-2157 | R.VGGEESEVTVGGLEPGR.K | |

# Detailed Protein Report

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## Protein 122: PREDICTED: E3 ubiquitin-protein ligase HUWE1 isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530426358 | **Score:** | 50.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 466.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | |
|---|---|---|---|
| ***WUP:QUP*** | **Median:** 0.97 | **CV:** 0.00 % | **No. of Peptides:** 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKVDRTKLKK | TPTEAPADCR | ALIDKLKVCN | DEQLLLELQQ | IKTWNIGKCE | LYHWVDLLDR | FDGILADAGQ | TVENMSWMLV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CDRPEREQLK | MLLLAVLNFT | ALLIEYSFSR | HLYSSIEHLT | TLLASSDMQV | VLAVLNLLYV | FSKRSNYITR | LGSDKRTPLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TRLQHLAESW | GGKENGFGLA | ECCRDLHMMK | YPPSATTLHF | EFYADPGAEV | KIEKRTTSNT | LHYIHIEQLD | KISESPSEIM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ESLTKMYSIP | KDKQMLLFTH | IRLAHGFSNH | RKRLQAVQAR | LHAISILVYS | NALQESANSI | LYNGLIEELV | DVLQITDKQL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MEIKAASLRT | LTSIVHLERT | PKLSSIIDCT | GTASYHGFLP | VLVRNCIQAM | IDPSMDPYPH | QFATALFSFL | YHLASYDAGG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EALVSCGMME | ALLKVIKFLG | DEQDQITFVT | RAVRVVDLIT | NLDMAAFQSH | SGLSIFIYRL | EHEVDLCRKE | CPFVIKPKIQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RPNTTQEGEE | METDMDGVQC | IPQRAALLKS | MLNFLKKAIQ | DPAFSDGIRH | VMDGSLPTSL | KHIISNAEYY | GPSLFLLATE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VVTVFVFQEP | SLLSSLQDNG | LTDVMLHALL | IKDVPATREV | LGSLPNVFSA | LCLNARGLQS | FVQCQPFERL | FKVLLSPDYL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PAMRRRRSSD | PLGDTASNLG | SAVDELMRHQ | PTLKTDATTA | IIKLLEEICN | LGRDPKYICQ | KPSIQKADGT | ATAPPPRSNH |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AAEEASSEDE | EEEEVQAMQS | FNSTQQNETE | PNQQVVGTEE | RIPIPLMDYI | LNVMKFVESI | LSNNTTDDHC | QEFVNQKGLL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PLVTILGLPN | LPIDFPTSAA | CQAVAGVCKS | ILTLSHEPKV | LQEGLLQLDS | ILSSLEPLHR | PIESPGGSVL | LRELACAGNV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ADATLSAQAT | PLLHALTAAH | AYIMMFVHTC | RVGQSEIRSI | SVNQWGSQLG | LSVLSKLSQL | YCSLVWESTV | LLSLCTPNSL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PSGCEFGQAD | MQKLVPKDEK | AGTTQGGKRS | DGEQDGAAGS | MDASTQGLLE | GIGLDGDTLA | PMETDEPTAS | DSKGKSKITP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AMAARIKQIK | PLLSASSRLG | RALAELFGLL | VKLCVGSPVR | QRRSHHAAST | TTAPTPAARS | TASALTKLLT | KGLSWQPPPY |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TPTPRFRLTF | FICSVGFTSP | MLFDERKYPY | HLMLQKFLCS | GGHNALFETF | NWALSMGGKV | PVSEGLEHSD | LPDGTGEFLD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| AWLMLVEKMV | NPTTVLESPH | SLPAKLPGGV | QNFPQFSALR | FLVVTQKAAF | TCIKNLWNRK | PLKVYGGRMA | ESMLAILCHI |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LRGEPVIRER | LSKEKEGSRG | EEDTGQEEGG | SRREPQVNQQ | QLQQLMDMGF | TREHAMEALL | NTSTMEQATE | YLLTHPPPIM |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| GGVVRDLSMS | EEDQMMRAIA | MSLGQDIPMD | QRAESPEEVA | CRKEEEERKA | REKQEEEEAK | CLEKFQDADP | LEQDELHTFT |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DTMLPGCFHL | LDELPDTVYR | VCDLIMTAIK | RNGADYRDMI | LKQVVNQVWE | AADVLIKAAL | PLTTSDTKTV | SEWISQMATL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PQASNLATRI | LLLTLLFEEL | KLPCAWVVES | SGILNVLIKL | LEVVQPCLQA | AKEQKEVQTP | KWITPVLLLI | DFYEKTAISS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KRRAQMTKYL | QSNSNNWRWF | DDRSGRWCSY | SASNNSTIDS | AWKSGETSVR | FTAGRRRYTV | QFTTMVQVNE | ETGNRRPVML |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| TLLRVPRLNK | NSKNSNGQEL | EKTLEESKEM | DIKRKENKGN | DTPLALESTN | TEKETSLEET | KIGEILIQGL | TEDMVTVLIR |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| ACVSMLGVPV | DPDTLHATLR | LCLRLTRDHK | YAMMFAELKS | TRMILNLTQS | SGFNGFTPLV | TLLLRHIIED | PCTLRHTMEK |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| VVRSAATSGA | GSTTSGVVSG | SLGSREINYI | LRVLGPAACR | NPDIFTEVAN | CCIRIALPAP | RGSGTASDDE | FENLRIKGPN |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| AVQLVKTTPL | KPSPLPVIPD | TIKEVIYDML | NALAAYHAPE | EADKSDPKPG | VMTQEVGQLL | QDMGDDVYQQ | YRSLTRQSSD |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| FDTQSGFSIN | SQVFAADGAS | TETSASGTSQ | GEASTPEESR | DGKKDKEGDR | ASEEGKQKGK | GSKPLMPTST | ILRLLAELVR |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| SYVGIATLIA | NYSYTVGQSE | LIKEDCSVLA | FVLDHLLPHT | QNAEDKDTPA | LARLFLASLA | AAGSGTDAQV | ALVNEVKAAL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2725 | 2 | 1045.0312 | 6.89 | 2 | 64.4 | 11.5 | 2 | 1715-1733 | R.KENKGNDTPLALESTNTEK.E | | |
| 2705 | 1 | 645.8441 | -36.29 | 2 | 64.1 | 10.1 | 1 | 3005-3015 | R.GVQYTRLAVQR.G | | WUP:QUP 0.97 |
| 355 | 1 | 658.3846 | -33.13 | 2 | 33.1 | 10.5 | 2 | 3311-3321 | R.RSSLLTEKLLR.L | | |

# Detailed Protein Report

## Protein 123: pyruvate kinase PKM isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|33286418 | **Score:** | 50.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 5.1 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.03 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530405979 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: pyruvate kinase PKM isoform X3 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSKPHSEAGT | AFIQTQQLHA | AMADTFLEHM | CRLDIDSPPI | TARNTGIICT | IGPASRSVET | LKEMIKSGMN | VARLNFSHGT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HEYHAETIKN | VRTATESFAS | DPILYRPVAV | ALDTKGPEIR | TGLIKGSGTA | EVELKKGATL | KITLDNAYME | KCDENILWLD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YKNICKVVEV | GSKIYVDDGL | ISLQVKQKGA | DFLVTEVENG | GSLGSKKGVN | LPGAAVDLPA | VSEKDIQDLK | FGVEQDVDMV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FASFIRKASD | VHEVRKVLGE | KGKNIKIISK | IENHEGVRRF | DEILEASDGI | MVARGDLGIE | IPAEKVFLAQ | KMMIGRCNRA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GKPVICATQM | LESMIKKPRP | TRAEGSDVAN | AVLDGADCIM | LSGETAKGDY | PLEAVRMQHL | IAREAEAAIY | HLQLFEELRR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LAPITSDPTE | ATAVGAVEAS | FKCCSGAIIV | LTKSGRSAHQ | VARYRPRAPI | IAVTRNPQTA | RQAHLYRGIF | PVLCKDPVQE |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| AWAEDVDLRV | NFAMNVGKAR | GFFKKGDVVI | VLTGWRPGSG | FTNTMRVVPV | P | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 773 | 1 | 599.4299 | 171.21 | 2 | 39.7 | 39.3 | 0 | 33-43 | R.LDIDSPPITAR.N | | |
| 183 | 1 | 628.6439 | 7.16 | 3 | 32.3 | 10.8 | 0 | 74-89 | R.LNFSHGTHEYHAETIK.N | | QU:MU 1.03 |

# Detailed Protein Report

## Protein 124: PREDICTED: regulator of G-protein signaling 3 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578817733 | **Score:** | 50.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 120.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MERSLHRVSL | GSRRAHPDLS | FYLTTFGQLR | LSIDAQDRVL | LLHIIEGKGL | ISKQPGTCDP | YVKISLIPED | SRLRHQKTQT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VPDCRDPAFH | EHFFFPVQEE | DDQKRLLVTV | WNRASQSRQS | GLIGCMSFGV | KSLLTPDKEI | SGWYYLLGEH | LGRTKHLKVA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RRRLRPLRDP | LLRMPGGGDT | ENGKKLKITI | PRGKDGFGFT | ICCDSPVRVQ | AVDSGGPAER | AGLQQLDTVL | QLNERPVEHW |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KCVELAHEIR | SCPSEIILLV | WRMVPQVKPG | PDGGVLRRAS | CKSTHDLQSP | PNKREKNCTH | GVQARPEQRH | SCHLVCDSSD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GLLLGGWERY | TEVAKRGGQH | TLPALSRATA | PTDPNYIILA | PLNPGSQLLR | PVYQEDTIPE | ESGSPSKGKS | YTGLGKKSRL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MKTVQTMKGH | GNYQNCPVVR | PHATHSSYGT | YVTLAPKVLV | FPVFVQPLDL | CNPARTLLLS | EELLLYEGRN | KAAEVTLFAY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SDLLLFTKED | EPGRCDVLRN | PLYLQSVKLQ | EGSSEDLKFC | VLYLAEKAEC | LFTLEAHSQE | QKKRVCWCLS | ENIAKQQQLA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ASPPDSKMFE | TEADEKREMA | LEEGKGPGAE | DSPPSKEPSP | GQELPPGQDL | PPNKDSPSGQ | EPAPSQEPLS | SKDSATSEGS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PPGPDAPPSK | DVPPCQEPPP | AQDLSPCQDL | PAGQEPLPHQ | DPLLTKDLPA | IQESPTRDLP | PCQDLPPSQV | SLPAKALTED |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TMSSGDLLAA | TGDPPAAPRP | AFVIPEVRLD | STYSQKAGAE | QGCSGDEEDA | EEAEEVEEGE | EGEEDEDEDT | SDDNYGERSE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AKRSSMIETG | QGAEGGLSLR | VQNSLRRRTH | SEGSLLQEPR | GPCFASDTTL | HCSDGEGAAS | TWGMPSPSTL | KKELGRNGGS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| MHHLSLFFTG | HRKMSGADTV | GDDDEASRKR | KSKNLAKDMK | NKLGIFRRRN | ESPGAPPAGK | ADKMMKSFKP | TSEEALKWGE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SLEKLLVHKY | GLAVFQAFLR | TEFSEENLEF | WLACEDFKKV | KSQSKMASKA | KKIFAEYIAI | QACKEVNLDS | YTREHTKDNL |
| 1050 | 1060 | 1070 | 1080 | 1090 | | | |
| QSVTRGCFDL | AQKRIFGLME | KDSYPRFLRS | DLYLDLINQK | KMSPPL | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 7 | 6 | 819.8312 | -118.35 | 2 | 29.5 | 14.6 | 2 | 73-85 | R.LRHQKTQTVPDCR.D | Carbamidomethyl: 12 |
| 512 | 1 | 593.1679 | -216.84 | 2 | 36.4 | 10.4 | 0 | 209-220 | R.VQAVDSGGPAER.A | |
| 1949 | 1 | 599.9043 | -89.98 | 3 | 52.7 | 12.8 | 0 | 877-892 | R.NGGSMHHLSLFFTGHR.K | |

# Detailed Protein Report

## Protein 125: PREDICTED: ubiquitin carboxyl-terminal hydrolase 24 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530362258 | **Score:** | 50.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 275.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 3 |

### Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.60 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.27 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDRCMPEAFK | KLLTSSAVHK | WGTEIHEGIY | NMLMLLIELV | AERIKQDPIP | TGLLGVLTMA | FNPDNEYHFK | NRMKVSQRNW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AEVFGEGNMF | AVSPVSTFQK | EPHGWVVDLV | NKFGELGGFA | AIQAKLHSED | IELGAVSALI | QPLGVCAEYL | NSSVVQPMLD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PVILTTIQDV | RSVEEKDLKD | KRLVSIPELL | SAVKLLCMRF | QPDLVTIVDD | LRLDILLRML | KSPHFSAKMN | SLKEVTKLIE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DSTLSKSVKN | AIDTDRLLDW | LVENSVLSIA | LEGNIDQAQY | CDRIKGIIEL | LGSKLSLDEL | TKIWKIQSGQ | SSTVIENIHT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IIAAAAVKFN | SDQLNHLFVL | IQKSWETESD | RVRQKLLSLI | GRIGREARFE | TTSGKVLDVL | WELAHLPTLP | SSLIQQALEE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HLTILSDAYA | VKEAIKRSYI | IKCIEDIKRP | GEWSGLEKNK | KDGFKSSQLN | NPQFVWVVPA | LRQLHEITRS | FIKQTYQKQD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KSIIQDLKKN | FEIVKLVTGS | LIACHRLAAA | VAGPGGLSGS | TLVDGRYTYR | EYLEAHLKFL | AFFLQEATLY | LGWNRAKEIW |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ECLVTGQDVC | ELDREMCFEW | FTKGQHDLES | DVQQQLFKEK | ILKLESYEIT | MNGFNLFKTF | FENVNLCDHR | LKRQGAQLYV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EKLELIGMDF | IWKIAMESPD | EEIANEAIQL | IINYSYINLN | PRLKKDSVSL | HKKFIADCYT | RLEAASSALG | GPTLTHAVTR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ATKMLTATAM | PTVATSVQSP | YRSTKLVIIE | RLLLLAERYV | ITIEDFYSVP | RTILPHGASF | HGHLLTLNVT | YESTKDTFTV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EAHSNETIGS | VRWKIAKQLC | SPVDNIQIFT | NDSLLTVNKD | QKLLHQLGFS | DEQILTVKTS | GSGTPSGSSA | DSSTSSSSSS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SGVFSSSYAM | EQEKSLPGVV | MALVCNVFDM | LYQLANLEEP | RITLRVRKLL | LLIPTDPAIQ | EALDQLDSLG | RKKTLLSESS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SQSSKSPSLS | SKQQHQPSAS | SILESLFRSF | APGMSTFRVL | YNLEVLSSKL | MPTADDDMAR | SCAKSFCENF | LKAGGLSLVV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| NVMQRDSIPS | EVDYETRQGV | YSICLQLARF | LLVGQTMPTL | LDEDLTKDGI | EALSSRPFRN | VSRQTSRQMS | LCGTPEKSSY |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RQLSVSDRSS | IRVEEIIPAA | RVAIQTMEVS | DFTSTVACFM | RLSWAAAAGR | LDLVGSSQPI | KESNSLCPAG | IRNRLSSSGS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| NCSSGSEGEP | VALHAGICVR | QQSVSTKDSL | IAGEALSLLV | TCLQLRSQQL | ASFYNLPCVA | DFIIDILLGS | PSAEIRRVAC |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DQLYTLSQTD | TSAHPDVQKP | NQFLLGVILT | AQLPLWSPTS | IMRGVNQRLL | SQCMEYFDLR | CQLLDDLTTS | EMEQLRISPA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| TMLEDEITWL | DNFEPNRTAE | CETSEADNIL | LAGHLRLIKT | LLSLCGAEKE | MLGSSLIKPL | LDDFLFRASR | IILNSHSPAG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SAAISQQDFH | PKCSTANSRL | AAYEVLVMLA | DSSPSNLQII | IKELLSMHHQ | PDPALTKEFD | YLPPVDSRSS | SGFVGLRNGG |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ATCYMNAVFQ | QLYMQPGLPE | SLLSVDDDTD | NPDDSVFYQV | QSLFGHLMES | KLQYYVPENF | WKIFKMWNKE | LYVREQQDAY |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| EFFTSLIDQM | DEYLKKMGRD | QIFKNTFQGI | YSDQKICKDC | PHRYEREEAF | MALNLGVTSC | QSLEISLDQF | VRGEVLEGSN |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| AYYCEKCKEK | RITVKRTCIK | SLPSVLVIHL | MRFGFDWESG | RSIKYDEQIR | FPWMLNMEPY | TVSGMARQDS | SSEVGENGRS |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| VDQGGGGSPR | KKVALTENYE | LVGVIVHSGQ | AHAGHYYSFI | KDRRGCGKGK | WYKFNDTVIE | EFDLNDETLE | YECFGGEYRP |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| KVYDQTNPYT | DVRRRYWNAY | MLFYQRVSDQ | NSPVLPKKSR | VSVVRQEAED | LSLSAPSSPE | ISPQSSPRPH | RPNNDRLSIL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| TKLVKKGEKK | GLFVEKMPAR | IYQMVRDENL | KFMKNRDVYS | SDYFSFVLSL | ASLNATKLKH | PYYPCMAKVS | LQLAIQFLFQ |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| TYLRTKKKLR | VDTEEWIATI | EALLSKSFDA | CQWLVEYFIS | SEGRELIKIF | LLECNVREVR | VAVATILEKT | LDSALFYQDK |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| LKSLHQLLEV | LLALLDKDVP | ENCKNCAQYF | FLFNTFVQKQ | GIRAGDLLLR | HSALRHMISF | LLGASRQNNQ | IRRWSSAQAR |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2676 | 1 | 585.8808 | 7.47 | 2 | 61.8 | 11.9 | 1 | 284-294 | R.IKGIIELLGSK.L | | |
| 2168 | 1 | 841.4140 | 51.38 | 2 | 57.5 | 11.5 | 1 | 1010-1024 | K.LMPTADDDMARSCAK.S | Carbamidomethyl: 13 | |
| 1965 | 1 | 572.7269 | -108.26 | 2 | 54.9 | 16.4 | 1 | 1760-1771 | R.SVDQGGGGSPRK.K | | WUP:QUP 2.27<br>QU:MU 0.60 |

# Detailed Protein Report

## Protein 126: apolipoprotein B-100 precursor [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|105990532 | **Score:** | 49.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 515.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 0.9 |
|  |  | **No. of unique Peptides:** | 1 |

### Quantitation

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.24 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.38 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDPPRPALLA | LLALPALLLL | LLAGARAEEE | MLENVSLVCP | KDATRFKHLR | KYTYNYEAES | SSGVPGTADS | RSATRINCKV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ELEVPQLCSF | ILKTSQCTLK | EVYGFNPEGK | ALLKKTKNSE | EFAAAMSRYE | LKLAIPEGKQ | VFLYPEKDEP | TYILNIKRGI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ISALLVPPET | EEAKQVLFLD | TVYGNCSTHF | TVKTRKGNVA | TEISTERDLG | QCDRFKPIRT | GISPLALIKG | MTRPLSTLIS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SSQSCQYTLD | AKRKHVAEAI | CKEQHLFLPF | SYKNKYGMVA | QVTQTLKLED | TPKINSRFFG | EGTKKMGLAF | ESTKSTSPPK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QAEAVLKTLQ | ELKKLTISEQ | NIQRANLFNK | LVTELRGLSD | EAVTSLLPQL | IEVSSPITLQ | ALVQCGQPQC | STHILQWLKR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VHANPLLIDV | VTYLVALIPE | PSAQQLREIF | NMARDQRSRA | TLYALSHAVN | NYHKTNPTGT | QELLDIANYL | MEQIQDDCTG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DEDYTYLILR | VIGNMGQTME | QLTPELKSSI | LKCVQSTKPS | LMIQKAAIQA | LRKMEPKDKD | QEVLLQTFLD | DASPGDKRLA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AYLMLMRSPS | QADINKIVQI | LPWEQNEQVK | NFVASHIANI | LNSEELDIQD | LKKLVKEALK | ESQLPTVMDF | RKFSRNYQLY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KSVSLPSLDP | ASAKIEGNLI | FDPNNYLPKE | SMLKTTLTAF | GFASADLIEI | GLEGKGFEPT | LEALFGKQGF | FPDSVNKALY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| WVNGQVPDGV | SKVLVDHFGY | TKDDKHEQDM | VNGIMLSVEK | LIKDLKSKEV | PEARAYLRIL | GEELGFASLH | DLQLLGKLLL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| MGARTLQGIP | QMIGEVIRKG | SKNDFFLHYI | FMENAFELPT | GAGLQLQISS | SGVIAPGAKA | GVKLEVANMQ | AELVAKPSVS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VEFVTNMGII | IPDFARSGVQ | MNTNFFHESG | LEAHVALKAG | KLKFIIPSPK | RPVKLLSGGN | TLHLVSTTKT | EVIPPLIENR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QSWSVCKQVF | PGLNYCTSGA | YSNASSTDSA | SYYPLTGDTR | LELELRPTGE | IEQYSVSATY | ELQREDRALV | DTLKFVTQAE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GAKQTEATMT | FKYNRQSMTL | SSEVQIPDFD | VDLGTILRVN | DESTEGKTSY | RLTLDIQNKK | ITEVALMGHL | SCDTKEERKI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KGVISIPRLQ | AEARSEILAH | WSPAKLLLQM | DSSATAYGST | VSKRVAWHYD | EEKIEFEWNT | GTNVDTKKMT | SNFPVDLSDY |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PKSLHMYANR | LLDHRVPQTD | MTFRHVGSKL | IVAMSSWLQK | ASGSLPYTQT | LQDHLNSLKE | FNLQNMGLPD | FHIPENLFLK |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SDGRVKYTLN | KNSLKIEIPL | PFGGKSSRDL | KMLETVRTPA | LHFKSVGFHL | PSREFQVPTF | TIPKLYQLQV | PLLGVLDLST |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| NVYSNLYNWS | ASYSGGNTST | DHFSLRARYH | MKADSVVDLL | SYNVQGSGET | TYDHKNTFTL | SCDGSLRHKF | LDSNIKFSHV |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EKLGNNPVSK | GLLIFDASSS | WGPQMSASVH | LDSKKKQHLF | VKEVKIDGQF | RVSSFYAKGT | YGLSCQRDPN | TGRLNGESNL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| RFNSSYLQGT | NQITGRYEDG | TLSLTSTSDL | QSGIIKNTAS | LKYENYELTL | KSDTNGKYKN | FATSNKMDMT | FSKQNALLRS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| EYQADYESLR | FFSLLSGSLN | SHGLELNADI | LGTDKINSGA | HKATLRIGQD | GISTSATTNL | KCSLLVLENE | LNAELGLSGA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| SMKLTTNGRF | REHNAKFSLD | GKAALTELSL | GSAYQAMILG | VDSKNIFNFK | VSQEGLKLSN | DMMGSYAEMK | FDHTNSLNIA |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| GLSLDFSSKL | DNIYSSDKFY | KQTVNLQLQP | YSLVTTLNSD | LKYNALDLTN | NGKLRLEPLK | LHVAGNLKGA | YQNNEIKHIY |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| AISSAALSAS | YKADTVAKVQ | GVEFSHRLNT | DIAGLASAID | MSTNYNSDSL | HFSNVFRSVM | APFTMTIDAH | TNGNGKLALW |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| GEHTGQLYSK | FLLKAEPLAF | TFSHDYKGST | SHHLVSRKSI | SAALEHKVSA | LLTPAEQTGT | WKLKTQFNNN | EYSQDLDAYN |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| TKDKIGVELT | GRTLADLTLL | DSPIKVPLLL | SEPINIIDAL | EMRDAVEKPQ | EFTIVAFVKY | DKNQDVHSIN | LPFFETLQEY |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| FERNRQTIIV | VLENVQRNLK | HINIDQFVRK | YRAALGKLPQ | QANDYLNSFN | WERQVSHAKE | KLTALTKKYR | ITENDIQIAL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 222 | 1 | 493.5794 | -31.61 | 3 | 32.8 | 10.5 | 0 | 513-525 | K.CVQSTKPSLMIQK.A | Oxidation: 10 | WUP:QUP 0.38<br>QU:MU 0.24 |

# Detailed Protein Report

## Protein 127: transitional endoplasmic reticulum ATPase [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|6005942 | **Score:** | 49.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 89.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASGADSKGD | DLSTAILKQK | NRPNRLIVDE | AINEDNSVVS | LSQPKMDELQ | LFRGDTVLLK | GKKRREAVCI | VLSDDTCSDE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KIRMNRVVRN | NLRVRLGDVI | SIQPCPDVKY | GKRIHVLPID | DTVEGITGNL | FEVYLKPYFL | EAYRPIRKGD | IFLVRGGMRA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VEFKVVETDP | SPYCIVAPDT | VIHCEGEPIK | REDEEESLNE | VGYDDIGGCR | KQLAQIKEMV | ELPLRHPALF | KAIGVKPPRG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ILLYGPPGTG | KTLIARAVAN | ETGAFFFLIN | GPEIMSKLAG | ESESNLRKAF | EEAEKNAPAI | IFIDELDAIA | PKREKTHGEV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ERRIVSQLLT | LMDGLKQRAH | VIVMAATNRP | NSIDPALRRF | GRFDREVDIG | IPDATGRLEI | LQIHTKNMKL | ADDVDLEQVA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NETHGHVGAD | LAALCSEAAL | QAIRKKMDLI | DLEDETIDAE | VMNSLAVTMD | DFRWALSQSN | PSALRETVVE | VPQVTWEDIG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GLEDVKRELQ | ELVQYPVEHP | DKFLKFGMTP | SKGVLFYGPP | GCGKTLLAKA | IANECQANFI | SIKGPELLTM | WFGESEANVR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EIFDKARQAA | PCVLFFDELD | SIAKARGGNI | GDGGGAADRV | INQILTEMDG | MSTKKNVFII | GATNRPDIID | PAILRPGRLD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QLIYIPLPDE | KSRVAILKAN | LRKSPVAKDV | DLEFLAKMTN | GFSGADLTEI | CQRACKLAIR | ESIESEIRRE | RERQTNPSAM |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EVEEDDPVPE | IRRDHFEEAM | RFARRSVSDN | DIRKYEMFAQ | TLQQSRGFGS | FRFPSGNQGG | AGPSQGSGGG | TGGSVYTEDN |
| 810 | | | | | | | |
| DDDLYG | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2857 | 1 | 1051.5637 | 82.66 | 2 | 66.2 | 14.5 | 1 | 678-696 | K.MTNGFSGADLTEICQRACK.L | Carbamidomethyl: 18 |

# Detailed Protein Report

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**Protein 128:** **syntaxin-binding protein 5 isoform b [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|189217915 | **Score:** | 49.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 127.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.1 |
| | | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRKFNIRKVL | DGLTAGSSSA | SQQQQQQHPP | GNREPEIQET | LQSEHFQLCK | TVRHGFPYQP | SALAFDPVQK | ILAVGTQTGA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LRLFGRPGVE | CYCQHDSGAA | VIQLQFLINE | GALVSALADD | TLHLWNLRQK | RPAILHSLKF | CRERVTFCHL | PFQSKWLYVG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TERGNIHIVN | VESFTLSGYV | IMWNKAIELS | SKSHPGPVVH | ISDNPMDEGK | LLIGFESGTV | VLWDLKSKKA | DYRYTYDEAI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HSVAWHHEGK | QFICSHSDGT | LTIWNVRSPA | KPVQTITPHG | KQLKDGKKPE | PCKPILKVEF | KTTRSGEPFI | ILSGGLSYDT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VGRRPCLTVM | HGKSTAVLEM | DYSIVDFLTL | CETPYPNDFQ | EPYAVVVLLE | KDLVLIDLAQ | NGYPIFENPY | PLSIHESPVT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CCEYFADCPV | DLIPALYSVG | ARQKRQGYSK | KEWPINGGNW | GLGAQSYPEI | IITGHADGSV | KFWDASAITL | QVLYKLKTSK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VFEKSRNKDD | RPNTDIVDED | PYAIQIISWC | PESRMLCIAG | VSAHVIIYRF | SKQEVITEVI | PMLEVRLLYE | INDVETPEGE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QPPPLPTPVG | GSNPQPIPPQ | SHPSTSSSSS | DGLRDNVPCL | KVKNSPLKQS | PGYQTELVIQ | LVWVGGEPPQ | QITSLAVNSS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| YGLVVFGNCN | GIAMVDYLQK | AVLLNLGTIE | LYGSNDPYRR | EPRSPRKSRQ | PSGAGLCDIS | EGTVVPEDRC | KSPTSGSSSP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HNSDDEQKMN | NFIEKVKTKS | RKFSKMVAND | IAKMSRKLSL | PTDLKPDLDV | KDNSFSRSRS | SSVTSIDKES | REAISALHFC |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ETFTRKTDSS | PSPCLWVGTT | LGTVLVIALN | LPPGGEQRLL | QPVIVSPSGT | ILRLKGAILR | MAFLDTTGCL | IPPAYEPWRE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| HNVPEEKDEK | EKLKKRRPVS | VSPSSSQEIS | ENQYAVICSE | KQAKVISLPT | QNCAYKQNIT | ETSFVLRGDI | VALSNSICLA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| CFCANGHIMT | FSLPSLRPLL | DVYYLPLTNM | RIARTFCFTN | NGQALYLVSP | TEIQRLTYSQ | ETCENLQEML | GELFTPVETP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EAPNRGFFKG | LFGGGAQSLD | REELFGESSS | GKASRSLAQH | IPGPGGIEGV | KGAASGVVGE | LARARLALDE | RGQKLGDLEE |
| 1130 | 1140 | 1150 | 1160 | | | | |
| RTAAMLSSAE | SFSKHAHEIM | LKYKDKKWYQ | F | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1682 | 1 | 796.3351 | -89.13 | 2 | 50.8 | 10.5 | 1 | 143-155 | R.ERVTFCHLPFQSK.W | |
| 1487 | 1 | 676.3270 | -69.10 | 2 | 48.8 | 11.5 | 2 | 742-753 | R.KFSKMVANDIAK.M | |
| 1944 | 1 | 665.3207 | -0.95 | 2 | 54.7 | 15.6 | 0 | 1122-1134 | R.TAAMLSSAESFSK.H | |

# Detailed Protein Report

## Protein 129: PREDICTED: rho GTPase-activating protein 26 isoform X6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530380462 | **Score:** | 49.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.1 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.68 | **CV:** | 70.11 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 0.77 | **CV:** | 223.20 % | **No. of Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MKRETRRSAF CVQGWSGGDP ARVVLWGSAG GRGRARHAGV PAVGPECRAR RSQRADPIVS TAPAPLGAEL LSLECPTVRM
        90        100        110        120        130        140        150        160
ERALPRGRCL PLGKDLSSAK RKFADSLNEF KFQCIGDAET DDEMCIARSL QEFATVLRNL EDERIRMIEN ASEVLITPLE
       170        180        190        200        210        220        230        240
KFRKEQIGAA KEAKKKYDKE TEKYCGILEK HLNLSSKKKE SQLQEADSQV DLVRQHFYEV SLEYVFKVQE VQERKMFEFV
       250        260        270        280        290        300        310        320
EPLLAFLQGL FTFYHHGYEL AKDFGDFKTQ LTISIQNTRN RFEGTRSEVE SLMKKMKENP LEHKTISPYT MEGYLYVQEK
       330        340        350        360        370        380        390        400
RHFGTSWVKH YCTYQRDSKQ ITMVPFDQKS GGKGGEDESV ILKSCTRRKT DSIEKRFCFD VEAVDRPGVI TMQALSEEDR
       410        420        430        440        450        460        470        480
RLWMEAMDGR EPVYNSNKDS QSEGTAQLDS IGFSIIRKCI HAVETRGINE QGLYRIVGVN SRVQKLLSVL MDPKTASETE
       490        500        510        520        530        540        550        560
TDICAEWEIK TITSALKTYL RMLPGPLMMY QFQRSFIKAA KLENQESRVS EIHSLVHRLP EKNRQMLQLL MNHLAKLIVP
       570        580        590        600        610        620
GTLKVTGSVD MGKSSISLLF KEMKLLKVRK QQMLERMWRN RNDFTLLVGV
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1925 | 2 | 710.2851 | -115.74 | 2 | 53.9 | 19.4 | 1 | 35-48 | R.ARHAGVPAVGPECR.A | | |
| 47 | 3 | 768.2750 | -160.02 | 2 | 30.4 | 15.4 | 1 | 340-353 | K.QITMVPFDQKSGGK.G | | WUP:QUP 0.20<br>QU:MU 1.27 |
| 1623 | 1 | 516.2455 | -93.79 | 2 | 50.5 | 14.5 | 0 | 466-474 | K.LLSVLMDPK.T | Oxidation: 6 | WUP:QUP 2.95<br>QU:MU 0.36 |

# Detailed Protein Report

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**Protein 130:** **PREDICTED: autophagy-related protein 2 homolog B isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578825925 | **Score:** | 49.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 232.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 2 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MPWPFSESIK KRACRYLLQR YLGHFLQEKL SLEQLSLDLY QGTGSLAQVP LDKWCLNEIL ESADAPLEVT EGFIQSISLS

        90        100        110        120        130        140        150        160
VPWGSLLQDN CALEVRGLEM VFRPRPRPAT GSEPMYWSSF MTSSMQLAKE CLSQKLTDEQ GEGSQPFEGL EKFAETIETV

       170        180        190        200        210        220        230        240
LRRVKVTFID TVLRIEHVPE NSKTGTALEI RIERTVYCDE TADESSGINV HQPTAFAHKL LQLSGVSLFW DEFSASAKSS

       250        260        270        280        290        300        310        320
PVCSTAPVET EPKLSPSWNP KIIYEPHPQL TRNLPEIAPS DPVQIGRLIG RLELSLTLKQ NEVLPGAKLD VDGQIDSIHL

       330        340        350        360        370        380        390        400
LLSPRQVHLL LDMLAAIAGP ENSSKIGLAN KDRKNRPMQQ EDEYRIQMEL NRYYLRKDSL SVGVSSEQSF YETETARTPS

       410        420        430        440        450        460        470        480
SREEVFFSMA DMDMSHSLSS LPPLGDPPNM DLELSLTSTY TNTPAGSPLS ATVLQPTWGE FLDHHKEQPV RGSTFPSNLV

       490        500        510        520        530        540        550        560
HPTPLQKTSL PSRSVSVDES RPELIFRLAV GTFSISVLHI DPLSPPETSQ NLNPLTPMAV AFFTCIEKID PARFSTEDFK

       570        580        590        600        610        620        630        640
SFRAVFAEAC SHDHLRFIGT GIKVSYEQRQ RSASRYFSTD MSIGQMEFLE CLFPTDFHSV PPHYTELLTF HSKEETGSHS

       650        660        670        680        690        700        710        720
PVCLQLHYKH SENRGPQGNQ ARLSSVPHKA ELQIKLNPVC CELDISIVDR LNSLLQPQKL ATVEMMASHM YTSYNKHISL

       730        740        750        760        770        780        790        800
HKAFTEVFLD DSHSPANCRI SVQVATPALN LSVRFPIPDL RSDQERGPWF KKSLQKEILY LAFTDLEFKT EFIGGSTPEQ

       810        820        830        840        850        860        870        880
IKLELTFREL IGSFQEEKGD PSIKFFHVSS GVDGDTTSSD DFDWPRIVLK INPPAMHSIL ERIAAEEEEE NDGHYQEEEE

       890        900        910        920        930        940        950        960
GGAHSLKDVC DLRRPAPSPF SSRRVMFENE QMVMPGDPVE MTEFQDKAIS NSHYVLELTL PNIYVTLPNK SFYEKLYNRI

       970        980        990       1000       1010       1020       1030       1040
FNDLLLWEPT APSPVETFEN ISYGIGLSVA SQLINTFNKD SFSAFKSAVH YDEESGSEEE TLQYFSTVDP NYRSRRKKKL

      1050       1060       1070       1080       1090       1100       1110       1120
DSQNKNSQSF LSVLLNINHG LIAVFTDVKQ DNGDLLENKH GEFWLEFNSG SLFCVTKYEG FDDKHYICLH SSSFSLYHKG

      1130       1140       1150       1160       1170       1180       1190       1200
IVNGVILPTE TRLPSSTRPH WLEPTIYSSE EDGLSKTSSD GVGGDSLNML SVAVKILSDK SESNTKEFLI AVGLKGATLQ

      1210       1220       1230       1240       1250       1260       1270       1280
HRMLPSGLSW HEQILYFLNI ADEPVLGYNP PTSFTTFHVH LWSCALDYRP LYLPIRSLLT VETFSVSSSV ALDKSSSTLR

      1290       1300       1310       1320       1330       1340       1350       1360
IILDEAALHL SDKCNTVTIN LSRDYVRVMD MGLLELTITA VKSDSDGEQT EPRFELHCSS DVVHIRTCSD SCAALMNLIQ

      1370       1380       1390       1400       1410       1420       1430       1440
YIASYGDLQT PNKADMKPGA FQRRSKVDSS GRSSSRGPVL PEADQQMLRD LMSDAMEEID MQQGTSSVKP QANGVLDEKS

      1450       1460       1470       1480       1490       1500       1510       1520
QIQEPCCSDL FLFPDESGNV SQESGPTYAS FSHHFISDAM TGVPTENDDF CILFAPKAAM QEKEEEPVIK IMVDDAIVIR

      1530       1540       1550       1560       1570       1580       1590       1600
DNYFSLPVNK TDTSKAPLHF PIPVIRYVVK EVSLVWHLYG GKDFGIVPPT SPAKSYISPH SSPSHTPTRH GRNTVCGGKG

      1610       1620       1630       1640       1650       1660       1670       1680
RNHDFLMEIQ LSKVKFQHEV YPPCKPDCDS SLSEHPVSRQ VFIVQDLEIR DRLATSQMNK FLYLYCSKEM PRKAHSNMLT

      1690       1700       1710       1720       1730       1740       1750       1760
VKALHVCPES GRSPQECCLR VSLMPLRLNI DQDALFFLKD FFTSLSAEVE LQMTPDPEVK KSPGADVTCS LPRHLSTSKE

      1770       1780       1790       1800       1810       1820       1830       1840
PNLVISFSGP KQPSQNDSAN SVEVVNGMEE KNFSAEEASF RDQPVFFREF RFTSEVPIRL DYHGKHVSMD QGTLAGILIG

      1850       1860       1870       1880       1890       1900       1910       1920
LAQLNCSELK LKRLSYRHGL LGVDKLFSYA ITEWLNDIKK NQLPGILGGV GPMHSLVQLV QGLKDLVWLP IEQYRKDGRI

      1930       1940       1950       1960       1970       1980       1990       2000
VRGFQRGAAS FGTSTAMAAL ELTNRMVQTI QAAAETAYDM VSPGTLSIEP KKTKRFPHHR LAHQPVDLRE GVAKAYSVVK

      2010       2020       2030       2040       2050       2060       2070       2080
EGITDTAQTI YETAAREHES RGVTGAVGEV LRQIPPAVVK PLIVATEATS NVLGGMRNQI RPDVRQDESQ KWRHGDD
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2278 | 1 | 713.2212 | -186.29 | 2 | 56.8 | 10.0 | 1 | 549-560 | K.IDPARFSTEDFK.S | |
| 1611 | 1 | 621.3254 | 12.46 | 2 | 50.4 | 11.2 | 2 | 1590-1601 | R.HGRNTVCGGKGR.N | |

# Detailed Protein Report

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## Protein 131: PREDICTED: probable E3 ubiquitin-protein ligase MYCBP2 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530402184 | **Score:** | 49.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 504.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 3 |

### Quantitation

| | | | |
|---|---|---|---|
| ***WUP:QUP*** | **Median:** 0.15 | **CV:** 0.00 % | **No. of Peptides:** 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMMCAATASP | AAASSGLGGD | GFYPAATFSS | SPAPGALFMP | VPDGSVAAAG | LGLGLPAADS | RGHYQLLLSG | RALADRYRRI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YTAALNDRDQ | GGGSAGHPAS | RNKKILNKKK | LKRKQKSKSK | VKTRSKSENL | ENTVIIPDIK | LHSNPSAFNI | YCNVRHCVLE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WQKKEISLAA | ASKNSVQSGE | SDSDEEEESK | EPPIKLPKII | EVGLCEVFEL | IKETRFSHPS | LCLRSLQALL | NVLQGQQPEG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LQSEPPEVLE | SLFQLLLEIT | VRSTGMNDST | GQSLTALSCA | CLFSLVASWG | ETGRTLQAIS | AILTNNGSHA | CQTIQVPTIL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NSLQRSVQAV | LVGKIQIQDW | FSNGIKKAAL | MHKWPLKEIS | VDEDDQCLLQ | NDGFFLYLLC | KDGLYKIGSG | YSGTVRGHIY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NSTSRIRNRK | EKKSWLGYAQ | GYLLYRDVNN | HSMTAIRISP | ETLEQDGTVM | LPDCHTEGQN | ILFTDGEYIN | QIAASRDDGF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VVRIFATSTE | PVLQQELQLK | LARKCLHACG | ISLFDLEKDL | HIISTGFDEE | SAILGAGREF | ALMKTANGKI | YYTGKYQSLG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IKQGGPSAGK | WVELPITKSP | KIVHFSVGHD | GSHALLVAED | GSIFFTGSAS | KGEDGESTKS | RRQSKPYKPK | KIIKMEGKIV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VYTACNNGSS | SVISKDGELY | MFGKDAIYSD | SSSLVTDLKG | HFVTQVAMGK | AHTCVLMKNG | EVWTFGVNNK | GQCGRDTGAM |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NQGGKGFGVE | NMATAMDEDL | EEELDEKDEK | SMMCPPGMHK | WKLEQCMVCT | VCGDCTGYGA | SCVSSGRPDR | VPGGICGCGS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GESGCAVCGC | CKACARELDG | QEARQRGILD | AVKEMIPLDL | LLAVPVPGVN | IEEHLQLRQE | EKRQRVIRRH | RLEEGRGPLV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| FAGPIFMNHR | EQALARLRSH | PAQLKHKRDK | HKDGSGERGE | KDASKITTYP | PGSVRFDCEL | RAVQVSCGFH | HSVVLMENGD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VYTFGYGQHG | QLGHGDVNSR | GCPTLVQALP | GPSTQVTAGS | NHTAVLLMDG | QVFTFGSFSK | GQLGRPILDV | PYWNAKPAPM |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PNIGSKYGRK | ATWIGASGDQ | TFLRIDEALI | NSHVLATSEI | FASKHIIGLV | PASISEPPPF | KCLLINKVDG | SCKTFNDSEQ |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EDLQGFGVCL | DPVYDVIWRF | RPNTRELWCY | NAVVADARLP | SAADMQSRCS | ILSPELALPT | GSRALTTRSH | AALHILGCLD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TLAAMQDLKM | GVASTEEETQ | AVMKVYSKED | YSVVNRFESH | GGGWGYSAHS | VEAIRFSADT | DILLGGLGLF | GGRGEYTAKI |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KLFELGPDGG | DHETDGDLLA | ETDVLAYDCA | AREKYAMMFD | EPVLLQAGWW | YVAWARVSGP | SSDCGSHGQA | SITTDDGVVF |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| QFKSSKKSNN | GTDVNAGQIP | QLLYRLPTSD | GSASKGKQQT | SEPVHILKRS | FARTVSVECF | ESLLSILHWS | WTTLVLGVEE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LRGLKGFQFT | ATLLDLERLR | FVGTCCLRLL | RVYTCEIYPV | SATGKAVVEE | TSKLAECIGK | TRTLLRKILS | EGVDHCMVKL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| DNDPQGYLSQ | PLSLLEAVLQ | ECHNTFTACF | HSFYPTPALQ | WACLCDLLNC | LDQDIQEANF | KTSSSRLLAA | VMSALCHTSV |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KLTSIFPIAY | DGEVLLRSIV | KQVSTENDST | LVHRFPLLVA | HMEKLSQSEE | NISGMTSFRE | VLEKMLVIVV | LPVRNSLRRE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| NELFSSHLVS | NTCGLLASIV | SELTASALGS | EVDGLNSLHS | VKASANRFTK | TSQGRSWNTG | NGSPDAICFS | VDKPGIVVVG |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| FSVYGGGGIH | EYELEVLVDD | SEHAGDSTHS | HRWTSLELVK | GTYTTDDSPS | DIAEIRLDKV | VPLKENVKYA | VRLRNYGSRT |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| ANGDGGMTTV | QCPDGVTFTF | STCSLSSNGT | NQTRGQIPQI | LYYRSEFDGD | LQSQLLSKAN | EEDKNCSRAL | SVVSTVVRAS |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| KDLLHRALAV | DADDIPELLS | SSSLFSMLLP | LIIAYIGPVA | AAIPKVAVEV | FGLVQQLLPS | VAILNQKYAP | PAFNPNQSTD |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| STTGNQPEQG | LSACTTSSHY | AVIESEHPYK | PACVMHYKVT | FPECVRWMTI | EFDPQCGTAQ | SEDVLRLLIP | VRTVQNSGYG |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| PKLTSVHENL | NSWIELKKFS | GSSGWPTMVL | VLPGNEALFS | LETASDYVKD | DKASFYGFKC | FAIGYEFSPG | PDEGVIQLEK |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1748 | 3 | 697.3510 | 1.93 | 3 | 50.2 | 15.7 | 1 | 680-698 | K.GHFVTQVAMGKAHTCVLMK.N | Oxidation: 9, 18 | |
| 2398 | 1 | 1023.7079 | 112.56 | 2 | 59.9 | 13.0 | 2 | 2442-2460 | K.VKDPPKGMIPPGTQLVKPK.S | Oxidation: 8 | |
| 2407 | 1 | 973.4149 | -88.00 | 2 | 60.6 | 10.4 | 1 | 3799-3817 | K.DGESTKIAGQISASVAQQR.N | | WUP:QUP 0.15 |

# Detailed Protein Report

**Protein 132:** **cytospin-B isoform 2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|75750474 | **Score:** | 49.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 110.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 6.0 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGNHSGRPED | PEPGAFTTTK | RTGIPAPREF | SVTVSRERSV | PRGPSNPRKS | VSSPTSSNTP | TPTKHLRTPS | TKPKQENEGG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EKAALESQVR | ELLAEAKAKD | SEINRLRSEL | KKYKEKRTLN | AEGTDALGPN | VDGTSVSPGD | TEPMIRALEE | KNKNFQKELS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DLEEENRVLK | EKLIYLEHSP | NSEGAASHTG | DSSCPTSITQ | ESSFGSPTGN | QMSSDIDEYK | KNIHGNALRT | SGSSSSDVTK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ASLSPDASDF | EHITAETPSR | PLSSTSNPFK | SSKCSTAGSS | PNSVSELSLA | SLTEKIQKME | ENHHSTAEEL | QATLQELSDQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QQMVQELTAE | NEKLVDEKTI | LETSFHQHRE | RAEQLSQENE | KLMNLLQERV | KNEEPTTQEG | KIIELEQKCT | GILEQGRFER |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EKLLNIQQQL | TCSLRKVEEE | NQGALEMIKR | LKEENEKLNE | FLELERHNNN | MMAKTLEECR | VTLEGLKMEN | GSLKSHLQGE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KQKATEASAV | EQTAESCEVQ | EMLKVARAEK | DLLELSCNEL | RQELLKANGE | IKHVSSLLAK | VEKDYSYLKE | ICDHQAEQLS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RTSLKLQEKA | SESDAEIKDM | KETIFELEDQ | VEQHRAVKLH | NNQLISELES | SVIKLEEQKS | DLERQLKTLT | KQMKEETEEW |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RRFQADLQTA | VVVANDIKCE | AQQELRTVKR | KLLEEEEKNA | RLQKELGDVQ | GHGRVVTSRA | APPPVDEEPE | SSEVDAAGRW |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PGVCVSRTSP | TPPESATTVK | SLIKSFDLGR | PGGAGQNISV | HKTPRSPLSG | IPVRTAPAAA | VSPMQRHSTY | SSVRPASRGV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TQRLDLPDLP | LSDILKGRTE | TLKPDPHLRK | SPSLESLSRP | PSLGFGDTRL | LSASTRAWKP | QSKLSVERKD | PLAALAREYG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GSKRNALLKW | CQKKTQGYAN | IDITNFSSSW | SDGLAFCALL | HTYLPAHIPY | QELNSQEKKR | NLLLAFEAAE | SVGIKPSLEL |
| 970 | 980 | 990 | | | | | |
| SEMLYTDRPD | WQSVMQYVAQ | IYKYFET | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 14 | 1 | 1103.5194 | -101.41 | 2 | 29.8 | 16.5 | 2 | 799-818 | R.GVTQRLDLPDLPLSDILKGR.T | |
| 29 | 1 | 1001.9624 | -50.81 | 2 | 30.0 | 16.6 | 0 | 831-849 | K.SPSLESLSRPPSLGFGDTR.L | |

# Detailed Protein Report

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**Protein 133:** **myomesin-1 isoform b [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|140560917 | **Score:** | 48.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 177.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSLPFYQRCH | QHYDLSYRNK | DVRSTVSHYQ | REKKRSAVYT | QGSTAYSSRS | SAAHRRESEA | FRRASASSSQ | QQASQHALSS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EVSRKAASAY | DYGSSHGLTD | SSLLLDDYSS | KLSPKPKRAK | HSLLSGEEKE | NLPSDYMVPI | FSGRQKHVSG | ITDTEEERIK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EAAAYIAQRN | LLASEEGITT | SKQSTASKQT | TASKQSTASK | QSTASKQSTA | SRQSTASRQS | VVSKQATSAL | QQEETSEKKS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RKVVIREKAE | RLSLRKTLEE | TETYHAKLNE | DHLLHAPEFI | IKPRSHTVWE | KENVKLHCSI | AGWPEPRVTW | YKNQVPINVH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ANPGKYIIES | RYGMHTLEIN | GCDFEDTAQY | RASAMNVKGE | LSAYASVVVK | RYKGEFDETR | FHAGASTMPL | SFGVTPYGYA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SRFEIHFDDK | FDVSFGREGE | TMSLGCRVVI | TPEIKHFQPE | IQWYRNGVPL | SPSKWVQTLW | SGERATLTFS | HLNKEDEGLY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TIRVRMGEYY | EQYSAYVFVR | DADAEIEGAP | AAPLDVKCLE | ANKDYIIISW | KQPAVDGGSP | ILGYFIDKCE | VGTDSWSQCN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DTPVKFARFP | VTGLIEGRSY | IFRVRAVNKM | GIGFPSRVSE | PVAALDPAEK | ARLKSRPSAP | WTGQIIVTEE | EPSEGIVPGP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PTDLSVTEAT | RSYVVLSWKP | PGQRGHEGIM | YFVEKCEAGT | ENWQRVNTEL | PVKSPRFALF | DLAEGKSYCF | RVRCSNSAGV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GEPSEATEVT | VVGDKLDIPK | APGKIIPSRN | TDTSVVVSWE | ESKDAKELVG | YYIEASVAGS | GKWEPCNNNP | VKGSRFTCHG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LVTGQSYIFR | VRAVNAAGLS | EYSQDSEAIE | VKAAIAPPSP | PCDITCLESF | RDSMVLGWKQ | PDKIGGAEIT | GYYVNYREVI |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DGVPGKWREA | NVKAVSEEAY | KISNLKENMV | YQFQVAAMNM | AGLGAPSAVS | ECFKCEEWTI | AVPGPPHSLK | CSEVRKDSLV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LQWKPPVHSG | RTPVTGYFVD | LKEAKAKEDQ | WRGLNEAAIK | NVYLKVRGLK | EGVSYVFRVR | AINQAGVGKP | SDLAGPVVAE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TRPGTKEVVV | NVDDDGVISL | NFECDKMTPK | SEFSWSKDYV | STEDSPRLEV | ESKGNKTKMT | FKDLGMDDLG | IYSCDVTDTD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GIASSYLIDE | EELKRLLALS | HEHKFPTVPV | KSELAVEILE | KGQVRFWMQA | EKLSGNAKVN | YIFNEKEIFE | GPKYKMHIDR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| NTGIIEMFME | KLQDEDEGTY | TFQLQDGKAT | NHSTVVLVGD | VFKKLQKEAE | FQRQEWIRKQ | GPHFVEYLSW | EVTGECNVLL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KCKVANIKKE | THIVWYKDER | EISVDEKHDF | KDGICTLLIT | EFSKKDAGIY | EVILKDDRGK | DKSRLKLVDE | AFKELMMEVC |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KKIALSATDL | KIQSTAEGIQ | LYSFVTYYVE | DLKVNWSHNG | SAIRYSDRVK | TGVTGEQIWL | QINEPTPNDK | GKYVMELFDG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KTGHQKTVDL | SGQAYDEAYA | EFQRLKQAAI | AEKNRARVLG | GLPDVVTIQE | GKALNLTCNV | WGDPPPEVSW | LKNEKALASD |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | |
| DHCNLKFEAG | RTAYFTINGV | STADSGKYGL | VVKNKYGSET | SDFTVSVFIP | EEEARMAALE | SLKGGKKAK | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 792 | 1 | 555.7879 | -13.08 | 2 | 38.3 | 14.3 | 0 | 697-706 | R.FALFDLAEGK.S | |
| 1871 | 2 | 621.3062 | -102.44 | 2 | 53.7 | 17.1 | 2 | 1465-1475 | R.LKQAAIAEKNR.A | |

# Detailed Protein Report

## Protein 134: nucleolar transcription factor 1 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|115529449 | **Score:** | 48.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 84.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 3 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|115529451 | refseq_human (refseq_human_20140103.fasta) | nucleolar transcription factor 1 isoform b [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNGEADCPTD | LEMAAPKGQD | RWSQEDMLTL | LECMKNNLPS | NDSSKFKTTE | SHMDWEKVAF | KDFSGDMCKL | KWVEISNEVR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KFRTLTELIL | DAQEHVKNPY | KGKKLKKHPD | FPKKPLTPYF | RFFMEKRAKY | AKLHPEMSNL | DLTKILSKKY | KELPEKKKMK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YIQDFQREKQ | EFERNLARFR | EDHPDLIQNA | KKSDIPEKPK | TPQQLWYTHE | KKVYLKVRPD | EIMRDYIQKH | PELNISEEGI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TKSTLTKAER | QLKDKFDGRP | TKPPPNSYSL | YCAELMANMK | DVPSTERMVL | CSQQWKLLSQ | KEKDAYHKKC | DQKKKDYEVE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LLRFLESLPE | EEQQRVLGEE | KMLNINKKQA | TSPASKKPAQ | EGGKGGSEKP | KRPVSAMFIF | SEEKRRQLQE | ERPELSESEL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TRLLARMWND | LSEKKKAKYK | AREAALKAQS | ERKPGGEREE | RGKLPESPKR | AEEIWQQSVI | GDYLARFKND | RVKALKAMEM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TWNNMEKKEK | LMWIKKAAED | QKRYERELSE | MRAPPAATNS | SKKMKFQGEP | KKPPMNGYQK | FSQELLSNGE | LNHLPLKERM |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VEIGSRWQRI | SQSQKEHYKK | LAEEQQKQYK | VHLDLWVKSL | SPQDRAAYKE | YISNKRKSMT | KLRGPNPKSS | RTTLQSKSES |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EEDDEEDEDD | EDEDEEEEDD | ENGDSSEDGG | DSSESSSEDE | SEDGDENEED | DEDEDDDEDD | DEDEDNESEG | SSSSSSSSGD |
| 730 | | | | | | | |
| SSDSDSN | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2859 | 3 | 856.9262 | 37.72 | 2 | 66.2 | 13.0 | 1 | 474-487 | K.ALKAMEMTWNNMEK.K | Oxidation: 5 |
| 2869 | 1 | 856.9447 | 59.29 | 2 | 66.4 | 17.0 | 1 | 474-487 | K.ALKAMEMTWNNMEK.K | Oxidation: 7 |
| 1591 | 1 | 472.2351 | -22.65 | 2 | 49.6 | 18.5 | 0 | 513-522 | R.APPAATNSSK.K | |

# Detailed Protein Report

## Protein 135: fibrinogen beta chain isoform 2 preproprotein [Homo sapiens]

**Accession:** gi|296080754
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl, Oxidation

**Score:** 48.5
**MW [kDa]:** 49.9
**pI:** 9.0
**Sequence Coverage [%]:** 8.6
**No. of unique Peptides:** 3

## Quantitation

***QU:MU*** **Median:** 0.90 **CV:** 0.00 % **No. of Peptides:** 1
***WUP:QUP*** **Median:** 0.69 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKRMVSWSFH | KLKTMKHLLL | LLLCVFLVKS | QGVNDNEEGF | FSARGHRPLD | KKREEALLQQ | ERPIRNSVDE | LNNNVEAVSQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TSSSSFQYMY | LLKDLWQKRQ | KQVKDNENVV | NEYSSELEKH | QLYIDETVNS | NIPTNLRVLR | SILENLRSKI | QKLESDVSAQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MEYCRTPCTV | SCNIPVVSGK | ECEEIIRKGG | ETSEMYLIQP | DSSVKPYRVY | CDMNTENGGW | TVIQNRQDGS | VDFGRKWDPY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KQGFGNVATN | TDGKNYCGLP | GEYWLGNDKI | SQLTRMGPTE | LLIEMEDWKG | DKVKAHYGGF | TVQNEANKYQ | ISVNKYRGTA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GNALMDGASQ | LMGENRTMTI | HNGMFFSTYD | RDNDGWLTSD | PRKQCSKEDG | GGWWYNRCHA | ANPNGRYYWG | GQYTWDMAKH |
| 410 | 420 | 430 | 440 | | | | |
| GTDDGVVWMN | WKGSWYSMRK | MSMKIRPFFP | QQ | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 590 | 2 | 809.8948 | -6.44 | 2 | 37.4 | 25.6 | 0 | 166-180 | R.TPCTVSCNIPVVSGK.E | Carbamidomethyl: 3, 7 | QU:MU 0.90<br>WUP:QUP 0.69 |
| 1919 | 1 | 862.3067 | -107.58 | 2 | 53.9 | 11.4 | 0 | 276-289 | R.MGPTELLIEMEDWK.G | Oxidation: 1, 10 | |
| 747 | 1 | 516.6531 | -255.12 | 2 | 37.8 | 11.5 | 0 | 425-432 | K.IRPFFPQQ.- | | |

# Detailed Protein Report

**Protein 136:** **kinesin-like protein KIF20B isoform 2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|46049114 | **Score:** | 48.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 206.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 3.8 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MESNFNQEGV | PRPSYVFSAD | PIARPSEINF | DGIKLDLSHE | FSLVAPNTEA | NSFESKDYLQ | VCLRIRPFTQ | SEKELESEGC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VHILDSQTVV | LKEPQCILGR | LSEKSSGQMA | QKFSFSKVFG | PATTQKEFFQ | GCIMQPVKDL | LKGQSRLIFT | YGLTNSGKTY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TFQGTEENIG | ILPRTLNVLF | DSLQERLYTK | MNLKPHRSRE | YLRLSSEQEK | EEIASKSALL | RQIKEVTVHN | DSDDTLYGSL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TNSLNISEFE | ESIKDYEQAN | LNMANSIKFS | VWVSFFEIYN | EYIYDLFVPV | SSKFQKRKML | RLSQDVKGYS | FIKDLQWIQV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SDSKEAYRLL | KLGIKHQSVA | FTKLNNASSR | SHSIFTVKIL | QIEDSEMSRV | IRVSELSLCD | LAGSERTMKT | QNEGERLRET |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GNINTSLLTL | GKCINVLKNS | EKSKFQQHVP | FRESKLTHYF | QSFFNGKGKI | CMIVNISQCY | LAYDETLNVL | KFSAIAQKVC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VPDTLNSSQE | KLFGPVKSSQ | DVSLDSNSNS | KILNVKRATI | SWENSLEDLM | EDEDLVEELE | NAEETQNVET | KLLDEDLDKT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LEENKAFISH | EEKRKLLDLI | EDLKKKLINE | KKEKLTLEFK | IREEVTQEFT | QYWAQREADF | KETLLQEREI | LEENAERRLA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IFKDLVGKCD | TREEAAKDIC | ATKVETEEAT | ACLELKFNQI | KAELAKTKGE | LIKTKEELKK | RENESDSLIQ | ELETSNKKII |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TQNQRIKELI | NIIDQKEDTI | NEFQNLKSHM | ENTFKCNDKA | DTSSLIINNK | LICNETVEVP | KDSKSKICSE | RKRVNENELQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QDEPPAKKGS | IHVSSAITED | QKKSEEVRPN | IAEIEDIRVL | QENNEGLRAF | LLTIENELKN | EKEEKAELNK | QIVHFQQELS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LSEKKNLTLS | KEVQQIQSNY | DIAIAELHVQ | KSKNQEQEEK | IMKLSNEIET | ATRSITNNVS | QIKLMHTKID | ELRTLDSVSQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ISNIDLLNLR | DLSNGSEEDN | LPNTQLDLLG | NDYLVSKQVK | EYRIQEPNRE | NSFHSSIEAI | WEECKEIVKA | SSKKSHQIEE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LEQQIEKLQA | EVKGYKDENN | RLKEKEHKNQ | DDLLKEKETL | IQQLKEELQE | KNVTLDVQIQ | HVVEGKRALS | ELTQGVTCYK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| AKIKELETIL | ETQKVECSHS | AKLEQDILEK | ESIILKLERN | LKEFQEHLQD | SVKNTKDLNV | KELKLKEEIT | QLTNNLQDMK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| HLLQLKEEEE | ETNRQETEKL | KEELSASSAR | TQNLKADLQR | KEEDYADLKE | KLTDAKKQIK | QVQKEVSVMR | DEDKLLRIKI |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| NELEKKKNQC | SQELDMKQRT | IQQLKEQLNN | QKVEEAIQQY | ERACKDLNVK | EKIIEDMRMT | LEEQEQTQVE | QDQVLEAKLE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| EVERLATELE | KWKEKCNDLE | TKNNQRSNKE | HENNTDVLGK | LTNLQDELQE | SEQKYNADRK | KWLEEKMMLI | TQAKEAENIR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| NKEMKKYAED | RERFFKQQNE | MEILTAQLTE | KDSDLQKWRE | ERDQLVAALE | IQLKALISSN | VQKDNEIEQL | KRIISETSKI |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ETQIMDIKPK | RISSADPDKL | QTEPLSTSFE | ISRNKIEDGS | VVLDSCEVST | ENDQSTRFPK | PELEIQFTPL | QPNKMAVKHP |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| GCTTPVTVKI | PKARKRKSNE | MEEDLVKCEN | KKNATPRTNL | KFPISDDRNS | SVKKEQKVAI | RPSSKKTYSL | RSQASIIGVN |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LATKKKEGTL | QKFGDFLQHS | PSILQSKAKK | IIETMSSSKL | SNVEASKENV | SQPKRAKRKL | YTSEISSPID | ISGQVILMDQ |
| 1770 | 1780 | 1790 | | | | | |
| KMKESDHQII | KRRLRTKTAK | | | | | | |

| Cmpd. | No. of | m/z meas. | Δ m/z | z | Rt | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

|  | Cmpds. |  | [ppm] |  | [min] |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|
| 20 | 1 | 1103.5042 | -42.73 | 2 | 29.9 | 14.1 | 2 | 93-112 | K.EPQCILGRLSEKSSGQMAQK.F | Oxidation: 17 |
| 1683 | 1 | 954.5011 | 22.43 | 3 | 51.3 | 10.8 | 1 | 448-471 | K.GKICMIVNISQCYLAYDETLNVLK.F | Carbamidomethyl: 4, 12;<br>Oxidation: 5 |

# Detailed Protein Report

## Protein 137: PREDICTED: neurobeachin-like protein 1 isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578804777 | **Score:** | 48.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 305.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASRERLFEL | WMLYCTKKDP | DYLKLWLDTF | VSSYEQFLDV | DFEKLPTRVD | DMPPGISLLP | DNILQVLRIQ | LLQCVQKMAD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GLEEQQQALS | ILLVKFFIIL | CRNLSNVEEI | GTCSYINYVI | TMTTLYIQQL | KSKKKEKEMA | DQTCIEEFVI | HALAFCESLY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DPYRNWRHRI | SGRILSTVEK | SRQKYKPASL | TVEFVPFFYQ | CFQESEHLKE | SLKCCLLHLF | GAIVAGGQRN | ALQAISPATM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EVLMRVLADC | DSWEDGDPEE | VGRKAELTLK | CLTEVVHILL | SSNSDQRQVE | TSTILENYFK | LLNSDHSALP | NQRRSRQWEN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RFIALQIKML | NTITAMLDCT | DRPVLQAIFL | NSNCFEHLIR | LLQNCKEVFK | ERIGYTHMLE | VLKSLGQPPL | ELLKELMNMA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VEGDHTSVGI | LGISNVQPLL | LLIQWLPELQ | SHDLQIFISD | WLKRICCINR | QSRTTCVNAN | MGIRIIETLD | LHSSLHQTCA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ENLIAIHGSL | GSQSVSSEEI | RRLLRLLRVD | ESESVHPYVT | PVTRAILTMA | RKLSLESALQ | YFNLSHSMAG | ISVPPIQKWP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GSAFSFSAWF | CLDQDQLTLG | IANKGGKRKQ | LYSFFTGSGM | GFEAFITHSG | MLVVAVCTKR | EYATVMLPDH | SFCDSLWHNI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TVVHMPGKRP | FGQSFVYIYD | NGQQKVSAPL | RFPAMNEPFT | SCCIGSAGQR | TTTPPPSQIP | DPPFSSPITP | HRTSFGGILS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SASWGGTIEK | SKLITKLISA | GTQDSEWGCP | TSLEGQLGSV | IIFYEPLQPP | QVKALYLAGP | NCLSPWKCQE | SDMADLPGNI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LLYYTAKACK | NSICLDLSTN | CLHGRLTGNK | VVNWDIKDII | NCIGGLNVLF | PLLEQISHFS | EGQIPEEKNE | STVPESVTPV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EGDWLVWTST | KASESRLERN | LVATFILIVK | HFIQRHPINQ | GNLIHSHGVA | TLGALLQKVP | STLMDVNVLM | AVQLLIEQVS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LEKNMQLLQQ | MYQYLLFDFR | IWNRGDFPFR | IGHIQYLSTI | IKDSRRVFRK | KYGVQFLLDT | LRIYYGNGCK | YNELSLDDIR |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TIRTSLYGLI | KYFLCKGGSH | EEIQSIMGYI | AATNEEEQLF | GILDVLFSLL | RTSPTRGQLF | LLLFEPGNAD | ILYALLLNQK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| YSDRLREIIF | KIMEQMLKCT | NVYERSKQHI | RLREVGYSGL | GLLLNEALVN | TSLIKNLTHQ | IINTDPVINF | KDLLSVVYIS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| HRAHINVRVA | ICRKVLQILQ | FQPDAAHQIS | QQVGWQDTLV | RLFLKAKFEN | GNTLHKHSRA | VLMKDNDKNM | STEDTKKNSD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| EKTDEEKITS | FASANVSSDQ | WSLEDRHSLD | SNTPLFPEDS | SVGELSFKSE | NQEEFWHSNP | SHLSLDLSGI | DSCEMSDSGS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| QVPDSLPSTP | SPVESTKSFS | VHSDRESSIT | NDMGFSDDFS | LLESQERCEE | ELLQLLTHIL | NYVMCKGLEK | SDDDTWIERG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| QVFSALSKPG | ISSELLRPSD | EIKLTLLQKM | LEWAISENRE | AKTNPVTAEN | AFRLVLIIQD | FLQSEGLVNS | NMWTEKLLED |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| MMLLFDCLSV | CYSESPVWVK | LSQIQIQLLL | GFIGRGNLQV | CAMASAKLNT | LLQTKVIENQ | DEACYILGKL | EHVLSQSIKE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QTEIYSFLIP | LVRTLVSKIY | ELLFMNLHLP | SLPFTNGSSS | FFEDFQEYCN | SNEWQVYIEK | YIVPYMKQYE | AHTFYDGHEN |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| MALYWKDCYE | ALMVNMHKRD | REGGESKLKF | QELFVEPFNR | KARQENLRYN | NMLKQLSSQQ | LATLRRWKAI | QLYLTCERGP |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| WAKRKQNPIH | WKLANVENYS | RMRLKLVPNY | NFKTHEEASA | LRDNLGIQHS | QPSSDTLLLE | VVKQVKVSDM | VEDKLDLPEE |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| DITARVNVDE | KEEQDQKEKL | VLMEDCELIT | IIDVIPGRLE | ITTQHIYFYD | GSIEKEDGVG | FDFKWPHSQI | REIHLRRYNL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| RRSALEIFHV | DQSNYFLNFK | KEVRNKIYSR | LLSLHSPNSY | YGSRSPQELF | KASGLTQKWV | NREISNFDYL | IQINTMAGRT |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| YNDLAQYPVF | PWILQDYTSE | ELDLNNPAVF | RDLSKPIGVV | NEKNAKAMRE | KYENFEDPMG | TIDKFHYGTH | YSNSAGVMHY |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| LIRVEPFTTL | HIQLQSGRFD | CADRQFHSIP | ATWQALMDNP | YDVKELIPEF | FYFPEFLENQ | NQFNLGRLQI | SKELVNDVIL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1799 | 1 | 1045.0496 | 94.89 | 2 | 50.8 | 15.5 | 0 | 672-690 | R.FPAMNEPFTSCCIGSAGQR.T | Carbamidomethyl: 12;<br>Oxidation: 4 |
| 2060 | 1 | 899.3817 | -81.00 | 2 | 54.1 | 19.6 | 0 | 713-730 | R.TSFGGILSSASWGGTIEK.S | |

## Protein 138: PREDICTED: protein transport protein Sec16A isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530426857 | **Score:** | 47.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 240.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 3 |

### Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.63 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.37 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGAAGLGLGP | TTCSLTLFKQ | VRNLTPERQM | LAEQIGPGAT | SAGLKLSLHR | LRPCWRGTDI | TPSLTSRRPS | WGQGWLPPRE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DLSRCWELSL | PRCHRAGTPT | TAPALWKEQQ | RKAAALPCPC | QAGVQLQLRN | SYILLPSVSS | IDLCKGSVMQ | PPPQTVPSGM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AGPPPAGNPR | SVFWASSPYR | RRANNNAAVA | PTTCPLQPVT | DPFAFSRQAL | QSTPLGSSSK | SSPPVLQGPA | PAGFSQHPGL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LVPHTHARDS | SQGPCEPLPG | PLTQPRAHAS | PFSGALTPSA | PPGPEMNRSA | EVGPSSEPEV | QTLPYLPHYI | PGVDPETSHG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GHPHGNMPGL | DRPLSRQNPH | DGVVTPAASP | SLPQPGLQMP | GQWGPVQGGP | QPSGQHRSPC | PEGPVPSGVP | CATSVPHFPT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PSILHQGPGH | EQHSPLVAPP | AALPSDGRDE | VSHLQSGSHL | ANNSDPESTF | RQNPRIVNHW | ASPELRQNPG | VKNEHRPASA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LVNPLARGDS | PENRTHHPLG | AGAGSGCAPL | EADSGASGAL | AMFFQGGETE | NEENLSSEKA | GLSGQADFDD | FCSSPGLGRP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PAPTHVGAGS | LCQALLPGPS | NEAAGDVWGD | TASTGVPDAS | GSQYENVENL | EFVQNQEVLP | SEPLNLDPSS | PSDQFRYGPL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PGPAVPRHGA | VCHTGAPDAT | LHTVHPDSVS | SSYSSRSHGR | LSGSARPQEL | VGTFIQQEVG | KPEDEASGSF | FKQIDSSPVG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GETDETTVSQ | NYRGSVSQPS | TPSPPKPTGI | FQTSANSSFE | PVKSHLVGVK | PFEADRANVV | GEVRETCVRQ | KQCRPAAALP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DASPGNLEQP | PDNMETLCAP | QVCPLPLNST | TEAVHMLPHA | GAPPLDTVYP | APEKRPSART | QGPVKCESPA | TTLWAQSELP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DFGGNVLLAP | AAPALYVCAK | PQPPVVQPPE | EAMSGQQSRN | PSSAAPVQSR | GGIGASENLE | NPPKMGEEEA | LQSQVTKDAQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GQPGLERAQQ | ELVPPQQQAS | PPQLPKAMFS | ELSNPESLPA | QGQAQNSAQS | PASLVLVDAG | QQLPPRPPQS | SSVSLVSSGS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GQAAVPSEQP | WPQPVPALAP | GPPPQDLAAY | YYYRPLYDAY | QPQYSLPYPP | EPGAASLYYQ | DVYSLYEPRY | RPYDGAASAY |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| AQNYRYPEPE | RPSSRASHSS | ERPPPRQGYP | EGYYSSKSGW | SSQSDYYASY | YSSQYDYGDP | GHWDRYHYSA | RVRDPRTYDR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| RYWCDAEYDA | YRREHSAFGD | RPEKRDNNWR | YDPRFTGSFD | DDPDPHRDPY | GEEVDRRSVH | SEHSARSLHS | AHSLASRRSS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LSSHSHQSQI | YRSHNVAAGS | YEAPLPPGSF | HGDFAYGTYR | SNFSSGPGFP | EYGYPADTVW | PAMEQVSSRP | TSPEKFSVPH |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VCARFGPGGQ | LIKVIPNLPS | EGQPALVEVH | SMEALLQHTS | EQEEMRAFPG | PLAKDDTHKV | DVINFAQNKA | MKCLQNENLI |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DKESASLLWN | FIVLLCRQNG | TVVGTDIAEL | LLRDHRTVWL | PGKSPNEANL | IDFTNEAVEQ | VEEEESGEAQ | LSFLTGGPAA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| AASSLERETE | RFRELLLYGR | KKDALESAMK | NGLWGHALLL | ASKMDSRTHA | RVMTRFANSL | PINDPLQTVY | QLMSGRMPAA |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| STCCGDEKWG | DWRPHLAMVL | SNLNNNMDVE | SRTMATMGDT | LASRGLLDAA | HFCYLMAQAG | FGVYTKKTTK | LVLIGSNHSL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| PFLKFATNEA | IQRTEAYEYA | QSLGAETCPL | PSFQVFKFIY | SCRLAEMGLA | TQAFHYCEAI | AKSILTQPHL | YSPVLISQLV |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| QMASQLRLFD | PQLKEKPEEE | SLAAPTWLVH | LQQVERQIKE | GAGVWHQDGA | LPQQCPGTPS | SEMEQLDRPG | LSQPGALGIA |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| NPLLAVPAPS | PEHSSPSVRL | LPSAPQTLPD | GPLASPARVP | MFPVPLPPGP | LEPGPGCVTP | GPALGFLEPS | GPGLPPGVPP |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LQERRHLLQE | ARSPDPGIVP | QEAPVGNSLS | ELSEENFDGK | FANLTPSRTV | PDSEAPPGWD | RADSGPTQPP | LSLSPAPETK |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| RPGQAAKKET | KEPKKGESWF | FRWLPGKKKT | EAYLPDDKNK | SIVWDEKKNQ | WVNLNEPEEE | KKAPPPPPTS | MPKTVQAAPP |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| ALPGPPGAPV | NMYSRRAAGT | RARYVDVLNP | SGTQRSEPAL | APADFVAPLA | PLPIPSNLFV | PTPDAEEPQL | PDGTGREGPA |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 118 | 1 | 635.6951 | -152.31 | 2 | 30.4 | 10.0 | 0 | 1633-1644 | R.TMATMGDTLASR.G | Oxidation: 2 | |
| 2722 | 2 | 607.3395 | -24.29 | 2 | 62.5 | 12.3 | 2 | 2001-2011 | K.RPGQAAKKETK.E | | QU:MU 1.63<br>WUP:QUP 0.37 |
| 2457 | 1 | 647.2076 | -173.21 | 2 | 61.2 | 14.3 | 1 | 2030-2040 | K.TEAYLPDDKNK.S | | |

# Detailed Protein Report

**Protein 139:** **PREDICTED: leucine-rich PPR motif-containing protein, mitochondrial isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578802653 | **Score:** | 47.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 119.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***QU:MU*** **Median:** 0.55 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MAALLRSARW LLRAGAAPRL PLSLRLLPGG PGRLHAASYL PAARAGPVAG GLLSPARLYA IAAKEKDIQE ESTFSSRKIS
        90        100        110        120        130        140        150        160
NQFDWALMRL DLSVRRTGRI PKKLLQKVFN DTCRSGGLGG SHALLLLRSC GSLLPELKLE ERTEFAHRIW DTLQKLGAVY
       170        180        190        200        210        220        230        240
DVSHYNALLK VYLQNEYKFS PTDFLAKMEE ANIQPNRVTY QRLIASYCNV GDIEGASKIL GFMKTKDLPV TEAVFSALVT
       250        260        270        280        290        300        310        320
GHARAGDMEN AENILTVMRD AGIEPGPDTY LALLNAYAEK GDIDHVKQTL EKVEKSELHL MDRDLLQIIF SFSKAGYPQY
       330        340        350        360        370        380        390        400
VSEILEKVTC ERRYIPDAMN LILLLVTEKL EDVALQILLA CPVSKEDGPS VFGSFFLQHC VTMNTPVEKL TDYCKKLKEV
       410        420        430        440        450        460        470        480
QMHSFPLQFT LHCALLANKT DLAKALMKAV KEEGFPIRPH YFWPLLVGRR KEKNVQGIIE ILKGMQELGV HPDQETYTDY
       490        500        510        520        530        540        550        560
VIPCFDSVNS ARAILQENGC LSDSDMFSQA GLRSEAANGN LDFVLSFLKS NTLPISLQSI RSSLLLGFRR SMNINLWSEI
       570        580        590        600        610        620        630        640
TELLYKDGRY CQEPRGPTEA VGYFLYNLID SMSDSEVQAK EEHLRQYFHQ LEKMNVKIPE NIYRGIRNLL ESYHVPELIK
       650        660        670        680        690        700        710        720
DAHLLVESKN LDFQKTVQLT SSELESTLET LKAENQPIRD VLKQLILVLC SEENMQKALE LKAKYESDMV TGGYAALINL
       730        740        750        760        770        780        790        800
CCRHDKVEDA LNLKEEFDRL DSSAVLDTGK YVGLVRVLAK HGKLQDAINI LKEMKEKDVL IKDTTALSFF HMLNGAALRG
       810        820        830        840        850        860        870        880
EIETVKQLHE AIVTLGLAEP STNISFPLVT VHLEKGDLST ALEVAIDCYE KYKVLPRIHD VLCKLVEKGE TDLIQKAMDF
       890        900        910        920        930        940        950        960
VSQEQGEMVM LYDLFFAFLQ TGNYKEAKKI IETPGIRARS ARLQWFCDRC VANNQVETLE KLVELTQKLF ECDRDQMYYN
       970        980        990       1000       1010       1020       1030       1040
LLKLYKINGD WQRADAVWNK IQEENVIPRE KTLRLLAEIL REGNQEVPFD VPELWYEDEK HSLNSSSAST TEPDFQKDIL
      1050       1060
IACRLNQKKR GI
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1368 | 1 | 428.2118 | -70.40 | 3 | 47.2 | 12.4 | 1 | 673-683 | K.AENQPIRDVLK.Q | | |
| 386 | 4 | 627.3328 | -88.01 | 2 | 34.8 | 18.2 | 2 | 909-919 | K.KIIETPGIRAR.S | | QU:MU 0.55 |

# Detailed Protein Report

## Protein 140: cation-independent mannose-6-phosphate receptor precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|119964726 | **Score:** | 47.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 274.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGAAAGRSPH | LGPAPARRPQ | RSLLLLQLLL | LVAAPGSTQA | QAAPFPELCS | YTWEAVDTKN | NVLYKINICG | SVDIVQCGPS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SAVCMHDLKT | RTYHSVGDSV | LRSATRSLLE | FNTTVSCDQQ | GTNHRVQSSI | AFLCGKTLGT | PEFVTATECV | HYFEWRTTAA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CKKDIFKANK | EVPCYVFDEE | LRKHDLNPLI | KLSGAYLVDD | SDPDTSLFIN | VCRDIDTLRD | PGSQLRACPP | GTAACLVRGH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QAFDVGQPRD | GLKLVRKDRL | VLSYVREEAG | KLDFCDGHSP | AVTITFVCPS | ERREGTIPKL | TAKSNCRYEI | EWITEYACHR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DYLESKTCSL | SGEQQDVSID | LTPLAQSGGS | SYISDGKEYL | FYLNVCGETE | IQFCNKKQAA | VCQVKKSDTS | QVKAAGRYHN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QTLRYSDGDL | TLIYFGGDEC | SSGFQRMSVI | NFECNKTAGN | DGKGTPVFTG | EVDCTYFFTW | DTEYACVKEK | EDLLCGATDG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KKRYDLSALV | RHAEPEQNWE | AVDGSQTETE | KKHFFINICH | RVLQEGKARG | CPEDAAVCAV | DKNGSKNLGK | FISSPMKEKG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NIQLSYSDGD | DCGHGKKIKT | NITLVCKPGD | LESAPVLRTS | GEGGCFYEFE | WHTAAACVLS | KTEGENCTVF | DSQAGFSFDL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SPLTKKNGAY | KVETKKYDFY | INVCGPVSVS | PCQPDSGACQ | VAKSDEKTWN | LGLSNAKLSY | YDGMIQLNYR | GGTPYNNERH |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TPRATLITFL | CDRDAGVGFP | EYQEEDNSTY | NFRWYTSYAC | PEEPLECVVT | DPSTLEQYDL | SSLAKSEGGL | GGNWYAMDNS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GEHVTWRKYY | INVCRPLNPV | PGCNRYASAC | QMKYEKDQGS | FTEVVSISNL | GMAKTGPVVE | DSGSLLLEYV | NGSACTTSDG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RQTTYTTRIH | LVCSRGRLNS | HPIFSLNWEC | VVSFLWNTEA | ACPIQTTTDT | DQACSIRDPN | SGFVFNLNPL | NSSQGYNVSG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| IGKIFMFNVC | GTMPVCGTIL | GKPASGCEAE | TQTEELKNWK | PARPVGIEKS | LQLSTEGFIT | LTYKGPLSAK | GTADAFIVRF |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VCNDDVYSGP | LKFLHQDIDS | GQGIRNTYFE | FETALACVPS | PVDCQVTDLA | GNEYDLTGLS | TVRKPWTAVD | TSVDGRKRTF |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| YLSVCNPLPY | IPGCQGSAVG | SCLVSEGNSW | NLGVVQMSPQ | AAANGSLSIM | YVNGDKCGNQ | RFSTRITFEC | AQISGSPAFQ |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LQDGCEYVFI | WRTVEACPVV | RVEGDNCEVK | DPRHGNLYDL | KPLGLNDTIV | SAGEYTYYFR | VCGKLSSDVC | PTSDKSKVVS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SCQEKREPQG | FHKVAGLLTQ | KLTYENGLLK | MNFTGGDTCH | KVYQRSTAIF | FYCDRGTQRP | VFLKETSDCS | YLFEWRTQYA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| CPPFDLTECS | FKDGAGNSFD | LSSLSRYSDN | WEAITGTGDP | EHYLINVCKS | LAPQAGTEPC | PPEAAACLLG | GSKPVNLGRV |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| RDGPQWRDGI | IVLKYVDGDL | CPDGIRKKST | TIRFTCSESQ | VNSRPMFISA | VEDCEYTFAW | PTATACPMKS | NEHDDCQVTN |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PSTGHLFDLS | SLSGRAGFTA | AYSEKGLVYM | SICGENENCP | PGVGACFGQT | RISVGKANKR | LRYVDQVLQL | VYKDGSPCPS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KSGLSYKSVI | SFVCRPEAGP | TNRPMLISLD | KQTCTLFFSW | HTPLACEQAT | ECSVRNGSSI | VDLSPLIHRT | GGYEAYDESE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| DDASDTNPDF | YINICQPLNP | MHGVPCPAGA | AVCKVPIDGP | PIDIGRVAGP | PILNPIANEI | YLNFESSTPC | LADKHFNYTS |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| LIAFHCKRGV | SMGTPKLLRT | SECDFVFEWE | TPVVCPDEVR | MDGCTLTDEQ | LLYSFNLSSL | STSTFKVTRD | SRTYSVGVCT |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| FAVGPEQGGC | KDGGVCLLSG | TKGASFGRLQ | SMKLDYRHQD | EAVVLSYVNG | DRCPPETDDG | VPCVFPFIFN | GKSYEECIIE |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| SRAKLWCSTT | ADYDRDHEWG | FCRHSNSYRT | SSIIFKCDED | EDIGRPQVFS | EVRGCDVTFE | WKTKVVCPPK | KLECKFVQKH |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| KTYDLRLLSS | LTGSWSLVHN | GVSYYINLCQ | KIYKGPLGCS | ERASICRRTT | TGDVQVLGLV | HTQKLGVIGD | KVVVTYSKGY |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| PCGGNKTASS | VIELTCTKTV | GRPAFKRFDI | DSCTYYFSWD | SRAACAVKPQ | EVQMVNGTIT | NPINGKSFSL | GDIYFKLFRA |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1181 | 1 | 955.7839 | 6.62 | 3 | 44.9 | 12.0 | 1 | 267-292 | R.EEAGKLDFCDGHSPAVTITFVCPSER.R | Carbamidomethyl: 22 |
| 2855 | 2 | 731.8691 | -0.65 | 2 | 66.1 | 13.0 | 2 | 471-483 | K.EDLLCGATDGKKR.Y | Carbamidomethyl: 5 |

# Detailed Protein Report

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**Protein 141:** **staphylococcal nuclease domain-containing protein 1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|77404397 | **Score:** | 47.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 101.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 5.9 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASSAQSGGS | SGGPAVPTVQ | RGIIKMVLSG | CAIIVRGQPR | GGPPPERQIN | LSNIRAGNLA | RRAAATQPDA | KDTPDEPWAF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PAREFLRKKL | IGKEVCFTIE | NKTPQGREYG | MIYLGKDTNG | ENIAESLVAE | GLATRREGMR | ANNPEQNRLS | ECEEQAKAAK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KGMWSEGNGS | HTIRDLKYTI | ENPRHFVDSH | HQKPVNAIIE | HVRDGSVVRA | LLLPDYYLVT | VMLSGIKCPT | FRREADGSET |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PEPFAAEAKF | FTESRLLQRD | VQIILESCHN | QNILGTILHP | NGNITELLLK | EGFARCVDWS | IAVYTRGAEK | LRAAERFAKE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RRLRIWRDYV | APTANLDQKD | KQFVAKVMQV | LNADAIVVKL | NSGDYKTIHL | SSIRPPRLEG | ENTQDKNKKL | RPLYDIPYMF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EAREFLRKKL | IGKKVNVTVD | YIRPASPATE | TVPAFSERTC | ATVTIGGINI | AEALVSKGLA | TVIRYRQDDD | QRSSHYDELL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AAEARAIKNG | KGLHSKKEVP | IHRVADISGD | TQKAKQFLPF | LQRAGRSEAV | VEYVFSGSRL | KLYLPKETCL | ITFLLAGIEC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PRGARNLPGL | VQEGEPFSEE | ATLFTKELVL | QREVEVEVES | MDKAGNFIGW | LHIDGANLSV | LLVEHALSKV | HFTAERSSYY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KSLLSAEEAA | KQKKEKVWAH | YEEQPVEEVM | PVLEEKERSA | SYKPVFVTEI | TDDLHFYVQD | VETGTQLEKL | MENMRNDIAS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HPPVEGSYAP | RRGEFCIAKF | VDGEWYRARV | EKVESPAKIH | VFYIDYGNRE | VLPSTRLGTL | SPAFSTRVLP | AQATEYAFAF |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IQVPQDDDAR | TDAVDSVVRD | IQNTQCLLNV | EHLSAGCPHV | TLQFADSKGD | VGLGLVKEGL | VMVEVRKEKQ | FQKVITEYLN |
| 890 | 900 | 910 | 920 | | | | |
| AQESAKSARL | NLWRYGDFRA | DDADEFGYSR | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2148 | 1 | 966.3470 | -130.61 | 2 | 56.7 | 12.8 | 2 | 161-177 | K.KGMWSEGNGSHTIRDLK.Y | Oxidation: 3 |
| 2741 | 1 | 656.8579 | 55.61 | 2 | 64.6 | 11.5 | 0 | 296-306 | R.CVDWSIAVYTR.G | |
| 297 | 2 | 626.2973 | 4.64 | 3 | 33.4 | 12.1 | 1 | 733-747 | R.GEFCIAKFVDGEWYR.A | Carbamidomethyl: 4 |

# Detailed Protein Report

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**Protein 142:** **PREDICTED: methylcytosine dioxygenase TET3 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530367326 | **Score:** | 47.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 193.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|566559863 | refseq_human (refseq_human_20140103.fasta) | methylcytosine dioxygenase TET3 [Homo sapiens] |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSQFQVPLAV | QPDLPGLYDF | PQRQVMVGSF | PGSGLSMAGS | ESQLRGGGDG | RKKRKRCGTC | EPCRRLENCG | ACTSCTNRRT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HQICKLRKCE | VLKKKVGLLK | EVEIKAGEGA | GPWGQGAAVK | TGSELSPVDG | PVPGQMDSGP | VYHGDSRQLS | ASGVPVNGAR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EPAGPSLLGT | GGPWRVDQKP | DWEAAPGPAH | TARLEDAHDL | VAFSAVAEAV | SSYGALSTRL | YETFNREMSR | EAGNNSRGPR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PGPEGCSAGS | EDLDTLQTAL | ALARHGMKPP | NCNCDGPECP | DYLEWLEGKI | KSVVMEGGEE | RPRLPGPLPP | GEAGLPAPST |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RPLLSSEVPQ | ISPQEGLPLS | QSALSIAKEK | NISLQTAIAI | EALTQLSSAL | PQPSHSTPQA | SCPLPEALSP | PAPFRSPQSY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LRAPSWPVVP | PEEHSSFAPD | SSAFPPATPR | TEFPEAWGTD | TPPATPRSSW | PMPRPSPDPM | AELEQLLGSA | SDYIQSVFKR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PEALPTKPKV | KVEAPSSSPA | PAPSPVLQRE | APTPSSEPDT | HQKAQTALQQ | HLHHKRSLFL | EQVHDTSFPA | PSEPSAPGWW |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PPPSSPVPRL | PDRPPKEKKK | KLPTPAGGPV | GTEKAAPGIK | PSVRKPIQIK | KSRPREAQPL | FPPVRQIVLE | GLRSPASQEV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QAHPPAPLPA | SQGSAVPLPP | EPSLALFAPS | PSRDSLLPPT | QEMRSPSPMT | ALQPGSTGPL | PPADDKLEEL | IRQFEAEFGD |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SFGLPGPPSV | PIQDPENQQT | CLPAPESPFA | TRSPKQIKIE | SSGAVTVLST | TCFHSEEGGQ | EATPTKAENP | LTPTLSGFLE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SPLKYLDTPT | KSLLDTPAKR | AQAEFPTCDC | VEQIVEKDEG | PYYTHLGSGP | TVASIRELME | ERYGEKGKAI | RIEKVIYTGK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EGKSSRGCPI | AKWVIRRHTL | EEKLLCLVRH | RAGHHCQNAV | IVILILAWEG | IPRSLGDTLY | QELTDTLRKY | GNPTSRRCGL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NDDRTCACQG | KDPNTCGASF | SFGCSWSMYF | NGCKYARSKT | PRKFRLAGDN | PKEEEVLRKS | FQDLATEVAP | LYKRLAPQAY |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QNQVTNEEIA | IDCRLGLKEG | RPFAGVTACM | DFCAHAHKDQ | HNLYNGCTVV | CTLTKEDNRC | VGKIPEDEQL | HVLPLYKMAN |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TDEFGSEENQ | NAKVGSGAIQ | VLTAFPREVR | RLPEPAKSCR | QRQLEARKAA | AEKKKIQKEK | LSTPEKIKQE | ALELAGITSD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PGLSLKGGLS | QQGLKPSLKV | EPQNHFSSFK | YSGNAVVESY | SVLGNCRPSD | PYSMNSVYSY | HSYYAQPSLT | SVNGFHSKYA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LPSFSYYGFP | SSNPVFPSQF | LGPGAWGHSG | SSGSFEKKPD | LHALHNSLSP | AYGGAEFAEL | PSQAVPTDAH | HPTPHHQQPA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| YPGPKEYLLP | KAPLLHSVSR | DPSPFAQSSN | CYNRSIKQEP | VDPLTQAEPV | PRDAGKMGKT | PLSEVSQNGG | PSHLWGQYSG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GPSMSPKRTN | GVGGSWGVFS | SGESPAIVPD | KLSSFGASCL | APSHFTDGQW | GLFPGEGQQA | ASHSGGRLRG | KPWSPCKFGN |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| STSALAGPSL | TEKPWALGAG | DFNSALKGSP | GFQDKLWNPM | KGEEGRIPAA | GASQLDRAWQ | SFGLPLGSSE | KLFGALKSEE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KLWDPFSLEE | GPAEEPPSKG | AVKEEKGGGG | AEEEEEELWS | DSEHNFLDEN | IGGVAVAPAH | GSILIECARR | ELHATTPLKK |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| PNRCHPTRIS | LVFYQHKNLN | QPNHGLALWE | AKMKQLAERA | RARQEEAARL | GLGQQEAKLY | GKKRKWGGTV | VAEPQQKEKK |
| 1770 | 1780 | 1790 | 1800 | | | | |
| GVVPTRQALA | VPTDSAVTVS | SYAYTKVTGP | YSRWI | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 806 | 1 | 546.9707 | -505.05 | 1 | 39.6 | 11.3 | 0 | 1562-1566 | K.GEEGR.I | |
| 1833 | 2 | 697.0345 | -7.09 | 3 | 51.3 | 12.9 | 2 | 1724-1742 | R.QEEAARLGLGQQEAKLYGK.K | |

# Detailed Protein Report

## Protein 143: PREDICTED: microtubule-actin cross-linking factor 1 isoform X29 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578798838 | **Score:** | 47.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 608.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 3 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSSDEETLS | ERSCRSERSC | RSERSYRSER | SGSLSPCPPG | DTLPWNLPLH | EQKKRKSQDS | VLDPAERAVV | RVADERDRVQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KKTFTKWVNK | HLMKVRKHIN | DLYEDLRDGH | NLISLLEVLS | GIKLPREKGR | MRFHRLQNVQ | IALDFLKQRQ | VKLVNIRNDD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ITDGNPKLTL | GLIWTIILHF | QISDIYISGE | SGDMSAKEKL | LLWTQKVTAG | YTGIKCTNFS | SCWSDGKMFN | ALIHRYRPDL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VDMERVQIQS | NRENLEQAFE | VAERLGVTRL | LDAEDVDVPS | PDEKSVITYV | SSIYDAFPKV | PEGGEGISAT | EVDSRWQEYQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SRVDSLIPWI | KQHTILMSDK | TFPQNPVELK | ALYNQYIHFK | ETEILAKERE | KGRIEELYKL | LEVWIEFGRI | KLPQGYHPND |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VEEEWGKLII | EMLEREKSLR | PAVERLELLL | QIANKIQNGA | LNCEEKLTLA | KNTLQADAAH | LESGQPVQCE | SDVIMYIQEC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EGLIRQLQVD | LQILRDENYY | QLEELAFRVM | RLQDELVTLR | LECTNLYRKG | HFTSLELVPP | STLTTTHLKA | EPLTKATHSS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| STSWFRKPMT | RAELVAISSS | EDEGNLRFVY | ELLSWVEEMQ | MKLERAEWGN | DLPSVELQLE | TQQHIHTSVE | ELGSSVKEAR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LYEGKMSQNF | HTSYAETLGK | LETQYCKLKE | TSSFRMRHLQ | SLHKFVSRAT | AELIWLNEKE | EEELAYDWSD | NNSNISAKRN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YFSELTMELE | EKQDVFRSLQ | DTAELLSLEN | HPAKQTVEAY | SAAVQSQLQW | MKQLCLCVEQ | HVKENTAYFQ | FFSDARELES |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FLRNLQDSIK | RKYSCDHNTS | LSRLEDLLQD | SMDEKEQLIQ | SKSSVASLVG | RSKTIVQLKP | RSPDHVLKNT | ISVKAVCDYR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QIEITICKND | ECVLEDNSQR | TKWKVISPTG | NEAMVPSVCF | LIPPPNKDAI | EMASRVEQSY | QKVMALWHQL | HVNTKSLISW |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NYLRKDLDLV | QTWNLEKLRS | SAPGECHQIM | KNLQAHYEDF | LQDSRDSVLF | SVADRLRLEE | EVEACKARFQ | HLMKSMENED |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KEETVAKMYI | SELKNIRLRL | EEYEQRVVKR | IQSLASSRTD | RDAWQDNALR | IAEQEHTQED | LQQLRSDLDA | VSMKCDSFLH |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QSPSSSSVPT | LRSELNLLVE | KMDHVYGLST | VYLNKLKTVD | VIVRSIQDAE | LLVKGYEIKL | SQEEVVLADL | SALEAHWSTL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| RHWLSDVKDK | NSVFSVLDEE | IAKAKVVAEQ | MSRLTPERNL | DLERYQEKGS | QLQERWHRVI | AQLEIRQSEL | ESIQEVLGDY |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| RACHGTLIKW | IEETTAQQEM | MKPGQAEDSR | VLSEQLSQQT | ALFAEIERNQ | TKLDQCQKFS | QQYSTIVKDY | ELQLMTYKAF |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VESQQKSPGK | RRRMLSSSDA | ITQEFMDLRT | RYTALVTLTT | QHVKYISDAL | RRLEEEEKVV | EEEKQEHVEK | VKELLGWVST |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LARNTQGKAT | SSETKESTDI | EKAILEQQVL | SEELTTKKEQ | VSEAIKTSQI | FLAKHGHKLS | EKEKKQISEQ | LNALNKAYHD |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| LCDGSANQLQ | QLQSQLAHQT | EQKTLQKQQN | TCHQQLEDLC | SWVGQAERAL | AGHQGRTTQQ | DLSALQKNQS | DLKDLQDDIQ |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| NRATSFATVV | KDIEGFMEEN | QTKLSPRELT | ALREKLHQAK | EQYEALQEET | RVAQKELEEA | VTSALQQETE | KSKAAKELAE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| NKKKIDALLD | WVTSVGSSGG | QLLTNLPGME | QLSGASLEKG | ALDTTDGYMG | VNQAPEKLDK | QCEMMKARHQ | ELLSQQQNFI |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| LATQSAQAFL | DQHGHNLTPE | EQQMLQQKLG | ELKEQYSTSL | AQSEAELKQV | QTLQDELQKF | LQDHKEFESW | LERSEKELEN |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| MHKGGSSPET | LPSLLKRQGS | FSEDVISHKG | DLRFVTISGQ | KVLDMENSFK | EGKEPSEIGN | LVKDKLKDAT | ERYTALHSKC |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| TRLGSHLNML | LGQYHQFQNS | ADSLQAWMQA | CEANVEKLLS | DTVASDPGVL | QEQLATTKQL | QEELAEHQVP | VEKLQKVARD |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| IMEIEGEPAP | DHRHVQETTD | SILSHFQSLS | YSLAERSSLL | QKAIAQSQSV | QESLESLLQS | IGEVEQNLEG | KQVSSLSSGV |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| IQEALATNMK | LKQDIARQKS | SLEATREMVT | RFMETADSTT | AAVLQGKLAE | VSQRFEQLCL | QQQEKESSLK | KLLPQAEMFE |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 91 | 2 | 1240.0402 | -66.65 | 2 | 31.1 | 23.4 | 2 | 1882-1903 | K.VLDMENSFKEGKEPSEIGNLVK.D | Oxidation: 4 |
| 371 | 1 | 625.3885 | 104.40 | 2 | 34.3 | 11.3 | 2 | 2836-2845 | R.LKDCMQKAQK.Y | Carbamidomethyl: 4 |
| 11 | 1 | 650.7452 | -159.65 | 2 | 29.7 | 12.6 | 2 | 4482-4491 | K.RAKQFHEAWK.K | |

# Detailed Protein Report

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**Protein 144:** **cadherin EGF LAG seven-pass G-type receptor 3 precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|145309304 | **Score:** | 47.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 358.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.24 | **CV:** | 52.77 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 0.72 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMARRPPWRG | LGGRSTPILL | LLLLSLFPLS | QEELGGGGHQ | GWDPGLAATT | GPRAHIGGGA | LALCPESSGV | REDGGPGLGV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| REPIFVGLRG | RRQSARNSRG | PPEQPNEELG | IEHGVQPLGS | RERETGQGPG | SVLYWRPEVS | SCGRTGPLQR | GSLSPGALSS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GVPGSGNSSP | LPSDFLIRHH | GPKPVSSQRN | AGTGSRKRVG | TARCCGELWA | TGSKGQGERA | TTSGAERTAP | RRNCLPGASG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SGPELDSAPR | TARTAPASGS | APRESRTAPE | PAPKRMRSRG | LFRCRFLPQR | PGPRPPGLPA | RPEARKVTSA | NRARFRRAAN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RHPQFPQYNY | QTLVPENEAA | GTAVLRVVAQ | DPDAGEAGRL | VYSLAALMNS | RSLELFSIDP | QSGLIRTAAA | LDRESMERHY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LRVTAQDHGS | PRLSATTMVA | VTVADRNDHS | PVFEQAQYRE | TLRENVEEGY | PILQLRATDG | DAPPNANLRY | RFVGPPAARA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AAAAAFEIDP | RSGLISTSGR | VDREHMESYE | LVVEASDQGQ | EPGPRSATVR | VHITVLDEND | NAPQFSEKRY | VAQVREDVRP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HTVVLRVTAT | DRDKDANGLV | HYNIISGNSR | GHFAIDSLTG | EIQVVAPLDF | EAEREYALRI | RAQDAGRPPL | SNNTGLASIQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VVDINDHIPI | FVSTPFQVSV | LENAPLGHSV | IHIQAVDADH | GENARLEYSL | TGVAPDTPFV | INSATGWVSV | SGPLDRESVE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HYFFGVEARD | HGSPPLSASA | SVTVTVLDVN | DNRPEFTMKE | YHLRLNEDAA | VGTSVVSVTA | VDRDANSAIS | YQITGGNTRN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RFAISTQGGV | GLVTLALPLD | YKQERYFKLV | LTASDRALHD | HCYVHINITD | ANTHRPVFQS | AHYSVSVNED | RPMGSTIVVI |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SASDDDVGEN | ARITYLLEDN | LPQFRIDADS | GAITLQAPLD | YEDQVTYTLA | ITARDNGIPQ | KADTTYVEVM | VNDVNDNAPQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FVASHYTGLV | SEDAPPFTSV | LQISATDRDA | HANGRVQYTF | QNGEDGDGDF | TIEPTSGIVR | TVRRLDREAV | SVYELTAYAV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| DRGVPPLRTP | VSIQVMVQDV | NDNAPVFPAE | EFEVRVKENS | IVGSVVAQIT | AVDPDEGPNA | HIMYQIVEGN | IPELFQMDIF |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SGELTALIDL | DYEARQEYVI | VVQATSAPLV | SRATVHVRLV | DQNDNSPVLN | NFQILFNNYV | SNRSDTFPSG | IIGRIPAYDP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DVSDHLFYSF | ERGNELQLLV | VNQTSGELRL | SRKLDNNRPL | VASMLVTVTD | GLHSVTAQCV | LRVVIITEEL | LANSLTVRLE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| NMWQERFLSP | LLGRFLEGVA | AVLATPAEDV | FIFNIQNDTD | VGGTVLNVSF | SALAPRGAGA | GAAGPWFSSE | ELQEQLYVRR |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| AALAARSLLD | VLPFDDNVCL | REPCENYMKC | VSVLRFDSSA | PFLASASTLF | RPIQPIAGLR | CRCPPGFTGD | FCETELDLCY |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SNPCRNGGAC | ARREGGYTCV | CRPRFTGEDC | ELDTEAGRCV | PGVCRNGGTC | TDAPNGGFRC | QCPAGGAFEG | PRCEVAARSF |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PPSSFVMFRG | LRQRFHLTLS | LSFATVQQSG | LLFYNGRLNE | KHDFLALELV | AGQVRLTYST | GESNTVVSPT | VPGGLSDGQW |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| HTVHLRYYNK | PRTDALGGAQ | GPSKDKVAVL | SVDDCDVAVA | LQFGAEIGNY | SCAAAGVQTS | SKKSLDLTGP | LLLGGVPNLP |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| ENFPVSHKDF | IGCMRDLHID | GRRVDMAAFV | ANNGTMAGCQ | AKLHFCDSGP | CKNSGFCSER | WGSFSCDCPV | GFGGKDCQLT |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| MAHPHHFRGN | GTLSWNFGSD | MAVSVPWYLG | LAFRTRATQG | VLMQVQAGPH | STLLCQLDRG | LLSVTVTRGS | GRASHLLLDQ |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| VTVSDGRWHD | LRLELQEEPG | GRRGHHVLMV | SLDFSLFQDT | MAVGSELQGL | KVKQLHVGGL | PPGSAEEAPQ | GLVGCIQGVW |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LGSTPSGSPA | LLPPSHRVNA | EPGCVVTNAC | ASGPCPPHAD | CRDLWQTFSC | TCQPGYYGPG | CVDACLLNPC | QNQGSCRHLP |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| GAPHGYTCDC | VGGYFGHHCE | HRMDQQCPRG | WWGSPTCGPC | NCDVHKGFDP | NCNKTNGQCH | CKEFHYRPRG | SDSCLPCDCY |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| PVGSTSRSCA | PHSGQCPCRP | GALGRQCNSC | DSPFAEVTAS | GCRVLYDACP | KSLRSGVWWP | QTKFGVLATV | PCPRGALGAA |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1349 | 4 | 942.4987 | 46.29 | 2 | 46.5 | 16.8 | 1 | 232-250 | R.RNCLPGASGSGPELDSAPR.T | | QU:MU 0.75 |
| 1065 | 3 | 470.5947 | -263.79 | 2 | 43.4 | 12.8 | 0 | 2331-2338 | R.MEHPSSPR.G | | |
| 587 | 2 | 459.6056 | -275.62 | 2 | 35.7 | 17.8 | 1 | 2636-2643 | R.NVDRGAMR.F | | WUP:QUP 0.72<br>QU:MU 2.03 |

# Detailed Protein Report

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## Protein 145: PREDICTED: centlein isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578816553 | **Score:** | 46.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 155.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| | | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***QU:MU*** **Median:** 0.85 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAARSPPSPH | PSPPARQLGP | RSPRVGRGAE | VHAMRSEASG | FAGAAREVVA | DESDKIWADK | EFVWSLWKRL | QVTNPDLTQV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VSLVVEREKQ | KSEAKDRKVL | EILQVKDAKI | QEFEQRESVL | KQEINDLVKR | KIAVDEENAF | LRKEFSDLEK | KFKDKSQEIK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DTKECVQNKE | EQNRLVIKNL | EEENKKLSTR | CTDLLNDLEK | LRKQEAHLRK | EKYSTDAKIK | TFEDNLIEAR | KEVEVSQSKY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NALSLQLSNK | QTELIQKDMD | ITLVRKELQE | LQNLYKQNST | HTAQQAELIQ | QLQVLNMDTQ | KVLRNQEDVH | TAESISYQKL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YNELHICFET | TKSNEAMLRQ | SVTNLQDQLL | QKEQENAKLK | EKLQESQGAP | LPLPQESDPD | YSAQVPHRPS | LSSLETLMVS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QKSEIEYLQE | KLKIANEKLS | ENISANKGFS | RKSIMTSAEG | KHKEPPVKRS | RSLSPKSSFT | DSEELQKLRK | AERKIENLEK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ALQLKSQEND | ELRDAHEKRK | ERLQMLQTNY | RAVKEQLKQW | EEGSGMTEIR | KIKRADPQQL | RQEDSDAVWN | ELAYFKRENQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ELMIQKMNLE | EELDELKVHI | SIDKAAIQEL | NRCVAERREE | QLFRSGEDDE | VKRSTPEKNG | KEMLEQTLQK | VTELENRLKS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FEKRSRKLKE | GNKKLMKEND | FLKSLLKQQQ | EDTETREKEL | EQIIKGSKDV | EKENTELQVK | ISELETEVTS | LRRQVAEANA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LRNENEELIN | PMEKSHQSAD | RAKSEMATMK | VRSGRYDCKT | TMTKVKFKAA | KKNCSVGRHH | TVLNHSIKVM | SNVFENLSKD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GWEDVSESSS | DSEAQTSQTL | GTIIVETSQK | ISPTEDGKDQ | KESDPTEDSQ | TQGKEIVQTY | LNIDGKTPKD | YFHDKNAKKP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TFQKKNCKMQ | KSSHTAVPTR | VNREKYKNIT | AQKSSSNIIL | LRERIISLQQ | QNSVLQNAKK | TAELSVKEYK | EVNEKLLHQQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QVSDQRFQTS | RQTIKKLNLD | LAGLRKEKED | LLKKLESSSE | ITSLAEENSQ | VTFPRIQVTS | LSPSRSMDLE | MKQLQYKLKN |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ATNELTKQSS | NVKTLKFELL | AKEEHIKEMH | EKISRMERDI | TMKRHLIEDL | KFRQKVNLES | NKSFSEMLQN | LDKKVKTLTE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ECSNKKVSID | SLKQRLNVAV | KEKSQYEQMY | QKSKEELEKK | DLKLTLLVSR | ISETESAMAE | IETAASKQLQ | ELALQSEQVL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EGAQKTLLLA | NEKVEEFTTF | VKALAKELQN | DVHVVRRQIR | ELKKMKKNRD | ACKTSTHKAQ | TLAASILNIS | RSDLEEILDT |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | |
| EDQVEIEKTK | IDAENDKEWM | LYIQKLLEGQ | LPFASYLLEA | VLEKINEKKK | LVEGYFTIMK | DIR | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 848 | 1 | 512.1520 | -290.70 | 2 | 40.7 | 15.4 | 1 | 1084-1091 | K.RHLIEDLK.F | | |
| 562 | 1 | 884.4457 | 29.69 | 2 | 37.0 | 19.0 | 0 | 1171-1187 | R.ISETESAMAEIETAASK.Q | | QU:MU 0.85 |

# Detailed Protein Report

**Protein 146:** **RNA polymerase II subunit A C-terminal domain phosphatase isoform 3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|321267522 | **Score:** | 46.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 92.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| | | **Sequence Coverage [%]:** | 7.1 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKGLCAECGQ | DLTQLQSKNG | KQQVPLSTAT | VSMVHSVPEL | MVSSEQAEQL | GREDQQRLHR | NRKLVLMVDL | DQTLIHTTEQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HCQQMSNKGI | FHFQLGRGEP | MLHTRLRPHC | KDFLEKIAKL | YELHVFTFGS | RLYAHTIAGF | LDPEKKLFSH | RILSRDECID |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PFSKTGNLRN | LFPCGDSMVC | IIDDREDVWK | FAPNLITVKK | YVYFQGTGDM | NAPPGSRESQ | TRKKVNHSRG | TEVSEPSPPV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RDPEGVTQAP | GVEPSNGLEK | PARELNGSEA | ATPRDSPRPG | KPDERDIWPP | AQAPTSSQEL | AGAPEPQGSC | AQGGRVAPGQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RPAQGATGTD | LDFDLSSDSE | SSSESEGTKS | SSSASDGESE | GKRGRQKPKA | APEGAGALAQ | GSSLEPGRPA | APSLPGEAEP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GAHAPDKEPE | LGGQEEGERD | GLCGLGNGCA | DRKEAETESQ | NSELSGVTAG | ESLDQSMEEE | EEEDTDEDDH | LIYLEEILVR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VHTDYYAKYD | RYLNKEIEEA | PDIRKIVPEL | KSKVLADVAI | IFSGLHPTNF | PIEKTREHYH | ATALGAKILT | RLVLSPDAPD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RATHLIAARA | GTEKVLQAQE | CGHLHVVNPD | WLWSCLERWD | KVEEQLFPLR | DDHTKAQREN | SPAAFPDREG | VPPTALFHPM |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PVLPKAQPGP | EVRIYDSNTG | KLIRTGARGP | PAPSSSLPIR | QEPSSFRAVP | PPQPQMFGEE | LPDAQDGEQP | GPSRRKRQPS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| MSETMPLYTL | CKEDLESMDK | EVDDILGEGS | DDSDSEKRRP | EEQEEEPQPR | KPGTRRERTL | GAPASSERSA | AGGRGPRGHK |
| 810 | 820 | 830 | 840 | 850 | | | |
| RKLNEEDAAS | ESSRESSNED | EGSSSEADEM | AKALEAELND | LM | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2677 | 1 | 973.4768 | -94.08 | 2 | 63.6 | 15.5 | 2 | 662-680 | K.LIRTGARGPPAPSSSLPIR.Q | |
| 1965 | 3 | 899.3643 | -116.81 | 2 | 52.9 | 16.3 | 2 | 779-797 | R.TLGAPASSERSAAGGRGPR.G | |

# Detailed Protein Report

## Protein 147: PREDICTED: G-protein coupled receptor 124 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578815277 | **Score:** | 46.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 140.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGAGGRRMRG | APARLLLPLL | PWLLLLLAPE | ARGAPGCPLS | IRSCKCSGER | PKGLSGGVPG | PARRRVVCSG | GDLPEPPEPG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LLPNGTVTLD | LRNNIISTVQ | PGAFLGLGEL | KRLDLSNNRI | GCLTSETFQG | LPRLLRLNIS | GNIFSSLQPG | VFDELPALKV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VDLGTEFLTC | DCHLRWLLPW | AQNRSLQLSE | HTLCAYPSAL | HAQALGSLQE | AQLCCEGALE | LHTHHLIPSL | RQVVFQGDRL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PFQCSASYLG | NDTRIRWYHN | RAPVEGDEQA | GILLAESLIH | DCTFITSELT | LSHIGVWASG | EWECTVSMAQ | GNASKKVEIV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VLETSASYCP | AERVANNRGD | FRWPRTLAGI | TAYQSCLQYP | FTSVPLGGGA | PGTRASRRCD | RAGRWEPGDY | SHCLYTNDIT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RVLYTFVLMP | INASNALTLA | HQLRVYTAEA | ASFSDMMDVV | YVAQMIQKFL | GYVDQIKELV | EVMVDMASNL | MLVDEHLLWL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AQREDKACSR | IVGALERIGG | AALSPHAQHI | SVNARNVALE | AYLIKPHSYV | GLTCTAFQRR | EGGVPGTRPG | SPGQNPPPEP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EPPADQQLRF | RCTTGRPNVS | LSSFHIKNSV | ALASIQLPPS | LFSSLPAALA | PPVPPDCTLQ | LLVFRNGRLF | HSHSNTSRPG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AAGPGKRRGV | ATPVIFAGTS | GCGVGNLTEP | VAVSLRHWAE | GAEPVAAWWS | QEGPGEAGGW | TSEGCQLRSS | QPNVSALHCQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HLGNVAVLME | LSAFPREVGG | AGAGLHPVVY | PCTALLLLCL | FATIITYILN | HSSIRVSRKG | WHMLLNLCFH | IAMTSAVFAG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GITLTNYQMV | CQAVGITLHY | SSLSTLLWMG | VKARVLHKEL | TWRAPPPQEG | DPALPTPSPM | LRFYLIAGGI | PLIICGITAA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VNIHNYRDHS | PYCWLVWRPS | LGAFYIPVAL | ILLITWIYFL | CAGLRLRGPL | AQNPKAGNSR | ASLEAGEELR | GSTRLRGSGP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LLSDSGSLLA | TGSARVGTPG | PPEDGDSLYS | PGVQLGALVT | THFLYLAMWA | CGALAVSQRW | LPRVVCSCLY | GVAASALGLF |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VFTHHCARRR | DVRASWRACC | PPASPAAPHA | PPRALPAAAE | DGSPVFGEGP | PSLKSSPSGS | SGHPLALGPC | KLTNLQLAQS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QVCEAGAAAG | GEGEPEPAGT | RGNLAHRHPN | NVHHGRRAHK | SRAKGHRAGE | ACGKNRLKAL | RGGAAGALEL | LSSESGSLHN |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SPTDSYLGSS | RNSPGAGLQL | EGEPMLTPSE | GSDTSAAPLS | EAGRAGQRRS | ASRDSLKGGG | ALEKESHRRS | YPLNAASLNG |
| 1290 | 1300 | 1310 | 1320 | | | | |
| APKGGKYDDV | TLMGAEVASG | GCMKTGLWKS | ETTV | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2732 | 2 | 673.3595 | 29.93 | 2 | 64.5 | 15.8 | 1 | 33-45 | R.GAPGCPLSIRSCK.C | Carbamidomethyl: 5 |
| 2870 | 9 | 673.3611 | 32.18 | 2 | 66.4 | 16.5 | 1 | 33-45 | R.GAPGCPLSIRSCK.C | Carbamidomethyl: 12 |
| 1660 | 1 | 716.0007 | 12.17 | 3 | 50.5 | 14.1 | 1 | 1284-1304 | K.GGKYDDVTLMGAEVASGGCMK.T | Carbamidomethyl: 19 |

# Detailed Protein Report

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**Protein 148:** **A disintegrin and metalloproteinase with thrombospondin motifs 19 preproprotein [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|112789555 | **Score:** | 46.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 134.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRLTHICCCC | LLYQLGFLSN | GIVSELQFAP | DREEWEVVFP | ALWRREPVDP | AGGSGGSADP | GWVRGVGGGG | SARAQAAGSS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| REVRSVAPVP | LEEPVEGRSE | SRLRPPPPSE | GEEDEELESQ | ELPRGSSGAA | ALSPGAPASW | QPPPPPQPPP | SPPPAQHAEP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DGDEVLLRIP | AFSRDLYLLL | RRDGRFLAPR | FAVEQRPNPG | PGPTGAASAP | QPPAPPDAGC | FYTGAVLRHP | GSLASFSTCG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GGLMGFIQLN | EDFIFIEPLN | DTMAITGHPH | RVYRQKRSME | EKVTEKSALH | SHYCGIISDK | GRPRSRKIAE | SGRGKRYSYK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LPQEYNIETV | VVADPAMVSY | HGADAARRFI | LTILNMVFNL | FQHKSLSVQV | NLRVIKLILL | HETPPELYIG | HHGEKMLESF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CKWQHEEFGK | KNDIHLEMST | NWGEDMTSVD | AAILITRKDF | CVHKDEPCDT | VGIAYLSGMC | SEKRKCIIAE | DNGLNLAFTI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AHEMGHNMGI | NHDNDHPSCA | DGLHIMSGEW | IKGQNLGDVS | WSRCSKEDLE | RFLRSKASNC | LLQTNPQSVN | SVMVPSKLPG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MTYTADEQCQ | ILFGPLASFC | QEMQHVICTG | LWCKVEGEKE | CRTKLDPPMD | GTDCDLGKWC | KAGECTSRTS | APEHLAGEWS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LWSPCSRTCS | AGISSRERKC | PGLDSEARDC | NGPRKQYRIC | ENPPCPAGLP | GFRDWQCQAY | SVRTSSPKHI | LQWQAVLDEE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KPCALFCSPV | GKEQPILLSE | KVMDGTSCGY | QGLDICANGR | CQKVGCDGLL | GSLAREDHCG | VCNGNGKSCK | IIKGDFNHTR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GAGYVEVLVI | PAGARRIKVV | EEKPAHSYLA | LRDAGKQSIN | SDWKIEHSGA | FNLAGTTVHY | VRRGLWEKIS | AKGPTTAPLH |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LLVLLFQDQN | YGLHYEYTIP | SDPLPENQSS | KAPEPLFMWT | HTSWEDCDAT | CGGGERKTTV | SCTKIMSKNI | SIVDNEKCKY |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LTKPEPQIRK | CNEQPCQTRW | MMTEWTPCSR | TCGKGMQSRQ | VACTQQLSNG | TLIRARERDC | IGPKPASAQR | CEGQDCMTVW |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EAGVWSECSV | KCGKGIRHRT | VRCTNPRKKC | VLSTRPREAE | DCEDYSKCYV | WRMGDWSKCS | ITCGKGMQSR | VIQCMHKITG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RHGNECFSSE | KPAAYRPCHL | QPCNEKINVN | TITSPRLAAL | TFKCLGDQWP | VYCRVIREKN | LCQDMRWYQR | CCETCRDFYA |
| 1210 | | | | | | | |
| QKLQQKS | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 109 | 1 | 1098.0910 | -64.88 | 3 | 31.1 | 12.4 | 2 | 619-647 | K.WCKAGECTSRTSAPEHLAGEWSLWSPCSR.T | Carbamidomethyl: 2 |

# Detailed Protein Report

## Protein 149: treslin [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|118421085 | **Score:** | 46.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 210.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MACCHKVMLL | LDTAGGAARH | SRVRRAALRL | LTYLSCRFGL | ARVHWAFKFF | DSQGARSRPS | RVSDFRELGS | RSWEDFEEEL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EARLEDRAHL | PGPAPRATHT | HGALMETLLD | YQWDRPEITS | PTKPILRSSG | RRLLDVESEA | KEAEAALGGL | VNAVFLLAPC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PHSQRELLQF | VSGCEAQAQR | LPPTPKQVME | KLLPKRVREV | MVARKITFYW | VDTTEWSKLW | ESPDHLGYWT | VCELLHHGGG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TVLPSESFSW | DFAQAGEMLL | RSGIKLSSEP | HLSPWISMLP | TDATLNRLLY | NSPEYEASFP | RMEGMLFLPV | EAGKEIQETW |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TVTLEPLAMH | QRHFQKPVRI | FLKGSVAQWS | LPTSSTLGTD | SWMLGSPEES | TATQRLLFQQ | LVSRLTAEEL | HLVADVDPGE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GRPPITGVIS | PLSASAMILT | VCRTKEAEFQ | RHVLQTAVAD | SPRDTASLFS | DVVDSILNQT | HDSLADTASA | ASPVPEWAQQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ELGHTTPWSP | AVVEKWFPFC | NISGASSDLM | ESFGLLQAAS | ANKEESSKTE | GELIHCLAEL | YQRKSREEST | IAHQEDSKKK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RGVPRTPVRQ | KMNTMCRSLK | MLNVARLNVK | AQKLHPDGSP | DVAGEKGIQK | IPSGRTVDKL | EDRGRTLRSS | KPKDFKTEEE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LLSYIRENYQ | KTVATGEIML | YACARNMIST | VKMFLKSKGT | KELEVNCLNQ | VKSSLLKTSK | SLRQNLGKKL | DKEDKVRECQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LQVFLRLEMC | LQCPSINEST | DDMEQVVEEV | TDLLRMVCLT | EDSAYLAEFL | EEILRLYIDS | IPKTLGNLYN | SLGFVIPQKL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AGVLPTDFFS | DDSMTQENKS | PLLSVPFLSS | ARRSVSGSPE | SDELQELRTR | SAKKRRKNAL | IRHKSIAEVS | QNLRQIEIPK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VSKRATKKEN | SHPAPQQPSQ | PVKDTVQEVT | KVRRNLFNQE | LLSPSKRSLK | RGLPRSHSVS | AVDGLEDKLD | NFKKNKGYHK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LLTKSVAETP | VHKQISKRLL | HRQIKGRSSD | PGPDIGVVEE | SPEKGDEISL | RRSPRIKQLS | FSRTHSASFY | SVSQPKSRSV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QRVHSFQQDK | SDQRENSPVQ | SIRSPKSLLF | GAMSEMISPS | EKGSARMKKR | SRNTLDSEVP | AAYQTPKKSH | QKSLSFSKTT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PRRISHTPQT | PLYTPERLQK | SPAKMTPTKQ | AAFKESLKDS | SSPGHDSPLD | SKITPQKRHT | QAGEGTSLET | KTPRTPKRQG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TQPPGFLPNC | TWPHSVNSSP | ESPSCPAPPT | SSTAQPRREC | LTPIRDPLRT | PPRAAAFMGT | PQNQTHQQPH | VLRAARAEEP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| AQKLKDKAIK | TPKRPGNSTV | TSSPPVTPKK | LFTSPLCDVS | KKSPFRKSKI | ECPSPGELDQ | KEPQMSPSVA | ASLSCPVPST |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PPELSQRATL | DTVPPPPPSK | VGKRCRKTSD | PRRSIVECQP | DASATPGVGT | ADSPAAPTDS | RDDQKGLSLS | PQSPPERRGY |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| PGPGLRSDWH | ASSPLLITSD | TEHVTLLSEA | EHHGIGDLKS | NVLSVEEGEG | LRTADAEKSS | LSHPGIPPSP | PSCGPGSPLM |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PSRDVHCTTD | GRQCQASAQL | DNLPASAWHS | TDSASPQTYE | VELEMQASGL | PKLRIKKIDP | SSSLEAEPLS | KEESSLGEES |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| FLPALSMPRA | SRSLSKPEPT | YVSPPCPRLS | HSTPGKSRGQ | TYICQACTPT | HGPSSTPSPF | QTDGVPWTPS | PKHSGKTTPD |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| IIKDWPRRKR | AVGCGAGSSS | GRGEVGADLP | GSLSLLESEG | KDHGLELSIH | RTPILEDFEL | EGVCQLPDQS | PPRNSMPKAE |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| EASSWGQFGL | SSRKRVLLAK | EEADRGAKRI | CDLREDSEVS | KSKEGSPSWS | AWQLPSTGDE | EVFVSGSTPP | PSCAVRSCLS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| ASALQALTQS | PLLFQGKTPS | SQSKDPRDED | VDVLPSTVED | SPFSRAFSRR | RPISRTYTRK | KLMGTWLEDL | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2455 | 1 | 669.2124 | -220.96 | 2 | 61.2 | 12.2 | 1 | 1311-1322 | K.LFTSPLCDVSKK.S | |

# Detailed Protein Report

## Protein 150: PREDICTED: SH3 domain-containing protein 21 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578799774 | **Score:** | 46.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 84.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 4.3 |
| | | **No. of unique Peptides:** | 2 |

### Quantitation

***WUP:QUP*** **Median:** 2.96 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MEVLVLAGYR AQKEDELSLA PGDVVRQVRW VPARGWLRGE FGGRYGLFPE RLVQEIPETL RGSGEARRPR CARRRGHPAK
        90        100        110        120        130        140        150        160
HPRPQRWCKV NFSYSPEQAD ELKLQAGEIV EMIKEIEDGW WLGKKNGQLG AFPSNFVELL DSGPPSLGNP DMPSVSPGPQ
       170        180        190        200        210        220        230        240
RPPKLSSLAY DSPPDYLQTV SHPEVYRVLF DYQPEAPDEL ALRRGDVVKV LSKTTEDKGW WEGECQGRRG VFPDNFVLPP
       250        260        270        280        290        300        310        320
PPIKKLVPRK VVSRESAPIK EPKKLMPKTS LPTVKKLATA TTGPSKAKTS RTPSRDSQKL TSRDSGPNGG FQSGGSYHPG
       330        340        350        360        370        380        390        400
RKRSKTQTPQ QRSVSSQEEE HSSPVKAPSV KRTPMPDKTA TPERPPAPEN APSSKKIPAP DKVPSPEKTL TLGDKASIPG
       410        420        430        440        450        460        470        480
NSTSGKIPAP DKVPTPEKMV TPEDKASIPE NSIIPEETLT VDKPSTPERV FSVEESPALE APPMDKVPNP KMAPLGDEAP
       490        500        510        520        530        540        550        560
TLEKVLTPEL SEEEVSTRDD IQFHHFSSEE ALQKVKYFVA KEDPSSQEEA HTPEAPPPQP PSSERCLGEM KCTLVRGDSS
       570        580        590        600        610        620        630        640
PRQAELKSGP ASRPALEKPH PHEEATTLPE EAPSNDERTP EEEAPPNEQR PLREEVLPKE GVASKEEVTL KEELPPKEEV
       650        660        670        680        690        700        710        720
APKEEVPPIE RAFAQKTRPI KPPPDSQETL ALPSLVPQNY TENKNEGVDV TSLRGEVESL RRALELMEEE ADRHLGGAEE
       730        740        750        760        770        780
REGAAPAAGG PVYEPRALWG QGDVCPGVCR GLPWPSQARW EKRQPCPGGF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 328 | 1 | 658.3980 | 85.56 | 2 | 32.8 | 13.8 | 2 | 62-73 | R.GSGEARRPRCAR.R | | |
| 2858 | 1 | 805.9291 | -2.54 | 2 | 66.2 | 12.9 | 2 | 751-763 | R.GLPWPSQARWEKR.Q | | WUP:QUP 2.96 |

# Detailed Protein Report

## Protein 151: PREDICTED: PDZ domain-containing protein 2 isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578809880 | **Score:** | 46.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 289.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.4 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 3 |

BRUKER

# Detailed Protein Report

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPITQDNAVL | HLPLLYQWLQ | NSLQEGGDGP | EQRLCQAAIQ | KLQEYIQLNF | AVDESTVPPD | HSPPEMEICT | VYLTKELGDT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ETVGLSFGNI | PVFGDYGEKR | RGGKKRKTHQ | GPVLDVGCIW | VTELRKNSPA | GKSGKVRLRD | EILSLNGQLM | VGVDVSGASY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LAEQCWNGGF | IYLIMLRRFK | HKAHSTYNGN | SSNSSEPGET | PTLELGDRTA | KKGKRTRKFG | VISRPPANKA | PEESKGSAGC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EVSSDPSTEL | ENGPDPELGN | GHVFQLENGP | DSLKEVAGPH | LERSEVDRGT | EHRIPKTDAP | LTTSNDKRRF | SKGGKTDFQS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SDCLAREEVG | RIWKMELLKE | SDGLGIQVSG | GRGSKRSPHA | IVVTQVKEGG | AAHRDGRLSL | GDELLVINGH | LLVGLSHEEA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VAILRSATGM | VQLVVASKEN | SAEDLLRLTS | KSLPDLTSSV | EDVSSWTDNE | DQEADGEEDE | GTSSSVQRAM | PGTDEPQDVC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GAEESKGNLE | SPKQGSNKIK | LKSRLSGGVH | RLESVEEYNE | LMVRNGDPRI | RMLEVSRDGR | KHSLPQLLDS | SSASQEYHIV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KKSTRSLSTT | QVESPWRLIR | PSVISIIGLY | KEKGKGLGFS | IAGGRDCIRG | QMGIFVKTIF | PNGSAAEDGR | LKEGDEILDV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NGIPIKGLTF | QEAIHTFKQI | RSGLFVLTVR | TKLVSPSLTP | CSTPTHMSRS | ASPNFNTSGG | ASAGGSDEGS | SSSLGRKTPG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PKDRIVMEVT | LNKEPRVGLG | IGACCLALEN | SPPGIYIHSL | APGSVAKMES | NLSRGDQILE | VNSVNVRHAA | LSKVHAILSK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| CPPGPVRLVI | GRHPNPKVSE | QEMDEVIARS | TYQESKEANS | SPGLGTPLKS | PSLAKKDSLI | SESELSQYFA | HDVPGPLSDF |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| MVAGSEDEDH | PGSGCSTSEE | GSLPPSTSTH | KEPGKPRANS | LVTLGSHRAS | GLFHKQVTVA | RQASLPGSPQ | ALRNPLLRQR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KVGCYDANDA | SDEEEFDREG | DCISLPGALP | GPIRPLSEDD | PRRVSISSSK | GMDVHNQEER | PRKTLESLGK | LTTGDACVST |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SCELASALSH | LDASHLTENL | PKAASELGQQ | PMTELDSSSD | LISSPGKKGA | AHPDPSKTSV | DTGQVSRPEN | PSQPASPRVT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KCKARSPVRL | PHEGSPSPGE | KAAAPPDYSK | TRSASETSTP | HNTRRVAALR | GAGPGAEGMT | PAGAVLPGDP | LTSQEQRQGA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PGNHSKALEM | TGIHAPESSQ | EPSLLEGADS | VSSRAPQASL | SMLPSTDNTK | EACGHVSGHC | CPGGSRESPV | TDIDSFIKEL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DASAARSPSS | QTGDSGSQEG | SAQGHPPAGA | GGGSSCRAEP | VPGGQTSSPR | RAWAAGAPAY | PQWASQPSVL | DSINPDKHFT |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VNKNFLSNYS | RNFSSFHEDS | TSLSGLGDST | EPSLSSMYGD | AEDSSSDPES | LTEAPRASAR | DGWSPPRSRV | SLHKEDPSES |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EEEQIEICST | RGCPNPPSSP | AHLPTQAAIC | PASAKVLSLK | YSTPRESVAS | PREKAACLPG | SYTSGPDSSQ | PSSLLEMSSQ |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| EHETHADIST | SQNHRPSCAE | ETTEVTSASS | AMENSPLSKV | ARHFHSPPII | LSSPNMVNGL | EHDLLDDETL | NQYETSINAA |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| ASLSSFSVDV | PKNGESVLEN | LHISESQDLD | DLLQKPKMIA | RRPIMAWFKE | INKHNQGTHL | RSKTEKEQPL | MPARSPDSKI |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| QMVSSSQKKG | VTVPHSPPQP | KTNLENKDLS | KKSPAEMLLT | NGQKAKCGPK | LKRLSLKGKA | KVNSEAPAAN | AVKAGGTDHR |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| KPLISPQTSH | KTLSKAVSQR | LHVADHEDPD | RNTTAAPRSP | QCVLESKPPL | ATSGPLKPSV | SDTSIRTFVS | PLTSPKPVPE |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| QGMWSRFHMA | VLSEPDRGCP | TTPKSPKCRA | EGRAPRADSG | PVSPAASRNG | MSVAGNRQSE | PRLASHVAAD | TAQPRPTGEK |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| GGNIMASDRL | ERTNQLKIVE | ISAEAVSETV | CGNKPAESDR | RGGCLAQGNC | QEKSEIRLYR | QVAESSTSHP | SSLPSHASQA |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| EQEMSRSFSM | AKLASSSSSL | QTAIRKAEYS | QGKSSLMSDS | RGVPRNSIPG | GPSGEDHLYF | TPRPATRTYS | MPAQFSSHFG |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| REGHPPHSLG | RSRDSQVPVT | SSVVPEAKAS | RGGLPSLANG | QGIYSVKPLL | DTSRNLPATD | EGDIISVQET | SCLVTDKIKV |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 892 | 1 | 675.8467 | 18.44 | 4 | 41.2 | 12.0 | 1 | 76-100 | K.ELGDTETVGLSFGNIPVFGDYGEKR.R | |
| 2006 | 1 | 917.8396 | -134.11 | 2 | 53.5 | 11.6 | 1 | 2474-2492 | R.KEGSGLGFSVAGGTDVEPK.S | |
| 444 | 1 | 848.1390 | 136.74 | 2 | 35.2 | 10.0 | 1 | 2606-2621 | R.IGRPTVLLGSSAVIRR.S | |

# Detailed Protein Report

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**Protein 152:** **leucine zipper protein 1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|216548085 | **Score:** | 46.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 120.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 5.9 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|216548091 | refseq_human<br>(refseq_human_20140103.fasta) | leucine zipper protein 1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAEFTSYKET | ASSRHLRFKL | QSLSRRLDEL | EEATKNLQKA | EDELLDLQDK | VIQAEGSNSS | MLAEIEVLRQ | RVLRIEGKDE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EIKRAEDLCR | LMKEKLEEEE | NLTRELKSEI | ERLQKRMAEL | EKLEEAFSRS | KNDCTQLCLS | LNEERNLTKK | ISSELEMLRV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KVKELESSED | RLDKTEQSLA | SELEKLKSLT | LSFVSERKYL | NEKEKENEKL | IKELTQKLEQ | NKKMNRDYTR | NASNLERNDL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RIEDGISSTL | PSKESRRKGG | LDYLKQVENE | TRNKSENEKN | RNQEDNKVKD | LNQEIEKLKT | QIKHFESLEE | ELKKMKSKNN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DLQDNYLSEQ | NKNKLLASQL | EEIKLQIKKQ | KELENGEVEG | EDAFLSSKGR | HERTKFRGHG | SEASVSKHTA | RELSPQHKRE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RLRNREFALN | NENYSLSNRQ | VSSPSFTNRR | AAKASHMGVS | TDSGTQETKK | TEDRFVPGSS | QSEGKKSREQ | PSVLSRYPPA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AQEHSKAWKG | TSKPGTESGL | KGKVEKTTRT | FSDTTHGSVP | SDPLGRADKA | SDTSSETVFG | KRGHVLGNGS | QVTQAANSGC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SKAIGALASS | RRSSSEGLSK | GKKAANGLEA | DNSCPNSKAP | VLSKYPYSCR | SQENILQGFS | TSHKEGVNQP | AAVVMEDSSP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HEALRCRVIK | SSGREKPDSD | DDLDIASLVT | AKLVNTTITP | EPEPKPQPNS | REKAKTRGAP | RTSLFENDKD | AGMENESVKS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VRASTNTMEL | PDTNGAGVKS | QRPFSPREAL | RSRAIIKPVI | VDKDVKKIMG | GSGTETTLEK | QKPVSKPGPN | KVTSSITIYP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SDSSSPRAAP | GEALRERHTS | TSNIQVGLAE | LTSVSNHVSS | PFELSIHKHD | ITLQLAEAER | MADGPLKDRP | ETVVSRSSII |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| IKPSDPVERN | SHAPPAETIR | WKSHSAPSEV | GFSDARHVTV | RNAWKSRRDL | KSLEDPPTRI | GKNVESTNSN | AYTQRSSTDF |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SELEQPRSCL | FEQGTRRVGP | SSGDAPEPSS | RRTQSSLTVS | EVLTRRNRVG | DTITVAAWNH | SASMEEEGED | CTLSVYRQLH |
| 1050 | 1060 | 1070 | 1080 | | | | |
| NSLDPSELPG | KQGLPESGRV | RAEERLRPTR | PCAEEN | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2080 | 1 | 1044.4112 | -88.13 | 2 | 55.9 | 13.0 | 1 | 510-529 | R.TFSDTTHGSVPSDPLGRADK.A | |
| 2108 | 1 | 698.2650 | -143.11 | 2 | 56.2 | 11.7 | 0 | 849-860 | K.HDITLQLAEAER.M | |

# Detailed Protein Report

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## Protein 153: cyclic AMP-dependent transcription factor ATF-5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|12597625 | **Score:** | 45.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 30.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|302370956 | refseq_human (refseq_human_20140103.fasta) | cyclic AMP-dependent transcription factor ATF-5 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSLLATLGLE | LDRALLPASG | LGWLVDYGKL | PPAPAPLAPY | EVLGGALEGG | LPVGGEPLAG | DGFSDWMTER | VDFTALLPLE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PPLPPGTLPQ | PSPTPPDLEA | MASLLKKELE | QMEDFFLDAP | PLPPPSPPPL | PPPPLPPAPS | LPLSLPSFDL | PQPPVLDTLD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLAIYCRNEA | GQEEVGMPPL | PPPQQPPPPS | PPQPSRLAPY | PHPATTRGDR | KQKKRDQNKS | AALRYRQRKR | AEGEALEGEC |
| 250 | 260 | 270 | 280 | 290 | | | |
| QGLEARNREL | KERAESVERE | IQYVKDLLIE | VYKARSQRTR | SC | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 533 | 1 | 625.6275 | 0.96 | 3 | 35.1 | 13.5 | 1 | 230-246 | K.RAEGEALEGECQGLEAR.N | Carbamidomethyl: 11 |

# Detailed Protein Report

## Protein 154: PREDICTED: fatty-acid amide hydrolase 2 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530426388 | **Score:** | 45.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 8.5 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MINGIVKYRF | EEAMKEAHAV | DQKLAEKQED | EATLENKWPF | LGVPLTVKEA | FQLQGMPNSS | GLMNRRDAIA | KTDATVVALL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KGAGAIPLGI | TNCSELCMWY | ESSNKIYGRS | NNPYDLQHIV | GGSSGGEGCT | LAAACSVIGV | GSDIGGSIRM | PAFFNGIFGH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KPSPGVVPNK | GQFPLAVGAQ | ELFLCTGPMC | RYAEDLAPML | KVMAGPGIKR | LKLDTKVHLK | DLKFYWMEHD | GGSFLMSKVD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QDLIMTQKKV | VVHLETILGA | SVQHVKLKKM | KYSFQLWIAM | MSAKGHDGKE | PVKFVDLLGD | HGKHVSPLWE | LIKWCLGLSV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YTIPSIGLAL | LEEKLRYSNE | KYQKFKAVEE | SLRKELVDML | GDDGVFLYPS | HPTVAPKHHV | PLTRPFNFAY | TGVFSALGLP |
| 410 | 420 | 430 | 440 | 450 | | | |
| VTQCPLGLNA | KGLPLGIQVV | AGPFNDHLTL | AVAQYLEKTF | GGWVCPGKF | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 701 | 1 | 1099.6923 | 17.73 | 2 | 38.7 | 22.7 | 2 | 249-268 | K.KVVVHLETILGASVQHVKLK.K | |
| 1689 | 3 | 1051.5326 | 35.47 | 2 | 50.9 | 22.8 | 1 | 272-289 | K.YSFQLWIAMMSAKGHDGK.E | Oxidation: 9, 10 |

# Detailed Protein Report

## Protein 155: CUB and sushi domain-containing protein 3 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|205277354 | **Score:** | 45.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 387.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 2 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKGIRKGESR | AKESKPWEPG | KRRCAKCGRL | DFILMKKMGI | KSGFTFWNLV | FLLTVSCVKG | FIYTCGGTLK | GLNGTIESPG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FPYGYPNGAN | CTWVIIAEER | NRIQIVFQSF | ALEEEYDYLS | LYDGHPHPTN | FRTRLTGFHL | PPPVTSTKSV | FSLRLTSDFA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VSAHGFKVYY | EELQSSSCGN | PGVPPKGVLY | GTRFDVGDKI | RYSCVTGYIL | DGHPQLTCIA | NSVNTASWDF | PVPICRAEDA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CGGTMRGSSG | IISSPSFPNE | YHNNADCTWT | IVAEPGDTIS | LIFTDFQMEE | KYDYLEIEGS | EPPTIWLSGM | NIPPPIISNK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NWLRLHFVTD | SNHRYRGFSA | PYQVKKAIDF | KSRGFKLFPG | KDNSNKFSIL | NEGGIKTASN | LCPDPGEPEN | GKRIGSDFSL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GSTVQFSCDE | DYVLQGAKSI | TCQRIAEVFA | AWSDHRPVCK | VKTCGSNLQG | PSGTFTSPNF | PFQYDSNAQC | VWVITAVNTN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KVIQINFEEF | DLEIGYDTLT | IGDGGEVGDP | RTVLQVLTGS | FVPDLIVSMS | SQMWLHLQTD | ESVGSVGFKV | NYKEIEKESC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GDPGTPLYGI | REGDGFSNRD | VLRFECQFGF | ELIGEKSIVC | QENNQWSANI | PICIFPCLSN | FTAPMGTVLS | PDYPEGYGNN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LNCIWTIISD | PGSRIHLSFN | DFDLESQFDF | LAVKDGDSPE | SPILGTFTGA | EVPSHLTSNS | HILRLEFQAD | HSMSGRGFNI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TYNTFGHNEC | PDPGIPINAR | RFGDNFQLGS | SISVICEEGF | IKTQGTETIT | CILMDGKVMW | SGLIPKCGAP | CGGHFSAPSG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VILSPGWPGY | YKDSLNCEWV | IEAEPGHSIK | ITFERFQTEL | NYDVLEVHDG | PNLLSPLLGS | YNGTQVPQFL | FSSSNFIYLL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| FTTDNSRSNN | GFKIHYESVT | VNTYSCLDPG | IPVHGRRYGH | DFSIGSTVSF | SCDSGYRLSH | EEPLLCEKNH | WWSHPLPTCD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ALCGGDVRGP | SGTILSPGYP | EFYPNSLNCT | WTVDVTHGKG | VQFNFHTFHL | EDHHDYLLIT | ENGSFTQPLA | RLTGSDLPPT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| INAGLYGNFR | AQLRFISDFS | ISYEGFNITF | SEYNLEPCED | PGIPQYGSRI | GFNFGIGDTL | TFSCSSGYRL | EGTSEIICLG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GGRRVWSAPL | PRCVAECGAS | ATNNEGILLS | PNYPLNYENN | HECIYSIQVQ | AGKGINISAR | TFHLAQGDVL | KIYDGKDKTT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| HLLGAFTGAS | MRGLTLSSTS | NQLWLEFNSD | TEGTDEGFQL | VYTSFELSHC | EDPGIPQFGY | KISDQGHFAG | STIIYGCNPG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| YTLHGSSLLK | CMTGERRAWD | YPLPSCIAEC | GGRFKGESSG | RILSPGYPFP | YDNNLRCMWM | IEVDPGNIVS | LQFLAFDTEA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| SHDILRVWDG | PPENDMLLKE | ISGSLIPEGI | HSTLNIVTIQ | FDTDFYISKS | GFAIQFSSSV | ATACRDPGVP | MNGTRNGDGR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EPGDTVVFQC | DPGYELQGEE | RITCIQVENR | YFWQPSPPVC | IAPCGGNLTG | SSGFILSPNF | PHPYPHSRDC | DWTITVNADY |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| VISLAFISFS | IEPNYDFLYI | YDGPDSNSPL | IGSFQDSKLP | ERIESSSNTM | HLAFRSDGSV | SYTGFHLEYK | AKLRESCFDP |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| GNIMNGTRLG | MDYKLGSTVT | YYCDAGYVLQ | GYSTLTCIMG | DDGRPGWNRA | LPSCHAPCGS | RSTGSEGTVL | SPNYPKNYSV |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| GHNCVYSIAV | PKEFVVFGQF | VFFQTSLHDV | VEVYDGPTQQ | SSLLSSLSGS | HSGESLPLSS | GNQITIRFTS | VGPITAKGFH |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| FVYQAVPRTS | STQCSSVPEP | RFGRRIGNEF | AVGSSVLFDC | NPGYILHGSI | AIRCETVPNS | LAQWNDSLPT | CIVPCGGILT |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| KRKGTILSPG | YPEPYDNNLN | CVWKITVPEG | AGIQVQVVSF | ATEHNWDSLD | FYDGGDNNAP | RLGSYSGTTI | PHLLNSTSNN |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LYLNFQSDIS | VSAAGFHLEY | TAIGLDSCPE | PQTPSSGIKI | GDRYMVGDVV | SFQCDQGYSL | QGHSHITCMP | GPVRRWNYPI |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| PICLAQCGGA | MSDFSGVILS | PGFPGNYPSS | LDCTWTINLP | IGFGVHLQFV | NFSTETIHDY | LEVRSGSSET | STVIGRLSGP |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| QIPSSLFSTT | HETSLYFHSD | YSQNKQGFHI | VYQAYQLQSC | PDPRPFRNGF | VIGNDFTVGQ | TISFECFPGY | TLIGNSALTC |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1865 | 1 | 897.8571 | -115.65 | 2 | 53.2 | 10.9 | 1 | 321-334 | K.NWLRLHFVTDSNHR.Y | |
| 1304 | 1 | 661.3930 | 144.57 | 1 | 46.4 | 11.2 | 0 | 2937-2941 | R.QPECK.A | Carbamidomethyl: 4 |

# Detailed Protein Report

## Protein 156: rho GTPase-activating protein 36 isoform 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|40255080 | **Score:** | 45.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 61.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 5.9 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGGCIPFLKA | ARALCPRIMP | PLLLLSAFIF | LVSVLGGAPG | HNPDRRTKMV | SIHSLSELER | LKLQETAYHE | LVARHFLSEF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KPDRALPIDR | PNTLDKWFLI | LRGQQRAVSH | KTFGISLEEV | LVNEFTRRKH | LELTATMQVE | EATGQAAGRR | RGNVVRRVFG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RIRRFFSRRR | NEPTLPREFT | RRGRRGAVSV | DSLAELEDGA | LLLQTLQLSK | ISFPIGQRLL | GSKRKMSLNP | IAKQIPQVVE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ACCQFIEKHG | LSAVGIFTLE | YSVQRVRQLR | EEFDQGLDVV | LDDNQNVHDV | AALLKEFFRD | MKDSLLPDDL | YMSFLLTATL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KPQDQLSALQ | LLVYLMPPCH | SDTLERLLKA | LHKITENCED | SIGIDGQLVP | GNRMTSTNLA | LVFGSALLKK | GKFGKRESRK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TKLGIDHYVA | SVNVVRAMID | NWDVLFQVPP | HIQRQVAKRV | WKSSPEALDF | IRRRNLRKIQ | SARIKMEEDA | LLSDPVETSA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | |
| EARAAVLAQS | KPSDEGSSEE | PAVPSGTARS | HDDEEGAGNP | PIPEQDRPLL | RVPREKEAKT | GVSYFFP | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1422 | 1 | 459.2842 | 44.39 | 2 | 47.9 | 16.9 | 0 | 211-218 | K.ISFPIGQR.L | |
| 2474 | 1 | 822.4025 | -186.55 | 1 | 61.5 | 16.1 | 1 | 347-353 | R.LLKALHK.I | |

# Detailed Protein Report

## Protein 157: PREDICTED: uncharacterized protein KIAA1551 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530399223 | **Score:** | 45.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 194.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNWNEKPKSA | TLPPLYPKSQ | PPFLHQSLIN | QITTTSQSSF | SYPGSNQEAC | MYPGNSNPIS | QPLLNIQNYP | QQISVSDMHN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GTVVASHTSV | ERITYANVNG | PKQLTHNLQM | SSGVTQNVWL | NSPMRNPVHS | HIGATVSHQT | DFGANVPNMP | ALQSQLITSD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TYSMQMQMIP | SNSTRLPVAY | QGNQGLNQSF | SEQQVDWTQQ | CISKGLTYPD | YRPPPKLYRY | SPQSFLPDST | IQKQNFIPHT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SLQVKNSQLL | NSVLTLPSRQ | TSAVPSQQYA | TQTDKRPPPP | PYNCRYGSQP | LQSTQHITKH | LSMEVPQSRE | MLSSEIRTSF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QQQWQNPNEN | VSTIGNFTNL | KVNTNSKQPF | NSPIRSSVDG | VQTLAQTNEE | KIMDSCNPTS | NQVLDTSVAK | EKLVRDIKTL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VEIKQKFSEL | ARKIKINKDL | LMAAGCIKMT | NTSYSEPAQN | SKLSLKQTAK | IQSGPQITPV | MPENAERQTP | TVVESAETNK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TQCMLNSDIQ | EVNCRRFNQV | DSVLPNPVYS | EKRPMPDSSH | DVKVLTSKTS | AVEMTQAVLN | TQLSSENVTK | VEQNSPAVCE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TISVPKSMST | EEYKSKIQNE | NMLLLALLSQ | ARKTQKTVLK | DANQTIQDSK | PDSCEMNPNT | QMTGNQLNLK | NMETPSTSNV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SGRVLDNSFC | SGQESSTKGM | PAKSDSSCSM | EVLATCLSLW | KKQPSDTAKE | KECDKLRTNT | TAVGISKPAN | IHVKSPCSVV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GNSNSQNKIS | NPSQQTALSM | VMHNYESSGI | NITKGTELQI | AVVSPLVLSE | VKTLSVKGIT | PAVLPETVYP | VIKEGSVCSL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QNQLAENAKA | TAALKVDVSG | PVASTATSTK | IFPLTQKEKQ | NESTNGNSEV | TPNVNQGKHN | KLESAIHSPM | NDQQISQESR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| NSTVVSSDTL | QIDNICSLVE | GDTSYNSQIA | KIFSSLPLKM | VEPQKPSLPN | QQGIGSREPE | KQLDNTTENK | DFGFQKDKPV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QCTDVSHKIC | DQSKSEPPLE | SSFNNLETNR | VILEKSSLEH | ATEKSTANDT | CSSAAIQEDI | YPQEIDASSN | YTPQDPARNE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| IHSDKAPVLY | LHDQLSELLK | EFPYGIEAVN | TREGSVGQQT | TYQTSEDQTA | DKTSSDSKDP | ADQIQITILS | SEQMKEIFPE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QDDQPYVVDK | LAEPQKEEPI | TEVVSQCDLQ | APAAGQSRDS | VILDSEKDDI | HCCALGWLSM | VYEGVPQCQC | NSIKNSSSEE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EKQKEQCSPL | DTNSCKQGER | TSDRDVTVVQ | FKSLVNNPKT | PPDGKSHFPE | LQDDSRKDTP | KTKHKSLPRT | EQELVAGQFS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SKCDKLNPLQ | NHKRKKLRFH | EVTFHSSNKM | TASYEQASQE | TRQKKHVTQN | SRPLKTKTAF | LPNKDVYKKH | SSLGQSLSPE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KIKLKLKSVS | FKQKRKLDQG | NVLDMEVKKK | KHDKQEQKGS | VGATFKLGDS | LSNPNERAIV | KEKMVSNTKS | VDTKASSSKF |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SRILTPKEYL | QRQKHKEALS | NKASKKICVK | NVPCDSEHMR | PSKLAVQVES | CGKSNEKHSS | GVQTSKESLN | GLTSHGKNLK |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| IHHSQESKTY | NILRNVKEKV | GGKQPDKIWI | DKTKLDKLTN | ISNEAQFSQM | PPQVKDQKKL | YLNRVGFKCT | ERESISLTKL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| ESSPRKLHKD | KRQENKHKTF | LPVKGNTEKS | NMLEFKLCPD | ILLKNTNSVE | ERKDVKPHPR | KEQAPLQVSG | IKSTKEDWLK |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | |
| FVATKKRTQK | DSQERDNVNS | RLSKRSFSAD | GFEMLQNPVK | DSKEMFQTYK | QMYLEKRSRS | LGSSPVK | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2006 | 1 | 1044.4022 | -89.89 | 2 | 55.0 | 16.6 | 1 | 957-974 | K.DKPVQCTDVSHKICDQSK.S | Carbamidomethyl: 6 |
| 120 | 1 | 585.2911 | -66.24 | 2 | 30.4 | 16.8 | 0 | 1662- | K.EQAPLQVSGIK.S | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | 1672 | | |

## Protein 158: heterogeneous nuclear ribonucleoprotein U-like protein 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|118601081 | **Score:** | 45.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 85.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| | | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.95 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.52 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MEVKRLKVTE LRSELQRRGL DSRGLKVDLA QRLQEALDAE MLEDEAGGGG AGPGGACKAE PRPVAASGGG PGGDEEEDEE
        90        100        110        120        130        140        150        160
EEEEDEEALL EDEDEEPPPA QALGQAAQPP PEPPEAAAME AAAEPDASEK PAEATAGSGG VNGGEEQGLG KREEDEPEER
       170        180        190        200        210        220        230        240
SGDETPGSEV PGDKAAEEQG DDQDSEKSKP AGSDGERRGV KRQRDEKDEH GRAYYEFREE AYHSRSKSPL PPEEEAKDEE
       250        260        270        280        290        300        310        320
EDQTLVNLDT YTSDLHFQVS KDRYGGQPLF SEKFPTLWSG ARSTYGVTKG KVCFEAKVTQ NLPMKEGCTE VSLLRVGWSV
       330        340        350        360        370        380        390        400
DFSRPQLGED EFSYGFDGRG LKAENGQFEE FGQTFGENDV IGCFANFETE EVELSFSKNG EDLGVAFWIS KDSLADRALL
       410        420        430        440        450        460        470        480
PHVLCKNCVV ELNFGQKEEP FFPPPEEFVF IHAVPVEERV RTAVPPKTIE ECEVILMVGL PGSGKTQWAL KYAKENPEKR
       490        500        510        520        530        540        550        560
YNVLGAETVL NQMRMKGLEE PEMDPKSRDL LVQQASQCLS KLVQIASRTK RNFILDQCNV YNSGQRRKLL LFKTFSRKVV
       570        580        590        600        610        620        630        640
VVVPNEEDWK KRLELRKEVE GDDVPESIML EMKANFSLPE KCDYMDEVTY GELEKEEAQP IVTKYKEEAR KLLPPSEKRT
       650        660        670        680        690        700        710        720
NRRNNRNKRN RQNRSRGQGY VGGQRRGYDN RAYGQQYWGQ PGNRGGYRNF YDRYRGDYDR FYGRDYEYNR YRDYYRQYNR
       730        740        750
DWQSYYYHHP QDRDRYYRNY YGYQGYR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 196 | 1 | 838.3951 | -57.68 | 2 | 32.2 | 16.3 | 1 | 507-521 | K.SRDLLVQQASQCLSK.L | | WUP:QUP 1.52<br>QU:MU 0.95 |

# Detailed Protein Report

## Protein 159: ADAMTS-like protein 1 isoform 4 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|154275767 | **Score:** | 45.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 193.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MECCRRATPG | TLLLFLAFLL | LSSRTARSEE | DRDGLWDAWG | PWSECSRTCG | GGASYSLRRC | LSSKSCEGRN | IRYRTCSNVD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CPPEAGDFRA | QQCSAHNDVK | HHGQFYEWLP | VSNDPDNPCS | LKCQAKGTTL | VVELAPKVLD | GTRCYTESLD | MCISGLCQIV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GCDHQLGSTV | KEDNCGVCNG | DGSTCRLVRG | QYKSQLSATK | SDDTVVAIPY | GSRHIRLVLK | GPDHLYLETK | TLQGTKGENS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LSSTGTFLVD | NSSVDFQKFP | DKEILRMAGP | LTADFIVKIR | NSGSADSTVQ | FIFYQPIIHR | WRETDFFPCS | ATCGGGYQLT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SAECYDLRSN | RVVADQYCHY | YPENIKPKPK | LQECNLDPCP | ASDGYKQIMP | YDLYHPLPRW | EATPWTACSS | SCGGGIQSRA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VSCVEEDIQG | HVTSVEEWKC | MYTPKMPIAQ | PCNIFDCPKW | LAQEWSPCTV | TCGQGLRYRV | VLCIDHRGMH | TGGCSPKTKP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HIKEECIVPT | PCYKPKEKLP | VEAKLPWFKQ | AQELEEGAAV | SEEPSFIPEA | WSACTVTCGV | GTQVRIVRCQ | VLLSFSQSVA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DLPIDECEGP | KPASQRACYA | GPCSGEIPEF | NPDETDGLFG | GLQDFDELYD | WEYEGFTKCS | ESCGGGVQEA | VVSCLNKQTR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EPAEENLCVT | SRRPPQLLKS | CNLDPCPARW | EIGKWSPCSL | TCGVGLQTRD | VFCSHLLSRE | MNETVILADE | LCRQPKPSTV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QACNRFNCPP | AWYPAQWQPC | SRTCGGGVQK | REVLCKQRMA | DGSFLELPET | FCSASKPACQ | QACKKDDCPS | EWLLSDWTEC |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| STSCGEGTQT | RSAICRKMLK | TGLSTVVNST | LCPPLPFSSS | IRPCMLATCA | RPGRPSTKHS | PHIAAARKVY | IQTRRQRKLH |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| FVVGGFAYLL | PKTAVVLRCP | ARRVRKPLIT | WEKDGQHLIS | STHVTVAPFG | YLKIHRLKPS | DAGVYTCSAG | PAREHFVIKL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| IGGNRKLVAR | PLSPRSEEEV | LAGRKGGPKE | ALQTHKHQNG | IFSNGSKAEK | RGLAANPGSR | YDDLVSRLLE | QGGWPGELLA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SWEAQDSAER | NTTSEEDPGA | EQVLLHLPFT | MVTEQRRLDD | ILGNLSQQPE | ELRDLYSKHL | VAQLAQEIFR | SHLEHQDTLL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KPSERRTSPV | TLSPHKHVSG | FSSSLRTSST | GDAGGGSRRP | HRKPTILRKI | SAAQQLSASE | VVTHLGQTVA | LASGTLSVLL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| HCEAIGHPRP | TISWARNGEE | VQFSDRILLQ | PDDSLQILAP | VEADVGFYTC | NATNALGYDS | VSIAVTLAGK | PLVKTSRMTV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| INTEKPAVTV | DIGSTIKTVQ | GVNVTINCQV | AGVPEAEVTW | FRNKSKLGSP | HHLHEGSLLL | TNVSSSDQGL | YSCRAANLHG |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ELTESTQLLI | LDPPQVPTQL | EDIRALLAAT | GPNLPSVLTS | PLGTQLVLDP | GNSALLGCPI | KGHPVPNITW | FHGGQPIVTA |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| TGLTHHILAA | GQILQVANLS | GGSQGEFSCL | AQNEAGVLMQ | KASLVIQDYW | WSVDRLATCS | ASCGNRGVQQ | PRLRCLLNST |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| EVNPAHCAGK | VRPAVQPIAC | NRRDCPSRWM | VTSWSACTRS | CGGGVQTRRV | TCQKLKASGI | STPVSNDMCT | QVAKRPVDTQ |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| ACNQQLCVEW | AFSSWGQCNG | PCIGPHLAVQ | HRQVFCQTRD | GITLPSEQCS | ALPRPVSTQN | CWSEACSVHW | RVSLWTLCTA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| TCGNYGFQSR | RVECVHARTN | KAVPEHLCSW | GPRPANWQRC | NITPCENMEC | RDTTRYCEKV | KQLKLCQLSQ | FKSRCCGTCG |
| 1770 | | | | | | | |
| KA | | | | | | | |

| Cmpd. | No. of | m/z meas. | Δ m/z | z | Rt | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

| | Cmpds. | | [ppm] | | [min] | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 1695 | 1 | 671.2184 | -97.93 | 3 | 51.5 | 14.6 | 1 | 172-189 | K.EDNCGVCNGDGSTCRLVR.G | Carbamidomethyl: 4, 7 |

# Detailed Protein Report

## Protein 160: voltage-dependent R-type calcium channel subunit alpha-1E isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|329663531 | **Score:** | 44.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 254.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 4.95 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.60 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MARFGEAVVA | RPGSGDGDSD | QSRNRQGTPV | PASGQAAAYK | QTKAQRARTM | ALYNPIPVRQ | NCFTVNRSLF | IFGEDNIVRK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YAKKLIDWPP | FEYMILATII | ANCIVLALEQ | HLPEDDKTPM | SRRLEKTEPY | FIGIFCFEAG | IKIVALGFIF | HKGSYLRNGW |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NVMDFIVVLS | GILATAGTHF | NTHVDLRTLR | AVRVLRPLKL | VSGIPSLQIV | LKSIMKAMVP | LLQIGLLLFF | AILMFAIIGL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EFYSGKLHRA | CFMNNSGILE | GFDPPHPCGV | QGCPAGYECK | DWIGPNDGIT | QFDNILFAVL | TVFQCITMEG | WTTVLYNTND |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ALGATWNWLY | FIPLIIIGSF | FVLNLVLGVL | SGEFAKERER | VENRRAFMKL | RRQQQIEREL | NGYRAWIDKA | EEVMLAEENK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NAGTSALEVL | RRATIKRSRT | EAMTRDSSDE | HCVDISSVGT | PLARASIKSA | KVDGVSYFRH | KERLLRISIR | HMVKSQVFYW |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IVLSLVALNT | ACVAIVHHNQ | PQWLTHLLYY | AEFLFLGLFL | LEMSLKMYGM | GPRLYFHSSF | NCFDFGVTVG | SIFEVVWAIF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RPGTSFGISV | LRALRLLRIF | KITKYWASLR | NLVVSLMSSM | KSIISLLFLL | FLFIVVFALL | GMQLFGGRFN | FNDGTPSANF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DTFPAAIMTV | FQILTGEDWN | EVMYNGIRSQ | GGVSSGMWSA | IYFIVLTLFG | NYTLLNVFLA | IAVDNLANAQ | ELTKDEQEEE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EAFNQKHALQ | KAKEVSPMSA | PNMPSIERER | RRRHHMSVWE | QRTSQLRKHM | QMSSQEALNR | EEAPTMNPLN | PLNPLSSLNP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LNAHPSLYRR | PRAIEGLALG | LALEKFEEER | ISRGGSLKGD | GGDRSSALDN | QRTPLSLGQR | EPPWLARPCH | GNCDPTQQEA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GGGEAVVTFE | DRARHRQSQR | RSRHRRVRTE | GKESSSASRS | RSASQERSLD | EAMPTEGEKD | HELRGNHGAK | EPTIQEERAQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DLRRTNSLMV | SRGSGLAGGL | DEADTPLVLP | HPELEVGKHV | VLTEQEPEGS | SEQALLGNVQ | LDMGRVISQS | EPDLSCITAN |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TDKATTESTS | VTVAIPDVDP | LVDSTVVHIS | NKTDGEASPL | KEAEIREDEE | EVEKKKQKKE | KRETGKAMVP | HSSMFIFSTT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| NPIRRACHYI | VNLRYFEMCI | LLVIAASSIA | LAAEDPVLTN | SERNKVLRYF | DYVFTGVFTF | EMVIKMIDQG | LILQDGSYFR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DLWNILDFVV | VVGALVAFAL | ANALGTNKGR | DIKTIKSLRV | LRVLRPLKTI | KRLPKLKAVF | DCVVTSLKNV | FNILIVYKLF |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| MFIFAVIAVQ | LFKGKFFYCT | DSSKDTEKEC | IGNYVDHEKN | KMEVKGREWK | RHEFHYDNII | WALLTLFTVS | TGEGWPQVLQ |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| HSVDVTEEDR | GPSRSNRMEM | SIFYVVYFVV | FPFFFVNIFV | ALIIITFQEQ | GDKMMEECSL | EKNERACIDF | AISAKPLTRY |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| MPQNRHTFQY | RVWHFVVSPS | FEYTIMAMIA | LNTVVLMMKY | YSAPCTYELA | LKYLNIAFTM | VFSLECVLKV | IAFGFLNYFR |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| DTWNIFDFIT | VIGSITEIIL | TDSKLVNTSG | FNMSFLKLFR | AARLIKLLRQ | GYTIRILLWT | FVQSFKALPY | VCLLIAMLFF |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| IYAIIGMQVF | GNIKLDEESH | INRHNNFRSF | FGSLMLLFRS | ATGEAWQEIM | LSCLGEKGCE | PDTTAPSGQN | ENERCGTDLA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| YVYFVSFIFF | CSFLMLNLFV | AVIMDNFEYL | TRDSSILGPH | HLDEFVRVWA | EYDRAACGRI | HYTEMYEMLT | LMSPPLGLGK |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| RCPSKVAYKR | LVLMNMPVAE | DMTVHFTSTL | MALIRTALDI | KIAKGGADRQ | QLDSELQKET | LAIWPHLSQK | MLDLLVPMPK |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| ASDLTVGKIY | AAMMIMDYYK | QSKVKKQRQQ | LEEQKNAPMF | QRMEPSSLPQ | EIIANAKALP | YLQQDPVSGL | SGRSGYPSMS |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| PLSPQDIFQL | ACMDPADDGQ | FQERQSLVVT | DPSSMRRSFS | TIRDKRSNSS | WLEEFSMERS | SENTYKSRRR | SYHSSLRLSA |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| HRLNSDSGHK | SDTHRSGGRE | RGRSKERKHL | LSPDVSRCNS | EERGTQADWE | SPERRQSRSP | SEGRSQTPNR | QGTGSLSESS |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| IPSVSDTSTP | RRSRRQLPPV | PPKPRPLLSY | SSLIRHAGSI | SPPADGSEEG | SPLTSQALES | NNACLTESSN | SPHPQQSQHA |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2785 | 1 | 973.5222 | 64.95 | 2 | 63.4 | 10.8 | 1 | 734-750 | K.EVSPMSAPNMPSIERER.R | Oxidation: 10 | |
| 183 | 1 | 823.9125 | -35.10 | 2 | 31.1 | 10.2 | 2 | 959-972 | R.AQDLRRTNSLMVSR.G | | QU:MU 4.95<br>WUP:QUP 0.60 |
| 27 | 1 | 814.2746 | -93.66 | 2 | 30.0 | 10.4 | 1 | 1296-1308 | K.FFYCTDSSKDTEK.E | Carbamidomethyl: 4 | |

# Detailed Protein Report

## Protein 161: sortilin-related receptor preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4507157 | **Score:** | 44.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 248.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.7 |
| | | **No. of unique Peptides:** | 2 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.72 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.65 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MATRSSRRES | RLPFLFTLVA | LLPPGALCEV | WTQRLHGGSA | PLPQDRGFLV | VQGDPRELRL | WARGDARGAS | RADEKPLRRK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RSAALQPEPI | KVYGQVSLND | SHNQMVVHWA | GEKSNVIVAL | ARDSLALARP | KSSDVYVSYD | YGKSFKKISD | KLNFGLGNRS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EAVIAQFYHS | PADNKRYIFA | DAYAQYLWIT | FDFCNTLQGF | SIPFRAADLL | LHSKASNLLL | GFDRSHPNKQ | LWKSDDFGQT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| WIMIQEHVKS | FSWGIDPYDK | PNTIYIERHE | PSGYSTVFRS | TDFFQSRENQ | EVILEEVRDF | QLRDKYMFAT | KVVHLLGSEQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QSSVQLWVSF | GRKPMRAAQF | VTRHPINEYY | IADASEDQVF | VCVSHSNNRT | NLYISEAEGL | KFSLSLENVL | YYSPGGAGSD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TLVRYFANEP | FADFHRVEGL | QGVYIATLIN | GSMNEENMRS | VITFDKGGTW | EFLQAPAFTG | YGEKINCELS | QGCSLHLAQR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LSQLLNLQLR | RMPILSKESA | PGLIIATGSV | GKNLASKTNV | YISSSAGARW | REALPGPHYY | TWGDHGGIIT | AIAQGMETNE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LKYSTNEGET | WKTFIFSEKP | VFVYGLLTEP | GEKSTVFTIF | GSNKENVHSW | LILQVNATDA | LGVPCTENDY | KLWSPSDERG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NECLLGHKTV | FKRRTPHATC | FNGEDFDRPV | VVSNCSCTRE | DYECDFGFKM | SEDLSLEVCV | PDPEFSGKSY | SPPVPCPVGS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TYRRTRGYRK | ISGDTCSGGD | VEARLEGELV | PCPLAEENEF | ILYAVRKSIY | RYDLASGATE | QLPLTGLRAA | VALDFDYEHN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| CLYWSDLALD | VIQRLCLNGS | TGQEVIINSG | LETVEALAFE | PLSQLLYWVD | AGFKKIEVAN | PDGDFRLTIV | NSSVLDRPRA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LVLVPQEGVM | FWTDWGDLKP | GIYRSNMDGS | AAYHLVSEDV | KWPNGISVDD | QWIYWTDAYL | ECIERITFSG | QQRSVILDNL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PHPYAIAVFK | NEIYWDDWSQ | LSIFRASKYS | GSQMEILANQ | LTGLMDMKIF | YKGKNTGSNA | CVPRPCSLLC | LPKANNSRSC |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RCPEDVSSSV | LPSGDLMCDC | PQGYQLKNNT | CVKEENTCLR | NQYRCSNGNC | INSIWWCDFD | NDCGDMSDER | NCPTTICDLD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TQFRCQESGT | CIPLSYKCDL | EDDCGDNSDE | SHCEMHQCRS | DEYNCSSGMC | IRSSWVCDGD | NDCRDWSDEA | NCTAIYHTCE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ASNFQCRNGH | CIPQRWACDG | DTDCQDGSDE | DPVNCEKKCN | GFRCPNGTCI | PSSKHCDGLR | DCSDGSDEQH | CEPLCTHFMD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| FVCKNRQQCL | FHSMVCDGII | QCRDGSDEDA | AFAGCSQDPE | FHKVCDEFGF | QCQNGVCISL | IWKCDGMDDC | GDYSDEANCE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| NPTEAPNCSR | YFQFRCENGH | CIPNRWKCDR | ENDCGDWSDE | KDCGDSHILP | FSTPGPSTCL | PNYYRCSSGT | CVMDTWVCDG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| YRDCADGSDE | EACPLLANVT | AASTPTQLGR | CDRFEFECHQ | PKTCIPNWKR | CDGHQDCQDG | RDEANCPTHS | TLTCMSREFQ |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| CEDGEACIVL | SERCDGFLDC | SDESDEKACS | DELTVYKVQN | LQWTADFSGD | VTLTWMRPKK | MPSASCVYNV | YYRVVGESIW |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KTLETHSNKT | NTVLKVLKPD | TTYQVKVQVQ | CLSKAHNTND | FVTLRTPEGL | PDAPRNLQLS | LPREAEGVIV | GHWAPPIHTH |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| GLIREYIVEY | SRSGSKMWAS | QRAASNFTEI | KNLLVNTLYT | VRVAAVTSRG | IGNWSDSKSI | TTIKGKVIPP | PDIHIDSYGE |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| NYLSFTLTME | SDIKVNGYVV | NLFWAFDTHK | QERRTLNFRG | SILSHKVGNL | TAHTSYEISA | WAKTDLGDSP | LAFEHVMTRG |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| VRPPAPSLKA | KAINQTAVEC | TWTGPRNVVY | GIFYATSFLD | LYRNPKSLTT | SLHNKTVIVS | KDEQYLFLVR | VVVPYQGPSS |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| DYVVVKMIPD | SRLPPRHLHV | VHTGKTSVVI | KWESPYDSPD | QDLLYAIAVK | DLIRKTDRSY | KVKSRNSTVE | YTLNKLEPGG |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| KYHIIVQLGN | MSKDSSIKIT | TVSLSAPDAL | KIITENDHVL | LFWKSLALKE | KHFNESRGYE | IHMFDSAMNI | TAYLGNTTDN |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| FFKISNLKMG | HNYTFTVQAR | CLFGNQICGE | PAILLYDELG | SGADASATQA | ARSTDVAAVV | VPILFLILLS | LGVGFAILYT |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 |  |  |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2231 | 1 | 599.9323 | -0.25 | 3 | 57.8 | 14.4 | 1 | 1239-1254 | K.CNGFRCPNGTCIPSSK.H | Carbamidomethyl: 1, 11 | |
| 1196 | 1 | 610.6448 | -210.75 | 2 | 43.2 | 10.3 | 0 | 1244-1254 | R.CPNGTCIPSSK.H | Carbamidomethyl: 1, 6 | WUP:QUP 0.65<br>QU:MU 0.72 |

# Detailed Protein Report

## Protein 162: PREDICTED: zinc finger protein 467 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578813954 | **Score:** | 44.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 66.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 9.3 |
| | | **No. of unique Peptides:** | 4 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKFPTPHPGL | PPSSLSPENR | ILPALSQVLW | PDPQEELLWV | TMRETLEALS | SLGFSVGQPE | MAPQSEPREG | SHNAQEQMSS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SREERALGVC | SGEEWMIRKV | KVEDEDQEAE | EEVEWPQHLS | LLPSPFPAPD | LGHLAAAYKL | EPGAPGALSG | LALSGWGPMP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EKPYGCGECE | RRFRDQLTLR | LHQRLHRGEG | PCACPDCGRS | FTQRAHMLLH | QRSHRGERPF | PCSECDKRFS | KKAHLTRHLR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| THTGERPYPC | AECGKRFSQK | IHLGSHQKTH | TGERPFPCTE | CEKRFRKKTH | LIRHQRIHTG | ERPYQCAQCA | RSFTHKQHLV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RHQRVHQTAG | PARPSPDSSA | SPHSTAPSPT | PSFPGPKPFA | CSDCGLSFGW | KKNLATHQCL | HRSEGRPFGC | DECALGATVD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| APAAKPLASA | PGGPGCGPGS | DPVVPQRAPS | GERSFFCPDC | GRGFSHGQHL | ARHPRVHTGE | RPFACTQCDR | RFGSRPNLVA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HSRAHSGARP | FACAQCGRRF | SRKSHLGRHQ | AVHTGSRPHA | CAVCARSFSS | KTNLVRHQAI | HTGSRPFSCP | QCGKSFSRKT |
| 570 | 580 | 590 | 600 | | | | |
| HLVRHQLIHG | EAAHAAPDAA | LAAPAWSAPP | EVAPPPLFF | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1902 | 1 | 785.7933 | -55.89 | 2 | 52.1 | 10.0 | 1 | 185-199 | R.LHRGEGPCACPDCGR.S | |
| 340 | 2 | 544.7855 | 123.91 | 2 | 32.9 | 10.7 | 0 | 434-442 | R.SFFCPDCGR.G | Carbamidomethyl: 7 |
| 1119 | 2 | 555.1856 | -176.56 | 2 | 44.1 | 13.3 | 0 | 443-452 | R.GFSHGQHLAR.H | |
| 2174 | 1 | 849.0086 | -71.63 | 3 | 57.0 | 10.8 | 1 | 537-558 | R.HQAIHTGSRPFSCPQCGKSFSR.K | Carbamidomethyl: 13, 16 |

# Detailed Protein Report

## Protein 163: ubiquitin carboxyl-terminal hydrolase 35 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|148746183 | **Score:** | 44.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 113.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.49 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.96 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDKILEAVVT | SSYPVSVKQG | LVRRVLEAAR | QPLEREQCLA | LLALGARLYV | GGAEELPRRV | GCQLLHVAGR | HHPDVFAEFF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SARRVLRLLQ | GGAGPPGPRA | LACVQLGLQL | LPEGPAADEV | FALLRREVLR | TVCERPGPAA | CAQVARLLAR | HPRCVPDGPH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RLLFCQQLVR | CLGRFRCPAE | GEEGAVEFLE | QAQQVSGLLA | QLWRAQPAAI | LPCLKELFAV | ISCAEEEPPS | SALASVVQHL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PLELMDGVVR | NLSNDDSVTD | SQMLTAISRM | IDWVSWPLGK | NIDKWIIALL | KGLAAVKKFS | ILIEVSLTKI | EKVFSKLLYP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IVRGAALSVL | KYMLLTFQHS | HEAFHLLLPH | IPPMVASLVK | EDSNSGTSCL | EQLAELVHCM | VFRFPGFPDL | YEPVMEAIKD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LHVPNEDRIK | QLLGQDAWTS | QKSELAGFYP | RLMAKSDTGK | IGLINLGNTC | YVNSILQALF | MASDFRHCVL | RLTENNSQPL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| MTKLQWLFGF | LEHSQRPAIS | PENFLSASWT | PWFSPGTQQD | CSEYLKYLLD | RLHEEEKTGT | RICQKLKQSS | SPSPPEEPPA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PSSTSVEKMF | GGKIVTRICC | LCCLNVSSRE | EAFTDLSLAF | PPPERCRRRR | LGSVMRPTED | ITARELPPPT | SAQGPGRVGP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RRQRKHCITE | DTPPTSLYIE | GLDSKEAGGQ | SSQEERIERE | EEGKEERTEK | EEVGEEEEST | RGEGEREKEE | EVEEEEEKVE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KETEKEAEQE | KEEDSLGAGT | HPDAAIPSGE | RTCGSEGSRS | VLDLVNYFLS | PEKLTAENRY | YCESCASLQD | AEKVVELSQG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PCYLILTLLR | FSFDLRTMRR | RKILDDVSIP | LLLRLPLAGG | RGQAYDLCSV | VVHSGVSSES | GHYYCYAREG | AARPAASLGT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ADRPEPENQW | YLFNDTRVSF | SSFESVSNVT | SFFPKDTAYV | LFYRQRPREG | PEAELGSSRV | RTEPTLHKDL | MEAISKDNIL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | | |
| YLQEQEKEAR | SRAAYISALP | TSPHWGRGFD | EDKDEDEGSP | GGCNPAGGNG | GDFHRLVF | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1261 | 1 | 1070.0005 | -62.40 | 2 | 45.9 | 12.2 | 1 | 131-150 | R.TVCERPGPAACAQVARLLAR.H | Carbamidomethyl: 3 | QU:MU 0.49<br>WUP:QUP 1.96 |

# Detailed Protein Report

## Protein 164: PREDICTED: collagen alpha-2(I) chain-like [Homo sapiens]

**Accession:** gi|530375734
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 44.7
**MW [kDa]:** 28.8
**pI:** 12.9
**Sequence Coverage [%]:** 11.6
**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MAPFHLSHAP AGARKVKLRH PRKWSPSGSP QPPAQLQPLE APRLPGEVRT SGRLATWFCR LLARRSAAQR KSKSRKDLNR

        90        100        110        120        130        140        150        160
RVQSPLTPHS FHYFSSQGIG GGGGGRDKFA GRLAWSNPRG WDRPRGSGGA LPRPEGDCGG ARPPAGGAGR WASPGAAGRW

       170        180        190        200        210        220        230        240
SLPGRVCGAF AQPAPCPHLT SSPPRPLGGP LRCAAQARSV AARAVRPRSL GQGPGAQGVG RAGRERGRPS TASGSARAGA

       250        260        270        280
ALPAAVRPRE GPRGPSACAL GRRRLCVGRP GGPRGTD
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1759 | 1 | 881.8978 | -107.69 | 2 | 50.4 | 14.1 | 1 | 204-221 | R.AVRPRSLGQGPGAQGVGR.A | |

## Protein 165: PREDICTED: lipopolysaccharide-responsive and beige-like anchor protein isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530378475 | **Score:** | 44.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 318.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 4 |

### Quantitation

| | | | |
|---|---|---|---|
| ***WUP:QUP*** | **Median:** 0.66 | **CV:** 0.00 % | **No. of Peptides:** 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASEDNRVPS | PPPTGDDGGG | GGREETPTEG | GALSLKPGLP | IRGIRMKFAV | LTGLVEVGEV | SNRDIVETVF | NLLVGGQFDL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EMNFIIQEGE | SINCMVDLLE | KCDITCQAEV | WSMFTAILKK | SIRNLQVCTE | VGLVEKVLGK | IEKVDNMIAD | LLVDMLGVLA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SYNLTVRELK | LFFSKLQGDK | GRWPPHAGKL | LSVLKHMPQK | YGPDAFFNFP | GKSAAAIALP | PIAKWPYQNG | FTFHTWLRMD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PVNNINVDKD | KPYLYCFRTS | KGLGYSAHFV | GGCLIVTSIK | SKGKGFQHCV | KFDFKPQKWY | MVTIVHIYNR | WKNSELRCYV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NGELASYGEI | TWFVNTSDTF | DKCFLGSSET | ADANRVFCGQ | MTAVYLFSEA | LNAAQIFAIY | QLGLGYKGTF | KFKAESDLFL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AEHHKLLLYD | GKLSSAIAFT | YNPRATDAQL | CLESSPKDNP | SIFVHSPHAL | MLQDVKAVLT | HSIQSAMHSI | GGVQVLFPLF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AQLDYRQYLS | DEIDLTICST | LLAFIMELLK | NSIAMQEQML | ACKGFLVIGY | SLEKSSKSHV | SRAVLELCLA | FSKYLSNLQN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GMPLLKQLCD | HVLLNPAIWI | HTPAKVQLML | YTYLSTEFIG | TVNIYNTIRR | VGTVLLIMHT | LKYYYWAVNP | QDRSGITPKG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LDGPRPNQKE | MLSLRAFLLM | FIKQLVMKDS | GVKEDELQAI | LNYLLTMHED | DNLMDVLQLL | VALMSEHPNS | MIPAFDQRNG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LRVIYKLLAS | KSEGIRVQAL | KAMGYFLKHL | APKRKAEVML | GHGLFSLLAE | RLMLQTNLIT | MTTYNVLFEI | LIEQIGTQVI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| HKQHPDPDSS | VKIQNPQILK | VIATLLRNSP | QCPESMEVRR | AFLSDMIKLF | NNSRENRRSL | LQCSVWQEWM | LSLCYFNPKN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SDEQKITEMV | YAIFRILLYH | AVKYEWGGWR | VWVDTLSITH | SKVTFEIHKE | NLANIFREQQ | GKVDEEIGLC | SSTSVQAASG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| IRRDINVSVG | SQQPDTKDSP | VCPHFTTNGN | ENSSIEKTSS | LESASNIELQ | TTNTSYEEMK | AEQENQELPD | EGTLEETLTN |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ETRNADDLEV | SSDIIEAVAI | SSNSFITTGK | DSMTVSEVTA | SISSPSEEDA | SEMPEFLDKS | IVEEEEDDDY | VELKVEGSPT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EEANLPTELQ | DNSLSPAASE | AGEKLDMFGN | DDKLIFQEGK | PVTEKQTDTE | TQDSKDSGIQ | TMTASGSSAM | SPETTVSQIA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VESDLGQMLE | EGKKATNLTR | ETKLINDCHG | SVSEASSEQK | IAKLDVSNVA | TDTERLELKA | SPNVEAPQPH | RHVLEISRQH |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| EQPGQGIAPD | AVNGQRRDSR | STVFRIPEFN | WSQMHQRLLT | DLLFSIETDI | QMWRSHSTKT | VMDFVNSSDN | VIFVHNTIHL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ISQVMDNMVM | ACGGILPLLS | AATSATHELE | NIEPTQGLSI | EASVTFLQRL | ISLVDVLIFA | SSLGFTEIEA | EKSMSSGGIL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| RQCLRLVCAV | AVRNCLECQQ | HSQLKTRGDK | ALKPMHSLIP | LGKSAAKSPV | DIVTGGISPV | RDLDRLLQDM | DINRLRAVVF |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| RDIEDSKQAQ | FLALAVVYFI | SVLMVSKYRD | ILEPQNERHS | QSCTETGSEN | ENVSLSEITP | AAFSTLTTAS | VEESESTSSA |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| RRRDSGIGEE | TATGLGSHVE | VTPHTAPPGV | SAGPDAISEV | LSTLSLEVNK | SPETKNDRGN | DLDTKATPSV | SVSKNVNVKD |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| ILRSLVNIPA | DGVTVDPALL | PPACLGALGD | LSVEQPVQFR | SFDRSVIVAA | KKSAVSPSTF | NTSIPTNAVS | VVSSVDSAQA |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SDMGGESPGS | RSSNAKLPSV | PTVDSVSQDP | VSNMSITERL | EHALEKAAPL | LREIFVDFAP | FLSRTLLGSH | GQELLIEGTS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| LVCMKSSSSV | VELVMLLCSQ | EWQNSIQKNA | GLAFIELVNE | GRLLSQTMKD | HLVRVANEAE | FILSRQRAED | IHRHAEFESL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| CAQYSADKRE | DEKMCDHLIR | AAKYRDHVTA | TQLIQKIINI | LTDKHGAWGN | SAVSRPLEFW | RLDYWEDDLR | RRRRFVRNPL |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| GSTHPEATLK | TAVEHATDED | ILAKGKQSIR | SQALGNQNSE | NEILLEGDDD | TLSSVDEKDL | ENLAGPVSLS | TPAQLVAPSV |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| VVKGTLSVTS | SELYFEVDEE | DPNFKKIDPK | ILAYTEGLHG | KWLFTEIRSI | FSRRYLLQNT | ALEIFMANRV | AVMFNFPDPA |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1142 | 1 | 555.2290 | -64.32 | 2 | 44.4 | 10.2 | 0 | 803-812 | K.QHPDPDSSVK.I | | |
| 1230 | 1 | 715.1053 | 93.99 | 3 | 43.7 | 12.4 | 1 | 821-839 | K.VIATLLRNSPQCPESMEVR.R | | |
| 1642 | 1 | 698.8555 | -54.14 | 2 | 50.8 | 10.1 | 0 | 1488-1501 | K.SPVDIVTGGISPVR.D | | |
| 2042 | 1 | 766.2799 | -83.49 | 2 | 55.4 | 11.9 | 0 | 2669-2684 | K.CSGIGDNPGSETAAPR.A | | WUP:QUP 0.66 |

# Detailed Protein Report

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## Protein 166: PREDICTED: lipoxygenase homology domain-containing protein 1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578832310 | **Score:** | 44.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 220.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 3 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.31 | **CV:** | 0.00 % | **No. of Peptides:** | 1 | |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMQLTLNTLF | PVVSTPAITY | IVTVFTGDVR | GAGTKSKIYL | VMYGARGNKN | SGKIFLEGGV | FDRGRTDIFH | IELAVLLSPL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SRVSVGHGNV | GVNRGWFCEK | VVILCPFTGI | QQTFPCSNWL | DEKKADGLIE | RQLYEMVSLR | KKRLKKFPWS | LWVWTTDLKK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AGTNSPIFIQ | IYGQKGRTDE | ILLNPNNKWF | KPGIIEKFRI | ELPDLGRFYK | IRVWHDKRSS | GSGWHLERMT | LMNTLNKDKY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NFNCNRWLDA | NEDDNEIVRE | MTAEGPTVRR | IMGMARYHVT | VCTGELEGAG | TDANVYLCLF | GDVGDTGERL | LYNCRNNTDL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FEKGNADEFT | IESVTMRNVR | RVRIRHDGKG | SGSGWYLDRV | LVREEGQPES | DNVEFPCLRW | LDKDKDDGQL | VRELLPSDSS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ATLKNFRYHI | SLKTGDVSGA | STDSRVYIKL | YGDKSDTIKQ | VLLVSDNNLK | DYFERGRVDE | FTLETLNIGN | INRLVIGHDS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TGMHASWFLG | SVQIRVPRQG | KQYTFPANRW | LDKNQADGRL | EVELYPSEVV | EIQKLVHYEV | EIWTGDVGGA | GTSARVYMQI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YGEKGKTEVL | FLSSRSKVFE | RASKDTFQLE | AADVGEVYKL | RLGHTGEGFG | PSWFVDTVWL | RHLVVREVDL | TPEEEARKKK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EKDKLRQLLK | KERLKAKLQR | KKKKRKGSDE | EDEGEEEESS | SSEESSSEEE | EMEEEEEEEE | FGPGMQEVIE | QHKFEAHRWL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ARGKEDNELV | VELVPAGKPG | PERNTYEVQV | VTGNVPKAGT | DANVYLTIYG | EEYGDTGERP | LKKSDKSNKF | EQGQTDTFTI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| YAIDLGALTK | IRIRHDNTGN | RAGWFLDRID | ITDMNNEITY | YFPCQRWLAV | EEDDGQLSRE | LLPVDESYVL | PQSEEGRGGG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DNNPLDNLAL | EQKDKSTTFS | VTIKTGVKKN | AGTDANVFIT | LFGTQDDTGM | TLLKSSKTNS | DKFERDSIEI | FTVETLDLGD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LWKVRLGHDN | TGKAPGWFVD | WVEVDAPSLG | KCMTFPCGRW | LAKNEDDGSI | IRDLFHAELQ | TRLYTPFVPY | EITLYTSDVF |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AAGTDANIFI | IIYGCDAVCT | QQKYLCTNKR | EQKQFFERKS | ASRFIVELED | VGEIIEKIRI | GHNNTGMNPG | WHCSHVDIRR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LLPDKDGAET | LTFPCDRWLA | TSEDDKKTIR | ELVPYDIFTE | KYMKDGSLRQ | VYKEVEEPLD | IVLYSVQIFT | GNIPGAGTDA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KVYITIYGDL | GDTGERYLGK | SENRTNKFER | GTADTFIIEA | ADLGVIYKIK | LRHDNSKWCA | DWYVEKVEIW | NDTNEDEFLF |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LCGRWLSLKK | EDGRLERLFY | EKEYTGDRSS | NCSSPADFWE | IALSSKMADV | DISTVTGPMA | DYVQEGPIIP | YYVSVTTGKH |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KDAATDSRAF | IFLIGEDDER | SKRIWLDYPR | GKRGFSRGSV | EEFYVAGLDV | GIIKKIEVLY | EMTVWTGDVV | GGGTDSNIFM |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| TLYGINGSTE | EMQLDKKKAR | FEREQNDTFI | MEILDIAPFT | KMRIRIDGLG | SRPEWFLERI | LLKNMNTGDL | TMFYYGDWLS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| QRKGKKTLVC | EMCAVIDEEE | MMEWTSYTVA | VKTSDILGAG | TDANVFIIIF | GENGDSGTLA | LKQSANWNKF | ERNNTDTFNF |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| PDMLSLGHLC | KLRVWHDNKG | IFPGWHLSYV | DVKDNSRDET | FHFQCDCWLS | KSEGDGQTVR | DFACANNKIC | DELEETTYEI |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| VIETGNGGET | RENVWLILEG | RKNRSKEFLM | ENSSRQRAFR | KGTTDTFEFD | SIYLGDIASL | CVGHLAREDR | FIPKRELAWH |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| VKTITITEME | YGNVYFFNCD | CLIPLKRKRK | YFKVFEVTKT | TESFASKVQS | LVPVKYEVIV | TTGYEPGAGT | DANVFVTIFG |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| ANGDTGKREL | KQKMRNLFER | GSTDRFFLET | LELGELRKVR | LEHDSSGYCS | GWLVEKVEVT | NTSTGVATIF | NCGRWLDKKR |
| 1930 | 1940 | | | | | | |
| GDGLTWRDLF | PSV | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2434 | 1 | 1045.2535 | -261.87 | 1 | 60.9 | 17.6 | 1 | 384-392 | K.DKDDGQLVR.E | | |
| 2071 | 1 | 1052.4367 | -86.97 | 2 | 56.3 | 14.8 | 2 | 1120-1137 | R.RLLPDKDGAETLTFPCDR.W | Carbamidomethyl: 16 | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1581 | 1 | 698.7063 | -184.90 | 2 | 50.0 | 12.1 | 1 | 1707-1717 | K.EFLMENSSRQR.A |  | QU:MU 1.31 |

# Detailed Protein Report

## Protein 167: PREDICTED: plexin-A1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578807485 | **Score:** | 44.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 212.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMLTPAGPEH | RGPRPQPAMP | LPPRSLQVLL | LLLLLLLLLP | GMWAEAGLPR | AGGGSQPPFR | TFSASDWGLT | HLVVHEQTGE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VYVGAVNRIY | KLSGNLTLLR | AHVTGPVEDN | EKCYPPPSVQ | SCPHGLGSTD | NVNKLLLLDY | AANRLLACGS | ASQGICQFLR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LDDLFKLGEP | HHRKEHYLSS | VQEAGSMAGV | LIAGPPGQGQ | AKLFVGTPID | GKSEYFPTLS | SRRLMANEED | ADMFGFVYQD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EFVSSQLKIP | SDTLSKFPAF | DIYYVYSFRS | EQFVYYLTLQ | LDTQLTSPDA | AGEHFFTSKI | VRLCVDDPKF | YSYVEFPIGC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EQAGVEYRLV | QDAYLSRPGR | ALAHQLGLAE | DEDVLFTVFA | QGQKNRVKPP | KESALCLFTL | RAIKEKIKER | IQSCYRGEGK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LSLPWLLNKE | LGCINSPLQI | DDDFCGQDFN | QPLGGTVTIE | GTPLFVDKDD | GLTAVAAYDY | RGRTVVFAGT | RSGRIRKILV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DLSNPGGRPA | LAYESVVAQE | GSPILRDLVL | SPNHQYLYAM | TEKQVTRVPV | ESCVQYTSCE | LCLGSRDPHC | GWCVLHSICS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RRDACERADE | PQRFAADLLQ | CVQLTVQPRN | VSVTMSQVPL | VLQAWNVPDL | SAGVNCSFED | FTESESVLED | GRIHCRSPSA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| REVAPITRGQ | GDQRVVKLYL | KSKETGKKFA | SVDFVFYNCS | VHQSCLSCVN | GSFPCHWCKY | RHVCTHNVAD | CAFLEGRVNV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SEDCPQILPS | TQIYVPVGVV | KPITLAARNL | PQPQSGQRGY | ECLFHIPGSP | ARVTALRFNS | SSLQCQNSSY | SYEGNDVSDL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PVNLSVVWNG | NFVIDNPQNI | QAHLYKCPAL | RESCGLCLKA | DPRFECGWCV | AERRCSLRHH | CAADTPASWM | HARHGSSRCT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DPKILKLSPE | TGPRQGGTRL | TITGENLGLR | FEDVRLGVRV | GKVLCSPVES | EYISAEQIVC | EIGDASSVRA | HDALVEVCVR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DCSPHYRALS | PKRFTFVTPT | FYRVSPSRGP | LSGGTWIGIE | GSHLNAGSDV | AVSVGGRPCS | FSWRNSREIR | CLTPPGQSPG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SAPIIININR | AQLTNPEVKY | NYTEDPTILR | IDPEWSINSG | GTLLTVTGTN | LATVREPRIR | AKYGGIEREN | GCLVYNDTTM |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| VCRAPSVANP | VRSPPELGER | PDELGFVMDN | VRSLLVLNST | SFLYYPDPVL | EPLSPTGLLE | LKPSSPLILK | GRNLLPPAPG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| NSRLNYTVLI | GSTPCTLTVS | ETQLLCEAPN | LTGQHKVTVR | AGGFEFSPGT | LQVYSDSLLT | LPAIVGIGGG | GGLLLLVIVA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VLIAYKRKSR | DADRTLKRLQ | LQMDNLESRV | ALECKEAFAE | LQTDIHELTN | DLDGAGIPFL | DYRTYAMRVL | FPGIEDHPVL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KEMEVQANVE | KSLTLFGQLL | TKKHFLLTFI | RTLEAQRSFS | MRDRGNVASL | IMTALQGEME | YATGVLKQLL | SDLIEKNLES |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KNHPKLLLRR | TESVAEKMLT | NWFTFLLYKF | LKECAGEPLF | MLYCAIKQQM | EKGPIDAITG | EARYSLSEDK | LIRQQIDYKT |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| LTLNCVNPEN | ENAPEVPVKG | LDCDTVTQAK | EKLLDAAYKG | VPYSQRPKAA | DMDLEWRQGR | MARIILQDED | VTTKIDNDWK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| RLNTLAHYQV | TDGSSVALVP | KQTSAYNISN | SSTFTKSLSR | YESMLRTASS | PDSLRSRTPM | ITPDLESGTK | LWHLVKNHDH |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LDQREGDRGS | KMVSEIYLTR | LLATKKFVDD | LFETIFSTAH | RGSALPLAIK | YMFDFLDEQA | DKHQIHDADV | RHTWKSNCLP |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| LRFWVNVIKN | PQFVFDIHKN | SITDACLSVV | AQTFMDSCST | SEHKLGKDSP | SNKLLYAKDI | PNYKSWVERY | YADIAKMPAI |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| SDQDMSAYLA | EQSRLHLSQF | NSMSALHEIY | SYITKYKDEI | LAALEKDEQA | RRQRLRSKLE | QVVDTMALSS | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1881 | 1 | 628.2724 | -43.47 | 2 | 53.9 | 15.1 | 0 | 1-11 | -.MMLTPAGPEHR.G | Oxidation: 1 |

# Detailed Protein Report

## Protein 168: fibrillin-2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|66346695 | **Score:** | 44.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 314.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.09 | **CV:** | 63.27 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 1.03 | **CV:** | 41.37 % | **No. of Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGRRRRLCLQ | LYFLWLGCVV | LWAQGTAGQP | QPPPPKPPRP | QPPPQQVRSA | TAGSEGGFLA | PEYREEGAAV | ASRVRRRGQQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DVLRGPNVCG | SRFHSYCCPG | WKTLPGGNQC | IVPICRNSCG | DGFCSRPNMC | TCSSGQISST | CGSKSIQQCS | VRCMNGGTCA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DDHCQCQKGY | IGTYCGQPVC | ENGCQNGGRC | IGPNRCACVY | GFTGPQCERD | YRTGPCFTQV | NNQMCQGQLT | GIVCTKTLCC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ATIGRAWGHP | CEMCPAQPQP | CRRGFIPNIR | TGACQDVDEC | QAIPGICQGG | NCINTVGSFE | CRCPAGHKQS | ETTQKCEDID |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ECSIIPGICE | TGECSNTVGS | YFCVCPRGYV | TSTDGSRCID | QRTGMCFSGL | VNGRCAQELP | GRMTKMQCCC | EPGRCWGIGT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IPEACPVRGS | EEYRRLCMDG | LPMGGIPGSA | GSRPGGTGGN | GFAPSGNGNG | YGPGGTGFIP | IPGGNGFSPG | VGGAGVGAGG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QGPIITGLTI | LNQTIDICKH | HANLCLNGRC | IPTVSSYRCE | CNMGYKQDAN | GDCIDVDECT | SNPCTNGDCV | NTPGSYYCKC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HAGFQRTPTK | QACIDIDECI | QNGVLCKNGR | CVNTDGSFQC | ICNAGFELTT | DGKNCVDHDE | CTTTNMCLNG | MCINEDGSFK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CICKPGFVLA | PNGRYCTDVD | ECQTPGICMN | GHCINSEGSF | RCDCPPGLAV | GMDGRVCVDT | HMRSTCYGGI | KKGVCVRPFP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GAVTKSECCC | ANPDYGFGEP | CQPCPAKNSA | EFHGLCSSGV | GITVDGRDIN | ECALDPDICA | NGICENLRGS | YRCNCNSGYE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PDASGRNCID | IDECLVNRLL | CDNGLCRNTP | GSYSCTCPPG | YVFRTETETC | EDINECESNP | CVNGACRNNL | GSFNCECSPG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SKLSSTGLIC | IDSLKGTCWL | NIQDSRCEVN | INGATLKSEC | CATLGAAWGS | PCERCELDTA | CPRGLARIKG | VTCEDVNECE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VFPGVCPNGR | CVNSKGSFHC | ECPEGLTLDG | TGRVCLDIRM | EQCYLKWDED | ECIHPVPGKF | RMDACCCAVG | AAWGTECEEC |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PKPGTKEYET | LCPRGAGFAN | RGDVLTGRPF | YKDINECKAF | PGMCTYGKCR | NTIGSFKCRC | NSGFALDMEE | RNCTDIDECR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ISPDLCGSGI | CVNTPGSFEC | ECFEGYESGF | MMMKNCMDID | ECERNPLLCR | GGTCVNTEGS | FQCDCPLGHE | LSPSREDCVD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| INECSLSDNL | CRNGKCVNMI | GTYQCSCNPG | YQATPDRQGC | TDIDECMIMN | GGCDTQCTNS | EGSYECSCSE | GYALMPDGRS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| CADIDECENN | PDICDGGQCT | NIPGEYRCLC | YDGFMASMDM | KTCIDVNECD | LNSNICMFGE | CENTKGSFIC | HCQLGYSVKK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| GTTGCTDVDE | CEIGAHNCDM | HASCLNIPGS | FKCSCREGWI | GNGIKCIDLD | ECSNGTHQCS | INAQCVNTPG | SYRCACSEGF |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| TGDGFTCSDV | DECAENINLC | ENGQCLNVPG | AYRCECEMGF | TPASDSRSCQ | DIDECSFQNI | CVFGTCNNLP | GMFHCICDDG |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| YELDRTGGNC | TDIDECADPI | NCVNGLCVNT | PGRYECNCPP | DFQLNPTGVG | CVDNRVGNCY | LKFGPRGDGS | LSCNTEIGVG |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| VSRSSCCCSL | GKAWGNPCET | CPPVNSTEYY | TLCPGGEGFR | PNPITIILED | IDECQELPGL | CQGGNCINTF | GSFQCECPQG |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| YYLSEDTRIC | EDIDECFAHP | GVCGPGTCYN | TLGNYTCICP | PEYMQVNGGH | NCMDMRKSFC | YRSYNGTTCE | NELPFNVTKR |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| MCCCTYNVGK | AWNKPCEPCP | TPGTADFKTI | CGNIPGFTFD | IHTGKAVDID | ECKEIPGICA | NGVCINQIGS | FRCECPTGFS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| YNDLLLVCED | IDECSNGDNL | CQRNADCINS | PGSYRCECAA | GFKLSPNGAC | VDRNECLEIP | NVCSHGLCVD | LQGSYQCICH |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| NGFKASQDQT | MCMDVDECER | HPCGNGTCKN | TVGSYNCLCY | PGFELTHNND | CLDIDECSSF | FGQVCRNGRC | FNEIGSFKCL |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| CNEGYELTPD | GKNCIDTNEC | VALPGSCSPG | TCQNLEGSFR | CICPPGYEVK | SENCIDINEC | DEDPNICLFG | SCTNTPGGFQ |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| CLCPPGFVLS | DNGRRCFDTR | QSFCFTNFEN | GKCSVPKAFN | TTKAKCCCSK | MPGEGWGDPC | ELCPKDDEVA | FQDLCPYGHG |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 186 | 1 | 806.9057 | 27.18 | 2 | 31.2 | 11.0 | 0 | 49-64 | R.SATAGSEGGFLAPEYR.E |  | QU:MU 0.61<br>WUP:QUP 0.69 |
| 2112 | 1 | 600.2270 | -134.67 | 3 | 54.8 | 15.6 | 2 | 77-92 | R.RGQQDVLRGPNVCGSR.F | Carbamidomethyl: 13 |  |
| 323 | 5 | 642.1545 | -201.52 | 2 | 33.7 | 17.8 | 1 | 2529-2539 | K.TCKDLDECQTK.Q |  | QU:MU 1.94<br>WUP:QUP 1.54 |

# Detailed Protein Report

## Protein 169: sushi, nidogen and EGF-like domain-containing protein 1 precursor [Homo sapiens]

**Accession:** gi|122937283
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 44.1
**MW [kDa]:** 152.1
**pI:** 6.6
**Sequence Coverage [%]:** 1.3
**No. of unique Peptides:** 3

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578804032 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: sushi, nidogen and EGF-like domain-containing protein 1 isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRHGVAWALL | VAAALGLGAR | GVRGAVALAD | FYPFGAERGD | AVTPKQDDGG | SGLRPLSVPF | PFFGAEHSGL | YVNNNGIISF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LKEVSQFTPV | AFPIAKDRCV | VAAFWADVDN | RRAGDVYYRE | ATDPAMLRRA | TEDVRHYFPE | LLDFNATWVF | VATWYRVTFF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GGSSSSPVNT | FQTVLITDGK | LSFTIFNYES | IVWTTGTHAS | SGGNATGLGG | IAAQAGFNAG | DGQRYFSIPG | SRTADMAEVE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TTTNVGVPGR | WAFRIDDAQV | RVGGCGHTTS | VCLALRPCLN | GGKCIDDCVT | GNPSYTCSCL | SGFTGRRCHL | DVNECASQPC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QNGGTCTHGI | NSFRCQCPAG | FGGPTCETAQ | SPCDTKECQH | GGQCQVENGS | AVCVCQAGYT | GAACEMDVDD | CSPDPCLNGG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SCVDLVGNYT | CLCAEPFKGL | RCETGDHPVP | DACLSAPCHN | GGTCVDADQG | YVCECPEGFM | GLDCRERVPD | DCECRNGGRC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LGANTTLCQC | PLGFFGLLCE | FEITAMPCNM | NTQCPDGGYC | MEHGGSYLCV | CHTDHNASHS | LPSPCDSDPC | FNGGSCDAHD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DSYTCECPRG | FHGKHCEKAR | PHLCSSGPCR | NGGTCKEAGG | EYHCSCPYRF | TGRHCEIGKP | DSCASGPCHN | GGTCFHYIGK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| YKCDCPPGFS | GRHCEIAPSP | CFRSPCVNGG | TCEDRDTDFF | CHCQAGYMGR | RCQAEVDCGP | PEEVKHATLR | FNGTRLGAVA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LYACDRGYSL | SAPSRIRVCQ | PHGVWSEPPQ | CLEIDECRSQ | PCLHGGSCQD | RVAGYLCLCS | TGYEGAHCEL | ERDECRAHPC |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RNGGSCRNLP | GAYVCRCPAG | FVGVHCETEV | DACDSSPCQH | GGRCESGGGA | YLCVCPESFF | GYHCETVSDP | CFSSPCGGRG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| YCLASNGSHS | CTCKVGYTGE | DCAKELFPPT | ALKMERVEES | GVSISWNPPN | GPAARQMLDG | YAVTYVSSDG | SYRRTDFVDR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TRSSHQLQAL | AAGRAYNISV | FSVKRNSNNK | NDISRPAVLL | ARTRPRPVEG | FEVTNVTAST | ISVQWALHRI | RHATVSGVRV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SIRHPEALRD | QATDVDRSVD | RFTFRALLPG | KRYTIQLTTL | SGLRGEEHPT | ESLATAPTHV | WTRPLPPANL | TAARVTATSA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| HVVWDAPTPG | SLLEAYVINV | TTSQSTKSRY | VPNGKLASYT | VRDLLPGRRY | QLSVIAVQST | ELGPQHSEPA | HLYIITSPRD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| GADRRWHQGG | HHPRVLKNRP | PPARLPELRL | LNDHSAPETP | TQPPRFSELV | DGRGRVSARF | GGSPSKAATV | RSQPTASAQL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| ENMEEAPKRV | SLALQLPEHG | SKDIGNVPGN | CSENPCQNGG | TCVPGADAHS | CDCGPGFKGR | RCELACIKVS | RPCTRLFSET |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | | |
| KAFPVWEGGV | CHHVYKRVYR | VHQDICFKES | CESTSLKKTP | NRKQSKSQTL | EKS | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2079 | 1 | 1044.9332 | 12.94 | 2 | 56.4 | 14.4 | 1 | 591-609 | R.NGGTCKEAGGEYHCSCPYR.F | Carbamidomethyl: 5 |
| 1667 | 1 | 1073.2934 | -127.64 | 2 | 49.2 | 19.6 | 1 | 591-609 | R.NGGTCKEAGGEYHCSCPYR.F | Carbamidomethyl: 5, 16 |
| 2019 | 1 | 715.9639 | 11.03 | 3 | 53.6 | 10.1 | 1 | 591-609 | R.NGGTCKEAGGEYHCSCPYR.F | Carbamidomethyl: 14, 16 |

# Detailed Protein Report

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## Protein 170: PREDICTED: coiled-coil domain-containing protein 88B isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578821335 | **Score:** | 44.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 173.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| | | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

***WUP:QUP*** **Median:** 4.17 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEGGKGPRLR | DFLSGSLATW | ALGLAGLVGE | AEDSEGEEEE | EEEEPPLWLE | KRFLRLSDGA | LLLRVLGIIA | PSSRGGPRML |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RGLDGPAAWR | VWNLNHLWGR | LRDFYQEELQ | LLILSPPPDL | QTLGFDPLSE | EAVEQLEGVL | RLLLGASVQC | EHRELFIRHI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QGLSLEVQSE | LAAAIQEVTQ | PGAGVVLALS | GPDPGELAPA | ELEMLSRSLM | GTLSKLARER | DLGAQRLAEL | LLEREPLCLR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PEAPSRAPAE | GPSHHLALQL | ANAKAQLRRL | RQELEEKAEL | LLDSQAEVQG | LEAEIRRLRQ | EAQALSGQAK | RAELYREEAE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ALRERAGRLP | RLQEELRRCR | ERLQAAEAYK | SQLEEERVLS | GVLEASKALL | EEQLEAARER | CARLHETQRE | NLLLRTRLGE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AHAELDSLRH | QVDQLAEENV | ELELELQRSL | EPPPGSPGEA | PLAGAAPSLQ | DEVREAEAGR | LRTLERENRE | LRGLLQVLQG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QPGGQHPLLE | APREDPVLPV | LEEAPQTPVA | FDHSPQGLVQ | KARDGGPQAL | DLAPPALDSV | LEASAECPQA | PDSDPQEAES |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PLQAAAMDPQ | ASDWSPQESG | SPVETQESPE | KAGRRSSLQS | PASVAPPQGP | GTKIQAPQLL | GGETEGREAP | QGELVPEAWG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LRQEGPEHKP | GPSEPSSVQL | EEQEGPNQGL | DLATGQAEAR | EHDQRLEGTV | RDPAWQKPQQ | KSEGALEVQV | WEGPIPGESL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ASGVAEQEAL | REEVAQLRRK | AEALGDELEA | QARKLEAQNT | EAARLSKELA | QARRAEAEAH | REAEAQAWEQ | ARLREAVEAA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GQELESASQE | REALVEALAA | AGRERRQWER | EGSRLRAQSE | AAEERMQVLE | SEGRQHLEEA | ERERREKEAL | QAELEKAVVR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GKELGDRLEH | LQRELEQAAL | ERQEFLREKE | SQHQRYQGLE | QRLEAELQAA | ATSKEEALME | LKTRALQLEE | ELFQLRQGPA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GLGPKKRAEP | QLVETQNVRL | IEVERSNAML | VAEKAALQGQ | LQHLEGQLGS | LQGRAQELLL | QSQRAQEHSS | RLQAEKSVLE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| IQGQELHRKL | EVLEEEVRAA | RQSQEETRGQ | QQALLRDHKA | LAQLQRRQEA | ELEGLLVRHR | DLKANMRALE | LAHRELQGRH |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EQLQAQRASV | EAQEVALLAE | RERLMQDGHR | QRGLEEELRR | LQSEHDRAQM | LLAELSRERG | ELQGERGELR | GRLARLELER |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| AQLEMQSQQL | RESNQQLDLS | ACRLTTQCEL | LTQLRSAQEE | ENRQLLAEVQ | ALSRENRELL | ERSLESRDHL | HREQREYLDQ |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LNALRREKQK | LVEKIMDQYR | VLEPVPLPRT | KKGSWLADKG | PLPRHPCAGP | RAPSACGMRP | WQAGSGGNSA | QGSRWGEALS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| HSALGTPLGN | DSDSAIQAPW | GRPSPTAKDL | VWDGRTPLRP | CRNTKQMPTE | RALRYRNRRN | VPSPHPSASD | TVGTAGLGVQ |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| PSRHWSVSGG | PRQPKSSGSQ | GPQGESLDKE | AWALRSSTVS | AGARRWSWDE | CVDRGDGWPP | RAAPGWSSGS | SRWLPLRQRS |
| 1530 | 1540 | 1550 | 1560 | 1570 | | | |
| LGDPPAEGGW | QELAREPPAL | SRWEAESQCW | GTVAWADLEP | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 245 | 1 | 715.7361 | -205.90 | 2 | 33.1 | 13.1 | 1 | 755-767 | K.LEAQNTEAARLSK.E | | |
| 2188 | 1 | 945.6234 | 129.84 | 2 | 57.8 | 19.6 | 2 | 1258-<br>1272 | R.ELLERSLESRDHLHR.E | | |
| 1580 | 1 | 781.3390 | -87.96 | 2 | 49.5 | 11.3 | 1 | 1470- | K.EAWALRSSTVSAGAR.R | | WUP:QUP 4.17 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | 1484 | | | |

# Detailed Protein Report

## Protein 171: G-protein coupled receptor 98 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|113722120 | **Score:** | 43.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 692.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.4 |
| | | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSVFLGPGMP | SASLLVNLLS | ALLILFVFGE | TEIRFTGQTE | FVVNETSTTV | IRLIIERIGE | PANVTAIVSL | YGEDAGDFFD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TYAAAFIPAG | ETNRTVYIAV | CDDDLPEPDE | TFIFHLTLQK | PSANVKLGWP | RTVTVTILSN | DNAFGIISFN | MLPSIAVSEP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KGRNESMPLT | LIREKGTYGM | VMVTFEVEGG | PNPPDEDLSP | VKGNITFPPG | RATVIYNLTV | LDDEVPENDE | IFLIQLKSVE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GGAEINTSRN | SIEIIIKKND | SPVRFLQSIY | LVPEEDHILI | IPVVRGKDNN | GNLIGSDEYE | VSISYAVTTG | NSTAHAQQNL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DFIDLQPNTT | VVFPPFIHES | HLKFQIVDDT | IPEIAESFHI | MLLKDTLQGD | AVLISPSVVQ | VTIKPNDKPY | GVLSFNSVLF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ERTVIIDEDR | ISRYEEITVV | RNGGTHGNVS | ANWVLTRNST | DPSPVTADIR | PSSGVLHFAQ | GQMLATIPLT | VVDDDLPEEA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EAYLLQILPH | TIRGGAEVSE | PAELLFYIQD | SDDVYGLITF | FPMENQKIES | SPGERYLSLS | FTRLGGTKGD | VRLLYSVLYI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PAGAVDPLQA | KEGILNISRR | NDLIFPEQKT | QVTTKLPIRN | DAFLQNGAHF | LVQLETVELL | NIIPLIPPIS | PRFGEICNIS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LLVTPAIANG | EIGFLSNLPI | ILHEPEDFAA | EVVYIPLHRD | GTDGQATVYW | SLKPSGFNSK | AVTPDDIGPF | NGSVLFLSGQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SDTTINITIK | GDDIPEMNET | VTLSLDRVNV | ENQVLKSGYT | SRDLIILEND | DPGGVFEFSP | ASRGPYVIKE | GESVELHIIR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SRGSLVKQFL | HYRVEPRDSN | EFYGNTGVLE | FKPGEREIVI | TLLARLDGIP | ELDEHYWVVL | SSHGERESKL | GSATIVNITI |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LKNDDPHGII | EFVSDGLIVM | INESKGDAIY | SAVYDVVRNR | GNFGDVSVSW | VVSPDFTQDV | FPVQGTVVFG | DQEFSKNITI |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| YSLPDEIPEE | MEEFTVILLN | GTGGAKVGNR | TTATLRIRRN | DDPIYFAEPR | VVRVQEGETA | NFTVLRNGSV | DVTCMVQYAT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KDGKATARER | DFIPVEKGET | LIFEVGSRQQ | SISIFVNEDG | IPETDEPFYI | ILLNSTGDTV | VYQYGVATVI | IEANDDPNGI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| FSLEPIDKAV | EEGKTNAFWI | LRHRGYFGSV | SVSWQLFQND | SALQPGQEFY | ETSGTVNFMD | GEEAKPIILH | AFPDKIPEFN |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EFYFLKLVNI | SGGSPGPGGQ | LAETNLQVTV | MVPFNDDPFG | VFILDPECLE | REVAEDVLSE | DDMSYITNFT | ILRQQGVFGD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VQLGWEILSS | EFPAGLPPMI | DFLLVGIFPT | TVHLQQHMRR | HHSGTDALYF | TGLEGAFGTV | NPKYHPSRNN | TIANFTFSAW |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VMPNANTNGF | IIAKDDGNGS | IYYGVKIQTN | ESHVTLSLHY | KTLGSNATYI | AKTTVMKYLE | ESVWLHLLII | LEDGIIEFYL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DGNAMPRGIK | SLKGEAITDG | PGILRIGAGI | NGNDRFTGLM | QDVRSYERKL | TLEEIYELHA | MPAKSDLHPI | SGYLEFRQGE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| TNKSFIISAR | DDNDEEGEEL | FILKLVSVYG | GARISEENTT | ARLTIQKSDN | ANGLFGFTGA | CIPEIAEEGS | TISCVVERTR |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| GALDYVHVFY | TISQIETDGI | NYLVDDFANA | SGTITFLPWQ | RSEVLNIYVL | DDDIPELNEY | FRVTLVSAIP | GDGKLGSTPT |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| SGASIDPEKE | TTDITIKASD | HPYGLLQFST | GLPPQPKDAM | TLPASSVPHI | TVEEEDGEIR | LLVIRAQGLL | GRVTAEFRTV |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SLTAFSPEDY | QNVAGTLEFQ | PGERYKYIFI | NITDNSIPEL | EKSFKVELLN | LEGGVAELFR | VDGSGSGDGD | MEFFLPTIHK |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| RASLGVASQI | LVTIAASDHA | HGVFEFSPES | LFVSGTEPED | GYSTVTLNVI | RHHGTLSPVT | LHWNIDSDPD | GDLAFTSGNI |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| TFEIGQTSAN | ITVEILPDED | PELDKAFSVS | VLSVSSGSLG | AHINATLTVL | ASDDPYGIFI | FSEKNRPVKV | EEATQNITLS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| IIRLKGLMGK | VLVSYATLDD | MEKPPYFPPN | LARATQGRDY | IPASGFALFG | ANQSEATIAI | SILDDDEPER | SESVFIELLN |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| STLVAKVQSR | SIPNSPRLGP | KVETIAQLII | IANDDAFGTL | QLSAPIVRVA | ENHVGPIINV | TRTGGAFADV | SVKFKAVPIT |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| AIAGEDYSIA | SSDVVLLEGE | TSKAVPIYVI | NDIYPELEES | FLVQLMNETT | GGARLGALTE | AVIIIEASDD | PYGLFGFQIT |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| KLIVEEPEFN | SVKVNLPIIR | NSGTLGNVTV | QWVATINGQL | ATGDLRVVSG | NVTFAPGETI | QTLLLEVLAD | DVPEIEEVIQ |
| 2330 | 2340 | 2350 | 2360 | 2370 | 2380 | 2390 | 2400 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1940 | 2 | 643.2750 | -74.26 | 2 | 54.6 | 11.3 | 0 | 4809-4819 | K.EQPIVTENAER.Q | |

BRUKER

# Detailed Protein Report

## Protein 172: FERM and PDZ domain-containing protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|239582741 | **Score:** | 43.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 173.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.37 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.06 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEELETSLFQ | TRKAHRIEQM | VARWLRRSRD | SSARAKVAAA | DGPARNPTQT | LIPVRHTVKI | DKDTLLQDYG | FHISESLPLT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VVAVTAGGSA | HGKLFPGDQI | LQMNNEPAED | LSWERAVDIL | REAEDSLSIT | VVRCTSGVPK | SSFLTEEKRA | RLKTNPVKVH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FAEEVLISGH | SQGNSLLCMP | NVLKLYLENG | QTKAFKFEAN | TTVKDIILTV | KEKLSIRSIE | YFALALEEQY | SISRLHLLHE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EELIQQVVER | EESHDYRCLF | RVCFVPKDPL | DLLKEDPVAF | EYLYLQSCSD | VLQERFAVEM | KCSSALRLAA | LHIQERIYAC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AQPQKISLKY | IEKDWGIENF | ISPTLLRNMK | GKDIKKAISF | HMKRNQNLLE | PRQKQLISAA | QLRLNYLQIL | GELKTYGGRI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FNATLMLQDR | ESYIALLVGA | KYGISQVINS | KLNIMSTLAE | FANISRVELT | EESEKVSVVK | VYLQDVKVLT | LLLESNSAKD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LACLIAGYYR | LLVDPVTSIF | LWPGNKQQAH | RVSAEEGYES | RACSDSEESS | EVDCVLEPLS | DRRLVKLAPC | RSLIKEEQPP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GNSPTPEVAR | RGPSTCGASS | TTDSAESEAS | DSANTESRGY | RTSGSSESMD | ALEEDDLDTC | SSSRSTFFHF | GSPGLAESID |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SDSQEERSGI | ETSGFLCLLD | LAQRANPQCQ | KTEFSESAAL | ETFGWAPELS | TVRLDPRLYE | GSHADYYSLC | SSVSPASYLS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DSSESTASRQ | GGAPPAWGQQ | GWTEAQPSSM | LEPLALHPPL | AFEDGSSDEE | YYDAADKLTP | PGPPSGPRDV | STAEPSATSL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QNKASTSSPE | NSLPCGPDGR | QPSRRGGVKK | YAKTLRKRRS | FLQTDYTSQV | SFPLVPSASL | ESVDDVCYYD | REPYLALGAP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SPTVSSLQDM | QGEPGLLETK | ALGLLAPLRE | TKSTNPASRV | MEMEPETMET | KSVIDSRVSS | ISAIRFRIDP | NNKENSGVVP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| AASSSASTPH | CSNPGSSGPD | TAQARPSQIL | PLSQDLDGIA | PKEPTIEHGD | SSFSLSSGDP | NPDRACLASN | PGLNNVSQGD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TLELQLEPHV | QLEMGLESFC | TNHIQETAPK | YTEPLLSPRD | EPRSDECGIN | PGEKIASIPT | KEEPQGQLSL | ERDREVTNKN |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GTNVFQEESR | KDSGDSPGDV | SNNVSQTLDI | SSPAGKIVTS | LSLDAPVTGT | EQIPPHPPRD | PQGQSREPPG | QGCQAQEQKL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| FVELDLDPDF | FLGKQTVSPA | VPPEGIKAEA | PNHVTGQDIA | PRDSPEWVCF | NPEPSLPEPL | PCPQEDPHLE | TSNHCLLSEG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KSDSSSICLS | AEKSFLCFAP | ESHPEVSASL | RVATSLGFAG | MNEMVAPRIG | MDQCSCQFSY | ATCFRGPQPE | TEEEDRDLEA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| HPMAPLTSPP | SAGSPVVLPW | RPARAHSCTT | APLSRKSHIW | PEYCSRALRQ | LKATPASTPE | GFIQLMESLL | ELQDILETSW |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GVGNKHPPEK | CTWHFTESRS | RLCMGSQKLL | SSCRHVIRMD | QSPEEMQGAV | RDTFQHLVQL | AGLCFQFTDC | SRCSARHREA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | | |
| AGNLRDVVYT | YHQFIEAAKS | TCERGYHDLS | VKLLARQCTA | LTAAVFCLTQ | KFRASTAL | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2745 | 1 | 849.4011 | -32.55 | 1 | 65.4 | 14.4 | 0 | 357-363 | K.AISFHMK.R | Oxidation: 6 | |
| 2634 | 1 | 994.5127 | -8.52 | 2 | 63.7 | 13.9 | 2 | 1462-1478 | R.LCMGSQKLLSSCRHVIR.M | Carbamidomethyl: 2 | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2077 | 1 | 1158.9066 | -123.27 | 2 | 55.9 | 15.3 | 1 | 1526-1544 | R.DVVYTYHQFIEAAKSTCER.G | Carbamidomethyl: 17 | QU:MU<br>WUP:QUP | 2.37<br>1.06 |

# Detailed Protein Report

**Protein 173:** **MAX gene-associated protein isoform 2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|256017159 | **Score:** | 43.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 315.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***WUP:QUP*** | **Median:** | 5.06 | **CV:** | 0.00 % | **No. of Peptides:** | 1 | |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MEEKQQIILA NQDGGTVAGA APTFFVILKQ PGNGKTDQGI LVTNQDACAL ASSVSSPVKS KGKICLPADC TVGGITVTLD
        90        100        110        120        130        140        150        160
NNSMWNEFYH RSTEMILTKQ GRRMFPYCRY WITGLDSNLK YILVMDISPV DNHRYKWNGR WWEPSGKAEP HVLGRVFIHP
       170        180        190        200        210        220        230        240
ESPSTGHYWM HQPVSFYKLK LTNNTLDQEG HIILHSMHRY LPRLHLVPAE KAVEVIQLNG PGVHTFTFPQ TEFFAVTAYQ
       250        260        270        280        290        300        310        320
NIQITQLKID YNPFAKGFRD DGLNNKPQRD GKQKNSSDQE GNNISSSSGH RVRLTEGQGS EIQPGDLDPL SRGHETSGKG
       330        340        350        360        370        380        390        400
LEKTSLNIKR DFLGFMDTDS ALSEVPQLKQ EISECLIASS FEDDSRVASP LDQNGSFNVV IKEEPLDDYD YELGECPEGV
       410        420        430        440        450        460        470        480
TVKQEETDEE TDVYSNSDDD PILEKQLKRH NKVDNPEADH LSSKWLPSSP SGVAKAKMFK LDTGKMPVVY LEPCAVTRST
       490        500        510        520        530        540        550        560
VKISELPDNM LSTSRKDKSS MLAELEYLPT YIENSNETAF CLGKESENGL RKHSPDLRVV QKYPLLKEPQ WKYPDISDSI
       570        580        590        600        610        620        630        640
STERILDDSK DSVGDSLSGK EDLGRKRTTM LKIATAAKVV NANQNASPNV PGKRGRPRKL KLCKAGRPPK NTGKSLISTK
       650        660        670        680        690        700        710        720
NTPVSPGSTF PDVKPDLEDV DGVLFVSFES KEALDIHAVD GTTEESSSLQ ASTTNDSGYR ARISQLEKEL IEDLKTLRHK
       730        740        750        760        770        780        790        800
QVIHPGLQEV GLKLNSVDPT MSIDLKYLGV QLPLAPATSF PFWNLTGTNP ASPDAGFPFV SRTGKTNDFT KIKGWRGKFH
       810        820        830        840        850        860        870        880
SASASRNEGG NSESSLKNRS AFCSDKLDEY LENEGKLMET SMGFSSNAPT SPVVYQLPTK STSYVRTLDS VLKKQSTISP
       890        900        910        920        930        940        950        960
STSYSLKPHS VPPVSRKAKS QNRQATFSGR TKSSYKSILP YPVSPKQKYS HVILGDKVTK NSSGIISENQ ANNFVVPTLD
       970        980        990       1000       1010       1020       1030       1040
ENIFPKQISL RQAQQQQQQQ QGSRPPGLSK SQVKLMDLED CALWEGKPRT YITEERADVS LTTLLTAQAS LKTKPIHTII
      1050       1060       1070       1080       1090       1100       1110       1120
RKRAPPCNND FCRLGCVCSS LALEKRQPAH CRRPDCMFGC TCLKRKVVLV KGGSKTKHFQ RKAAHRDPVF YDTLGEEARE
      1130       1140       1150       1160       1170       1180       1190       1200
EEEGIREEEE QLKEKKKRKK LEYTICETEP EQPVRHYPLW VKVEGEVDPE PVYIPTPSVI EPMKPLLLPQ PEVLSPTVKG
      1210       1220       1230       1240       1250       1260       1270       1280
KLLTGIKSPR SYTPKPNPVI REEDKDPVYL YFESMMTCAR VRVYERKKED QRQPSSSSSP SPSFQQQTSC HSSPENHNNA
      1290       1300       1310       1320       1330       1340       1350       1360
KEPDSEQQPL KQLTCDLEDD SDKLQEKSWK SSCNEGESSS TSYMHQRSPG GPTKLIEIIS DCNWEEDRNK ILSILSQHIN
      1370       1380       1390       1400       1410       1420       1430       1440
SNMPQSLKVG SFIIELASQR KSRGEKNPPV YSSRVKISMP SCQDQDDMAE KSGSETPDGP LSPGKMEDIS PVQTDALDSV
      1450       1460       1470       1480       1490       1500       1510       1520
RERLHGGKGL PFYAGLSPAG KLVAYKRKPS SSTSGLIQVA SNAKVAASRK PRTLLPSTSN SKMASSSGTA TNRPGKNLKA
      1530       1540       1550       1560       1570       1580       1590       1600
FVPAKRPIEN AAQIPVATPQ VSPNTVKRAG PRLLLIPVQQ GSPTLRPVSN TQLQGHRMVL QPVRSPSGMN LFRHPNGQIV
      1610       1620       1630       1640       1650       1660       1670       1680
QLLPLHQLRG SNTQPNLQPV MFRNPGSVMG IRLPAPSKPS ETPPSSTSSS AFSVMNPVIQ AVGSSSAVNV ITQAPSLLSS
      1690       1700       1710       1720       1730       1740       1750       1760
GASFVSQAGT LTLRISPPEP QSFASKTGSE TKITYSSGGQ PVGTASLIPL QSGSFALLQL PGQKPVPSSI LQHVASLQMK
      1770       1780       1790       1800       1810       1820       1830       1840
RESQNPDQKD ETNSIKREQE TKKVLQSEGE AVDPEANVIK QNSGAATSEE TLNDSLEDRG DHLDEECLPE EGCATVKPSE
      1850       1860       1870       1880       1890       1900       1910       1920
HSCITGSHTD QDYKDVNEEY GARNRKSSKE KVAVLEVRTI SEKASNKTVQ NLSKVQHQKL GDVKVEQQKG FDNPEENSSE
      1930       1940       1950       1960       1970       1980       1990       2000
FPVTFKEESK FELSGSKVME QQSNLQPEAK EKECGDSLEK DRERWRKHLK GPLTRKCVGA SQECKKEADE QLIKETKTCQ
      2010       2020       2030       2040       2050       2060       2070       2080
ENSDVFQQEQ GISDLLGKSG ITEDARVLKT ECDSWSRISN PSAFSIVPRR AAKSSRGNGH FQGHLLLPGE QIQPKQEKKG
      2090       2100       2110       2120       2130       2140       2150       2160
GRSSADFTVL DLEEDDEDDN EKTDDSIDEI VDVVSDYQSE EVDDVEKNNC VEYIEDDEEH VDIETVEELS EEINVAHLKT
      2170       2180       2190       2200       2210       2220       2230       2240
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2438 | 1 | 611.7346 | -126.77 | 2 | 60.9 | 12.8 | 0 | 1054-1065 | R.LGCVCSSLALEK.R | | |
| 939 | 1 | 583.7035 | -110.96 | 2 | 41.3 | 10.6 | 1 | 1976-1985 | R.KCVGASQECK.K | Carbamidomethyl: 2, 9 | WUP:QUP 5.06 |

# Detailed Protein Report

## Protein 174: PREDICTED: RING finger protein 17 isoform X10 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578824967 | **Score:** | 43.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 168.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLDTNTAEEI | DEALNTAHHS | FEQLSIAGKA | LEHMQKQTIE | ERERVIEVVE | KQFDQLLAFF | DSRKKNLCEE | FARTTDDYLS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NLIKAKSYIE | EKKNNLNAAM | NIARALQLSP | SLRTYCDLNQ | IIRTLQLTSD | SELAQVSSPQ | LRNPPRLSVN | CSEIICMFNN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MGKIEFRDST | KCYPQENEIR | QNVQKKYNNK | KELSCYDTYP | PLEKKKVDMS | VLTSEAPPPP | LQPETNDVHL | EAKNFQPQKD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VATASPKTIA | VLPQMGSSPD | VIIEEIIEDN | VESSAELVFV | SHVIDPCHFY | IRKYSQIKDA | KVLEKKVNEF | CNRSSHLDPS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DILELGARIF | VSSIKNGMWC | RGTITELIPI | EGRNTRKPCS | PTRLFVHEVA | LIQIFMVDFG | NSEVLIVTGV | VDTHVRPEHS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AKQHIALNDL | CLVLRKSEPY | TEGLLKDIQP | LAQPCSLKDI | VPQNSNEGWE | EEAKVEFLKM | VNNKAVSMKV | FREEDGVLIV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DLQKPPPNKI | SSDMPVSLRD | ALVFMELAKF | KSQSLRSHFE | KNTTLHYHPP | ILPKEMTDVS | VTVCHINSPG | DFYLQLIEGL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DILFLLKTIE | EFYKSEDGEN | LEILCPVQDQ | ACVAKFEDGI | WYRAKVIGLP | GHQEVEVKYV | DFGNTAKITI | KDVRKIKDEF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LNAPEKAIKC | KLAYIEPYKR | TMQWSKEAKE | KFEEKAQDKF | MTCSVIKILE | DNVLLVELFD | SLGAPEMTTT | SINDQLVKEG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LASYEIGYIL | KDNSQKHIEV | WDPSPEEIIS | NEVHNLNPVS | AKSLPNENFQ | SLYNKELPVH | ICNVISPEKI | YVQWLLTENL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LNSLEEKMIA | AYENSKWEPV | KWENDMHCAV | KIQDKNQWRR | GQIIRMVTDT | LVEVLLYDVG | VELVVNVDCL | RKLEENLKTM |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GRLSLECSLV | DIRPAGGSDK | WTATACDCLS | LYLTGAVATI | ILQVDSEENN | TTWPLPVKIF | CRDEKGERVD | VSKYLIKKGL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ALRERRINNL | DNSHSLSEKS | LEVPLEQEDS | VVTNCIKTNF | DPDKKTADII | SEQKVSEFQE | KILEPRTTRG | YKPPAIPNMN |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VFEATVSCVG | DDGTIFVVPK | LSEFELIKMT | NEIQSNLKCL | GLLEPYFWKK | GEACAVRGSD | TLWYRGKVME | VVGGAVRVQY |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LDHGFTEKIP | QCHLYPILLY | PDIPQFCIPC | QLHNTTPVGN | VWQPDAIEVL | QQLLSKRQVD | IHIMELPKNP | WEKLSIHLYF |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DGMSLSYFMA | YYKYCTSEHT | EEMLKEKPRS | DHDKKYEEEQ | WEIRFEELLS | AETDTPLLPP | YLSSSLPSPG | ELYAVQVKHV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VSPNEVYICL | DSIETSNQSN | QHSDTDDSGV | SGESESESLD | EALQRVNKKV | EALPPLTDFR | TEMPCLAEYD | DGLWYRAKIV |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| AIKEFNPLSI | LVQFVDYGST | AKLTLNRLCQ | IPSHLMRYPA | RAIKVLLAGF | KPPLRDLGET | RIPYCPKWSM | EALWAMIDCL |
| 1450 | 1460 | 1470 | 1480 | 1490 | | | |
| QGKQLYAVSM | APAPEQIVTL | YDDEQHPVHM | PLVEMGLADK | DE | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 200 | 1 | 642.8816 | 92.45 | 2 | 32.2 | 16.1 | 1 | 596-605 | K.FEDGIWYRAK.V | |

## Protein 175: PREDICTED: uncharacterized protein LOC285556 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578809699 | **Score:** | 43.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 190.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 2 |

### Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.47 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.21 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578809701 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: uncharacterized protein LOC285556 isoform X2 [Homo sapiens] |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLSFHFWKSR | GQPTDAASSV | ADGIQTPRCC | RRCQANNWTG | QLSYRTLATV | SAGAAAPQPQ | TTSTASSRSL | PTSLRLAAAP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PQGLKNWEVV | AAVAAVPTAL | GPVQIRGTLL | RATLQPLRGQ | RRTQDFPSDH | HCLFLSLKPG | QGLIMEAAPP | ELNSKARQAE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VGDGVSSAQD | SQELKQQLWP | LPKPSASSQR | EAKYVDMCAS | AEVQRESPQT | MKLTLGHCPG | GQRASRSPKE | KAQDEPSSKT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PSPQNNPASS | QLSRSQHSAS | EEGGNFSSSS | SSSPMNKAEE | DGLSKMEDST | TSTGALATSS | SSLGFESESG | ESEGCQAVGG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EGEKISGGGG | GGKGGGGGGA | GDGTECRDII | AKSQGSRDPP | KVEEAHYITT | HEIQLSEVEQ | DMDFDVGLAS | RWDFEDNNVI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YSFVDYASFG | GSDETPGDIT | SLTEEDDDNS | CYLSTTPSTN | TTRTPSPTSS | DLARPNAGRS | GRDTSSTEVG | SGPSDSGPTP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PPTGPGTAPL | TEPLPETPEA | ASGAAAAAAS | SCGSAASQIL | LSIKPASRAI | NEPSNVRAKQ | NIIYAAKHEG | DMSLRVSTAA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EHNSSSLKQN | PAAAVAQDHA | KKFIAVPARL | QTRCGAIRAK | ELVDYSSGAS | SAVSELDDAD | KEVRNLTSRA | FRSLAYPYFE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ALNISSRESS | TTLSEVGFGR | WSTFLDLKCG | GVGARVEQSL | LRSSAASVAA | GLRKGSGARA | TADQLYIQSK | KSQTKALEFV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VSKVEGEIKH | VETPLCFQKQ | VQTGSRVVTL | LEPLNVRSES | KASSAPGPGR | ATKGPGKGPG | SAYTDDGSET | SEGSKPTSRA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DGPQKSKFAS | SLLKNVISKK | MQREHEFKME | RGEVMDTSHH | LSGTSKETEG | ARGSERQRER | GLQRQSSRHS | EAGSEYTVVS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| MSDAGGEGSV | AGSKSPVFKA | STPRERNAGP | GRNFTDGHTE | VCEIKKSASE | TVKGIFLRSQ | NSAFRSWKEK | EAEKREEQAP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| IGKLKLPKGG | DWRADLGEIS | ASKNTIMSRL | FVPNIQQTPK | DKQPRKQATK | YPAAQATSTA | VIRPKAPEIK | IRLGSVQQPS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SDFNIAKLLT | PKLAGGSASN | LFKTIEDNSR | AQQKLFRGDN | LEKVPHFQVR | DIRDKSKAQG | PLHQVRDVRK | LIKGSGDSSD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KGSVTPEQGL | TGPKPRQLSA | AAGGSGSLSP | MVITCQAVVN | QREDSMDREP | RESMGKGGGS | RVLNSSSPEG | TVLVHRASGR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LPVATIAPNK | PEQGSYLPVL | KIVSKASTQK | TPEKLKEEEV | KEEGKATKPA | RNALEKLTAA | VRSMEELYSF | NRNEWKRKSD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PLPMMMDSHV | LSLIASEERE | GVVVADGDHD | KLSKRLGEVE | ERGTGNKAGV | VLRGAPIERL | QRRNSNPSAE | SVSARAAAFE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| NLARERPRSL | YIPPVHKDVE | RTQPLQPLPP | LPSNRNVFTV | SASSIQKTGG | VAGKFPQGPS | PESPSAAKGI | KSQGLRSLKI |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SPATRAPPDE | VTNRKSGSNL | EKSNSDCENY | LTIPLKGSSA | AGELLSRPGA | SREGPPNSSA | ATLCSLPPLS | ARSQVPSSSK |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| GSQVSGTSRP | AWRTKPDNPR | ETVAAPPGPQ | SPEHPPTTIY | HQPPLPFTLQ | GAQPQVLCFS | PPSMPAPAPA | ASAPVPTDPF |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QQAQPQQTQR | KMLLDVTTGQ | YYLVDTPVQP | MTRRLFDPET | GQYVDVPMTS | QQQAVAPMSI | SVPPLALSPG | AYGPTYMIYP |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| GFLPTVLPTN | ALQPTPIARA | PRGSELSPMV | AEPSSKEAAA | TFTEAPYFMA | SGQSPASSTS | SAPAATSQLL | GAKAFAQLHG |
| 1770 | 1780 | 1790 | 1800 | | | | |
| KPVISITSQP | LGPRIIAPPS | FDGTTMSFVV | EHR | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 886 | 1 | 575.7576 | 46.75 | 2 | 40.6 | 12.5 | 0 | 334-347 | K.GGGGGGAGDGTECR.D | | |
| 1984 | 1 | 634.7974 | -113.89 | 2 | 54.7 | 11.7 | 2 | 955-965 | K.REEQAPIGKLK.L | | WUP:QUP 2.21<br>QU:MU 0.47 |

## Protein 176: tau-tubulin kinase 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|58761548 | **Score:** | 43.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 142.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.66 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.21 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQCLAAALKD | ETNMSGGGEQ | ADILPANYVV | KDRWKVLKKI | GGGGFGEIYE | AMDLLTRENV | ALKVESAQQP | KQVLKMEVAV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LKKLQGKDHV | CRFIGCGRNE | KFNYVVMQLQ | GRNLADLRRS | QPRGTFTLST | TLRLGKQILE | SIEAIHSVGF | LHRDIKPSNF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AMGRLPSTYR | KCYMLDFGLA | RQYTNTTGDV | RPPRNVAGFR | GTVRYASVNA | HKNREMGRHD | DLWSLFYMLV | EFAVGQLPWR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KIKDKEQVGM | IKEKYEHRML | LKHMPSEFHL | FLDHIASLDY | FTKPDYQLIM | SVFENSMKER | GIAENEAFDW | EKAGTDALLS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TSTSTPPQQN | TRQTAAMFGV | VNVTPVPGDL | LRENTEDVLQ | GEHLSDQENA | PPILPGRPSE | GLGPSPHLVP | HPGGPEAEVW |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EETDVNRNKL | RINIGKSPCV | EEEQSRGMGV | PSSPVRAPPD | SPTTPVRSLR | YRRVNSPESE | RLSTADGRVE | LPERRSRMDL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PGSPSRQACS | SQPAQMLSVD | TGHADRQASG | RMDVSASVEQ | EALSNAFRSV | PLAEEEDFDS | KEWVIIDKET | ELKDFPPGAE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PSTSGTTDEE | PEELRPLPEE | GEERRRLGAE | PTVRPRGRSM | QALAEEDLQH | LPPQPLPPQL | SQGDGRSETS | QPPTPGSPSH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SPLHSGPRPR | RRESDPTGPQ | RQVFSVAPPF | EVNGLPRAVP | LSLPYQDFKR | DLSDYRERAR | LLNRVRRVGF | SHMLLTTPQV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PLAPVQPQAN | GKEEEEEEEE | DEEEEEEDEE | EEEEEEEEEE | EEEEEEEEEE | EAAAAVALGE | VLGPRSGSSS | EGSERSTDRS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QEGAPSTLLA | DDQKESRGRA | SMADGDLEPE | EGSKTLVLVS | PGDMKKSPVT | AELAPDPDLG | TLAALTPQHE | RPQPTGSQLD |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VSEPGTLSSV | LKSEPKPPGP | GAGLGAGTVT | TGVGGVAVTS | SPFTKVERTF | VHIAEKTHLN | VMSSGGQALR | SEEFSAGGEL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GLELASDGGA | VEEGARAPLE | NGLALSGLNG | AEIEGSALSG | APRETPSEMA | TNSLPNGPAL | ADGPAPVSPL | EPSPEKVATI |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SPRRHAMPGS | RPRSRIPVLL | SEEDTGSEPS | GSLSAKERWS | KRARPQQDLA | RLVMEKRQGR | LLLRLASGAS | SSSSEEQRRA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SETLSGTGSE | EDTPASEPAA | ALPRKSGRAA | ATRSRIPRPI | GLRMPMPVAA | QQPASRSHGA | APALDTAITS | RLQLQTPPGS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ATAADLRPKQ | PPGRGLGPGR | AQAGARPPAP | RSPRLPASTS | AARNASASPR | SQSLSRRESP | SPSHQARPGV | PPPRGVPPAR |
| 1290 | 1300 | 1310 | 1320 | 1330 | | | |
| AQPDGTPSPG | GSKKGPRGKL | QAQRATTKGR | AGGAEGRAGA | R | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1658 | 1 | 697.8038 | -143.18 | 2 | 50.5 | 11.5 | 1 | 124-136 | R.GTFTLSTTLRLGK.Q | | |
| 1595 | 1 | 932.5310 | 13.94 | 2 | 50.2 | 20.1 | 0 | 1192-1209 | R.LQLQTPPGSATAADLRPK.Q | | QU:MU 0.66<br>WUP:QUP 1.21 |

# Detailed Protein Report

## Protein 177: PREDICTED: serine/threonine-protein kinase WNK2 isoform X12 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578817784 | **Score:** | 43.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 227.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 2 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDGDGGRRDV | PGTLMEPGRG | AGPAGMAEPR | AKAARPGPQR | FLRRSVVESD | QEEPPGLEAA | EAPGPQPPQP | LQRRVLLLCK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TRRLIAERAR | GRPAAPAPAA | LVAQPGAPGA | PADAGPEPVG | TQEPGPDPIA | AAVETAPAPD | GGPREEAAAT | VRKEDEGAAE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AKPEPGRTRR | DEPEEEEDDE | DDLKAVATSL | DGRFLKFDIE | LGRGSFKTVY | KGLDTETWVE | VAWCELQDRK | LTKLERQRFK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EEAEMLKGLQ | HPNIVRFYDF | WESSAKGKRC | IVLVTELMTS | GTLKTYLKRF | KVMKPKVLRS | WCRQILKGLL | FLHTRTPPII |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HRDLKCDNIF | ITGPTGSVKI | GDLGLATLKR | ASFAKSVIGT | PEFMAPEMYE | EHYDESVDVY | AFGMCMLEMA | TSEYPYSECQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NAAQIYRKVT | CGIKPASFEK | VHDPEIKEII | GECICKNKEE | RYEIKDLLSH | AFFAEDTGVR | VELAEEDHGR | KSTIALRLWV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EDPKKLKGKP | KDNGAIEFTF | DLEKETPDEV | AQEMIESGFF | HESDVKIVAK | SIRDRVALIQ | WRRERIWPAL | QPKEQQDVGS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PDKARGPPVP | LQVQVTYHAQ | AGQPGPPEPE | EPEADQHLLP | PTLPTSATSL | ASDSTFDSGQ | GSTVYSDSQS | SQQSVMLGSL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ADAAPSPAQC | VCSPPVSEGP | VLPQSLPSLG | AYQQPTAAPG | LPVGSVPAPA | CPPSLQQHFP | DPAMSFAPVL | PPPSTPMPTG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PGQPAPPGQQ | PPPLAQPTPL | PQVLAPQPVV | PLQPVPPHLP | PYLAPASQVG | APAQLKPLQM | PQAPLQPLAQ | VPPQMPPIPV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VPPITPLAGI | DGLPPALPDL | PTATVPPVPP | PQYFSPAVIL | PSLAAPLPPA | SPALPLQAVK | LPHPPGAPLA | MPCRTIVPNA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PATIPLLAVA | PPGVAALSIH | SAVAQLPGQP | VYPAAFPQMA | PTDVPPSPHH | TVQNMRATPP | QPALPPQPTL | PPQPVLPPQP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TLPPQPVLPP | QPTRPPQPVL | PPQPMLPPQP | VLPPQPALPV | RPEPLQPHLP | EQAAPAATPG | SQILLGHPAP | YAVDVAAQVP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TVPVPPAAVL | SPPLPEVLLP | AAPELLPQFP | SSLATVSASV | QSVPTQTATL | LPPANPPLPG | GPGIASPCPT | VQLTVEPVQE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EQASQDKPPG | LPQSCESYGG | SDVTSGKELS | DSCEGAFGGG | RLEGRAARKH | HRRSTRARSR | QERASRPRLT | ILNVCNTGDK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| MVECQLETHN | HKMVTFKFDL | DGDAPDEIAT | YMVEHDFILQ | AERETFIEQM | KDVMDKAEDM | LSEDTDADRG | SDPGTSPPHL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| STCGLGTGEE | SRQSQANAPV | YQQNVLHTGK | RWFIICPVAE | HPAPEAPESS | PPLPLSSLPP | EASQDSAPYK | DQLSSKEQPS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| FLASQQLLSQ | AGPSNPPGAP | PAPLAPSSPP | VTALPQDGAA | PATSTMPEPA | SGTASQAGGP | GTPQGLTSEL | ETSQPLAETH |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EAPLAVQPLV | VGLAPCTPAP | EAASTRDASA | PREPLPPPAP | EPSPHSGTPQ | PALGQPAPLL | PAAVGAVSLA | TSQLPSPPLG |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PTVPPQPPSA | LESDGEGPPP | RVGFVDSTIK | SLDEKLRTLL | YQEHVPTSSA | SAGTPVEVGD | RDFTLEPLRG | DQPRSEVCGG |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| DLALPPVPKE | AVSGRVQLPQ | PLVEKSELAP | TRGAVMEQGT | SSSMTAESSP | RSMLGYDRDG | RQVASDSHVV | PSVPQDVPAF |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| VRPARVEPTD | RDGGEAGESS | AEPPPSDMGT | VGGQASHPQT | LGARALGSPR | KRPEQQDVSS | PAKTVGRFSV | VSTQDEWTLA |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SPHSLRYSAP | PDVYLDEAPS | SPDVKLAVRR | AQTASSIEVG | VGEPVSSDSG | DEGPRARPPV | QKQASLPVSG | SVAGDFVKKA |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| TAFLQRPSRA | GSLGPETPSR | VGMKVPTISV | TSFHSQSSYI | SSDNDSELED | ADIKKELQSL | REKHLKEISE | LQSQQKQEIE |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| ALYRRLGKPL | PPNVGFFHTA | PPTGRRRKTS | KSKLKAGKLL | NPLVRQLKVV | ASSTGSSTSS | LAPGPEPGPQ | PALHVQAQVN |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| NSNNKKGTFT | DDLHKLVDEW | TSKTVGAAQL | KPTLNQLKQT | QKLQDMEAQA | GWAAPGEARA | MTAPRAGVGM | PRLPPAPGPL |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | |
| STTVIPGAAP | TLSVPTPDGA | LGTARRNQVW | FGLRVPPTAC | CGHSTQPRGG | QRVGSKTASF | AASDPVRS | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2405 | 1 | 904.4370 | -32.64 | 2 | 60.5 | 15.1 | 1 | 323-339 | R.DLKCDNIFITGPTGSVK.I | |
| 1286 | 1 | 945.9319 | -64.24 | 2 | 46.2 | 11.9 | 2 | 2129-2147 | R.GGQRVGSKTASFAASDPVR.S | |

# Detailed Protein Report

## Protein 178: probable G-protein coupled receptor 179 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|93352554 | **Score:** | 43.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 257.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.19 | **CV:** | 73.29 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 0.17 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGTRGAVMPP | PMWGLLGCCF | VCAWALGGPR | PIRSLPPLSS | QVKPGSVPMQ | VPLEGAEAAL | AYLYSGDAQQ | LSQVNCSERY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EARGAGAMPG | LPPSLQGAAG | TLAQAANFLN | MLLQANDIRE | SSVEEDVEWY | QALVRSVAEG | DPRVYRALLT | FNPPPGASHL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QLALQATRTG | EETILQDLSG | NWVQEENPPG | DLDTPALKKR | VLTNDLGSLG | SPKWPQADGY | VGDTQQVRLS | PPFLECQEGR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LRPGWLITLS | ATFYGLKPDL | SPEVRGQVQM | DVDLQSVDIN | QCASGPGWYS | NTHLCDLNST | QCVPLESQGF | VLGRYLCRCR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PGFYGASPSG | GLEESDFQTT | GQFGFPEGRS | GRLLQCLPCP | EGCTSCMDAT | PCLVEEAAVL | RAAVLACQAC | CMLAIFLSML |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VSYRCRRNKR | IWASGVVLLE | TVLFGFLLLY | FPVFILYFKP | SVFRCIALRW | VRLLGFAIVY | GTIILKLYRV | LQLFLSRTAQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RSALLSSGRL | LRRLGLLLLP | VLGFLAVWTV | GALERGIQHA | PLVIRGHTPS | GRHFYLCHHD | RWDYIMVVAE | LLLLCWGSFL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| CYATRAVLSA | FHEPRYMGIA | LHNELLLSAA | FHTARFVLVP | SLHPDWTLLL | FFFHTHSTVT | TTLALIFIPK | FWKLGAPPRE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EMVDEVCEDE | LDLQHSGSYL | GSSIASAWSE | HSLDPGDIRD | ELKKLYAQLE | VHKTKEMAAN | NPHLPKKRGS | SCQGLGRSFM |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RYLAEFPEAL | ARQHSRDSGS | PGHGSLPGSS | RRRLLSSSLQ | EPEGTPALHK | SRSTYDQRRE | QDPPLLDSLL | RRKLAKKASR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TESRESVEGP | PALGFRSASA | HNLTVGERLP | RARPASLQKS | LSVASSREKA | LLMASQAYLE | ETYRQAKERE | ERKKAKAAMA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SLVRRPSARR | LERPRGAPLS | APPSPAKSSS | VDSSHTSGRL | HEEARRRLPH | PPIRHQVSTP | ILALSGGLGE | PRMLSPTSTL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| APALLPALAP | TPAPALAPVP | VSPQSPNLLT | YICPWENAEL | PAKQENVPQE | GPSGPERGHH | SPAPARARLW | RALSVAVEKS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RAGENEMDAE | DAHHQREAND | VDEDRPKIFP | KSHSLKAPVQ | QGSMRSLGLA | IKALTRSRST | YREKESVEES | PEGQNSGTAG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ESMGAPSRSP | RLGRPKAVSK | QAALIPSDDK | ESLQNQQNAH | TSRMLQVCQR | EGSREQEDRG | RRMTQGLGER | KAERAGKTGL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| AMLRQVSRDK | NIKQSKETPV | GWQELPKAGL | QSLGSADHRV | AEVCPWEVTE | SETRQPDSGN | KAEICPWETS | EGAPESRALR |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| QDPGDSQKKR | GEARGKSEPI | DVVPMMRKKP | ERLVREQEAV | CPWESADRGG | LSPGSAPQDP | GRIRDKSEAG | DSVEARKVEK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PGWEAAGPEA | HTPDITKAEP | CPWEASEGGE | DGKPAQEAVK | DLPQEKQKTR | KATFWKEQKP | GGDLESLCPW | ESTDFRGPSA |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| VSIQAPGSSE | CSGSLGSGIA | EVCLWEAGDA | PAIQKAEICP | WELDDNVMGQ | EMLSLGTGRE | SLQEKEKASR | KGSFGEMGEQ |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| TVKAVQKLSQ | QQESVCPRES | TVPGHSSPCL | DNSSSKAGSQ | FLCNGGSRAT | QVCPQEDLRP | EAQEATPAKT | EICPWEVNER |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| TREEWTSAQV | PRGGESQKDK | EKMPGKSEIE | DVTAWEKPEG | QIQKQEAVGP | WESVDPGSFS | PQPRPQDTER | PQTLLQMSGS |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| VGSKAADICP | LDVEENLTAG | KAEICPWEVG | AGAGEERALG | AEAIRKSPND | TGKVSADLGP | RERAVTAPEK | PQKPTPEWEV |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| ACPWGSVGPG | ACSQHPGTLD | ADGPKAGFQE | LDHMGCRPGE | VCPWEAQEAA | TSEKAKICPW | EVSEGTTGKG | LDQKAGSESA |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| EQREKALEKG | RLTSLGEDVS | KGMAKLCQQQ | ETICIWENKD | LRESPAQAPK | ISDLPSSMSS | EVAEGHSLEA | TEKGDLRQDP |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| KTGSFPEHIT | QEKAPAADTE | EFTTEDGEKT | SHELQSVCPW | ETTAPADSVS | HLDRQRPDQP | KASSQRLVST | GGRAADVCPW |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| DVPDAGVYKS | DSSAKAETCP | WEVTERIPVK | GVSRQDGKGD | SQEEKGRAPE | KSEPKGVPVQ | KKPEMADFRQ | QEAVCPWESQ |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| DGKGLSPQPA | PDASDRSRGS | SEAAGSVETR | VAEVCLWEVV | EAPSAKKAEI | CPWEAGGGAA | EEGEQERESQ | GQGEMFLQKA |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 671 | 1 | 648.3571 | -64.53 | 2 | 36.8 | 12.2 | 2 | 1129-1140 | R.SPRLGRPKAVSK.Q | | |
| 479 | 1 | 475.6002 | -274.91 | 2 | 35.6 | 13.9 | 0 | 1164-1170 | R.MLQVCQR.E | Carbamidomethyl: 5;<br>Oxidation: 1 | QU:MU 1.14 |
| 813 | 7 | 509.1525 | -284.31 | 2 | 38.6 | 17.2 | 1 | 1195-1204 | R.AGKTGLAMLR.Q | | WUP:QUP 0.17<br>QU:MU 4.21 |

# Detailed Protein Report

## Protein 179: conserved oligomeric Golgi complex subunit 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21237783 | **Score:** | 43.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 108.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.1 |
| | | **No. of unique Peptides:** | 3 |

### Quantitation

***WUP:QUP*** **Median:** 0.28 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MATAATSPAL | KRLDLRDPAA | LFETHGAEEI | RGLERQVRAE | IEHKKEELRQ | MVGERYRDLI | EAADTIGQMR | RCAVGLVDAV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KATDQYCARL | RQAGSAAPRP | PRAQQPQQPS | QEKFYSMAAQ | IKLLLEIPEK | IWSSMEASQC | LHATQLYLLC | CHLHSLLQLD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SSSSRYSPVL | SRFPILIRQV | AAASHFRSTI | LHESKMLLKC | QGVSDQAVAE | ALCSIMLLEE | SSPRQALTDF | LLARKATIQK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LLNQPHHGAG | IKAQICSLVE | LLATTLKQAH | ALFYTLPEGL | LPDPALPCGL | LFSTLETITG | QHPAGKGTGV | LQEEMKLCSW |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FKHLPASIVE | FQPTLRTLAH | PISQEYLKDT | LQKWIHMCNE | DIKNGITNLL | MYVKSMKGLA | GIRDAMWELL | TNESTNHSWD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VLCRRLLEKP | LLFWEDMMQQ | LFLDRLQTLT | KEGFDSISSS | SKELLVSALQ | ELESSTSNSP | SNKHIHFEYN | MSLFLWSESP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NDLPSDAAWV | SVANRGQFAS | SGLSMKAQAI | SPCVQNFCSA | LDSKLKVKLD | DLLAYLPSDD | SSLPKDVSPT | QAKSSAFDRY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ADAGTVQEML | RTQSVACIKH | IVDCIRAELQ | SIEEGVQGQQ | DALNSAKLHS | VLFMARLCQS | LGELCPHLKQ | CILGKSESSE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KPAREFRALR | KQGKVKTQEI | IPTQAKWQEV | KEVLLQQSVM | GYQVWSSAVV | KVLIHGFTQS | LLLDDAGSVL | ATATSWDELE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| IQEEAESGSS | VTSKIRLPAQ | PSWYVQSFLF | SLCQEINRVG | GHALPKVTLQ | EMLKSCMVQV | VAAYEKLSEE | KQIKKEGAFP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VTQNRALQLL | YDLRYLNIVL | TAKGDEVKSG | RSKPDSRIEK | VTDHLEALID | PFDLDVFTPH | LNSNLHRLVQ | RTSVLFGLVT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GTENQLAPRS | STFNSQEPHN | ILPLASSQIR | FGLLPLSMTS | TRKAKSTRNI | ETKAQVVPPA | RSTAGDPTVP | GSLFRQLVSE |
| 970 | 980 | 990 | | | | | |
| EDNTSAPSLF | KLGWLSSMTK | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2917 | 1 | 724.8590 | 4.01 | 2 | 65.2 | 12.8 | 0 | 58-70 | R.DLIEAADTIGQMR.R | Oxidation: 12 | WUP:QUP 0.28 |
| 2511 | 1 | 941.9690 | 8.39 | 2 | 62.0 | 16.9 | 1 | 72-89 | R.CAVGLVDAVKATDQYCAR.L | | |
| 1712 | 1 | 1045.0032 | -51.34 | 2 | 49.7 | 13.3 | 1 | 527-545 | K.VKLDDLLAYLPSDDSSLPK.D | | |

# Detailed Protein Report

## Protein 180: PREDICTED: uncharacterized aarF domain-containing protein kinase 1 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530404248 | **Score:** | 43.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 52.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 9.8 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***WUP:QUP*** **Median:** 1.03 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MARKALKLAS | WTSMALAASG | IYFYSNKYLD | PNDFGAVRVG | RAVATTAVIS | YDYLTSLKSV | PYGSEEYLQL | RSKVHLRSAR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RLCELCCANR | GTFIKVGQHL | GALDYLLPEE | YTSTLKVLHS | QAPQSSMQEI | RQVIREDLGK | EIHDLFQSFD | DTPLGTASLA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QVHKAVLHDG | RTVAVKVQHP | KVRAQSSKDI | LLMEVLVLAV | KQLFPEFEFM | WLVDEAKKNL | PLELDFLNEG | RNAEKVSQML |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RHFDFLKVPR | IHWDLSTERV | LLMEFVDGGQ | VNDRDYMERN | KIDVNEISRH | LGKMYSEMIF | VNGFVHCDPH | PGNVLVRKHP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GTGKAEIVLL | DHGLYQDLEI | RNNAANYLPQ | ISHLLNHVPR | QMLLILKTND | LLRGIEAALG | TRASASSFLN | MSRCCIRALA |
| 410 | 420 | 430 | 440 | 450 | 460 | | |
| EHKKKNTCSF | FRRTQISFSE | AFNLWQINLH | ELILRVKGLK | LADRVLALIC | WLFPAPL | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2471 | 1 | 588.1664 | -250.34 | 2 | 61.4 | 20.5 | 1 | 232-241 | R.NAEKVSQMLR.H | | |
| 5 | 1 | 1205.0356 | -39.18 | 2 | 29.0 | 11.7 | 2 | 383-403 | R.ASASSFLNMSRCCIRALAEHK.K | Carbamidomethyl: 12, 13 | WUP:QUP 1.03 |

# Detailed Protein Report

## Protein 181: probable G-protein coupled receptor 125 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|59823631 | **Score:** | 42.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 146.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 3.4 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEPPGRRRGR | AQPPLLLPLS | LLALLALLGG | GGGGGAAALP | AGCKHDGRPR | GAGRAAGAAE | GKVVCSSLEL | AQVLPPDTLP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NRTVTLILSN | NKISELKNGS | FSGLSLLERL | DLRNNLISSI | DPGAFWGLSS | LKRLDLTNNR | IGCLNADIFR | GLTNLVRLNL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SGNLFSSLSQ | GTFDYLASLR | SLEFQTEYLL | CDCNILWMHR | WVKEKNITVR | DTRCVYPKSL | QAQPVTGVKQ | ELLTCDPPLE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LPSFYMTPSH | RQVVFEGDSL | PFQCMASYID | QDMQVLWYQD | GRIVETDESQ | GIFVEKNMIH | NCSLIASALT | ISNIQAGSTG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NWGCHVQTKR | GNNTRTVDIV | VLESSAQYCP | PERVVNNKGD | FRWPRTLAGI | TAYLQCTRNT | HGSGIYPGNP | QDERKAWRRC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DRGGFWADDD | YSRCQYANDV | TRVLYMFNQM | PLNLTNAVAT | ARQLLAYTVE | AANFSDKMDV | IFVAEMIEKF | GRFTKEEKSK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ELGDVMVDIA | SNIMLADERV | LWLAQREAKA | CSRIVQCLQR | IATYRLAGGA | HVYSTYSPNI | ALEAYVIKST | GFTGMTCTVF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QKVAASDRTG | LSDYGRRDPE | GNLDKQLSFK | CNVSNTFSSL | ALKNTIVEAS | IQLPPSLFSP | KQKRELRPTD | DSLYKLQLIA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FRNGKLFPAT | GNSTNLADDG | KRRTVVTPVI | LTKIDGVNVD | THHIPVNVTL | RRIAHGADAV | AARWDFDLLN | GQGGWKSDGC |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HILYSDENIT | TIQCYSLSNY | AVLMDLTGSE | LYTQAASLLH | PVVYTTAIIL | LLCLLAVIVS | YIYHHSLIRI | SLKSWHMLVN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LCFHIFLTCV | VFVGGITQTR | NASICQAVGI | ILHYSTLATV | LWVGVTARNI | YKQVTKKAKR | CQDPDEPPPP | PRPMLRFYLI |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GGGIPIIVCG | ITAAANIKNY | GSRPNAPYCW | MAWEPSLGAF | YGPASFITFV | NCMYFLSIFI | QLKRHPERKY | ELKEPTEEQQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RLAANENGEI | NHQDSMSLSL | ISTSALENEH | TFHSQLLGAS | LTLLLYVALW | MFGALAVSLY | YPLDLVFSFV | FGATSLSFSA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| FFVVHHCVNR | EDVRLAWIMT | CCPGRSSYSV | QVNVQPPNSN | GTNGEAPKCP | NSSAESSCTN | KSASSFKNSS | QGCKLTNLQA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| AAAQCHANSL | PLNSTPQLDN | SLTEHSMDND | IKMHVAPLEV | QFRTNVHSSR | HHKNRSKGHR | ASRLTVLREY | AYDVPTSVEG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SVQNGLPKSR | LGNNEGHSRS | RRAYLAYRER | QYNPPQQDSS | DACSTLPKSS | RNFEKPVSTT | SKKDALRKPA | VVELENQQKS |
| 1290 | 1300 | 1310 | 1320 | 1330 | | | |
| YGLNLAIQNG | PIKSNGQEGP | LLGTDSTGNV | RTGLWKHETT | V | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2747 | 1 | 1045.5347 | -21.10 | 2 | 65.5 | 16.6 | 2 | 211-229 | R.DTRCVYPKSLQAQPVTGVK.Q | |
| 430 | 1 | 706.0114 | 194.46 | 2 | 33.9 | 10.5 | 0 | 366-378 | R.TLAGITAYLQCTR.N | |

# Detailed Protein Report

## Protein 182: estrogen sulfotransferase [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4885617 | **Score:** | 42.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 35.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 13.3 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MNSELDYYEK FEEVHGILMY KDFVKYWDNV EAFQARPDDL VIATYPKSGT TWVSEIVYMI YKEGDVEKCK EDVIFNRIPF
        90        100        110        120        130        140        150        160
LECRKENLMN GVKQLDEMNS PRIVKTHLPP ELLPASFWEK DCKIIYLCRN AKDVAVSFYY FFLMVAGHPN PGSFPEFVEK
       170        180        190        200        210        220        230        240
FMQGQVPYGS WYKHVKSWWE KGKSPRVLFL FYEDLKEDIR KEVIKLIHFL ERKPSEELVD RIIHHTSFQE MKNNPSTNYT
       250        260        270        280        290        300
TLPDEIMNQK LSPFMRKGIT GDWKNHFTVA LNEKFDKHYE QQMKESTLKF RTEI
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2243 | 1 | 945.9550 | -47.59 | 2 | 58.5 | 10.9 | 2 | 78-93 | R.IPFLECRKENLMNGVK.Q | |

# Detailed Protein Report

**Protein 183:** **synaptojanin-1 isoform d [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|237757326 | **Score:** | 42.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 168.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.4 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAFSKGFRIY | HKLDPPPFSL | IVETRHKEEC | LMFESGAVAV | LSSAEKEAIK | GTYSKVLDAY | GLLGVLRLNL | GDTMLHYLVL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VTGCMSVGKI | QESEVFRVTS | TEFISLRIDS | SDEDRISEVR | KVLNSGNFYF | AWSASGISLD | LSLNAHRSMQ | EQTTDNRFFW |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NQSLHLHLKH | YGVNCDDWLL | RLMCGGVEIR | TIYAAHKQAK | ACLISRLSCE | RAGTRFNVRG | TNDDGHVANF | VETEQVVYLD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DSVSSFIQIR | GSVPLFWEQP | GLQVGSHRVR | MSRGFEANAP | AFDRHFRTLK | NLYGKQIIVN | LLGSKEGEHM | LSKAFQSHLK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ASEHAADIQM | VNFDYHQMVK | GGKAEKLHSV | LKPQVQKFLD | YGFFYFNGSE | VQRCQSGTVR | TNCLDCLDRT | NSVQAFLGLE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MLAKQLEALG | LAEKPQLVTR | FQEVFRSMWS | VNGDSISKIY | AGTGALEGKA | KAGKLKDGAR | SVTRTIQNNF | FDSSKQEAID |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VLLLGNTLNS | DLADKARALL | TTGSLRASSK | VLKSMCENFY | KYSKPKKIRV | CVGTWNVNGG | KQFRSIAFKN | QTLTDWLLDA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PKLAGIQEFQ | DKRSKPTDIF | AIGFEEMVEL | NAGNIVSAST | TNQKLWAVEL | QKTISRDNKY | VLLASEQLVG | VCLFVFIRPQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HAPFIRDVAV | DTVKTGMGGA | TGNKGAVAIR | MLFHTTSLCF | VCSHFAAGQS | QVKERNEDFI | EIARKLSFPM | GRMLFSHDYV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| FWCGDFNYRI | DLPNEEVKEL | IRQQNWDSLI | AGDQLINQKN | AGQVFRGFLE | GKVTFAPTYK | YDLFSDDYDT | SEKCRTPAWT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DRVLWRRRKW | PFDRSAEDLD | LLNASFQDES | KILYTWTPGT | LLHYGRAELK | TSDHRPVVAL | IDIDIFEVEA | EERQNIYKEV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| IAVQGPPDGT | VLVSIKSSLP | ENNFFDDALI | DELLQQFASF | GEVILIRFVE | DKMWVTFLEG | SSALNVLSLN | GKELLNRTIT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| IALKSPDWIK | NLEEEMSLEK | ISIALPSSTS | STLLGEDAEV | AADFDMEGDV | DDYSAEVEEL | LPQHLQPSSS | SGLGTSPSSS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PRTSPCQSPT | ISEGPVPSLP | IRPSRAPSRT | PGPPSAQSSP | IDAQPATPLP | QKDPAQPLEP | KRPPPPRPVA | PPTRPAPPQR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PPPPSGRSQP | SPQAGLAGPG | PAGYSTARPT | IPPRAGVISA | PQSHARASAG | RLTPESQSKT | SETSKGSTFL | PEPLKPQAAF |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PPQSSLPPPA | QRLQEPLVPV | AAPMPQSGPQ | PNLETPPQPP | PRSRSSHSLP | SEASSQPQVK | TNGISDGKRE | SPLKIDPFED |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LSFNLLAVSK | AQLSVQTSPV | PTPDPKRLIQ | LPSATQSNVL | SSVSCMPTMP | PIPARSQSQE | NMRSSPNPFI | TGLTRTNPFS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| DRTAAPGNPF | RAKSEESEAT | SWFSKEEPVT | ISPFPSLQPL | GHNKSRASSS | LDGFKDSFDL | QGQSTLKISN | PKGWVTFEEE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EDFGVKGKSK | SACSDLLGNQ | PSSFSGSNLT | LNDDWNKGTN | VSFCVLPSRR | PPPPPVPLLP | PGTSPPVDPF | TTLASKASPT |
| 1530 | | | | | | | |
| LDFTER | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1994 | 1 | 1044.9084 | -141.16 | 2 | 55.3 | 14.4 | 2 | 182-200 | R.LMCGGVEIRTIYAAHKQAK.A | |
| 2282 | 1 | 614.2542 | -33.53 | 3 | 59.0 | 16.0 | 1 | 374-389 | R.CQSGTVRTNCLDCLDR.T | Carbamidomethyl: 10 |
| 1652 | 1 | 626.6317 | -42.50 | 3 | 50.4 | 12.3 | 1 | 1416-1432 | K.DSFDLQGQSTLKISNPK.G | |

# Detailed Protein Report

## Protein 184: PREDICTED: zinc finger protein 175 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530417172 | **Score:** | 42.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***WUP:QUP*** **Median:** 1.03 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPADVNLSQK | PQVLGPEKQD | GSCEASVSFE | DVTVDFSREE | WQQLDPAQRC | LYRDVMLELY | SHLFAVGYHI | PNPEVIFRML |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KEKEPRVEEA | EVSHQRCQES | LKLNLEVNGQ | NESNDTEQLD | DVVGSGQLFS | HSSSDACSKN | IHTGETFCKG | NQCRKVCGHK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QSLKQHQIHT | QKKPDGCSEC | GGSFTQKSHL | FAQQRIHSVG | NLHECGKCGK | AFMPQLKLSV | YLTDHTGDIP | CICKECGKVF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IQRSELLTHQ | KTHTRKKPYK | CHDCGKAFFQ | MLSLFRHQRT | HSREKLYECS | ECGKGFSQNS | TLIIHQKIHT | GERQYACSEC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GKAFTQKSTL | SLHQRIHSGQ | KSYVCIECGQ | AFIQKAHLIV | HQRSHTGEKP | YQCHNCGKSF | ISKSQLDIHH | RIHTGEKPYE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CSDCGKTFTQ | KSHLNIHQKI | HTGERHHVCS | ECGKAFNQKS | ILSMHQRIHT | GEKPYKCSEC | GKAFTSKSQF | KEHQRIHTGE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KPYVCTECGK | AFNGRSNFHK | HQITHTRERP | FVCYKCGKAF | VQKSELITHQ | RTHMGEKPYE | CLDCGKSFSK | KPQLKVHQRI |
| 570 | 580 | 590 | 600 | 610 | | | |
| HTGERPYVCS | ECGKAFNNRS | NFNKHQTTHT | RDKSYKCSYS | VKGFTKQ | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 22 | 1 | 1205.0462 | -16.45 | 2 | 30.0 | 19.7 | 1 | 218-238 | K.LSVYLTDHTGDIPCICKECGK.V | Carbamidomethyl: 14, 16 | WUP:QUP | 1.03 |
| 6 | 2 | 1205.0350 | -25.71 | 2 | 29.5 | 22.9 | 1 | 218-238 | K.LSVYLTDHTGDIPCICKECGK.V | Carbamidomethyl: 14, 19 | | |

# Detailed Protein Report

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## Protein 185: ectodysplasin-A isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|54112101 | **Score:** | 42.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 8.7 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGYPEVERRE | LLPAAAPRER | GSQGCGCGGA | PARAGEGNSC | LLFLGFFGLS | LALHLLTLCC | YLELRSELRR | ERGAESRLGG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SGTPGTSGTL | SSLGGLDPDS | PITSHLGQPS | PKQQPLEPGE | AALHSDSQDG | HQMALLNFFF | PDEKPYSEEE | SRRVRRNKRS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KSNEGADGPV | KNKKKGKKAG | PPGPNGPPGP | PGPPGPQGPP | GIPGIPGIPG | TTVMGPPGPP | GPPGPQGPPG | LQGPSGAADK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AGTRENQPAV | VHLQGQGSAI | QVKNDLSGGV | LNDWSRITMN | PKVFKLHPRS | GELEVLVDGT | YFIYSQVYYI | NFTDFASYEV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| VVDEKPFLQC | TRSIETGKTN | YNTCYTAGVC | LLKARQKIAV | KMVHADISIN | MSKHTTFFGA | IRLGEAPAS | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1964 | 4 | 703.2668 | -56.59 | 2 | 52.9 | 13.6 | 1 | 19-33 | R.ERGSQGCGCGGAPAR.A | |
| 1518 | 3 | 1059.0796 | 50.76 | 2 | 48.7 | 16.6 | 1 | 264-282 | K.NDLSGGVLNDWSRITMNPK.V | |

# Detailed Protein Report

| | | | |
|---|---|---|---|
| **Protein 186:** | **PREDICTED: talin-2 isoform X15 [Homo sapiens]** | | |
| **Accession:** | gi\|578827491 | **Score:** | 42.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 267.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 1.45 | **CV:** 0.00 % | **No. of Peptides:** 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVALSLKICV | RHCNVVKTMQ | FEPSTAVYDA | CRVIRERVPE | AQTGQASDYG | LFLSDEDPRK | GIWLEAGRTL | DYYMLRNGDI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LEYKKKQRPQ | KIRMLDGSVK | TVMVDDSKTV | GELLVTICSR | IGITNYEEYS | LIQETIEEKK | EEGTGTLKKD | RTLLRDERKM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EKLKAKLHTD | DDLNWLDHSR | TFREQGVDEN | ETLLLRRKFF | YSDQNVDSRD | PVQLNLLYVQ | ARDDILNGSH | PVSFEKACEF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GGFQAQIQFG | PHVEHKHKPG | FLDLKEFLPK | EYIKQRGAEK | RIFQEHKNCG | EMSEIEAKVK | YVKLARSLRT | YGVSFFLVKE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KMKGKNKLVP | RLLGITKDSV | MRVDEKTKEV | LQEWPLTTVK | RWAASPKSFT | LDFGEYQESY | YSVQTTEGEQ | ISQLIAGYID |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IILKKKQSKD | RFGLEGDEES | TMLEESVSPK | KSTILQQQFN | RTGKAEHGSV | ALPAVMRSGS | SGPETFNVGS | MPSPQQQVMV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GQMHRGHMPP | LTSAQQALMG | TINTSMHAVQ | QAQDDLSELD | SLPPLGQDMA | SRVWVQNKVD | ESKHEIHSQV | DAITAGTASV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VNLTAGDPAD | TDYTAVGCAI | TTISSNLTEM | SKGVKLLAAL | MDDEVGSGED | LLRAARTLAG | AVSDLLKAVQ | PTSGEPRQTV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LTAAGSIGQA | SGDLLRQIGE | NETDERFQDV | LMSLAKAVAN | AAAMLVLKAK | NVAQVAEDTV | LQNRVIAAAT | QCALSTSQLV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ACAKVVSPTI | SSPVCQEQLI | EAGKLVDRSV | ENCVRACQAA | TTDSELLKQV | SAAASVVSQA | LHDLLQHVRQ | FASRGEPIGR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| YDQATDTIMC | VTESIFSSMG | DAGEMVRQAR | VLAQATSDLV | NAMRSDAEAE | IDMENSKKLL | AAAKLLADST | ARMVEAAKGA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| AANPENEDQQ | QRLREAAEGL | RVATNAAAQN | AIKKKIVNRL | EVAAKQAAAA | ATQTIAASQN | AAVSNKNPAA | QQQLVQSCKA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VADHIPQLVQ | GVRGSQAQAE | DLSAQLALII | SSQNFLQPGS | KMVSSAKAAV | PTVSDQAAAM | QLSQCAKNLA | TSLAELRTAS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QKAHEACGPM | EIDSALNTVQ | TLKNELQDAK | MAAVESQLKP | LPGETLEKCA | QDLGSTSKAV | GSSMAQLLTC | AAQGNEHYTG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| VAARETAQAL | KTLAQAARGV | AASTTDPAAA | HAMLDSARDV | MEGSAMLIQE | AKQALIAPGD | AERQQRLAQV | AKAVSHSLNN |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| CVNCLPGQKD | VDVALKSIGE | SSKKLLVDSL | PPSTKPFQEA | QSELNQAAAD | LNQSAGEVVH | ATRGQSGELA | AASGKFSDDF |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DEFLDAGIEM | AGQAQTKEDQ | IQVIGNLKNI | SMASSKLLLA | AKSLSVDPGA | PNAKNLLAAA | ARAVTESINQ | LITLCTQQAP |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| GQKECDNALR | ELETVKGMLD | NPNEPVSDLS | YFDCIESVME | NSKVLGESMA | GISQNAKTGD | LPAFGECVGI | ASKALCGLTE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| AAAQAAYLVG | ISDPNSQAGH | QGLVDPIQFA | RANQAIQMAC | QNLVDPGSSP | SQVLSAATIV | AKHTSALCNA | CRIASSKTAN |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PVAKRHFVQS | AKEVANSTAN | LVKTIKALDG | DFSEDNRNKC | RIATAPLIEA | VENLTAFASN | PEFVSIPAQI | SSEGSQAQEP |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| ILVSAKTMLE | SSSYLIRTAR | SLAINPKDPP | TWSVLAGHSH | TVSDSIKSLI | TSIRDKAPGQ | RECDYSIDGI | NRCIRDIEQA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| SLAAVSQSLA | TRDDISVEAL | QEQLTSVVQE | IGHLIDPIAT | AARGEAAQLG | HKVTQLASYF | EPLILAAVGV | ASKILDHQQQ |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| MTVLDQTKTL | AESALQMLYA | AKEGGGNPKA | QHTHDAITEA | AQLMKEAVDD | IMVTLNEAAS | EVGLVGGMVD | AIAEAMSKLD |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| EGTPPEPKGT | FVDYQTTVVK | YSKAIAVTAQ | EMIGFQIRTR | VQDLGHGCIF | LVQKAGALQV | CPTDSYTKRE | LIECARAVTE |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| KVSLVLSALQ | AGNKGTQACI | TAATAVSGII | ADLDTTIMFA | TAGTLNAENS | ETFADHRENI | LKTAKALVED | TKLLVSGAAS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| TPDKLAQAAQ | SSAATITQLA | EVVKLGAASL | GSDDPETQVV | LINAIKDVAK | ALSDLISATK | GAASKPVDDP | SMYQLKGAAK |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| VMVTNVTSLL | KTVKAVEDEA | TRGTRALEAT | IECIKQELTV | FQSKDVPEKT | SSPEESIRMT | KGITMATAKA | VAAGNSCRQE |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| DVIATANLSR | KAVSDMLTAC | KQASFHPDVS | DEVRTALRLF | GTECTLGYLD | LLEHVLVILQ | KPTPEFKQQL | AAFSKRVAGA |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| VTELIQAAEA | MKGTEWVDPE | DPTVIAETEL | LGAAASIEAA | AKKLEQLKPR | AKPKQADETL | DFEEQILEAA | KSIAAATSAL |
| 2330 | 2340 | 2350 | 2360 | 2370 | 2380 | 2390 | 2400 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2049 | 1 | 812.3468 | -109.11 | 2 | 56.0 | 14.1 | 1 | 442-457 | R.TGKAEHGSVALPAVMR.S |  | QU:MU 1.45 |

# Detailed Protein Report

**Protein 187:** **dematin isoform 3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|166706885 | **Score:** | 42.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MERLQKAKMD NQVLGYKDLA AIPKDKAILD IERPDLMIYE PHFTYSLLEH VELPRSRERS LSPKSTSPPP SPEVWADSRS

        90        100        110        120        130        140        150        160
PGIISQASAP RTTGTPRTSL PHFHHPETSR PDSNIYKKPP IYKQRESVGG SPQTKHLIED LIIESSKFPA AQPPDPNQPA

       170        180        190        200        210        220        230        240
KIETDYWPCP PSLAVVETEW RKRKASRRGA EEEEEEEDDD SGEEMKALRE RQREELSKVT SNLGKMILKE EMEKSLPIRR

       250        260        270        280        290        300        310        320
KTRSLPDRTP FHTSLHQGTS KSSSLPAYGR TTLSRLQSTE FSPSGSETGS PGLQIYPYEM LVVTNKGRTK LPPGVDRMRL

       330        340        350        360
ERHLSAEDFS RVFAMSPEEF GKLALWKRNE LKKKASLF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 953 | 1 | 531.2210 | -62.44 | 2 | 40.3 | 19.5 | 0 | 323-331 | R.HLSAEDFSR.V | |

# Detailed Protein Report

## Protein 188: PREDICTED: partitioning defective 3 homolog isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530392319 | **Score:** | 42.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 149.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MKVTVCFGRT RVVVPCGDGH MKVFSLIQQA VTRYRKAIAK DPNYWIQVHR LEHGDGGILD LDDILCDVAD DKDRLVAVFD
        90        100        110        120        130        140        150        160
EQDPHHGGDG TSASSTGTQS PEIFGSELGT NNVSAFQPYQ ATSEIEVTPS VLRANMPLHV RRSSDPALIG LSTSVSDSNF
       170        180        190        200        210        220        230        240
SSEEPSRKNP TRWSTTAGFL KQNTAGSPKT CDRKKDENYR SLPRDTSNWS NQFQRDNARS SLSASHPMVG KWLEKQEQDE
       250        260        270        280        290        300        310        320
DGTEEDNSRV EPVGHADTGL EHIPNFSLDD MVKLVEVPND GGPLGIHVVP FSARGGRTLG LLVKRLEKGG KAEHENLFRE
       330        340        350        360        370        380        390        400
NDCIVRINDG DLRNRRFEQA QHMFRQAMRT PIIWFHVVPA ANKEQYEQLS QSEKNNYYSS RFSPDSQYID NRSVNSAGLH
       410        420        430        440        450        460        470        480
TVQRAPRLNH PPEQIDSHSR LPHSAHPSGK PPSAPASAPQ NVFSTTVSSG YNTKKIGKRL NIQLKKGTEG LGFSITSRDV
       490        500        510        520        530        540        550        560
TIGGSAPIYV KNILPRGAAI QDGRLKAGDR LIEVNGVDLV GKSQEEVVSL LRSTKMEGTV SLLVFRQEDA FHPRELNAEP
       570        580        590        600        610        620        630        640
SQMQIPKETK AEDEDIVLTP DGTREFLTFE VPLNDSGSAG LGVSVKGNRS KENHADLGIF VKSIINGGAA SKDGRLRVND
       650        660        670        680        690        700        710        720
QLIAVNGESL LGKTNQDAME TLRRSMSTEG NKRGMIQLIV ARRISKCNEL KSPGSPPGPE LPIETALDDR ERRISHSLYS
       730        740        750        760        770        780        790        800
GIEGLDESPS RNAALSRIMG KYQLSPTVNM PQDDTVIIED DRLPVLPPHL SDQSSSSSHD DVGFVTADAG TWAKAAISDS
       810        820        830        840        850        860        870        880
ADCSLSPDVD PVLAFQREGF GRQSMSEKRT KQFSDASQLD FVKTRKSKSM DLGSSPSRDV GPSLGLKKSS SLESLQTAVA
       890        900        910        920        930        940        950        960
EVTLNGDIPF HRPRPRIIRG RGCNESFRAA IDKSYDKPAV DDDDEGMETL EEDTEESSRS GRESVSTASD QPSHSLERQM
       970        980        990       1000       1010       1020       1030       1040
NGNQEKGDKT DRKKDKTGKE KKKDRDKEKD KMKAKKGMLK GLGDMFRFGK HRKDDKIEKT GKIKIQESFT SEEERIRMKQ
      1050       1060       1070       1080       1090       1100       1110       1120
EQERIQAKTR EFRERQARER DYAEIQDFHR TFGCDDELMY GGVSSYEGSM ALNARPQSPR EGHMMDALYA QVKKPRNSKP
      1130       1140       1150       1160       1170       1180       1190       1200
SPVDSNRSTP SNHDRIQRLR QEFQQAKQDE DVEDRRRTYS FEQPWPNARP ATQSGRHSVS VEVQMQRQRQ EERESSQQAQ
      1210       1220       1230       1240       1250       1260       1270       1280
RQYSSLPRQS RKNASSVSQD SWEQNYSPGE GFQSAKENPR YSSYQGSRNG YLGGHGFNAR VMLETQELLR QEQRRKEQQM
      1290       1300       1310       1320       1330       1340
KKQPPSEGPS NYDSYKKVQD PSYAPPKGPF RQDVPPSPSQ VARLNRLQTP EKGRPFYS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2795 | 1 | 729.3498 | -56.43 | 2 | 66.1 | 14.8 | 1 | 610-622 | R.SKENHADLGIFVK.S | |
| 2354 | 1 | 711.9476 | -118.31 | 3 | 59.3 | 10.7 | 2 | 847-867 | K.SKSMDLGSSPSRDVGPSLGLK.K | Oxidation: 4 |

# Detailed Protein Report

## Protein 189: endothelin-2 preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4503463 | **Score:** | 42.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 19.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 14.0 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MVSVPTTWCS VALALLVALH EGKGQAAATL EQPASSSHAQ GTHLRLRRCS CSSWLDKECV YFCHLDIIWV NTPEQTAPYG
        90        100        110        120        130        140        150        160
LGNPPRRRRR SLPRRCQCSS ARDPACATFC LRRPWTEAGA VPSRKSPADV FQTGKTGATT GELLQRLRDI STVKSLFAKR
       170        180
QQEAMREPRS THSRWRKR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2946 | 1 | 1051.5610 | 95.12 | 2 | 65.6 | 10.9 | 2 | 95-112 | R.RCQCSSARDPACATFCLR.R | Carbamidomethyl: 4, 12 |

# Detailed Protein Report

## Protein 190: PREDICTED: protein FAM186A isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578823289 | **Score:** | 42.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 262.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFFKMKNEID | NDPESEKCIK | DSTIMRREPQ | NILSPLMLPN | LEIPFSVKDI | ISRIERAQLH | RAREDIDMQL | SEIMNNVHRI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MTRYTLVFNS | SSERNVSLTE | HKKKQRTNFL | EKMATYAKTI | EIREKTLANI | LAWLEEWNDV | LSEMTLMDVD | EHHHWIAQME |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLPDTLKAIE | NNVKILSRFS | TSFLDEKKKQ | KKKILSRGTL | WKSWKERVIK | RPSTARALRP | DQMISDQLAT | NTKVSEIQGM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LQELIGTTMF | STLENNAIKY | ISSTIVNLST | ALSMLNDELK | CVNFQSSTVY | AHETSEAEKE | LSLKIIRDLS | NENEMLQQKL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QDAEEKCEQL | IRSKIVIEQL | YAKLSTSSTL | KVLPGPSPQS | SRAIIKVGDT | EDNMDNILDK | ELENIVDEVQ | RKETKDSGIK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| WDSTISYTAQ | AERTPDLTEL | RQQPVASEDI | SEDSTKDNVS | LKKGDFYQED | ETDEYQSWKR | SHKKATYVYE | TSGPNLSDNK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SGQKVSEAKP | SQYYELQVLK | KKRKEMKSFS | EDKSKSPTEA | KRKHLSLTET | KSQGGKSGTS | MMMLEQFRKV | KRESPFDKRP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TAAEIKVEPT | TESLDKEGKG | EIRSLVEPLS | MIQFDDTAEP | QKGKIKGKKH | HISSGTITSK | EEKTEEKEEL | TKQVKSHQLV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KSLSRVAKET | SESTRVLESP | DGKSEQSNLE | EFQEAIMAFL | KQKIDNIGKA | FDKKTVPKEE | ELLKRAEAEK | LGIIKAKMEE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YFQKVAETVT | KILRKYKDTK | KEEQVGEKPI | KQKKVVSFMP | GLHFQKSPIS | AKSESSTLLS | YESTDPVINN | LIQMILAEIE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SERDIPTVST | VQKDHKEKEK | QRQEQYLQEG | QEQMSGMSLK | QQLLGERNLL | KEHYEKISEN | WEEKKAWLQM | KEGKQEQQSQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KQWQEEEMWK | EEQKQATPKQ | AEQEEKQKQR | GQEEEELPKS | SLQRLEEGTQ | KMKTQGLLLE | KENGQMRQIQ | KEAKHLGPHR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RREKGKEKQK | PERGLEDLER | QIKTKDQMQM | KETQPKELEK | MVIQTPMTLS | PRWKSVLKDV | QRSYEGKEFQ | RNLKTLENLP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| DEKEPISITP | PPSLQYSLPG | ALPISGQPLT | KCIHLTPQQA | QEVGITLTPQ | QAQAQGITLT | LQQAQELGIP | LTPQQAQALE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ILFTPQQAQA | LGIPLTPQQT | QVQGITLTPQ | QDQAPGISLT | TQQAQKLGIP | LTPQQAQALG | IPLTPQQAQE | LGIPLTPQQA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| QALRVSLTPQ | QAQELGIPLT | PQQAQALGIT | LTLQQAQQLG | IPLTPQQAQA | LGITLTPKQV | QELGIPLTPQ | QAQALGITLT |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PKQAQELGIP | LNPQQAQTLG | IPLTPKQAQA | LGIPFTPQQA | QALGIPLTPQ | QAQTQEITLT | PQQAQALGMP | LTTQQAQELG |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| IPLTPQHAQA | LGMPLTTQQA | QELGIPLTPQ | QAQALGMPLT | TQQAQELGIP | LTPQQAQELG | IPFTPQQAQA | QEITLTPQQA |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| QALGMPLTAQ | QAQELGITLT | PQQAQELGIP | LTPQQAQALG | IPLIPPQAQE | LGIPLTPQQA | QALGILLIPP | QAQELGIPLT |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PQQAQALGIP | LIPPQAQELG | IPLTPQQVQA | LGIPLIPPQA | QELEIPLTPQ | QAQALGIPLT | PQQAQELGIP | LTPQQAQELG |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| IPLTPQQAQA | QGIPLTPQQA | QALGISLTPQ | QAQAQGITLT | PQQAQALGVP | ITPVNAWVSA | VTLTSEQTHA | LESPMNLEQA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| QEQLLKLGVP | LTLDKAHTLG | SPLTLKQVQW | SHRPFQKSKA | SLPTGQSIIS | RLSPSLRLSL | ASSAPTAEKS | SIFGVSSTPL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| QISRVPLNQG | PFAPGKPLEM | GILSEPGKLG | APQTLRSSGQ | TLVYGGQSTS | AQFPAPQAPP | SPGQLPISRA | PPTPGQPFIA |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| GVPPTSGQIP | SLWAPLSPGQ | PLVPEASSIP | GDLLESGPLT | FSEQLQEFQP | PATAEQSPYL | QAPSTPGQHL | ATWTLPGRAS |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| SLWIPPTSRH | PPTLWPSPAP | GKPQKSWSPS | VAKKRLAIIS | SLKSKSVLIH | PSAPDFKVAQ | VPFTTKKFQM | SEVSDTSEET |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| QILRDTFAIE | SFRTFQSHFT | KYRTPVYQTP | YTDERALLTL | MKPTTSPSSL | TTLLRTSQIS | PLEWYQKSRF | PPIDKPWILS |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| SVSDTKKPKV | MVPPSSPQEL | EEKRYFVDVE | AQKKNLILLN | QAIKTCGLPS | QLHTMARTLI | IEILHMDTVQ | LGYLFRKYIA |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| YRLIQHARNN | IMKRLKAIQN | TGKGYEARNL | HMMLSRLDDY | GKKVMQVWTE | KQKSLGQKRN | QCLKKMIHVF | NQLKKIHELN |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| LSQPIPLIIE | EKQIPASTTF | VQKPFLKLLM | EEDRTSDICK | KFRQQEDQTE | AIWNVDLSTS | SYPIAEKTSM | HSLWAQLGGY |
| 2330 | 2340 | 2350 | | | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1615 | 1 | 781.3837 | 27.46 | 2 | 49.9 | 12.0 | 1 | 537-549 | K.SGTSMMMLEQFRK.V | Oxidation: 6 |

# Detailed Protein Report

## Protein 191: PREDICTED: nesprin-1 isoform X19 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578812604 | **Score:** | 42.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 1002.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 0.7 |
| | | **No. of unique Peptides:** | 3 |

### Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 0.70 | **CV:** 0.00 % | **No. of Peptides:** 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MATSRGASRC | PRDIANVMQR | LQDEQEIVQK | RTFTKWINSH | LAKRKPPMVV | DDLFEDMKDG | VKLLALLEVL | SGQKLPCEQG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RRMKRIHAVA | NIGTALKFLE | GRKSMHRGSP | IKLVNINSTD | IADGRPSIVL | GLMWTIILYF | QIEELTSNLP | QLQSLSSSAS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SVDSIVSSET | PSPPSKRKVT | TKIQGNAKKA | LLKWVQYTAG | KQTGIEVKDF | GKSWRSGVAF | HSVIHAIRPE | LVDLETVKGR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SNRENLEDAF | TIAETELGIP | RLLDPEDVDV | DKPDEKSIMT | YVAQFLKHYP | DIHNASTDGQ | EDDEILPGFP | SFANSVQNFK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| REDRVIFKEM | KVWIEQFERD | LTRAQMVESN | LQDKYQSFKH | FRVQYEMKRK | QIEHLIQPLH | RDGKLSLDQA | LVKQSWDRVT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SRLFDWHIQL | DKSLPAPLGT | IGAWLYRAEV | ALREEITVQQ | VHEETANTIQ | RKLEQHKDLL | QNTDAHKRAF | HEIYRTRSVN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GIPVPPDQLE | DMAERFHFVS | STSELHLMKM | EFLELKYRLL | SLLVLAESKL | KSWIIKYGRR | ESVEQLLQNY | VSFIENSKFF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EQYEVTYQIL | KQTAEMYVKA | DGSVEEAENV | MKFMNETTAQ | WRNLSVEVRS | VRSMLEEVIS | NWDRYGNTVA | SLQAWLEDAE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KMLNQSENAK | KDFFRNLPHW | IQQHTAMNDA | GNFLIETCDE | MVSRDLKQQL | LLLNGRWREL | FMEVKQYAQA | DEMDRMKKEY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TDCVVTLSAF | ATEAHKKLSE | PLEVSFMNVK | LLIQDLEDIE | QRVPVMDAQY | KIITKTAHLI | TKESPQEEGK | EMFATMSKLK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EQLTKVKECY | SPLLYESQQL | LIPLEELEKQ | MTSFYDSLGK | INEIITVLER | EAQSSALFKQ | KHQELLACQE | NCKKTLTLIE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KGSQSVQKFV | TLSNVLKHFD | QTRLQRQIAD | IHVAFQSMVK | KTGDWKKHVE | TNSRLMKKFE | ESRAELEKVL | RIAQEGLEEK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GDPEELLRRH | TEFFSQLDQR | VLNAFLKACD | ELTDILPEQE | QQGLQEAVRK | LHKQWKDLQG | EAPYHLLHLK | IDVEKNRFLA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SVEECRTELD | RETKLMPQEG | SEKIIKEHRV | FFSDKGPHHL | CEKRLQLIEE | LCVKLPVRDP | VRDTPGTCHV | TLKELRAAID |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| STYRKLMEDP | DKWKDYTSRF | SEFSSWISTN | ETQLKGIKGE | AIDTANHGEV | KRAVEEIRNG | VTKRGETLSW | LKSRLKVLTE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VSSENEAQKQ | GDELAKLSSS | FKALVTLLSE | VEKMLSNFGD | CVQYKEIVKN | SLEELISGSK | EVQEQAEKIL | DTENLFEAQQ |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LLLHHQQKTK | RISAKKRDVQ | QQIAQAQQGE | GGLPDRGHEE | LRKLESTLDG | LERSRERQER | RIQVTLRKWE | RFETNKETVV |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| RYLFQTGSSH | ERFLSFSSLE | SLSSELEQTK | EFSKRTESIA | VQAENLVKEA | SEIPLGPQNK | QLLQQQAKSI | KEQVKKLEDT |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LEEDIKTMEM | VKTKWDHFGS | NFETLSVWIT | EKEKELNALE | TSSSAMDMQI | SQIKVTIQEI | ESKLSSIVGL | EEEAQSFAQF |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| VTTGESARIK | AKLTQIRRYG | EELREHAQCL | EGTILGHLSQ | QQKFEENLRK | IQQSVSEFED | KLAVPIKICS | SATETYKVLQ |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| EHMDLCQALE | SLSSAITAFS | ASARKVVNRD | SCVQEAAALQ | QQYEDILRRA | KERQTALENL | LAHWQRLEKE | LSSFLTWLER |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| GEAKASSPEM | DISADRVKVE | GELQLIQALQ | NEVVSQASFY | SKLLQLKESL | FSVASKDDVK | MMKLHLEQLD | ERWRDLPQII |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| NKRINFLQSV | VAEHQQFDEL | LLSFSVWIKL | FLSELQTTSE | ISIMDHQVAL | TRHKDHAAEV | ESKKGELQSL | QGHLAKLGSL |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| GRAEDLHLLQ | GKAEDCFQLF | EEASQVVERR | QLALSHLAEF | LQSHASLSGI | LRQLRQTVEA | TNSMNKNESD | LIEKDLNDAL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| QNAKALESAA | VSLDGILSKA | QYHLKIGSSE | QRTSCRATAD | QLCGEVERIQ | NLLGTKQSEA | DALAVLKKAF | QDQKEELLKS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| IEDIEERTDK | ERLKEPTRQA | LQQRLRVFNQ | LEDELNSHEH | ELCWLKDKAK | QIAQKDVAFA | PEVDREINRL | EVTWDDTKRL |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| IHENQGQCCG | LIDLMREYQN | LKSAVSKVLE | NASSVIVTRT | TIKDQEDLKW | AFSKHETAKN | KMNYKQKDLD | NFTSKGKHLL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 280 | 1 | 607.8593 | -49.80 | 2 | 33.5 | 10.5 | 1 | 3327-3337 | R.TLKLEALLSVK.Q | | QU:MU 0.70 |
| 2894 | 1 | 724.8707 | 49.22 | 2 | 64.9 | 10.6 | 1 | 4576-4586 | K.EDFDKACHWLK.Q | Carbamidomethyl: 7 | |
| 2810 | 1 | 1024.4996 | -15.58 | 3 | 65.5 | 10.3 | 2 | 6575-6600 | K. LQDMYDELMMIIGSRRSGLNQNLT S | Oxidation: 9, 10 | |

# Detailed Protein Report

## Protein 192: utrophin [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|110611228 | **Score:** | 42.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 394.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| | | **Sequence Coverage [%]:** | 0.6 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***WUP:QUP*** | **Median:** | 0.40 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530384033 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: utrophin isoform X4 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAKYGEHEAS | PDNGQNEFSD | IIKSRSDEHN | DVQKKTFTKW | INARFSKSGK | PPINDMFTDL | KDGRKLLDLL | EGLTGTSLPK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ERGSTRVHAL | NNVNRVLQVL | HQNNVELVNI | GGTDIVDGNH | KLTLGLLWSI | ILHWQVKDVM | KDVMSDLQQT | NSEKILLSWV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RQTTRPYSQV | NVLNFTTSWT | DGLAFNAVLH | RHKPDLFSWD | KVVKMSPIER | LEHAFSKAQT | YLGIEKLLDP | EDVAVQLPDK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KSIIMYLTSL | FEVLPQQVTI | DAIREVETLP | RKYKKECEEE | AINIQSTAPE | EEHESPRAET | PSTVTEVDMD | LDSYQIALEE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VLTWLLSAED | TFQEQDDISD | DVEEVKDQFA | THEAFMMELT | AHQSSVGSVL | QAGNQLITQG | TLSDEEEFEI | QEQMTLLNAR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| WEALRVESMD | RQSRLHDVLM | ELQKKQLQQL | SAWLTLTEER | IQKMETCPLD | DDVKSLQKLL | EEHKSLQSDL | EAEQVKVNSL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| THMVVIVDEN | SGESATAILE | DQLQKLGERW | TAVCRWTEER | WNRLQEINIL | WQELLEEQCL | LKAWLTEKEE | ALNKVQTSNF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KDQKELSVSV | RRLAILKEDM | EMKRQTLDQL | SEIGQDVGQL | LDNSKASKKI | NSDSEELTQR | WDSLVQRLED | SSNQVTQAVA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KLGMSQIPQK | DLLETVRVRE | QAITKKSKQE | LPPPPPPKKR | QIHVDIEAKK | KFDAISAELL | NWILKWKTAI | QTTEIKEYMK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| MQDTSEMKKK | LKALEKEQRE | RIPRADELNQ | TGQILVEQMG | KEGLPTEEIK | NVLEKVSSEW | KNVSQHLEDL | ERKIQLQEDI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NAYFKQLDEL | EKVIKTKEEW | VKHTSISESS | RQSLPSLKDS | CQRELTNLLG | LHPKIEMARA | SCSALMSQPS | APDFVQRGFD |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SFLGRYQAVQ | EAVEDRQQHL | ENELKGQPGH | AYLETLKTLK | DVLNDSENKA | QVSLNVLNDL | AKVEKALQEK | KTLDEILENQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KPALHKLAEE | TKALEKNVHP | DVEKLYKQEF | DDVQGKWNKL | KVLVSKDLHL | LEEIALTLRA | FEADSTVIEK | WMDGVKDFLM |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KQQAAQGDDA | GLQRQLDQCS | AFVNEIETIE | SSLKNMKEIE | TNLRSGPVAG | IKTWVQTRLG | DYQTQLEKLS | KEIATQKSRL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SESQEKAANL | KKDLAEMQEW | MTQAEEEYLE | RDFEYKSPEE | LESAVEEMKR | AKEDVLQKEV | RVKILKDNIK | LLAAKVPSGG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| QELTSELNVV | LENYQLLCNR | IRGKCHTLEE | VWSCWIELLH | YLDLETTWLN | TLEERMKSTE | VLPEKTDAVN | EALESLESVL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| RHPADNRTQI | RELGQTLIDG | GILDDIISEK | LEAFNSRYED | LSHLAESKQI | SLEKQLQVLR | ETDQMLQVLQ | ESLGELDKQL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| TTYLTDRIDA | FQVPQEAQKI | QAEISAHELT | LEELRRNMRS | QPLTSPESRT | ARGGSQMDVL | QRKLREVSTK | FQLFQKPANF |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EQRMLDCKRV | LDGVKAELHV | LDVKDVDPDV | IQTHLDKCMK | LYKTLSEVKL | EVETVIKTGR | HIVQKQQTDN | PKGMDEQLTS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| LKVLYNDLGA | QVTEGKQDLE | RASQLARKMK | KEAASLSEWL | SATETELVQK | STSEGLLGDL | DTEISWAKNV | LKDLEKRKAD |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LNTITESSAA | LQNLIEGSEP | ILEERLCVLN | AGWSRVRTWT | EDWCNTLMNH | QNQLEIFDGN | VAHISTWLYQ | AEALLDEIEK |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| KPTSKQEEIV | KRLVSELDDA | NLQVENVRDQ | ALILMNARGS | SSRELVEPKL | AELNRNFEKV | SQHIKSAKLL | IAQEPLYQCL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| VTTETFETGV | PFSDLEKLEN | DIENMLKFVE | KHLESSDEDE | KMDEESAQIE | EVLQRGEEML | HQPMEDNKKE | KIRLQLLLLH |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| TRYNKIKAIP | IQQRKMGQLA | SGIRSSLLPT | DYLVEINKIL | LCMDDVELSL | NVPELNTAIY | EDFSFQEDSL | KNIKDQLDKL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| GEQIAVIHEK | QPDVILEASG | PEAIQIRDTL | TQLNAKWDRI | NRMYSDRKGC | FDRAMEEWRQ | FHCDLNDLTQ | WITEAEELLV |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| DTCAPGGSLD | LEKARIHQQE | LEVGISSHQP | SFAALNRTGD | GIVQKLSQAD | GSFLKEKLAG | LNQRWDAIVA | EVKDRQPRLK |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| GESKQVMKYR | HQLDEIICWL | TKAEHAMQKR | STTELGENLQ | ELRDLTQEME | VHAEKLKWLN | RTELEMLSDK | SLSLPERDKI |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 36 | 1 | 721.8221 | -42.42 | 2 | 30.3 | 16.3 | 2 | 24-35 | K.SRSDEHNDVQKK.T | | |
| 467 | 5 | 607.8289 | -91.67 | 2 | 35.5 | 25.9 | 2 | 997-1006 | K.WNKLKVLVSK.D | | WUP:QUP 0.40 |

# Detailed Protein Report

## Protein 193: A disintegrin and metalloproteinase with thrombospondin motifs 16 preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|110735441 | **Score:** | 42.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 136.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 3.8 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKPRARGWRG | LAALWMLLAQ | VAEQAPACAM | GPAAAAPGSP | SVPRPPPPAE | RPGWMEKGEY | DLVSAYEVDH | RGDYVSHEIM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HHQRRRRAVP | VSEVESLHLR | LKGSRHDFHM | DLRTSSSLVA | PGFIVQTLGK | TGTKSVQTLP | PEDFCFYQGS | LRSHRNSSVA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LSTCQGLSGM | IRTEEADYFL | RPLPSHLSWK | LGRAAQGSSP | SHVLYKRSTE | PHAPGASEVL | VTSRTWELAH | QPLHSSDLRL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GLPQKQHFCG | RRKKYMPQPP | KEDLFILPDE | YKSCLRHKRS | LLRSHRNEEL | NVETLVVVDK | KMMQNHGHEN | ITTYVLTILN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MVSALFKDGT | IGGNINIAIV | GLILLEDEQP | GLVISHHADH | TLSSFCQWQS | GLMGKDGTRH | DHAILLTGLD | ICSWKNEPCD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TLGFAPISGM | CSKYRSCTIN | EDTGLGLAFT | IAHESGHNFG | MIHDGEGNMC | KKSEGNIMSP | TLAGRNGVFS | WSPCSRQYLH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KFLSTAQAIC | LADQPKPVKE | YKYPEKLPGE | LYDANTQCKW | QFGEKAKLCM | LDFKKDICKA | LWCHRIGRKC | ETKFMPAAEG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TICGHDMWCR | GGQCVKYGDE | GPKPTHGHWS | DWSSWSPCSR | TCGGGVSHRS | RLCTNPKPSH | GGKFCEGSTR | TLKLCNSQKC |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PRDSVDFRAA | QCAEHNSRRF | RGRHYKWKPY | TQVEDQDLCK | LYCIAEGFDF | FFSLSNKVKD | GTPCSEDSRN | VCIDGICERV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GCDNVLGSDA | VEDVCGVCNG | NNSACTIHRG | LYTKHHHTNQ | YYHMVTIPSG | ARSIRIYEMN | VSTSYISVRN | ALRRYYLNGH |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| WTVDWPGRYK | FSGTTFDYRR | SYNEPENLIA | TGPTNETLIV | ELLFQGRNPG | VAWEYSMPRL | GTEKQPPAQP | SYTWAIVRSE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| CSVSCGGGQM | TVREGCYRDL | KFQVNMSFCN | PKTRPVTGLV | PCKVSACPPS | WSVGNWSACS | RTCGGGAQSR | PVQCTRRVHY |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DSEPVPASLC | PQPAPSSRQA | CNSQSCPPAW | SAGPWAECSH | TCGKGWRKRA | VACKSTNPSA | RAQLLPDAVC | TSEPKPRMHE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ACLLQRCHKP | KKLQWLVSAW | SQCSVTCERG | TQKRFLKCAE | KYVSGKYREL | ASKKCSHLPK | PSLELERACA | PLPCPRHPPF |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| AAAGPSRGSW | FASPWSQCTA | SCGGGVQTRS | VQCLAGGRPA | SGCLLHQKPS | ASLACNTHFC | PIAEKKDAFC | KDYFHWCYLV |
| 1210 | 1220 | 1230 | | | | | |
| PQHGMCSHKF | YGKQCCKTCS | KSNL | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1904 | 1 | 724.3383 | -56.32 | 2 | 54.2 | 12.7 | 2 | 631-642 | R.TLKLCNSQKCPR.D | Carbamidomethyl: 10 |
| 2449 | 1 | 1025.1077 | -9.04 | 3 | 60.5 | 13.5 | 2 | 1186-1209 | K.KDAFCKDYFHWCYLVPQHGMCSHK.F | Carbamidomethyl: 5, 12; Oxidation: 20 |
| 1728 | 1 | 636.2813 | 0.97 | 2 | 51.9 | 15.9 | 2 | 1214-1224 | K.QCCKTCSKSNL.- | Carbamidomethyl: 2 |

# Detailed Protein Report

## Protein 194: PREDICTED: dedicator of cytokinesis protein 11 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530422336 | **Score:** | 42.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 235.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFKEKAKVVE | PLDYENVIAQ | RKTQIYSDPL | RDLLMFPMED | ISISVIGRQR | RTVQSTVPED | AEKRAQSLFV | KECIKTYSTD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| WHVVNYKYED | FSGDFRMLPC | KSLRPEKIPN | HVFEIDEDCE | KDEDSSSLCS | QKGGVIKQGW | LHKANVNSTI | TVTMKVFKRR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YFYLTQLPDG | SYILNSYKDE | KNSKESKGCI | YLDACIDVVQ | CPKMRRHAFE | LKMLDKYSHY | LAAETEQEME | EWLITLKKII |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QINTDSLVQE | KKETVETAQD | DETSSQGKAE | NIMASLERSM | HPELMKYGRE | TEQLNKLSRG | DGRQNLFSFD | SEVQRLDFSG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IEPDIKPFEE | KCNKRFLVNC | HDLTFNILGQ | IGDNAKGPPT | NVEPFFINLA | LFDVKNNCKI | SADFHVDLNP | PSVREMLWGS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| STQLASDGSP | KGSSPESYIH | GIAESQLRYI | QQGIFSVTNP | HPEIFLVARI | EKVLQGNITH | CAEPYIKNSD | PVKTAQKVHR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TAKQVCSRLG | QYRMPFAWAA | RPIFKDTQGS | LDLDGRFSPL | YKQDSSKLSS | EDILKLLSEY | KKPEKTKLQI | IPGQLNITVE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| CVPVDLSNCI | TSSYVPLKPF | EKNCQNITVE | VEEFVPEMTK | YCYPFTIYKN | HLYVYPLQLK | YDSQKTFAKA | RNIAVCVEFR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DSDESDASAL | KCIYGKPAGS | VFTTNAYAVV | SHHNQNPEFY | DEIKIELPIH | LHQKHHLLFT | FYHVSCEINT | KGTTKKQDTV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ETPVGFAWVP | LLKDGRIITF | EQQLPVSANL | PPGYLNLNDA | ESRRQCNVDI | KWVDGAKPLL | KIKSHLESTI | YTQDLHVHKF |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FHHCQLIQSG | SKEVPGELIK | YLKCLHAMEI | QVMIQFLPVI | LMQLFRVLTN | MTHEDDVPIN | CTMVLLHIVS | KCHEEGLDSY |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LRSFIKYSFR | PEKPSAPQAQ | LIHETLATTM | IAILKQSADF | LSINKLLKYS | WFFFEIIAKS | MATYLLEENK | IKLPRGQRFP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ETYHHVLHSL | LLAIIPHVTI | RYAEIPDESR | NVNYSLASFL | KRCLTLMDRG | FIFNLINDYI | SGFSPKDPKV | LAEYKFEFLQ |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TICNHEHYIP | LNLPMAFAKP | KLQRVQDFFS | FAVDRLTSVD | SNLEYSLSDE | YCKHHFLVGL | LLRETSIALQ | DNYEIRYTAI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SVIKNLLIKH | AFDTRYQHKN | QQAKIAQLYL | PFVGLLLENI | QRLAGRDTLY | SCAAMPNSAS | RDEFPCGFTS | PANRGSLSTD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KDTAYGSFQN | GHGIKREDSR | GSLIPEGATG | FPDQGNTGEN | TRQSSTRSSV | SQYNRLDQYE | IRSLLMCYLY | IVKMISEDTL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LTYWNKVSPQ | ELINILILLE | VCLFHFRYMG | KRNIARVHDA | WLSKHFGIDR | KSQTMPALRN | RSGVMQARLQ | HLSSLESSFT |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LNHSSTTTEA | DIFHQALLEG | NTATEVSLTV | LDTISFFTQC | FKTQLLNNDG | HNPLMKKVFD | IHLAFLKNGQ | SEVSLKHVFA |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SLRAFISKFP | SAFFKGRVNM | CAAFCYEVLK | CCTSKISSTR | NEASALLYLL | MRNNFEYTKR | KTFLRTHLQI | IIAVSQLIAD |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| VALSGGSRFQ | ESLFIINNFA | NSDRPMKATA | FPAEVKDLTK | RIRTVLMATA | QMKEHEKDPE | MLIDLQYSLA | KSYASTPELR |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KTWLDSMAKI | HVKNGDFSEA | AMCYVHVAAL | VAEFLHRKKL | FPNGCSAFKK | ITPNIDEEGA | MKEDAGMMDV | HYSEEVLLEL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LEQCVDGLWK | AERYEIISEI | SKLIVPIYEK | RREFEKLTQV | YRTLHGAYTK | ILEVMHTKKR | LLGTFFRVAF | YGQSFFEEED |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| GKEYIYKEPK | LTGLSEISLR | LVKLYGEKFG | TENVKIIQDS | DKVNAKELDP | KYAHIQVTYV | KPYFDDKELT | ERKTEFERNH |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| NISRFVFEAP | YTLSGKKQGC | IEEQCKRRTI | LTTSNSFPYV | KKRIPINCEQ | QINLKPIDVA | TDEIKDKTAE | LQKLCSSTDV |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| DMIQLQLKLQ | GCVSVQVNAG | PLAYARAFLN | DSQASKYPPK | KVSELKDMFR | KFIQACSIAL | ELNERLIKED | QVEYHEGLKS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | | |
| NFRDMVKELS | DIIHEQILQE | DTMHSPWMSN | TLHVFCAISG | TSSDRGYGSP | RYAEV | | |

| Cmpd. | No. of | m/z meas. | Δ m/z | z | Rt | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

| | Cmpds. | | [ppm] | | [min] | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 180 | 1 | 1043.9250 | -79.30 | 2 | 32.2 | 13.4 | 1 | 269-286 | K.AENIMASLERSMHPELMK.Y | |
| 2146 | 4 | 682.9130 | 127.21 | 2 | 57.2 | 18.0 | 1 | 279-289 | R.SMHPELMKYGR.E | Oxidation: 7 |
| 2045 | 1 | 731.3221 | -60.47 | 2 | 56.0 | 10.6 | 1 | 1650-1662 | K.KITPNIDEEGAMK.E | Oxidation: 12 |

# Detailed Protein Report

## Protein 195: putative tyrosine-protein phosphatase auxilin isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|379030617 | **Score:** | 41.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 98.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEPSYGGGLF | DMVKGGAGRL | FSNLKDNLKD | TLKDTSSRVI | QSVTSYTKGD | LDFTYVTSRI | IVMSFPLDNV | DIGFRNQVDD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IRSFLDSRHL | DHYTVYNLSP | KSYRTAKFHS | RVSECSWPIR | QAPSLHNLFA | VCRNMYNWLL | QNPKNVCVVH | CLDGRAASSI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LVGAMFIFCN | LYSTPGPAIR | LLYAKRPGIG | LSPSHRRYLG | YMCDLLADKP | YRPHFKPLTI | KSITVSPIPF | FNKQRNGCRP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YCDVLIGETK | IYSTCTDFER | MKEYRVQDGK | IFIPLNITVQ | GDVVVSMYHL | RSTIGSRLQA | KVTNTQIFQL | QFHTGFIPLD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TTVLKFTKPE | LDACDVPEKY | PQLFQVTLDV | ELQPHDKVID | LTPPWEHYCT | KDVNPSILFS | SHQEHQDTLA | LGGQAPIDIP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PDNPRHYGQS | GFFASLCWQD | QKSEKSFCEE | DHAALVNQES | EQSDDELLTL | SSPHGNANGD | KPHGVKKPSK | KQQEPAAPPP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PEDVDLLGLE | GSAMSNSFSP | PAAPPTNSEL | LSDLFGGGGA | AGPTQAGQSG | VEDVFHPSGP | ASTQSTPRRS | ATSTSASPTL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RVGEGATFDP | FGAPSKPSGQ | DLLGSFLNTS | SASSDPFLQP | TRSPSPTVHA | SSTPAVNIQP | DVSGGWDWHA | KPGGFGMGSK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SAATSPTGSS | HGTPTHQSKP | QTLDPFADLG | TLGSSSFASK | PTTPTGLGGG | FPPLSSPQKA | SPQPMGGGWQ | QGGAYNWQQP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QPKPQPSMPH | SSPQNRPNYN | VSFSAMPGGQ | NERGKGSSNL | EGKQKAADFE | DLLSGQGFNA | HKDKKGPRTI | AEMRKEEMAK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EMDPEKLKIL | EWIEGKERNI | RALLSTMHTV | LWAGETKWKP | VGMADLVTPE | QVKKVYRKAV | LVVHPDKATG | QPYEQYAKMI |
| 890 | 900 | 910 | | | | | |
| FMELNDAWSE | FENQGQKPLY | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1549 | 1 | 1052.1533 | -35.54 | 3 | 49.1 | 11.3 | 2 | 108-133 | K.FHSRVSECSWPIRQAPSLHNLFAVCR.N | Carbamidomethyl: 8, 25 |

# Detailed Protein Report

## Protein 196: PREDICTED: zinc finger protein 407 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578832590 | **Score:** | 41.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 180.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MMDSENKPEN | DEDEKINKEA | QDLTKLSSHN | EDGGPVSDVI | ASFPENSMGK | RGFSESSNSD | SVVIGEDRNK | HASKRRKLDE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AEPLKSGKQG | ICRLETSESS | VTEGGIALDE | TGKETFLSDC | TVGGTCLPNA | LSPSCNFSTI | DVVSLKTDTE | KTSAQEMVSL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DLERESPFPP | KEISVSCTIG | NVDTVLKCSI | CGHLFSSCSD | LEKHAESHMQ | QPKEHTCCHC | SHKAESSSAL | HMHIKQAHGP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QKVFSCDLCG | FQCSEENLLN | AHYLGKTHLR | RQNLAARGGF | VQILTKQPFP | KKSRTMATKN | VHSKPRTSKS | IAKNSDSKGL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RNVGSTFKDF | RGSISKQSGS | SSELLVEMMP | SRNTLSQEVE | IVEEHVTSLG | LAQNPENQSR | KLDTLVTSEG | LLEKLESTKN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TLQAAHGNSV | TSRPRPERNI | LVLGNSFRRR | SSTFTLKGQA | KKRFNLLGIK | RGTSETQRMY | MKHLRTQMKT | HDAESVLKHL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EACSSVQRVC | VTTSETQEAE | QGQGSARPPD | SGLHSLTVKP | ASGSQTLCAC | TDCGQVATNR | TDLEIHVKRC | HAREMKFYCR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TCDFSSMSRR | DLDEHLHSNQ | HQQTASVLSC | QCCSFISLDE | INLRDHMKEK | HNMHFLCTPC | NLFFLSEKDV | EEHKATEKHI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NSLVQPKTLQ | SSNSDLVLQT | LPLSTLESEN | AKESMDDSGK | ASQEEPLKSR | VSHGNEVRHS | SKPQFQCKKC | FYKTRSSTVL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TRHIKLRHGQ | DYHFLCKACN | LYSLSKEGME | KHIKRSKHLE | NAKKNNIGLS | FEECIERVCI | GANDKKEEFD | VSGNGRIEGH |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IGVQLQEHSY | LEKGMLASEE | LSQSGGSTKD | DELASTTTPK | RGRPKGNISR | TCSHCGLLAS | SITNLTVHIR | RKHSHQYSYL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| CKVCKYYTVT | KGDMERHCAT | KKHKGRVEIE | ASGKHSSDII | VGPEGGSLEA | GKKNAGSAVT | MSDEHANKPA | ESPTSVLEKP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DRGNSIEAEV | ENVFHSLDGE | VNSHLLDKKE | QISSEPEDFA | QPGDVYSQRD | VTGTGENKCL | HCEFSAHSSA | SLELHVKRKH |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TKEFEFYCMA | CDYYAVTRRE | MTRHAATEKH | KMKRQSYLNS | ANVEAGSADM | SKNIIMPEEE | HQQNSEEFQI | ISGQPSDTLK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SRNAADCSIL | NENTNLDMSK | VLCAADSVEV | ETEEESNFNE | DHSFCETFQQ | APVKDKVRKP | EEMMSLTMSS | NYGSPSRFQN |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ENSGSSALNC | ETAKKNHEIS | NDAGELRVHC | EGEGGNAGDG | GGVVPHRHLC | PVTLDGERSA | ESPVLVVTRI | TREQGNLESG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| GQNRVARGHG | LEDLKGVQED | PVLGNKEILM | NSQHETEFIL | EEDGPASDST | VESSDVYETI | ISIDDKGQAM | YSFGRFDSSI |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| IRIKNPEDGE | LIDQSEEGLI | ATGVRISELP | LKDCAQGVKK | KKSEGSSIGE | STRIRCDDCG | FLADGLSGLN | VHIAMKHPTK |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EKHFHCLLCG | KSFYTESNLH | QHLASAGHMR | NEQASVEELP | EGGATFKCVK | CTEPFDSEQN | LFLHIKGQHE | ELLREVNKYI |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| VEDTEQINRE | REENQGNVCK | YCGKMCRSSN | SMAFLAHIRT | HTGSKPFKCK | ICHFATAQLG | DARNHVKRHL | GMREYKCHVC |
| 1610 | 1620 | 1630 | | | | | |
| GVAFVMKKHL | NTHLLGKHGV | GTPKERQI | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2427 | 1 | 1103.9913 | -10.11 | 2 | 58.6 | 12.6 | 2 | 1541-1559 | K.YCGKMCRSSNSMAFLAHIR.T | Oxidation: 5, 12 |

# Detailed Protein Report

## Protein 197: DNA-directed RNA polymerase III subunit RPC5 isoform 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|384475537 | **Score:** | 41.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 75.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.4 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.76 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.02 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MANEEDDPVV | QEIKPKQQKV | ELEMAIDTLN | PNYCRSKGEQ | IALNVDGACA | DETSTYSSKL | MDKQTFCSSQ | TTSNTSRYAA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ALYRQGELHL | TPLHGILQLR | PSFSYLDKAD | AKHREREAAN | EAGDSSQDEA | EDDVKQITVR | FSRPESEQAR | QRRVQSYEFL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QKKHAEEPWV | HLHYYGLRDS | RSEHERQYLL | CPGSSGVENT | ELVKSPSEYL | MMLMPPSQEE | EKDKPVAPSN | VLSMAQLRTL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PLADQIKILM | KNVKVMPFAN | LMSLLGPSID | SVAVLRGIQK | VAMLVQGNWV | VKSDILYPKD | SSSPHSGVPA | EVLCRGRDFV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MWKFTQSRWV | VRKEVATVTK | LCAEDVKDFL | EHMAVVRINK | GWEFILPYDG | EFIKKHPDVV | QRQHMLWTGI | QAKLEKVYNL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VKETMPKKPD | AQSGPAGLVC | GDQRIQVAKT | KAQQNHALLE | RELQRRKEQL | RVPAVPPGVR | IKEEPVSEEG | EEDEEQEAEE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EPMDTSPSGL | HSKLANGLPL | GRAAGTDSFN | GHPPQGCAST | PVARELKAFV | EATFQRQFVL | TLSELKRLFN | LHLASLPPGH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TLFSGISDRM | LQDTVLAAGC | KQILVPFPPQ | TAASPDEQKV | FALWESGDMS | DQHRQVLLEI | FSKNYRVRRN | MIQSRLTQEC |
| 650 | 660 | 670 | 680 | | | | |
| GEDLSKQEVD | KVLKDCCVSY | GGMWYLKGTV | QS | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 887 | 1 | 491.6754 | -177.12 | 2 | 40.6 | 13.5 | 2 | 109-116 | K.ADAKHRER.E | | |
| 2616 | 1 | 742.3664 | -111.86 | 2 | 62.8 | 14.6 | 1 | 239-251 | R.TLPLADQIKILMK.N | | |
| 828 | 1 | 897.4861 | 96.86 | 2 | 40.4 | 13.7 | 0 | 600-614 | K.VFALWESGDMSDQHR.Q | Oxidation: 10 | WUP:QUP 2.02<br>QU:MU 0.76 |

# Detailed Protein Report

## Protein 198: PREDICTED: uncharacterized protein KIAA1109 isoform X7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530378301 | **Score:** | 41.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 553.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 2 |

### Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 2.25 | **CV:** 0.00 % | **No. of Peptides:** 1 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MDQRKNESIV PSITQLEDFL TEHNSNVVWL LVATILSCGW IIYLTYYNSR NVGLILTLVL NRLYKHGYIH IGSFSFSVLS
        90        100        110        120        130        140        150        160
GKVMVREIYY ITEDMSIRIQ DGFIIFRWWK MYNPKQKQHD PKAETRLYIT VNDFEFHVYN RSDLYGRLQE LFGLEPTIIP
       170        180        190        200        210        220        230        240
PKKDDDKTRE IGRTRTQSKI ERVKVKTESQ DPTSSWRSLI PVIKVNVSTG RLAFGNHYQP QTLCINFDDA FLTYTTKPPS
       250        260        270        280        290        300        310        320
SHLDQFMHIV KGKLENVRVM LVPSPRYVGL QNDEPPRLMG EGFVVMQSND VDIYYYMDEP GLVPEETEEN IEGEMSSEDC
       330        340        350        360        370        380        390        400
KLQDLPPCWG LDIVCGKGTD FNYGPWADRQ RDCLWKFFFP PDYQVLKVSE IAQPGRPRQI LAFELRMNII ADATIDLLFT
       410        420        430        440        450        460        470        480
KNRETNAVHV NVGAGSYLEI NIPMTVEENG YTPAIKGQLL HVDATTSMQY RTLLEAEMLA FHINASYPRI WNMPQTWQCE
       490        500        510        520        530        540        550        560
LEVYKATYHF IFAQKNFFTD LIQDWSSDSP PDIFSFVPYT WNFKIMFHQF EMIWAANQHN WIDCSTKQQE NVYLAACGET
       570        580        590        600        610        620        630        640
LNIDFSLPFT DFVPATCNTK FSLRGEDVDL HLFLPDCHPS KYSLFMLVKN CHPNKMIHDT GIPAECQSGQ KTVKPKWRNV
       650        660        670        680        690        700        710        720
TQEKSGWVEC WTVPSVMLTI DYTWHPIYPQ KADEQLKQSL SEMEETMLSV LRPSQKTSDR VVSSPSTSSR PPIDPSELPP
       730        740        750        760        770        780        790        800
DKLHVEMELS PDSQITLYGP LLNAFLCIKE NYFGEDDMYM DFEEVISSPV LSLSTSSSSG WTAVGMENDK KENEGSAKSI
       810        820        830        840        850        860        870        880
HPLALRPWDI TVLVNLYKVH GRLPVHGTTD GPECPTAFLE RLCFEMKKGF RETMLQLILS PLNVFVSDNY QQRPPVDEVL
       890        900        910        920        930        940        950        960
REGHINLSGL QLRAHAMFSA EGLPLGSDSL EYAWLIDVQA GSLTAKVTAP QLACLLEWGQ TFVFHVVCRE YELERPKSVI
       970        980        990       1000       1010       1020       1030       1040
ICQHGIDRRF CESKLSCIPG PCPTSDDLKY TMIRLAVDGA DIYIVEHGCA TNIKMGAIRV ANCNLHNQSV GEGISAAIQD
      1050       1060       1070       1080       1090       1100       1110       1120
FQVRQYIEQL NNCRIGLQPA VLRRAYWLEA GSANLGLITV DIALAADHHS KHEAQRHFLE THDARTKRLW FLWPDDILKN
      1130       1140       1150       1160       1170       1180       1190       1200
KRCRNKCGCL GGCRFFGGTV TGLDFFKLEE LTPSSSSAFS STSAESDMYY GQSLLQPGEW IITKEIPKII DGNVNGMKRK
      1210       1220       1230       1240       1250       1260       1270       1280
EWENKSVGIE VERKTQHLSL QVPLRSHSSS SSSEENSSSS AAQPLLAGEK ESPSSVADDH LVQKEFLHGT KRDDGQASIP
      1290       1300       1310       1320       1330       1340       1350       1360
TEISGNSPVS PNTQDKSVGQ SPLRSPLKRQ ASVCSTRLGS TKSLTAAFYG DKQPVTVGVQ FSSDVSRSDE NVLDSPKQRR
      1370       1380       1390       1400       1410       1420       1430       1440
SFGSFPYTPS ADSNSFHQYR SMDSSMSMAD SEAYFSAAEE FEPISSDEGP GTYPGRKKKK KQTQQIDYSR GSIYHSVEGP
      1450       1460       1470       1480       1490       1500       1510       1520
LTGHGESIQD SRTLPFKTHP SQASFVSALG GEDDVIEHLY IVEGEKTVES EQITPQQPVM NCYQTYLTQF QVINWSVKHP
      1530       1540       1550       1560       1570       1580       1590       1600
TNKRTSKSSL HRPLDLDTPT SEESSSSFEQ LSVPTFKVIK QGLTANSLLD RGMQLSGSTS NTPYTPLEKK LADNTDDETL
      1610       1620       1630       1640       1650       1660       1670       1680
TEEWTLDQPV SQTRTTAIVE VKGTVDIVLT PLVAEALDRY IEAMVHCAST RHPAAIVDDL HAKVLREAVQ NSKTTFSENL
      1690       1700       1710       1720       1730       1740       1750       1760
SSKQDIRGTK TEQSTIGTTN QGQAQTNLTM KQDNVTIKGL QTNVSIPKVN LCLLQASVEE SPTTAPSRSV THVSLVALCF
      1770       1780       1790       1800       1810       1820       1830       1840
DRIATQVRMN RGVVEETSNN AEPGRTSNFD RYVHATKMQP QSSGSLRSNA GAEKGKEIAA KLNIHRVHGQ LRGLDTTDIG
      1850       1860       1870       1880       1890       1900       1910       1920
TCAITAIPFE KSKVLFTLEE LDEFTFVDET DQQAVPDVTR IGPSQEKWGW IMFECGLENL TIKGGRQSGA VLYNSFGIMG
      1930       1940       1950       1960       1970       1980       1990       2000
KASDTERGGV LTSNNSSDSP TGSGYNTDVS DDNLPCDRTS PSSDLNGNSV SDEQDEGVES DDLKKDLPLM PPPPDSCSMK
      2010       2020       2030       2040       2050       2060       2070       2080
LTIKEIWFSF AAPTNVRSHT HAFSRQLNLL STATPAVGAW LVPIDQLKSS LNKLETEGTL RICAVMGCIM TEALENKSVH
      2090       2100       2110       2120       2130       2140       2150       2160
FPLRSKYNRL TKVARFLQEN PSCLLCNILH HYLHQANYSI IDDATMSDGL PALVTLKKGL VALARQWMKF IVVTPAFKGV
      2170       2180       2190       2200       2210       2220       2230       2240
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 117 | 1 | 774.3916 | -26.77 | 3 | 31.2 | 15.7 | 1 | 66-86 | K.HGYIHIGSFSFSVLSGKVMVR.E | | |
| 1348 | 1 | 669.3232 | -39.50 | 2 | 46.5 | 13.8 | 2 | 116-126 | K.QKQHDPKAETR.L | | QU:MU 2.25 |

# Detailed Protein Report

## Protein 199: ubiquitin carboxyl-terminal hydrolase 32 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|22550104 | **Score:** | 41.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 181.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.46 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 4.63 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGAKESRIGF | LSYEEALRRV | TDVELKRLKD | AFKRTCGLSY | YMGQHCFIRE | VLGDGVPPKV | AEVIYCSFGG | TSKGLHFNNL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IVGLVLLTRG | KDEEKAKYIF | SLFSSESGNY | VIREEMERML | HVVDGKVPDT | LRKCFSEGEK | VNYEKFRNWL | FLNKDAFTFS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RWLLSGGVYV | TLTDDSDTPT | FYQTLAGVTH | LEESDIIDLE | KRYWLLKAQS | RTGRFDLETF | GPLVSPPIRP | SLSEGLFNAF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DENRDNHIDF | KEISCGLSAC | CRGPLAERQK | FCFKVFDVDR | DGVLSRVELR | DMVVALLEVW | KDNRTDDIPE | LHMDLSDIVE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GILNAHDTTK | MGHLTLEDYQ | IWSVKNVLAN | EFLNLLFQVC | HIVLGLRPAT | PEEEGQIIRG | WLERESRYGL | QAGHNWFIIS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MQWWQQWKEY | VKYDANPVVI | EPSSVLNGGK | YSFGTAAHPM | EQVEDRIGSS | LSYVNTTEEK | FSDNISTASE | ASETAGSGFL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YSATPGADVC | FARQHNTSDN | NNQCLLGANG | NILLHLNPQK | PGAIDNQPLV | TQEPVKATSL | TLEGGRLKRT | PQLIHGRDYE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MVPEPVWRAL | YHWYGANLAL | PRPVIKNSKT | DIPELELFPR | YLLFLRQQPA | TRTQQSNIWV | NMGNVPSPNA | PLKRVLAYTG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CFSRMQTIKE | IHEYLSQRLR | IKEEDMRLWL | YNSENYLTLL | DDEDHKLEYL | KIQDEQHLVI | EVRNKDMSWP | EEMSFIANSS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KIDRHKVPTE | KGATGLSNLG | NTCFMNSSIQ | CVSNTQPLTQ | YFISGRHLYE | LNRTNPIGMK | GHMAKCYGDL | VQELWSGTQK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NVAPLKLRWT | IAKYAPRFNG | FQQQDSQELL | AFLLDGLHED | LNRVHEKPYV | ELKDSDGRPD | WEVAAEAWDN | HLRRNRSIVV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DLFHGQLRSQ | VKCKTCGHIS | VRFDPFNFLS | LPLPMDSYMH | LEITVIKLDG | TTPVRYGLRL | NMDEKYTGLK | KQLSDLCGLN |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SEQILLAEVH | GSNIKNFPQD | NQKVRLSVSG | FLCAFEIPVP | VSPISASSPT | QTDFSSSPST | NEMFTLTTNG | DLPRPIFIPN |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GMPNTVVPCG | TEKNFTNGMV | NGHMPSLPDS | PFTGYIIAVH | RKMMRTELYF | LSSQKNRPSL | FGMPLIVPCT | VHTRKKDLYD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| AVWIQVSRLA | SPLPPQEASN | HAQDCDDSMG | YQYPFTLRVV | QKDGNSCAWC | PWYRFCRGCK | IDCGEDRAFI | GNAYIAVDWD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PTALHLRYQT | SQERVVDEHE | SVEQSRRAQA | EPINLDSCLR | AFTSEEELGE | NEMYYCSKCK | THCLATKKLD | LWRLPPILII |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| HLKRFQFVNG | RWIKSQKIVK | FPRESFDPSA | FLVPRDPALC | QHKPLTPQGD | ELSEPRILAR | EVKKVDAQSS | AGEEDVLLSK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| SPSSLSANII | SSPKGSPSSS | RKSGTSCPSS | KNSSPNSSPR | TLGRSKGRLR | LPQIGSKNKL | SSSKENLDAS | KENGAGQICE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LADALSRGHV | LGGSQPELVT | PQDHEVALAN | GFLYEHEACG | NGYSNGQLGN | HSEEDSTDDQ | REDTRIKPIY | NLYAISCHSG |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ILGGGHYVTY | AKNPNCKWYC | YNDSSCKELH | PDEIDTDSAY | ILFYEQQGID | YAQFLPKTDG | KKMADTSSMD | EDFESDYKKY |
| 1610 | | | | | | | |
| CVLQ | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 598 | 1 | 823.8884 | -6.53 | 2 | 37.5 | 15.8 | 0 | 1432-1447 | K.ENGAGQICELADALSR.G |  | WUP:QUP 4.63<br>QU:MU 0.46 |

# Detailed Protein Report

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**Protein 200:** **cGMP-specific 3',5'-cyclic phosphodiesterase isoform 1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|61744435 | **Score:** | 41.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 99.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.6 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MERAGPSFGQ | QRQQQQPQQQ | KQQQRDQDSV | EAWLDDHWDF | TFSYFVRKAT | REMVNAWFAE | RVHTIPVCKE | GIRGHTESCS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CPLQQSPRAD | NSAPGTPTRK | ISASEFDRPL | RPIVVKDSEG | TVSFLSDSEK | KEQMPLTPPR | FDHDEGDQCS | RLLELVKDIS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SHLDVTALCH | KIFLHIHGLI | SADRYSLFLV | CEDSSNDKFL | ISRLFDVAEG | STLEEVSNNC | IRLEWNKGIV | GHVAALGEPL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NIKDAYEDPR | FNAEVDQITG | YKTQSILCMP | IKNHREEVVG | VAQAINKKSG | NGGTFTEKDE | KDFAAYLAFC | GIVLHNAQLY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ETSLLENKRN | QVLLDLASLI | FEEQQSLEVI | LKKIAATIIS | FMQVQKCTIF | IVDEDCSDSF | SSVFHMECEE | LEKSSDTLTR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EHDANKINYM | YAQYVKNTME | PLNIPDVSKD | KRFPWTTENT | GNVNQQCIRS | LLCTPIKNGK | KNKVIGVCQL | VNKMEENTGK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VKPFNRNDEQ | FLEAFVIFCG | LGIQNTQMYE | AVERAMAKQM | VTLEVLSYHA | SAAEEETREL | QSLAAAVVPS | AQTLKITDFS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FSDFELSDLE | TALCTIRMFT | DLNLVQNFQM | KHEVLCRWIL | SVKKNYRKNV | AYHNWRHAFN | TAQCMFAALK | AGKIQNKLTD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LEILALLIAA | LSHDLDHRGV | NNSYIQRSEH | PLAQLYCHSI | MEHHHFDQCL | MILNSPGNQI | LSGLSIEEYK | TTLKIIKQAI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LATDLALYIK | RRGEFFELIR | KNQFNLEDPH | QKELFLAMLM | TACDLSAITK | PWPIQQRIAE | LVATEFFDQG | DRERKELNIE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PTDLMNREKK | NKIPSMQVGF | IDAICLQLYE | ALTHVSEDCF | PLLDGCRKNR | QKWQALAEQQ | EKMLINGESG | QAKRN |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1989 | 1 | 616.7715 | -62.66 | 2 | 54.8 | 10.4 | 1 | 2-12 | M.ERAGPSFGQQR.Q | |
| 2072 | 1 | 1071.4033 | -85.02 | 2 | 56.3 | 13.5 | 1 | 70-88 | K.EGIRGHTESCSCPLQQSPR.A | Carbamidomethyl: 10 |

# Detailed Protein Report

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## Protein 201: cingulin-like protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|31982906 | **Score:** | 41.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 149.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 3.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|356874770 | refseq_human(refseq_human_20140103.fasta) | cingulin-like protein 1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MELYFGEYQH | VQQEYGVHLR | LASDDTQKSR | SSQNSKAGSY | GVSIRVQGID | GHPYIVLNNT | ERCLAGTSFS | ENGPPFPPPV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| INNLPLHSSN | GSVPKENSEE | LQLPENPYAQ | PSPIRNLKQP | LLHEGKNGVL | DRKDGSVKPS | HLLNFQRHPE | LLQPYDPEKN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ELNLQNHQPS | ESNWLKTLTE | EGINNKKPWT | CFPKPSNSQP | TSPSLEDPAK | SGVTAIRLCS | SVVIEDPKKQ | TSVCVNVQSC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TKERVGEEAL | FTSGRPLTAH | SPHAHPETKK | TRPDVLPFRR | QDSAGPVLDG | ARSRRSSSSS | TTPTSANSLY | RFLLDDQECA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IHADNVNRHE | NRRYIPFLPG | TGRDIDTGSI | PGVDQLIEKF | DQKPGLQRRG | RSGKRNRINT | DDRKRSRSVD | SAFPFGLQGN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SEYLIEFSRN | LGKSSEHLLR | PSQVCPQRPL | SQERRGKQSV | GRTFAKLQGA | AHGASCAHSR | PPQPNIDGKV | LETEGSQEST |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VIRAPSLGAQ | SKKEEEVKTA | TATLMLQNRA | TATSPDSGAK | KISVKTFPSA | SNTQATPDLL | KGQQELTQQT | NEETAKQILY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NYLKEGSTDN | DDATKRKVNL | VFEKIQTLKS | RAAGSAQGNN | QACNSTSEVK | DLLEQKSKLT | IEVAELQRQL | QLEVKNQQNI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KEERERMRAN | LEELRSQHNE | KVEENSTLQQ | RLEESEGELR | KNLEELFQVK | MEREQHQTEI | RDLQDQLSEM | HDELDSAKRS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EDREKGALIE | ELLQAKQDLQ | DLLIAKEEQE | DLLRKREREL | TALKGALKEE | VSSHDQEMDK | LKEQYDAELQ | ALRESVEEAT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KNVEVLASRS | NTSEQDQAGT | EMRVKLLQEE | NEKLQGRSEE | LERRVAQLQR | QIEDLKGDEA | KAKETLKKYE | GEIRQLEEAL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VHARKEEKEA | VSARRALENE | LEAAQGNLSQ | TTQEQKQLSE | KLKEESEQKE | QLRRLKNEME | NERWHLGKTI | EKLQKEMADI |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VEASRTSTLE | LQNQLDEYKE | KNRRELAEMQ | RQLKEKTLEA | EKSRLTAMKM | QDEMRLMEEE | LRDYQRAQDE | ALTKRQLLEQ |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TLKDLEYELE | AKSHLKDDRS | RLVKQMEDKV | SQLEMELEEE | RNNSDLLSER | ISRSREQMEQ | LRNELLQERA | ARQDLECDKI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SLERQNKDLK | SRIIHLEGSY | RSSKEGLVVQ | MEARIAELED | RLESEERDRA | NLQLSNRRLE | RKVKELVMQV | DDEHLSLTDQ |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KDQLSLRLKA | MKRQVEEAEE | EIDRLESSKK | KLQRELEEQM | DMNEHLQGQL | NSMKKDLRLK | KLPSKVLDDM | DDDDDLSTDG |
| 1290 | 1300 | 1310 | | | | | |
| GSLYEAPVSY | TFSKDSTVAS | QI | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1287 | 1 | 611.9489 | -57.31 | 3 | 46.2 | 10.8 | 1 | 494-509 | K.EEEVKTATATLMLQNR.A | |

# Detailed Protein Report

**Protein 202:** **PREDICTED: neuroblastoma breakpoint family member 4 isoform X2 [Homo sapiens]**

| | | | | |
|---|---|---|---|---|
| **Accession:** | gi\|578798443 | | **Score:** | 41.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | | **MW [kDa]:** | 70.3 |
| **Database Date:** | 2015-11-30 | | **pI:** | 4.9 |
| | | | **Sequence Coverage [%]:** | 5.9 |
| | | | **No. of unique Peptides:** | 3 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTPPPSNSVI | ATADRYLVRW | LLPPSLLSES | ELQAVPSALS | SGIPVPVFAV | KDSKVLCRVH | QLFLNFPGST | SSATNVSMVV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SADPLSSERA | EMNILEINQE | LRSQLAESNQ | QFRDLKEKFL | ITQATAYSLA | NQLKKYKCEE | YKDIIDSVLR | DELQSMEKLA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EKLRQAEELR | QYKALVHSQA | KELTQLREKL | REGRDASRWL | NKHLKTLLTP | DDPDKSQGQD | LREQLAEGHR | LAEHLVHKLS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PENDEDEDED | EDDKDEEVEK | VQESPAPRHH | DKSNSYRHRE | VSFLALDEQK | VCSAQDVARD | YSNPKWDETS | LGFLEKQSDL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EEVKGQETVA | PRLSRGPLRV | DKHEIPQESL | DGCCLTPSIL | PDLTPSYHPY | WSTLYSFEDK | QVSLALVDKI | KKDQEEIEDQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SPPCPRLSQE | LPEVKEQEVP | EDSVNEVYLT | PSVHHDVSDC | HQPYSSTLSS | LEDQLACSAL | DVASPTEAAC | PQGTWSGDLS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HHQSEVQVSQ | AQLEPSTLVP | SCLRLQLDQG | FHCGNGLAQR | GLSSTTCSFS | ANADSGNQWP | FQELVLEPSL | GMKNPPQLED |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| DALEGSASNT | QGRQVTGRIR | ASLVLILKTI | RRRLPFSKWR | LAFRFAGPHA | ESAEIPNTAG | RTQRMAG | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2547 | 4 | 1044.5458 | -3.00 | 2 | 62.5 | 15.8 | 1 | 1-19 | -.MTPPPSNSVIATADRYLVR.W | |
| 573 | 2 | 666.3169 | -41.31 | 2 | 37.1 | 12.9 | 2 | 192-202 | R.EGRDASRWLNK.H | |
| 601 | 1 | 460.1164 | -243.14 | 2 | 35.9 | 12.8 | 1 | 273-279 | K.SNSYRHR.E | |

# Detailed Protein Report

## Protein 203: DC-STAMP domain-containing protein 1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|219521926 | **Score:** | 41.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 77.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 10.0 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDIKHHQNGT | RGQRRKQPHT | TVQRLLTWGL | PVSCSWFLWR | QPGEFPVTAL | LLGAGAGGLL | AIGLGAMGWG | TSPHIRCASL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LLVPKMLGKE | GRLFVLGYAL | AAIYVGPVAN | LRHNLNNVIA | SLGCTVELQI | NNTRAAWRIS | TAPLRAMFKD | LLSSKELLRA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ETRNISATFE | DLDAQVNSET | GYTPEDTMDS | GETAQGREAR | QAPASRLHLS | TQKMYELKTK | LRCSYVVNQA | ILSCRRWFDR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KHEQCMKHIW | VPLLTHLLCL | PMKFKFFCGI | AKVMEVWCRN | RIPVEGNFGQ | TYDSLNQSIR | GLDGEFSANI | DFKEEKQAGV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LGLNTSWERV | STEVRDYVYR | QEARLEWALG | LLHVLLSCTF | LLVLHASFSY | MDSYNHDIRF | DNIYISTYFC | QIDDRRKKLG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KRTLLPLRKA | EEKTVIFPCK | PTIQASEMSN | VVRELLETLP | ILLLLVVLCG | LDWALYSIFD | TIRHHSFLQY | SFRSSHKLEV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KVGGDSMLAR | LLRKTIGALN | TSSETVMESN | NMPCLPQPVG | LDARAYWRAA | VPIGLLVCLC | LLQAFGYRLR | RVIAAFYFPK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| REKKRILFLY | NDLLKKRAAF | TKLRRAAILR | RERQQKAPRH | PLADILHRGC | PLLRRWLCRR | CVVCQAPETP | ESYVCRTLDC |
| 650 | 660 | 670 | 680 | 690 | | | |
| EAVYCWSCWD | DMRQRCPVCT | PREELSSSAF | SDSNDDTAYA | G | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2414 | 1 | 964.4799 | -71.72 | 3 | 60.6 | 15.7 | 2 | 86-112 | K.MLGKEGRLFVLGYALAAIYVGPVANLR.H | |
| 748 | 1 | 1010.1872 | -33.67 | 3 | 39.3 | 12.9 | 2 | 248-272 | K.HIWVPLLTHLLCLPMKFKFFCGIAK.V | Carbamidomethyl: 21;<br>Oxidation: 15 |
| 2267 | 1 | 920.9067 | 1.92 | 2 | 58.8 | 12.9 | 0 | 621-636 | R.CVVCQAPETPESYVCR.T | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 204: E3 ubiquitin-protein ligase listerin [Homo sapiens]

**Accession:** gi|231573214
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 41.5
**MW [kDa]:** 205.0
**pI:** 6.1
**Sequence Coverage [%]:** 1.4
**No. of unique Peptides:** 2

```
        10          20          30          40          50          60          70          80
MDRVGGGKGP  GGSYYRVSSS  AARSRKLCPG  RVNRGLSAQS  TAATATMGGK  NKQRTKGNLR  PSNSGRAAEL  LAKEQGTVPG
        90         100         110         120         130         140         150         160
FIGFGTSQSD  LGYVPAIQGA  EEIDSLVDSD  FRMVLRKLSK  KDVTTKLKAM  QEFGTMCTER  DTETVKGVLP  YWPRIFCKIS
       170         180         190         200         210         220         230         240
LDHDRRVREA  TQQAFEKLIL  KVKKQLAPYL  KSLMGYWLMA  QCDTYTPAAF  AAKDAFEAAF  PPSKQPEAIA  FCKDEITSVL
       250         260         270         280         290         300         310         320
QDHLIKETPD  TLSDPQTVPE  EEREAKFYRV  VTCSLLALKR  LLCLLPDNEL  DSLEEKFKSL  LSQNKFWKYG  KHSVPQIRSA
       330         340         350         360         370         380         390         400
YFELVSALCQ  RIPQLMKEEA  SKVSPSVLLS  IDDSDPIVCP  ALWEAVLYTL  TTIEDCWLHV  NAKKSVFPKL  STVIREGGRG
       410         420         430         440         450         460         470         480
LATVIYPYLL  PFISKLPQSI  TNPKLDFFKN  FLTSLVAGLS  TERTKTSSLE  SSAVISAFFE  CLRFIMQQNL  GEEEIEQMLV
       490         500         510         520         530         540         550         560
NDQLIPFIDA  VLKDPGLQHG  QLFNHLAETL  SSWEAKADTE  KDEKTAHNLE  NVLIHFWERL  SEICVAKISE  PEADVESVLG
       570         580         590         600         610         620         630         640
VSNLLQVLQK  PKSSLKSSKK  KNGKVRFADE  ILESNKENEK  CVSSEGEKIE  GWELTTEPSL  THNSSGLLSP  LRKKPLEDLV
       650         660         670         680         690         700         710         720
CKLADISINY  VNERKSEQHL  RFLSTLLDSF  SSSRVFKMLL  GDEKQSIVQA  KPLEIAKLVQ  KNPAVQFLYQ  KLIGWLNEDQ
       730         740         750         760         770         780         790         800
RKDFGFLVDI  LYSALRCCDN  DMERKKVLDD  LTKVDLKWNS  LLKIIEKACP  SSDKHALVTP  WLKGDILGEK  LVNLADCLCN
       810         820         830         840         850         860         870         880
EDLESRVSSE  SHFSERWTLL  SLVLSQHVKN  DYLIGDVYVE  RIIVRLHETL  FKTKKLSEAE  SSDSSVSFIC  DVAYNYFSSA
       890         900         910         920         930         940         950         960
KGCLLMPSSE  DLLLTLFQLC  AQSKEKTHLP  DFLICKLKNT  WLSGVNLLVH  QTDSSYKEST  FLHLSALWLK  NQVQASSLDI
       970         980         990        1000        1010        1020        1030        1040
NSLQVLLSAV  DDLLNTLLES  EDSYLMGVYI  GSVMPNDSEW  EKMRQSLPMQ  WLHRPLLEGR  LSLNYECFKT  DFKEQDIKTL
      1050        1060        1070        1080        1090        1100        1110        1120
PSHLCTSALL  SKMVLIALRK  ETVLENNELE  KIIAELLYSL  QWCEELDNPP  IFLIGFCEIL  QKMNITYDNL  RVLGNTSGLL
      1130        1140        1150        1160        1170        1180        1190        1200
QLLFNRSREH  GTLWSLIIAK  LILSRSISSD  EVKPHYKRKE  SFFPLTEGNL  HTIQSLCPFL  SKEEKKEFSA  QCIPALLGWT
      1210        1220        1230        1240        1250        1260        1270        1280
KKDLCSTNGG  FGHLAIFNSC  LQTKSIDDGE  LLHGILKIII  SWKKEHEDIF  LFSCNLSEAS  PEVLGVNIEI  IRFLSLFLKY
      1290        1300        1310        1320        1330        1340        1350        1360
CSSPLAESEW  DFIMCSMLAW  LETTSENQAL  YSIPLVQLFA  CVSCDLACDL  SAFFDSTTLD  TIGNLPVNLI  SEWKEFFSQG
      1370        1380        1390        1400        1410        1420        1430        1440
IHSLLLPILV  TVTGENKDVS  ETSFQNAMLK  PMCETLTYIS  KEQLLSHKLP  ARLVADQKTN  LPEYLQTLLN  TLAPLLLFRA
      1450        1460        1470        1480        1490        1500        1510        1520
RPVQIAVYHM  LYKLMPELPQ  YDQDNLKSYG  DEEEEPALSP  PAALMSLLSI  QEDLLENVLG  CIPVGQIVTI  KPLSEDFCYV
      1530        1540        1550        1560        1570        1580        1590        1600
LGYLLTWKLI  LTFFKAASSQ  LRALYSMYLR  KTKSLNKLLY  HLFRLMPENP  TYAETAVEVP  NKDPKTFFTE  ELQLSIRETT
      1610        1620        1630        1640        1650        1660        1670        1680
MLPYHIPHLA  CSVYHMTLKD  LPAMVRLWWN  SSEKRVFNIV  DRFTSKYVSS  VLSFQEISSV  QTSTQLFNGM  TVKARATTRE
      1690        1700        1710        1720        1730        1740        1750        1760
VMATYTIEDI  VIELIIQLPS  NYPLGSIIVE  SGKRVGVAVQ  QWRNWMLQLS  TYLTHQNGSI  MEGLALWKNN  VDKRFEGVED
      1770        1780        1790        1800        1810        1820
CMICFSVIHG  FNYSLPKKAC  RTCKKKFHSA  CLYKWFTSSN  KSTCPLCRET  FF
```

| Cmpd. | No. of | m/z meas. | Δ m/z | z | Rt | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

| | Cmpds. | | [ppm] | | [min] | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 57 | 1 | 731.6721 | -129.70 | 3 | 30.4 | 30.4 | 2 | 1127-1145 | R.SREHGTLWSLIIAKLILSR.S | |
| 2506 | 2 | 817.4892 | 80.15 | 1 | 61.9 | 11.1 | 0 | 1620-1626 | K.DLPAMVR.L | Oxidation: 5 |

# Detailed Protein Report

## Protein 205: PREDICTED: palladin isoform X5 [Homo sapiens]

**Accession:** gi|530377424
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 41.5
**MW [kDa]:** 138.1
**pI:** 8.0
**Sequence Coverage [%]:** 3.1
**No. of unique Peptides:** 2

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 3.61 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.29 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSGTSSHESF | YDSLSDMQEE | SKNTDFFPGL | SAFLSQEEIN | KSLDLARRAI | ADSETEDFDS | EKEISQIFST | SPASLCEHPS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HKETKLGEHA | SRRPQDNRST | PVQPLAEKQT | KSISSPVSKR | KPAMSPLLTR | PSYIRSLRKA | EKRGAKTPST | NVKPKTPHQR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KGGPQSQLCD | KAANLIEELT | SIFKAAKPRN | RSPNGESSSP | DSGYLSPKNQ | PSALLSASAS | QSPMEDQGEM | EREVKSPGAR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HCYQDNQDLA | VPHNRKSHPQ | PHSALHFPAA | PRFIQKLRSQ | EVAEGSRVYL | ECRVTGNPTP | RVRWFCEGKE | LHNTPDIQIH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CEGGDLHTLI | IAEAFEDDTG | RYTCLATNPS | GSDTTSAEVF | IEGASSTDSD | SESLAFKSRA | GAMPQAQKKT | TSVSLTIGSS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SPKTGVTTAV | IQPLSVPVQQ | VHSPTSYLCR | PDGTTTAYFP | PVFTKELQNT | AVAEGQVVVL | ECRVRGAPPL | QVQWFRQGSE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IQDSPDFRIL | QKKPRSTAEP | EEICTLVIAE | TFPEDAGIFT | CSARNDYGSA | TSTAQLVVTS | ANTENCSYES | MGESNNDHFQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HFPPPPPILE | TSSLELASKK | PSEIQQVNNP | ELGLSRAALQ | MQFNAAERET | NGVHPSRGVN | GLINGKANSN | KSLPTPAVLL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SPTKEPPPLL | AKPKLDPLKL | QQLQNQIRLE | QEAGARQPPP | APRSAPPSPP | FPPPPAFPEL | AACTPPASPE | PMSALASRSA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PAMQSSGSFN | YARPKQFIAA | QNLGPASGHG | TPASSPSSSS | LPSPMSPTPR | QFGRAPVPPF | AQPFGAEPEA | PWGSSSPSPP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PPPPPVFSPT | AAFPVPDVFP | LPPPPPPLPS | PGQASHCSSP | ATRFGHSQTP | AAFLSALLPS | QPPPAAVNAL | GLPKGVTPAG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| FPKKASRTAR | IASDEEIQGT | KDAVIQDLER | KLRFKEDLLN | NGQPIYWFKD | GKQISPKSDH | YTIQRDLDGT | CSLHTTASTL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DDDGNYTIMA | ANPQGRISCT | GRLMVQAVNQ | RGRSPRSPSG | HPHVRRPRSR | SRDSGDENEP | IQERFFRPHF | LQAPGDLTVQ |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EGKLCRMDCK | VSGLPTPDLS | WQLDGKPVRP | DSAHKMLVRE | NGVHSLIIEP | VTSRDAGIYT | CIATNRAGQN | SFSLELVVAA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KEAHKPPVFI | EKLQNTGVAD | GYPVRLECRV | LGVPPPQIFW | KKENESLTHS | TDRVSMHQDN | HGYICLLIQG | ATKEDAGWYT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VSAKNEAGIV | SCTARLDVYT | QWHQQSQSTK | PKKVRPSASR | YAALSDQGLD | IKAAFQPEAN | PSHLTLNTAL | VESEDL |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2009 | 2 | 945.8529 | -132.43 | 2 | 55.0 | 12.3 | 1 | 1133-1149 | K.LQNTGVADGYPVRLECR.V | | |
| 684 | 1 | 450.6291 | -317.71 | 2 | 37.0 | 12.1 | 1 | 1233-1240 | K.KVRPSASR.Y | | WUP:QUP 0.29<br>QU:MU 3.61 |

# Detailed Protein Report

## Protein 206: PREDICTED: forkhead box protein P3 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578838031 | **Score:** | 41.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.7 |
| | | **Sequence Coverage [%]:** | 9.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTRKGQRKKP | KISKFPFKSH | NQEKEKHRER | EKKNYENPSP | PRDYQRTHSS | KKIWIIRRER | SAASTPYSVV | FLLGIKAKLF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LIRDSFPQAR | LILFCQSTSP | SLPLDKDPMP | NPRPGKPSAP | SLALGPSPGA | SPSWRAAPKA | SDLLGARGPG | GTFQGRDLRG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GAHASSSSLN | PMPPSQLQLS | TVDAHARTPV | LQVHPLESPA | MISLTPPTTA | TGVFSLKARP | GLPPGINVAS | LEWVSREPAL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LCTFPNPSAP | RKDSTLSAVP | QSSYPLLANG | VCKWPGCEKV | FEEPEDFLKH | CQADHLLDEK | GRAQCLLQRE | MVQSLEQQLV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LEKEKLSAMQ | AHLAGKMALT | KASSVASSDK | GSCCIVAAGS | QGPVVPAWSG | PREAPDSLFA | VRRHLWGSHG | NSTFPEFLHN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MDYFKFHNMR | PPFTYATLIR | WAILEAPEKQ | RTLNEIYHWF | TRMFAFFRNH | PATWKNAIRH | NLSLHKCFVR | VESEKGAVWT |
| 490 | 500 | 510 | | | | | |
| VDELEFRKKR | SQRPSRCSNP | TPGP | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 14 | 1 | 712.9876 | -118.49 | 3 | 29.1 | 16.9 | 2 | 59-78 | R.ERSAASTPYSVVFLLGIKAK.L | |

# Detailed Protein Report

**Protein 207:** **endonuclease 8-like 3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|157388969 | **Score:** | 41.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 67.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVEGPGCTLN | GEKIRARVLP | GQAVTGVRGS | ALRSLQGRAL | RLAASTVVVS | PQAAALNNDS | SQNVLSLFNG | YVYSGVETLG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KELFMYFGPK | ALRIHFGMKG | FIMINPLEYK | YKNGASPVLE | VQLTKDLICF | FDSSVELRNS | MESQQRIRMM | KELDVCSPEF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SFLRAESEVK | KQKGRMLGDV | LMDQNVLPGV | GNIIKNEALF | DSGLHPAVKV | CQLTDEQIHH | LMKMIRDFSI | LFYRCRKAGL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ALSKHYKVYK | RPNCGQCHCR | ITVCRFGDNN | RMTYFCPHCQ | KENPQHVDIC | KLPTRNTIIS | WTSSRVDHVM | DSVARKSEEH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WTCVVCTLIN | KPSSKACDAC | LTSRPIDSVL | KSEENSTVFS | HLMKYPCNTF | GKPHTEVKIN | RKTAFGTTTL | VLTDFSNKSS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TLERKTKQNQ | ILDEEFQNSP | PASVCLNDIQ | HPSKKTTNDI | TQPSSKVNIS | PTISSESKLF | SPAHKKPKTA | QYSSPELKSC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NPGYSNSELQ | INMTDGPRTL | NPDSPRCSKH | NRLCILRVVR | KDGENKGRQF | YACPLPREAQ | CGFFEWADLS | FPFCNHGKRS |
| 570 | 580 | 590 | 600 | 610 | | | |
| TMKTVLKIGP | NNGKNFFVCP | LGKEKQCNFF | QWAENGPGIK | IIPGC | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1708 | 1 | 735.0267 | -63.51 | 3 | 51.1 | 14.2 | 2 | 564-583 | K.TVLKIGPNNGKNFFVCPLGK.E | Carbamidomethyl: 16 |

# Detailed Protein Report

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**Protein 208:** **PREDICTED: insulin-like growth factor 1 receptor isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530407102 | **Score:** | 41.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 141.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 3 |

```
        10         20         30         40         50         60         70         80
MTNLKDIGLY NLRNITRGAI RIEKNADLCY LSTVDWSLIL DAVSNNYIVG NKPPKECGDL CPGTMEEKPM CEKTTINNEY
        90        100        110        120        130        140        150        160
NYRCWTTNRC QKMCPSTCGK RACTENNECC HPECLGSCSA PDNDTACVAC RHYYYAGVCV PACPPNTYRF EGWRCVDRDF
       170        180        190        200        210        220        230        240
CANILSAESS DSEGFVIHDG ECMQECPSGF IRNGSQSMYC IPCEGPCPKV CEEEKKTKTI DSVTSAQMLQ GCTIFKGNLL
       250        260        270        280        290        300        310        320
INIRRGNNIA SELENFMGLI EVVTGYVKIR HSHALVSLSF LKNLRLILGE EQLEGNYSFY VLDNQNLQQL WDWDHRNLTI
       330        340        350        360        370        380        390        400
KAGKMYFAFN PKLCVSEIYR MEEVTGTKGR QSKGDINTRN NGERASCESD VLHFTSTTTS KNRIIITWHR YRPPDYRDLI
       410        420        430        440        450        460        470        480
SFTVYYKEAP FKNVTEYDGQ DACGSNSWNM VDVDLPPNKD VEPGILLHGL KPWTQYAVYV KAVTLTMVEN DHIRGAKSEI
       490        500        510        520        530        540        550        560
LYIRTNASVP SIPLDVLSAS NSSSQLIVKW NPPSLPNGNL SYYIVRWQRQ PQDGYLYRHN YCSKDKIPIR KYADGTIDIE
       570        580        590        600        610        620        630        640
EVTENPKTEV CGGEKGPCCA CPKTEAEKQA EKEEAEYRKV FENFLHNSIF VPRPERKRRD VMQVANTTMS SRSRNTTAAD
       650        660        670        680        690        700        710        720
TYNITDPEEL ETEYPFFESR VDNKERTVIS NLRPFTLYRI DIHSCNHEAE KLGCSASNFV FARTMPAEGA DDIPGPVTWE
       730        740        750        760        770        780        790        800
PRPENSIFLK WPEPENPNGL ILMYEIKYGS QVEDQRECVS RQEYRKYGGA KLNRLNPGNY TARIQATSLS GNGSWTDPVF
       810        820        830        840        850        860        870        880
FYVQAKTGYE NFIHLIIALP VAVLLIVGGL VIMLYVFHRK RNNSRLGNGV LYASVNPEYF SAADVYVPDE WEVAREKITM
       890        900        910        920        930        940        950        960
SRELGQGSFG MVYEGVAKGV VKDEPETRVA IKTVNEAASM RERIEFLNEA SVMKEFNCHH VVRLLGVVSQ GQPTLVIMEL
       970        980        990       1000       1010       1020       1030       1040
MTRGDLKSYL RSLRPEMENN PVLAPPSLSK MIQMAGEIAD GMAYLNANKF VHRDLAARNC MVAEDFTVKI GDFGMTRDIY
      1050       1060       1070       1080       1090       1100       1110       1120
ETDYYRKGGK GLLPVRWMSP ESLKDGVFTT YSDVWSFGVV LWEIATLAEQ PYQGLSNEQV LRFVMEGGLL DKPDNCPDML
      1130       1140       1150       1160       1170       1180       1190       1200
FELMRMCWQY NPKMRPSFLE IISSIKEEME PGFREVSFYY SEENKLPEPE ELDLEPENME SVPLDPSASS SSLPLPDRHS
      1210       1220       1230       1240       1250
GHKAENGPGP GVLVLRASFD ERQPYAHMNG GRKNERALPL PQSSTC
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1849 | 3 | 1045.0301 | 118.60 | 2 | 51.5 | 16.2 | 0 | 56-73 | K.ECGDLCPGTMEEKPMCEK.T | Carbamidomethyl: 16; Oxidation: 10, 15 |
| 1628 | 1 | 716.0279 | 112.96 | 3 | 50.1 | 12.0 | 0 | 56-73 | K.ECGDLCPGTMEEKPMCEK.T | Carbamidomethyl: 2, 16; Oxidation: 10, 15 |
| 1529 | 1 | 669.8325 | -70.94 | 2 | 49.3 | 13.1 | 0 | 271-282 | R.HSHALVSLSFLK.N | |

# Detailed Protein Report

**Protein 209:** **PREDICTED: ubiquitin carboxyl-terminal hydrolase 40 isoform X4 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530371419 | **Score:** | 41.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 125.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***WUP:QUP*** **Median:** 1.84 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MRQHDVQELN RILFSALETS LVGTSGHDLI YRLYHGTIVN QIVCKECKNV SERQEDFLDL TVAVKNVSGL EDALWNMYVE
        90        100        110        120        130        140        150        160
EEVFDCDNLY HCGTCDRLVK AAKSAKLRKL PPFLTVSLLR FNFDFVKCER YKETSCYTFP LRINLKPFCE QSELDDLEYI
       170        180        190        200        210        220        230        240
YDLFSVIIHK GGCYGGHYHV YIKDVDHLGN WQFQEEKSKP DVNLKDLQSE EEIDHPLMIL KAILLEEENN LIPVDQLGQK
       250        260        270        280        290        300        310        320
LLKKIGISWN KKYRKQHGPL RKFLQLHSQI FLLSSDESTV RLLKNSSLQA ESDFQRNDQQ IFKMLPPESP GLNNSISCPH
       330        340        350        360        370        380        390        400
WFDINDSKVQ PIREKDIEQQ FQGKESAYML FYRKSQLQRP PEARANPRYG VPCHLLNEMD AANIELQTKR AECDSANNTF
       410        420        430        440        450        460        470        480
ELHLHLGPQY HFFNGALHPV VSQTESVWDL TFDKRKTLGD LRQSIFQLLE FWEGDMVLSV AKLVPAGLHI YQSLGGDELT
       490        500        510        520        530        540        550        560
LCETEIADGE DIFVWNGVEV GGVHIQTGID CEPLLLNVLH LDTSSDGEKC CQVIESPHVF PANAEVGTVL TALAIPAGVI
       570        580        590        600        610        620        630        640
FINSAGCPGG EGWTAIPKED MRKTFREQGL RNGSSILIQD SHDDNSLLTK EEKWVTSMNE IDWLHVKNLC QLESEEKQVK
       650        660        670        680        690        700        710        720
ISATVNTMVF DIRIKAIKEL KLMKELADNS CLRPIDRNGK LLCPVPDSYT LKEAELKMGS SLGLCLGKAP SSSQLFLFFA
       730        740        750        760        770        780        790        800
MGSDVQPGTE MEIVVEETIS VRDCLKLMLK KSGLQGDAWH LRKMDWCYEA GEPLCEEDAT LKELLICSGD TLLLIEGQLP
       810        820        830        840        850        860        870        880
PLGFLKVPIW WYQLQGPSGH WESHQDQTNC TSSWGRVWRA TSSQGASGNE PAQVSLLYLG DIEISEDATL AELKSQAMTL
       890        900        910        920        930        940        950        960
PPFLEFGVPS PAHLRAWTVE RKRPGRLLRT DRQPLREYKL GRRIEICLEP LQKGENLGPQ DVLLRTQVRI PGERTYAPAL
       970        980        990       1000       1010       1020       1030       1040
DLVWNAAQGG TAGSLRQRVA DFYRLPVEKI EIAKYFPEKF EWLPISSWNQ QITKRKKKKK QDYLQGAPYY LKDGDTIGVK
      1050       1060       1070       1080       1090       1100       1110
NLLIDDDDDF STIRDDTGKE KQKQRALGRR KSQEALHEQS SYILSSAETP ARPRAPETSL SIHVGSFR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2293 | 1 | 937.4457 | -41.72 | 2 | 57.0 | 11.2 | 1 | 662-677 | K.LMKELADNSCLRPIDR.N | | WUP:QUP 1.84 |
| 2823 | 1 | 826.4280 | 41.02 | 2 | 65.7 | 30.1 | 0 | 1041-1054 | K.NLLIDDDDDFSTIR.D | | |

# Detailed Protein Report

## Protein 210: histone H4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4504301 | **Score:** | 41.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 11.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.8 |
| | | **Sequence Coverage [%]:** | 7.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.36 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.44 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|77539758 | refseq_human (refseq_human_20140103.fasta) | histone H4 [Homo sapiens] |
| gi\|28173560 | refseq_human (refseq_human_20140103.fasta) | histone H4 [Homo sapiens] |
| gi\|11415030 | refseq_human (refseq_human_20140103.fasta) | histone H4 [Homo sapiens] |
| gi\|4504323 | refseq_human (refseq_human_20140103.fasta) | histone H4 [Homo sapiens] |
| gi\|4504321 | refseq_human (refseq_human_20140103.fasta) | histone H4 [Homo sapiens] |
| gi\|4504317 | refseq_human (refseq_human_20140103.fasta) | histone H4 [Homo sapiens] |
| gi\|4504315 | refseq_human (refseq_human_20140103.fasta) | histone H4 [Homo sapiens] |
| gi\|4504313 | refseq_human (refseq_human_20140103.fasta) | histone H4 [Homo sapiens] |
| gi\|4504311 | refseq_human (refseq_human_20140103.fasta) | histone H4 [Homo sapiens] |
| gi\|4504309 | refseq_human (refseq_human_20140103.fasta) | histone H4 [Homo sapiens] |
| gi\|4504307 | refseq_human (refseq_human_20140103.fasta) | histone H4 [Homo sapiens] |
| gi\|4504305 | refseq_human (refseq_human_20140103.fasta) | histone H4 [Homo sapiens] |
| gi\|4504303 | refseq_human (refseq_human_20140103.fasta) | histone H4 [Homo sapiens] |

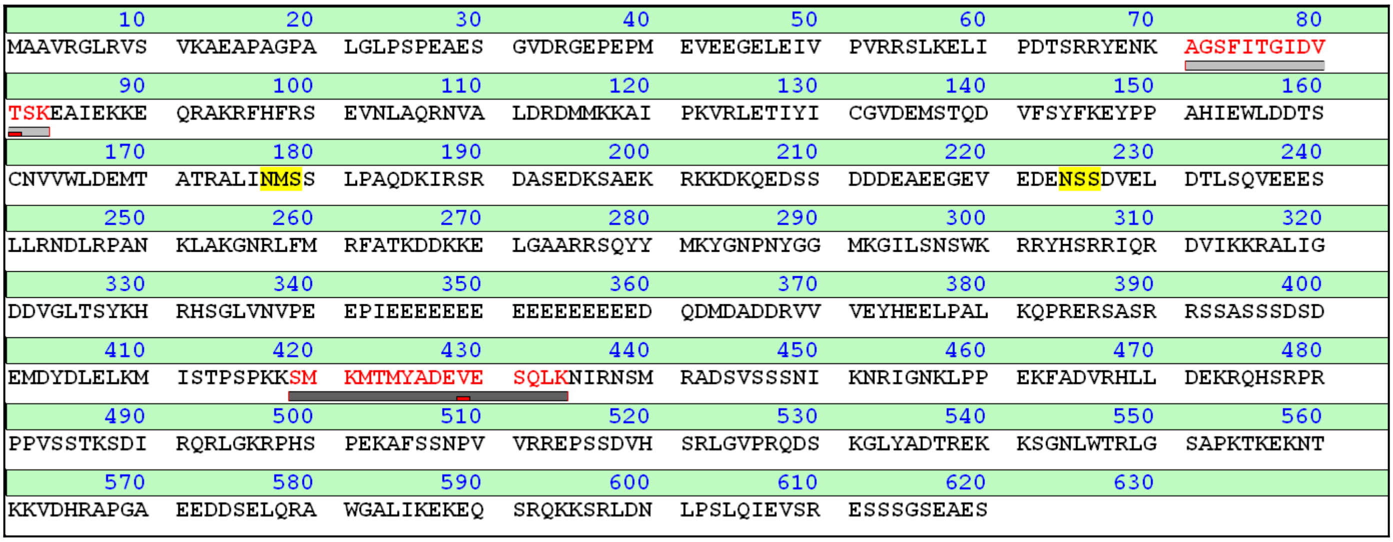
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSGRGKGGKG | LGKGGAKRHR | KVLRDNIQGI | TKPAIRRLAR | RGGVKRISGL | IYEETRGVLK | VFLENVIRDA | VTYTEHAKRK |
| **90** | **100** | **110** | | | | | |
| TVTAMDVVYA | LKRQGRTLYG | FGG | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1293 | 9 | 495.1457 | -296.53 | 2 | 45.8 | 41.1 | 0 | 61-68 | K.VFLENVIR.D | | QU:MU 1.36<br>WUP:QUP 1.44 |

# Detailed Protein Report

## Protein 211: uncharacterized protein C17orf85 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|166295179 | **Score:** | 40.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 70.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 6.0 |
| | | **No. of unique Peptides:** | 2 |



| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAAVRGLRVS | VKAEAPAGPA | LGLPSPEAES | GVDRGEPEPM | EVEEGELEIV | PVRRSLKELI | PDTSRRYENK | AGSFITGIDV |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| TSKEAIEKKE | QRAKRFHFRS | EVNLAQRNVA | LDRDMMKKAI | PKVRLETIYI | CGVDEMSTQD | VFSYFKEYPP | AHIEWLDDTS |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| CNVVWLDEMT | ATRALINMSS | LPAQDKIRSR | DASEDKSAEK | RKKDKQEDSS | DDDEAEEGEV | EDENSSDVEL | DTLSQVEEES |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| LLRNDLRPAN | KLAKGNRLFM | RFATKDDKKE | LGAARRSQYY | MKYGNPNYGG | MKGILSNSWK | RRYHSRRIQR | DVIKKRALIG |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| DDVGLTSYKH | RHSGLVNVPE | EPIEEEEEEE | EEEEEEEEED | QDMDADDRVV | VEYHEELPAL | KQPRERSASR | RSSASSSDSD |
| **410** | **420** | **430** | **440** | **450** | **460** | **470** | **480** |
| EMDYDLELKM | ISTPSPKKSM | KMTMYADEVE | SQLKNIRNSM | RADSVSSSNI | KNRIGNKLPP | EKFADVRHLL | DEKRQHSRPR |
| **490** | **500** | **510** | **520** | **530** | **540** | **550** | **560** |
| PPVSSTKSDI | RQRLGKRPHS | PEKAFSSNPV | VRREPSSDVH | SRLGVPRQDS | KGLYADTREK | KSGNLWTRLG | SAPKTKEKNT |
| **570** | **580** | **590** | **600** | **610** | **620** | **630** | |
| KKVDHRAPGA | EEDDSELQRA | WGALIKEKEQ | SRQKKSRLDN | LPSLQIEVSR | ESSSGSEAES | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2859 | 1 | 648.3692 | 36.16 | 2 | 64.5 | 11.7 | 0 | 71-83 | K.AGSFITGIDVTSK.E | |
| 2116 | 1 | 945.7998 | -143.91 | 2 | 56.8 | 14.7 | 1 | 419-434 | K.SMKMTMYADEVESQLK.N | |

# Detailed Protein Report

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## Protein 212: PREDICTED: peregrin isoform X6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530373123 | **Score:** | 40.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 78.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.9 |
| | | **Sequence Coverage [%]:** | 4.4 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.67 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 3.92 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGVDFDVKTF | CHNLRATKPP | YECPVETCRK | VYKSYSGIEY | HLYHYDHDNP | PPPQQTPLRK | HKKKGRQSRP | ANKQSPSPSE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VSQSPGREVM | SYAQAQRMVE | VDLHGRVHRI | SIFDNLDVVS | EDEEAPEEAP | ENGSNKENTE | TPAATPKSGK | HKNKEKRKDS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NHHHHHNVSA | STTPKLPEVV | YRELEQDTPD | APPRPTSYYR | YIEKSAEELD | EEVEYDMDEE | DYIWLDIMNE | RRKTEGVSPI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PQEIFEYLMD | RLEKESYFES | HNKGDPNALV | DEDAVCCICN | DGECQNSNVI | LFCDMCNLAV | HQECYGVPYI | PEGQWLCRRC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LQSPSRAVDC | ALCPNKGGAF | KQTDDGRWAH | VVCALWIPEV | CFANTVFLEP | IDSIEHIPPA | RWKLTCYICK | QRGSGACIQC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HKANCYTAFH | VTCAQQAGLY | MKMEPVRETG | ANGTSFSVRK | TAYCDIHTPP | GSARRLPALS | HSEGEEDEDE | EEDEGKGWSS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EKVKKAKAKS | RIKMKKARKI | LAEKRAAAPV | VSVPCIPPHR | LSKITNRLTI | QRKSQFMQRL | HSYWTLKRQS | RNGVPLLRRL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QTHLQSQRNC | DQVGRDSEDK | NWALKEQLKS | WQRLRHDLER | ARLLVELIRK | REKLKRETIK | VQQIAMEMQL | TPFLILLRKT |
| 650 | 660 | 670 | 680 | 690 | | | |
| LEQLQEKDTG | NIFSEPVPLS | EGPEWEAVCT | PSPEAGTESA | K | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 256 | 1 | 715.8400 | -27.55 | 2 | 33.2 | 17.3 | 1 | 137-150 | K.ENTETPAATPKSGK.H | | QU:MU 1.67<br>WUP:QUP 3.92 |
| 1974 | 1 | 757.2741 | -191.30 | 2 | 55.1 | 10.7 | 0 | 506-520 | R.AAAPVVSVPCIPPHR.L | | |

# Detailed Protein Report

## Protein 213: fibrocystin isoform 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|126131102 | **Score:** | 40.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 446.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTAWLISLMS | IEVLLLAVRH | LSLHIEPEEG | SLAGGTWITV | IFDGLELGVL | YPNNGSQLEI | HLVNVNMVVP | ALRSVPCDVF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PVFLDLPVVT | CRTRSVLSEA | HEGLYFLEAY | FGGQLVSSPN | PGPRDSCTFK | FSKAQTPIVH | QVYPPSGVPG | KLIHVYGWII |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TGRLETFDFD | AEYIDSPVIL | EAQGDKWVTP | CSLINRQMGS | CYPIQEDHGL | GTLQCHVEGD | YIGSQNVSFS | VFNKGKSMVH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KKAWLISAKQ | DLFLYQTHSE | ILSVFPETGS | LGGRTNITIT | GDFFDNSAQV | TIAGIPCDIR | HVSPRKIECT | TRAPGKDVRL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TTPQPGNRGL | LFEVGDAVEG | LELTEATPGY | RWQIVPNASS | PFGFWSQEGQ | PFRARLSGFF | VAPETNNYTF | WIQADSQASL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HFSWSEEPRT | KVKVASISVG | TADWFDSWEQ | NRDEGTWQQK | TPKLELLGGA | MYYLEAEHHG | IAPSRGMRIG | VQIHNTWLNP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DVVTTYLREK | HQIRVRAQRL | PEVQVLNVSG | RGNFFLTWDN | VSSQPIPANA | TAHLIQTTIE | ELLAVKCKLE | PLWSNILLRL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GFERGPEVSN | SDGDLTSGTE | PFCGRFSLRQ | PRHLVLTPPA | AQKGYRLDQY | THLCLAYKGH | MNKILKMIVS | FTIGFQNMVK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NTTCDWSLTR | TSPESWQFDC | TDLWETCVRC | FGDLQPPPAN | SPVLVHQINL | LPLAQETGLF | YVDEIIIADT | NVTVSQADSG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TARPGGNLVE | SVSVVGSPPV | YSVTSWLAGC | GTELPLITAR | SVPTEGTEEG | SGLVLVTTQR | RQRTSPPLGG | HFRIQLPNTV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ISDVPVQISA | HHLHQLLQNN | ADDFTSRYLN | ASDFTVKEDL | YTCYEHVWTL | SWSTQIGDLP | NFIRVSDENL | TGVNPAAATR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VVYDGGVFLG | PIFGDMLATA | NQHTQVVVRV | NDVPAHCPGS | CSFQYLQGST | PCVHSVWYSI | DGDINLMIYI | TGTGFSGDSQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FLQVTVNKTS | CKVIFSNQTN | VVCQTDLLPV | GMHRILMLVR | PSGLAISATG | EDLFLNVKPR | LDMVEPSRAA | DIGGLWATIR |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GSSLEGVSLI | LFGSYSCAIN | VATSNSSRIQ | CKVPPRGKDG | RIVNVTVIRG | DYSAVLPRAF | TYVSSLNPVI | VTLSRNISNI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| AGGETLVIGV | ARLMNYTDLD | VEVHVQDALA | PVHTQSAWGL | EVALPPLPAG | LHRISVSING | VSIHSQGVDL | HIQYLTEVFS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| IEPCCGSLLG | GTILSISGIG | FSRDPALVWV | LVGNRSCDIV | NLTEASIWCE | TLPAPQIPDA | GAPTVPAAVE | VWAGNRFFAR |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| GPSPSLVGKG | FTFMYEAAAT | PVVTAMQGEI | TNSSLSLHVG | GSNLSNSVIL | LGNLNCDVET | QSFQGNVSLS | GCSIPLHSLE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| AGIYPLQVRQ | KQMGFANMSV | VLQQFAVMPR | IMAIFPSQGS | ACGGTILTVR | GLLLNSRRRS | VRVDLSGPFT | CVILSLGDHT |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ILCQVSLEGD | PLPGASFSLN | VTVLVNGLTS | ECQGNCTLFI | REEASPVMDA | LSTNTSGSLT | TVLIRGQRLA | TTADEPMVFV |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| DDQLPCNVTF | FNASHVVCQT | RDLAPGPHYL | SVFYTRNGYA | CSGNVSRHFY | IMPQVFHYFP | KNFSLHGGSL | LTIEGTGLRG |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QNTTSVYIDQ | QTCLTVNIGA | ELIRCIVPTG | NGSVALEIEV | DGLWYHIGVI | GYNKAFTPEL | ISISQSDDIL | TFAVAQISGA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| ANIDIFIGMS | PCVGVSGNHT | VLQCVVPSLP | AGEYHVRGYD | CIRGWASSAL | VFTSRVIITA | VTENFGCLGG | RLVHVFGAGF |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SPGNVSAAVC | GAPCRVLANA | TVSAFSCLVL | PLDVSLAFLC | GLKREEDSCE | AARHTYVQCD | LTVAMATEQL | LESWPYLYIC |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| EESSQCLFVP | DHWAESMFPS | FSGLFISPKL | ERDEVLIYNS | SCNITMETEA | EMECETPNQP | ITVKITEIRK | RWGQNTQGNF |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| SLQFCRRWSR | THSWFPERLP | QDGDNVTVEN | GQLLLLDTNT | SILNLLHIKG | GKLIFMAPGP | IELRAHAILV | SDGGELRIGS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| EDKPFQGRAQ | ITLYGSSYST | PFFPYGVKFL | AVRNGTLSLH | GSLPEVIVTC | LRATAHALDT | VLALEDAVDW | NPGDEVVIIS |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| GTGVKGAKPM | EEIVTVETVQ | DTDLYLKSPL | RYSHNFTENW | VAGEHHILKA | TVALLSRSIT | IQGNLTNERE | KLLVSCQEAN |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2756 | 1 | 1023.5380 | 40.37 | 2 | 63.0 | 11.3 | 1 | 1718-1735 | R.GYDCIRGWASSALVFTSR.V | Carbamidomethyl: 4 |

# Detailed Protein Report

**Protein 214:** **myosin-IIIa [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|145275208 | **Score:** | 40.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 186.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFPLIGKTII | FDNFPDPSDT | WEITETIGKG | TYGKVFKVLN | KKNGQKAAVK | ILDPIHDIDE | EIEAEYNILK | ALSDHPNVVR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FYGIYFKKDK | VNGDKLWLVL | ELCSGGSVTD | LVKGFLKRGE | RMSEPLIAYI | LHEALMGLQH | LHNNKTIHRD | VKGNNILLTT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EGGVKLVDFG | VSAQLTSTRH | RRNTSVGTPF | WMAPEVIACE | QQLDTTYDAR | CDTWSLGITA | IELGDGDPPL | ADLHPMRALF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KIPRNPPPKL | RQPELWSAEF | NDFISKCLTK | DYEKRPTVSE | LLQHKFITQI | EGKDVMLQKQ | LTEFIGIHQC | MGGTEKARRE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RIHTKKGNFN | RPLISNLKDV | DDLATLEILD | ENTVSEQLEK | CYSRDQIYVY | VGDILIALNP | FQSLGLYSTK | HSKLYIGSKR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TASPPHIFAM | ADLGYQSMIT | YNSDQCIVIS | GESGAGKTEN | AHLLVQQLTV | LGKANNRTLQ | EKILQVNNLV | EAFGNACTII |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NDNSSRFGKY | LEMKFTSSGA | VVGAQISEYL | LEKSRVIHQA | IGEKNFHIFY | YIYAGLAEKK | KLAHYKLPEN | KPPRYLQNDH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LRTVQDIMNN | SFYKSQYELI | EQCFKVIGFT | MEQLGSIYSI | LAAILNVGNI | EFSSVATEHQ | IDKSHISNHT | ALENCASLLC |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IRADELQEAL | TSHCVVTRGE | TIIRPNTVEK | ATDVRDAMAK | TLYGRLFSWI | VNCINSLLKH | DSSPSGNGDE | LSIGILDIFG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| FENFKKNSFE | QLCINIANEQ | IQYYYNQHVF | AWEQNEYLNE | DVDARVIEYE | DNWPLLDMFL | QKPMGLLSLL | DEESRFPKAT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DQTLVEKFEG | NLKSQYFWRP | KRMELSFGIH | HYAGKVLYNA | SGFLAKNRDT | LPTDIVLLLR | SSDNSVIRQL | VNHPLTKTGN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LPHSKTKNVI | NYQMRTSEKL | INLAKGDTGE | ATRHARETTN | MKTQTVASYF | RYSLMDLLSK | MVVGQPHFVR | CIKPNSERQA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RKYDKEKVLL | QLRYTGILET | ARIRRLGFSH | RILFANFIKR | YYLLCYKSSE | EPRMSPDTCA | TILEKAGLDN | WALGKTKVFL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KYYHVEQLNL | MRKEAIDKLI | LIQACVRAFL | CSRRYQKIQE | KRKESAIIIQ | SAARGHLVRK | QRKEIVDMKN | TAVTTIQTSD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QEFDYKKNFE | NTRESFVKKQ | AENAISANER | FISAPNNKGS | VSVVKTSTFK | PEEETTNAVE | SNNRVYQTPK | KMNNVYEEEV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KQEFYLVGPE | VSPKQKSVKD | LEENSNLRKV | EKEEAMIQSY | YQRYTEERNC | EESKAAYLER | KAISERPSYP | VPWLAENETS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| FKKTLEPTLS | QRSIYQNANS | MEKEKKTSVV | TQRAPICSQE | EGRGRLRHET | VKERQVEPVT | QAQEEEDKAA | VFIQSKYRGY |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KRRQQLRKDK | MSSFKHQRIV | TTPTEVARNT | HNLYSYPTKH | EEINNIKKKD | NKDSKATSER | EACGLAIFSK | QISKLSEEYF |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ILQKKLNEMI | LSQQLKSLYL | GVSHHKPINR | RVSSQQCLSG | VCKGEEPKIL | RPPRRPRKPK | TLNNPEDSTY | YYLLHKSIQE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| EKRRPRKDSQ | GKLLDLEDFY | YKEFLPSRSG | PKEHSPSLRE | RRPQQELQNQ | CIKANERCWA | AESPEKEEER | EPAANPYDFR |
| 1610 | 1620 | | | | | | |
| RLLRKTSQRR | RLVQQS | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 875 | 1 | 648.3760 | 105.34 | 2 | 41.0 | 11.8 | 0 | 1472-<br>1483 | R.VSSQQCLSGVCK.G | Carbamidomethyl: 6 |

# Detailed Protein Report

## Protein 215: filamin-A isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|116063573 | **Score:** | 40.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 279.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 2 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSSHSRAGQ | SAAGAAPGGG | VDTRDAEMPA | TEKDLAEDAP | WKKIQQNTFT | RWCNEHLKCV | SKRIANLQTD | LSDGLRLIAL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LEVLSQKKMH | RKHNQRPTFR | QMQLENVSVA | LEFLDRESIK | LVSIDSKAIV | DGNLKLILGL | IWTLILHYSI | SMPMWDEEED |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EEAKKQTPKQ | RLLGWIQNKL | PQLPITNFSR | DWQSGRALGA | LVDSCAPGLC | PDWDSWDASK | PVTNAREAMQ | QADDWLGIPQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VITPEEIVDP | NVDEHSVMTY | LSQFPKAKLK | PGAPLRPKLN | PKKARAYGPG | IEPTGNMVKK | RAEFTVETRS | AGQGEVLVYV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EDPAGHQEEA | KVTANNDKNR | TFSVWYVPEV | TGTHKVTVLF | AGQHIAKSPF | EVYVDKSQGD | ASKVTAQGPG | LEPSGNIANK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TTYFEIFTAG | AGTGEVEVVI | QDPMGQKGTV | EPQLEARGDS | TYRCSYQPTM | EGVHTVHVTF | AGVPIPRSPY | TVTVGQACNP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SACRAVGRGL | QPKGVRVKET | ADFKVYTKGA | GSGELKVTVK | GPKGEERVKQ | KDLGDGVYGF | EYYPMVPGTY | IVTITWGGQN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IGRSPFEVKV | GTECGNQKVR | AWGPGLEGGV | VGKSADFVVE | AIGDDVGTLG | FSVEGPSQAK | IECDDKGDGS | CDVRYWPQEA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GEYAVHVLCN | SEDIRLSPFM | ADIRDAPQDF | HPDRVKARGP | GLEKTGVAVN | KPAEFTVDAK | HGGKAPLRVQ | VQDNEGCPVE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ALVKDNGNGT | YSCSYVPRKP | VKHTAMVSWG | GVSIPNSPFR | VNVGAGSHPN | KVKVYGPGVA | KTGLKAHEPT | YFTVDCAEAG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QGDVSIGIKC | APGVVGPAEA | DIDFDIIRND | NDTFTVKYTP | RGAGSYTIMV | LFADQATPTS | PIRVKVEPSH | DASKVKAEGP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GLSRTGVELG | KPTHFTVNAK | AAGKGKLDVQ | FSGLTKGDAV | RDVDIIDHHD | NTYTVKYTPV | QQGPVGVNVT | YGGDPIPKSP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FSVAVSPSLD | LSKIKVSGLG | EKVDVGKDQE | FTVKSKGAGG | QGKVASKIVG | PSGAAVPCKV | EPGLGADNSV | VRFLPREEGP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| YEVEVTYDGV | PVPGSPFPLE | AVAPTKPSKV | KAFGPGLQGG | SAGSPARFTI | DTKGAGTGGL | GLTVEGPCEA | QLECLDNGDG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TCSVSYVPTE | PGDYNINILF | ADTHIPGSPF | KAHVVPCFDA | SKVKCSGPGL | ERATAGEVGQ | FQVDCSSAGS | AELTIEICSE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| AGLPAEVYIQ | DHGDGTHTIT | YIPLCPGAYT | VTIKYGGQPV | PNFPSKLQVE | PAVDTSGVQC | YGPGIEGQGV | FREATTEFSV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DARALTQTGG | PHVKARVANP | SGNLTETYVQ | DRGDGMYKVE | YTPYEEGLHS | VDVTYDGSPV | PSSPFQVPVT | EGCDPSRVRV |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| HGPGIQSGTT | NKPNKFTVET | RGAGTGGLGL | AVEGPSEAKM | SCMDNKDGSC | SVEYIPYEAG | TYSLNVTYGG | HQVPGSPFKV |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| PVHDVTDASK | VKCSGPGLSP | GMVRANLPQS | FQVDTSKAGV | APLQVKVQGP | KGLVEPVDVV | DNADGTQTVN | YVPSREGPYS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ISVLYGDEEV | PRSPFKVKVL | PTHDASKVKA | SGPGLNTTGV | PASLPVEFTI | DAKDAGEGLL | AVQITDPEGK | PKKTHIQDNH |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| DGTYTVAYVP | DVTGRYTILI | KYGGDEIPFS | PYRVRAVPTG | DASKCTVTGA | GIGPTIQIGE | ETVITVDTKA | AGKGKVTCTV |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| CTPDGSEVDV | DVVENEDGTF | DIFYTAPQPG | KYVICVRFGG | EHVPNSPFQV | TALAGDQPSV | QPPLRSQQLA | PQYTYAQGGQ |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| QTWAPERPLV | GVNGLDVTSL | RPFDLVIPFT | IKKGEITGEV | RMPSGKVAQP | TITDNKDGTV | TVRYAPSEAG | LHEMDIRYDN |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| MHIPGSPLQF | YVDYVNCGHV | TAYGPGLTHG | VVNKPATFTV | NTKDAGEGGL | SLAIEGPSKA | EISCTDNQDG | TCSVSYLPVL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| PGDYSILVKY | NEQHVPGSPF | TARVTGDDSM | RMSHLKVGSA | ADIPINISET | DLSLLTATVV | PPSGREEPCL | LKRLRNGHVG |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| ISFVPKETGE | HLVHVKKNGQ | HVASSPIPVV | ISQSEIGDAS | RVRVSGQGLH | EGHTFEPAEF | IIDTRDAGYG | GLSLSIEGPS |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| KVDINTEDLE | DGTCRVTYCP | TEPGNYIINI | KFADQHVPGS | PFSVKVTGEG | RVKESITRRR | RAPSVANVGS | HCDLSLKIPE |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1673 | 1 | 694.3984 | 51.21 | 2 | 51.2 | 15.2 | 1 | 1451-1464 | K.VKCSGPGLSPGMVR.A | |
| 418 | 1 | 686.6239 | -116.77 | 3 | 33.8 | 10.2 | 1 | 2339-2359 | K.VNQPASFAVSLNGAKGAIDAK.V | |

# Detailed Protein Report

| | | | |
|---|---|---|---|
| **Protein 216:** | **PREDICTED: chromodomain-helicase-DNA-binding protein 4 isoform X6 [Homo sapiens]** | | |
| **Accession:** | gi\|578822562 | **Score:** | 40.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 216.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASGLGSPSP | CSAGSEEEDM | DALLNNSLPP | PHPENEEDPE | EDLSETETPK | LKKKKKPKKP | RDPKIPKSKR | QKKERMLLCR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QLGDSSGEGP | EFVEEEEEVA | LRSDSEGSDY | TPGKKKKKKL | GPKKEKKSKS | KRKEEEEEED | DDDDSKEPKS | SAQLLEDWGM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EDIDHVFSEE | DYRTLTNYKA | FSQFVRPLIA | AKNPKIAVSK | MMMVLGAKWR | EFSTNNPFKG | SSGASVAAAA | AAAVAVVESM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VTATEVAPPP | PPVEVPIRKA | KTKEGKGPNA | RRKPKGSPRV | PDAKKPKPKK | VAPLKIKLGG | FGSKRKRSSS | EDDDLDVESD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FDDASINSYS | VSDGSTSRSS | RSRKKLRTTK | KKKKDHQDYC | EVCQQGGEII | LCDTCPRAYH | MVCLDPDMEK | APEGKWSCPH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CEKEGIQWEA | KEDNSEGEEI | LEEVGGDLEE | EDDHHMEFCR | VCKDGGELLC | CDTCPSSYHI | HCLNPPLPEI | PNGEWLCPRC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TCPALKGKVQ | KILIWKWGQP | PSPTPVPRPP | DADPNTPSPK | PLEGRPERQF | FVKWQGMSYW | HCSWVSELQL | ELHCQVMFRN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YQRKNDMDEP | PSGDFGGDEE | KSRKRKNKDP | KFAEMEERFY | RYGIKPEWMM | IHRILNHSVD | KKGHVHYLIK | WRDLPYDQAS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| WESEDVEIQD | YDLFKQSYWN | HRELMRGEEG | RPGKKLKKVK | LRKLERPPET | PTVDPTVKYE | RQPEYLDATG | GTLHPYQMEG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LNWLRFSWAQ | GTDTILADEM | GLGKTVQTAV | FLYSLYKEGH | SKGPFLVSAP | LSTIINWERE | FEMWAPDMYV | VTYVGDKDSR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AIIRENEFSF | EDNAIRGGKK | ASRMKKEASV | KFHVLLTSYE | LITIDMAILG | SIDWACLIVD | EAHRLKNNQS | KFFRVLNGYS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LQHKLLLTGT | PLQNNLEELF | HLLNFLTPER | FHNLEGFLEE | FADIAKEDQI | KKLHDMLGPH | MLRRLKADVF | KNMPSKTELI |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VRVELSPMQK | KYYKYILTRN | FEALNARGGG | NQVSLLNVVM | DLKKCCNHPY | LFPVAAMEAP | KMPNGMYDGS | ALIRASGKLL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LLQKMLKNLK | EGGHRVLIFS | QMTKMLDLLE | DFLEHEGYKY | ERIDGGITGN | MRQEAIDRFN | APGAQQFCFL | LSTRAGGLGI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| NLATADTVII | YDSDWNPHND | IQAFSRAHRI | GQNKKVMIYR | FVTRASVEER | ITQVAKKKMM | LTHLVVRPGL | GSKTGSMSKQ |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ELDDILKFGT | EELFKDEATD | GGGDNKEGED | SSVIHYDDKA | IERLLDRNQD | ETEDTELQGM | NEYLSSFKVA | QYVVREEEMG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| EEEEVEREII | KQEESVDPDY | WEKLLRHHYE | QQQEDLARNL | GKGKRIRKQV | NYNDGSQEDR | DWQDDQSDNQ | SDYSVASEEG |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| DEDFDERSEA | PRRPSRKGLR | NDKDKPLPPL | LARVGGNIEV | LGFNARQRKA | FLNAIMRYGM | PPQDAFTTQW | LVRDLRGKSE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KEFKAYVSLF | MRHLCEPGAD | GAETFADGVP | REGLSRQHVL | TRIGVMSLIR | KKVQEFEHVN | GRWSMPELAE | VEENKKMSQP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| GSPSPKTPTP | STPGDTQPNT | PAPVPPAEDG | IKIEENSLKE | EESIEGEKEV | KSTAPETAIE | CTQAPAPASE | DEKVVVEPPE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| GEEKVEKAEV | KERTEEPMET | EPKGKGAADV | EKVEEKSAID | LTPIVVEDKE | EKKEEEEKKE | VMLQNGETPK | DLNDEKQKKN |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| IKQRFMFNIA | DGGFTELHSL | WQNEERAATV | TKKTYEIWHR | RHDYWLLAGI | INHGYARWQD | IQNDPRYAIL | NEPFKGEMNR |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| GNFLEIKNKF | LARRFKLLEQ | ALVIEEQLRR | AAYLNMSEDP | SHPSMALNTR | FAEVECLAES | HQHLSKESMA | GNKPANAVLH |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | |
| KGILKQLEEL | LSDMKADVTR | LPATIARIPP | VAVRLQMSER | NILSRLANRA | PEPTPQQVAQ | QQ | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2366 | 1 | 649.8737 | -146.01 | 3 | 59.4 | 13.6 | 0 | 1005-1021 | K.CCNHPYLFPVAAMEAPK.M | Carbamidomethyl: 1 |
| 505 | 1 | 699.1373 | 103.36 | 3 | 35.9 | 10.8 | 2 | 1868-1885 | R.IPPVAVRLQMSERNILSR.L | Oxidation: 10 |

# Detailed Protein Report

## Protein 217: PREDICTED: beta-enolase isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530410063 | **Score:** | 40.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 48.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 10.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAVMRTLRAM | AMQKIFAREI | LDSRGNPTVE | VDLHTAKGRF | RAAVPSGAST | GIYEALELRD | GDKGRYLGKG | VLKAVENINN |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| TLGPALLQKK | LSVVDQEKVD | KFMIELDGTE | NKSKFGANAI | LGVSLAVCKA | GAAEKGVPLY | RHIADLAGNP | DLILPVPAFN |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| VINGGSHAGN | KLAMQEFMIL | PVGASSFKEA | MRIGAEVYHH | LKGVIKAKYG | KDATNVGDEG | GFAPNILENN | EALELLKTAI |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| QAAGYPDKVV | IGMDVAASEF | YRNGKYDLDF | KSPDDPARHI | TGEKLGELYK | SFIKNYPVVS | IEDPFDQDDW | ATWTSFLSGV |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| NIQIVGDDLT | VTNPKRIAQA | VEKKACNCLL | LKVNQIGSVT | ESIQACKLAQ | SNGWGVMVSH | RSGETEDTFI | ADLVVGLCTG |
| **410** | **420** | **430** | **440** | **450** | | | |
| QIKTGAPCRS | ERLAKYNQLM | RIEEALGDKA | IFAGRKFRNP | KAK | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2482 | 1 | 835.4239 | 2.22 | 2 | 61.6 | 10.7 | 2 | 1-14 | -.MAVMRTLRAMAMQK.I | Oxidation: 4, 10 |

# Detailed Protein Report

## Protein 218: unconventional myosin-Ih [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|254028267 | **Score:** | 40.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 117.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 4.4 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***WUP:QUP*** **Median:** 6.53 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEGALTARDK | VGVQDFVLLD | AYTSESAFVD | NLRKRFSENL | IYTYIGTLLV | SVNPYQELGI | YTVSQMELYQ | GVNFFELPPH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VYAIADNAYR | MMCAELNNHF | ILISGESGAG | KTEASKKILE | YFAVTCPMTQ | SLQIARDRLL | FSNPVLEAFG | NARTLRNDNS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SRFGKYMDIQ | FDFQGIPVGG | HIISYLIEKS | RVVYQNEGER | NFHIFYQLLA | GGEEERLSYL | GLERDPQLYK | YLSQGHCAKE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SSISDKNDWK | TVSNAFSVID | FTEADLENLF | GIIASVLHLG | NIGFEEDDQG | CATIPDTHEI | KWIAKLLGVH | PSVLLEALTH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RKIEAKTEEV | ICPLTLELSV | YARDAMAKAV | YGRTFTWLVN | KINSSLVNKD | FTRKTVIGLL | DIYGFEVFDK | NGFEQFCINY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CNEKLQQLLI | ERTLKAEQAE | YEMEGIEWEP | IKYFNNKIIC | DLVEERHKGI | ISILDEECIR | PGPATDLSFL | EKLEEKVGKH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AHFETRKLAG | PKGRKRIGWM | EFRLLHYAGE | VTYCTKGFLE | KNNDLLYRHL | KEVLCKSKNI | ILRECFLLAE | LENRRRPPTV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GTQFKNSLSS | LLETLISKEP | SYIRCIKPND | RKEPSKFDDF | LIRHQIKYLG | LMEHLRVRRA | GFAYRRKYEH | FLQRYKSLCP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DTWPHWHGPP | AEGVERLIKY | IGYKPEEYKL | GKTKIFIRFP | RTLFATEDAF | EFSKHQLVAR | IQATYKRCLG | RREYVKKRQA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AIKLEAHWRG | ALARKAIQRR | KWAVRIIRKF | IKGFISRNKP | LCPDNEEFIV | FVRKNYILNL | RYHLPKTVLD | KSWLRPPGIL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ENASDLLRKM | CVRNLVQKYC | RGITAERKAM | MQQKVVTSEI | FRGRKDGYTE | SLNQPFVNSR | IDEGDINPKV | LQLISHEKIQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| YGVPVIKYDR | KGFKARQRQL | ILTQKAAYVV | ELAKIKQKIE | YSALKGVSTS | NLSDGILVIH | VSPEDSKQKG | DAVLQCGHVF |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | |
| EAVTKLVMLV | KKENIVNVVQ | GSLQFFISPG | KEGTIVFDTG | LEEQVYKNKN | GQLTVVSVRR | KS | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 354 | 1 | 1026.5219 | 53.51 | 2 | 34.4 | 10.0 | 0 | 416-432 | K.AEQAEYEMEGIEWEPIK.Y | | WUP:QUP 6.53 |
| 1186 | 1 | 863.9897 | 97.78 | 2 | 44.4 | 16.8 | 0 | 846-860 | K.DGYTESLNQPFVNSR.I | | |

# Detailed Protein Report

**Protein 219:** **PREDICTED: bromodomain adjacent to zinc finger domain protein 2A isoform X11 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578823227 | **Score:** | 40.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 170.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEVACILHTR | GGVQKTGERR | EMEANDHFNF | TGLPPAPAAS | GLKPSPSSGE | GLYTNGSPMN | FPQQGKSLNG | DVNVNGLSTV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SHTTTSGILN | SAPHSSSTSH | LHHPSVAYDC | LWNYSQYPSA | NPGSNLKDPP | LLSQFSGGQY | PLNGILGGSR | QPSSPSHNTN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LRAGSQEFWA | NGTQSPMGLN | FDSQELYDSF | PDQNFEVMPN | GPPSFFTSPQ | TSPMLGSSIQ | TFAPSQEVGS | GIHPDEAAEK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EMTSVVAENG | TGLVGSLELE | EEQPELKMCG | YNGSVPSVES | LHQEVSVLVP | DPTVSCLDDP | SHLPDQLEDT | PILSEDSLEP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FNSLAPEPVS | GGLYGIDDTE | LMGAEDKLPL | EDSPVISALD | CPSLNNATAF | SLLADDSQTS | TSIFASPTSP | PVLGESVLQD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NSFDLNNGSD | AEQEEMETQS | SDFPPSLTQP | APDQSSTIQL | HPATSPAVSP | TTSPAVSLVV | SPAASPEISP | EVCPAASTVV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SPAVFSVVSP | ASSAVLPAVS | LEVPLTASVT | SPKASPVTSP | AAAFPTASPA | NKDVSSFLET | TADVEEITGE | GLTASGSGDV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MRRRIATPEE | VRLPLQHGWR | REVRIKKGSH | RWQGETWYYG | PCGKRMKQFP | EVIKYLSRNV | VHSVRREHFS | FSPRMPVGDF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FEERDTPEGL | QWVQLSAEEI | PSRIQAITGK | RGRPRNTEKA | KTKEVPKVKR | GRGRPPKVKI | TELLNKTDNR | PLKKLEAQET |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LNEEDKAKIA | KSKKKMRQKV | QRGECQTTIQ | GQARNKRKQE | TKSLKQKEAK | KKSKAEKEKG | KTKQEKLKEK | VKREKKEKVK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| MKEKEEVTKA | KPACKADKTL | ATQRRLEERQ | RQQMILEEMK | KPTEDMCLTD | HQPLPDFSRV | PGLTLPSGAF | SDCLTIVEFL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| HSFGKVLGFD | PAKDVPSLGV | LQEGLLCQGD | SLGEVQDLLV | RLLKAALHDP | GFPSYCQSLK | ILGEKVSEIP | LTRDNVSEIL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RCFLMAYGVE | PALCDRLRTQ | PFQAQPPQQK | AAVLAFLVHE | LNGSTLIINE | IDKTLESMSS | YRKNKWIVEG | RLRRLKTVLA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KRTGRSEVEM | EGPEECLGRR | RSSRIMEETS | GMEEEEEEES | IAAVPGRRGR | RDGEVDATAS | SIPELERQIE | KLSKRQLFFR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KKLLHSSQML | RAVSLGQDRY | RRRYWVLPYL | AGIFVEGTEG | NLVPEEVIKK | ETDSLKVAAH | ASLNPALFSM | KMELAGSNTT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ASSPARARGR | PRKTKPGSMQ | PRHLKSPVRG | QDSEQPQAQL | QPEAQLHAPA | QPQPQLQLQL | QSHKGFLEQE | GSPLSLGQSQ |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| HDLSQSAFLS | WLSQTQSHSS | LLSSSVLTPD | SSPGKLDPAP | SQPPEEPEPD | EAESSPDPQA | LWFNISAQMP | CNAAPTPPPA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VSEDQPTPSP | QQLASSKPMN | RPSAANPCSP | VQFSSTPLAG | LAPKRRAGDP | GEMPQSPTGL | GQPKRRGRPP | SKFFKQMEQR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| YLTQLTAQPV | PPEMCSGWWW | IRDPEMLDAM | LKALHPRGIR | EKALHKHLNK | HRDFLQEVCL | RPSADPIFEP | RQLPAFQEGI |
| 1530 | 1540 | 1550 | 1560 | | | | |
| MSWSPKEKTY | ETDLAVLQWV | EELEQRVIMS | DLQIR | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2577 | 1 | 941.5794 | 21.02 | 2 | 62.2 | 13.8 | 2 | 698-713 | K.VKITELLNKTDNRPLK.K | |
| 778 | 1 | 830.6256 | 153.36 | 1 | 39.7 | 11.3 | 0 | 700-706 | K.ITELLNK.T | |

# Detailed Protein Report

**Protein 220:** **PREDICTED: plasma membrane calcium-transporting ATPase 3 isoform X5 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530422822 | **Score:** | 40.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 127.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGDMANSSIE | FHPKPQQQRD | VPQAGGFGCT | LAELRTLMEL | RGAEALQKIE | EAYGDVSGLC | RRLKTSPTEG | LADNTNDLEK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RRQIYGQNFI | PPKQPKTFLQ | LVWEALQDVT | LIILEVAAIV | SLGLSFYAPP | GEESEACGNV | SGGAEDEGEA | EAGWIEGAAI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLSVICVVLV | TAFNDWSKEK | QFRGLQSRIE | QEQKFTVIRN | GQLLQVPVAA | LVVGDIAQVK | YGDLLPADGV | LIQANDLKID |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ESSLTGESDH | VRKSADKDPM | LLSGTHVMEG | SGRMVVTAVG | VNSQTGIIFT | LLGAGGEEEE | KKDKKAKKQD | GAVAMEMQPL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KSAEGGEMEE | REKKKANAPK | KEKSVLQGKL | TKLAVQIGKA | GLVMSAITVI | ILVLYFVIET | FVVEGRTWLA | ECTPVYVQYF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VKFFIIGVTV | LVVAVPEGLP | LAVTISLAYS | VKKMMKDNNL | VRHLDACETM | GNATAICSDK | TGTLTTNRMT | VVQSYLGDTH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YKEIPAPSAL | TPKILDLLVH | AISINSAYTT | KILPPEKEGA | LPRQVGNKTE | CALLGFVLDL | KRDFQPVREQ | IPEDKLYKVY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TFNSVRKSMS | TVIRMPDGGF | RLFSKGASEI | LLKKCTNILN | SNGELRGFRP | RDRDDMVRKI | IEPMACDGLR | TICIAYRDFS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AGQEPDWDNE | NEVVGDLTCI | AVVGIEDPVR | PEVPEAIRKC | QRAGITVRMV | TGDNINTARA | IAAKCGIIQP | GEDFLCLEGK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EFNRRIRNEK | GEIEQERLDK | VWPKLRVLAR | SSPTDKHTLV | KGIIDSTTGE | QRQVVAVTGD | GTNDGPALKK | ADVGFAMGIA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GTDVAKEASD | IILTDDNFTS | IVKAVMWGRN | VYDSISKFLQ | FQLTVNVVAV | IVAFTGACIT | QDSPLKAVQM | LWVNLIMDTF |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ASLALATEPP | TESLLLRKPY | GRDKPLISRT | MMKNILGHAV | YQLAIIFTLL | FVGELFFDID | SGRNAPLHSP | PSEHYTIIFN |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TFVMMQLFNE | INARKIHGER | NVFDGIFSNP | IFCTIVLGTF | GIQIVIVQFG | GKPFSCSPLS | TEQWLWCLFV | GVGELVWGQV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| IATIPTSQLK | CLKEAGHGPG | KDEMTDEELA | EGEEEIDHAE | RELRRGQILW | FRGLNRIQTQ | MEVVSTFKRS | GSVQGAVRRR |
| 1130 | 1140 | 1150 | 1160 | | | | |
| SSVLSQLHDV | TNLSTPTHAI | LSAANPTSAA | GNPGGESVP | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2715 | 1 | 725.3796 | 55.65 | 2 | 65.1 | 12.1 | 0 | 309-321 | K.QDGAVAMEMQPLK.S | Oxidation: 7, 9 |
| 70 | 1 | 877.8816 | -104.57 | 2 | 30.6 | 11.7 | 1 | 757-772 | K.HTLVKGIIDSTTGEQR.Q | |

# Detailed Protein Report

## Protein 221: stAR-related lipid transfer protein 9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|270265793 | **Score:** | 40.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 516.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MANVQVAVRV | RPLSKRETKE | GGRIIVEVDG | KVAKIRNLKV | DNRPDGFGDS | REKVMAFGFD | YCYWSVNPED | PQYASQDVVF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QDLGMEVLSG | VAKGYNICLF | AYGQTGSGKT | YTMLGTPASV | GLTPRICEGL | FVREKDCASL | PSSCRIKVSF | LEIYNERVRD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLKQSGQKKS | YTLRVREHPE | MGPYVQGLSQ | HVVTNYKQVI | QLLEEGIANR | ITAATHVHEA | SSRSHAIFTI | HYTQAILENN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LPSEMASKIN | LVDLAGSERA | DPSYCKDRIA | EGANINKSLV | TLGIVISTLA | QNSQVFSSCQ | SLNSSVSNGG | DSGILSSPSG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TSSGGAPSRR | QSYIPYRDSV | LTWLLKDSLG | GNSKTIMVAT | VSPAHTSYSE | TMSTLRYASS | AKNIINKPRV | NEDANLKLIR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ELREEIERLK | ALLLSFELRN | FSSLSDENLK | ELVLQNELKI | DQLTKDWTQK | WNDWQALMEH | YSVDINRRRA | GVVIDSSLPH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LMALEDDVLS | TGVVLYHLKE | GTTKIGRIDS | DQEQDIVLQG | QWIERDHCTI | TSACGVVVLR | PARGARCTVN | GREVTASCRL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TQGAVITLGK | AQKFRFNHPA | EAAVLRQRRQ | VGEAAAGRGS | LEWLDLDGDL | AASRLGLSPL | LWKERRALEE | QCDEDHQTPR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DGETSHRAQI | QQQQSYVEDL | RHQILAEEIR | AAKELEFDQA | WISQQIKENQ | QCLLREETWL | ASLQQQQQED | QVAEKELEAS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VALDAWLQTD | PEIQPSPFVQ | SQKRVVHLQL | LRRHTLRAAE | RNVRRKKVSF | QLERIIKKQR | LLEAQKRLEK | LTTLCWLQDD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| STQEPPYQVL | SPDATVPRPP | CRSKLTSCSS | LSPQRLCSKH | MPQLHSIFLS | WDPSTTLPPR | PDPTHQTSEK | TSSEEHLPQA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ASYPARTGCL | RKNGLHSSGH | GQPCTARAAL | ARKGASAPDA | CLTMSPNSVG | IQEMEMGVKQ | PHQMVSQGLA | SLRKSANKLK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PRHEPKIFTS | TTQTRGAKGL | ADPSHTQAGW | RKEGNLGTHK | AAKGASCNSL | YPHGPRQTAG | HGKAVKTFWT | EYKPPSPSRA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SKRHQRVLAT | RVRNITKKSS | HLPLGSPLKR | QQNTRDPDTM | VPLTDFSPVM | DHSREKDNDL | SDTDSNYSLD | SLSCVYAKAL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| IEPLKPEERK | WDFPEPENSE | SDDSQLSEDS | LAEKRYQSPK | NRLGGNRPTN | NRGQPRTRTR | ASVRGFTAAS | DSDLLAQTHR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SFSLDSLIDA | EEELGEDQQE | EPFPGSADEI | PTETFWHLED | SSLPVMDQEA | ICRLGPINYR | TAARLDAVLP | MSSSFYLDPQ |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| FQPHCELQPH | CELQPHCELQ | PHCEQAESQV | EPSYSEQADS | LQGMQLSRES | PLMSMDSWFS | CDSKINPSSP | PGIVGSLCPS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PDMQEFHSCK | GERPGYWPNT | EELKPSDAET | VLPYSSKLHQ | GSTELLCSAR | DEHTASAADT | SRLSLWGIQR | LIQPGADGTF |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| QGRCIPDMTQ | QGSSEASHNS | SVSNVLAASA | TTLTHVGSTH | ERDWSALQQK | YLLELSCPVL | EAIGAPKPAY | PYLEEDSGSL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| AQASSKGGDT | LLPVGPRVSS | NLNLNNFPVH | LSRIRRLRAE | KEQDSLNAKL | EGVSDFFSTS | EKEASYDETY | SADLESLSAS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| RSTNAQVFAT | ENAIPDSMTE | ACEVKQNNLE | ECLQSCRKPG | LMTSSDEDFF | QKNACHSNVT | TATKADHWSQ | GWAPLRKNSA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| VQPGQLSPDS | HYPLEEEKTD | CQESSKEAVR | RHINVSFALP | SGPELYLHSA | PWNPLSSSLQ | PPLLETFYVT | KSRDALTETA |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| LEIPACREVR | VPSPPPREAW | GFGHNHQALQ | GAYLKNNLPV | LLQNQNSKIA | SSQQVTAEIP | VDLNTREVIR | ESGKCPGNIT |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| EESHDSVYSS | VTQNRHFLPS | TSTKVCEFEN | QVVILNKKHS | FPALEGGEVT | AQSCCGASSD | STESGKSLLF | RESEAREEEE |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LDQNTVLRQT | INVSLEKDMP | GESAVSLKSR | SVDRRVSSPV | MVAQGGGPTP | KWEGKNETGL | LEKGLRPKDS | SEEFKLPGTK |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| PAYERFQLVA | CPQERNPSEC | KSQEMLNPNR | EPSGKKQNKR | VNNTDEMARL | IRSVMQLENG | ILEIESKQNK | QVHASHTPGT |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| DKELVFQDQK | EQEKTDHAFR | PDSSGNPLPS | KDQPSSPRQT | DDTVFRDSEA | GAMEVNSIGN | HPQVQKITPN | PFRSREGVRE |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| SEPVREHTHP | AGSDRPARDI | CDSLGKHTTC | REFTNTSLHP | QRMKALARAL | PLQPRLERSS | KNNGQFVKAS | ASLKGQPWGL |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| GSLEELETVK | GFQESQVAEH | VSSSNQEEPK | AQGKVEEMPM | QRGGSLQEEN | KVTQKFPSLS | QLCRDTFFRQ | ETVSPLLSRT |
| 2330 | 2340 | 2350 | 2360 | 2370 | 2380 | 2390 | 2400 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 387 | 1 | 1294.0546 | -62.74 | 2 | 34.8 | 12.0 | 2 | 136-157 | K.DCASLPSSCRIKVSFLEIYNER.V | Carbamidomethyl: 2 |

# Detailed Protein Report

## Protein 222: MAP kinase-activating death domain protein isoform j [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|209863002 | **Score:** | 40.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 170.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530395946 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: MAP kinase-activating death domain protein isoform X18 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVQKKKFCPR | LLDYLVIVGA | RHPSSDSVAQ | TPELLRRYPL | EDHTEFPLPP | DVVFFCQPEG | CLSVRQRRMS | LRDDTSFVFT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LTDKDTGVTR | YGICVNFYRS | FQKRISKEKG | EGGAGSRGKE | GTHATCASEE | GGTESSESGS | SLQPLSADST | PDVNQSPRGK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RRAKAGSRSR | NSTLTSLCVL | SHYPFFSTFR | ECLYTLKRLV | DCCSERLLGK | KLGIPRGVQR | DTMWRIFTGS | LLVEEKSSAL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LHDLREIEAW | IYRLLRSPVP | VSGQKRVDIE | VLPQELQPAL | TFALPDPSRF | TLVDFPLHLP | LELLGVDACL | QVLTCILLEH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KVVLQSRDYN | ALSMSVMAFV | AMIYPLEYMF | PVIPLLPTCM | ASAEQLLLAP | TPYIIGVPAS | FFLYKLDFKM | PDDVWLVDLD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SNRVIAPTNA | EVLPILPEPE | SLELKKHLKQ | ALASMSLNTQ | PILNLEKFHE | GQEIPLLLGR | PSNDLQSTPS | TEFNPLIYGN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DVDSVDVATR | VAMVRFFNSA | NVLQGFQMHT | RTLRLFPRPV | VAFQAGSFLA | SRPRQTPFAE | KLARTQAVEY | FGEWILNPTN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YAFQRIHNNM | FDPALIGDKP | KWYAHQLQPI | HYRVYDSNSQ | LAEALSVPPE | RDSDSEPTDD | SGSDSMDYDD | SSSSYSSLGD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FVSEMMKCDI | NGDTPNVDPL | THAALGDASE | VEIDELQNQK | EAEEPGPDSE | NSQENPPLRS | SSSTTASSSP | STVIHGANSE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PADSTEMDDK | AAVGVSKPLP | SVPPSIGKSN | VDRRQAEIGE | GAQKLLRPNS | LRLASDSDAE | SDSRASSPNS | TVSNTSTEGF |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GGIMSFASSL | YRNHSTSFSL | SNLTLPTKGA | REKATPFPSL | KGNRRALVDQ | KSSVIKHSPT | VKREPPSPQG | RSSNSSENQQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| FLKEVVHSVL | DGQGVGWLNM | KKVRRLLESE | QLRVFVLSKL | NRMVQSEDDA | RQDIIPDVEI | SRKVYKGMLD | LLKCTVLSLE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QSYAHAGLGG | MASIFGLLEI | AQTHYYSKEP | DKRKRSPTES | VNTPVGKDPG | LAGRGDPKAM | AQLRVPQLGP | RAPSATGKGP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KELDTRSLKE | ENFIASIGPE | VIKPVFDLGE | TEEKKSQISA | DSGVSLTSSS | QRTDQDSVIG | VSPAVMIRSS | SQDSEVSNSS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GETLGADSDL | SSNAGDGPGG | EGSVHLASSR | GTLSDSEIET | NSATSTIFGK | AHSLKPSIKE | KLAGSPIRTS | EDVSQRVYLY |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EGLLGKERST | LWDQMQFWED | AFLDAVMLER | EGMGMDQGPQ | EMIDRYLSLG | EHDRKRLEDD | EDRLLATLLH | NLISYMLLMK |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VNKNDIRKKV | RRLMGKSHIG | LVYSQQINEV | LDQLANLNGR | DLSIWSSGSR | HMKKQTFVVH | AGTDTNGDIF | FMEVCDDCVV |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LRSNIGTVYE | RWWYEKLINM | TYCPKTKVLC | LWRRNGSETQ | LNKFYTKKCR | ELYYCVKDSM | ERAAARQQSI | KPGPELGGEF |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| PVQDLKTGEG | GLLQVTLEGI | NLKFMHNQVF | IELNHIKKCN | TVRGVFVLEE | FVPEIKEVVS | HKYKTPMAHE | ICYSVLCLFS |
| 1530 | 1540 | 1550 | | | | | |
| YVAAVHSSEE | DLRTPPRPVS | S | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 974 | 1 | 547.7654 | -198.26 | 2 | 40.5 | 10.2 | 2 | 207-216 | R.LLGKKLGIPR.G | |

# Detailed Protein Report

## Protein 223: multicilin [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|299782571 | **Score:** | 40.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 6.5 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQACGGGAAG | RRAFDSICPN | RMLALPGRAL | LCKPGKPERK | FAPPRKFFPG | CTGGSPVSVY | EDPPDAEPTA | LPALTTIDLQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DLADCSSLLG | SDAPPGGDLA | ASQNHSHQTE | ADFNLQDFRD | TVDDLISDSS | SMMSPTLASG | DFPFSPCDIS | PFGPCLSPPL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DPRALQSPPL | RPPDVPPPEQ | YWKEVADQNQ | RALGDALVEN | NQLHVTLTQK | QEEIASLKER | NVQLKELASR | TRHLASVLDK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LMITQSRDCG | AAAEPFLLKA | KAKRSLEELV | SAAGQDCAEV | DAILREISER | CDEALQSRDP | KRPRLLPEPA | NTDTRPGNLH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| GAFRGLRTDC | SRSALNLSHS | ELEEGGSFST | RIRSHSTIRT | LAFPQGNAFT | IRTANGGYKF | RWVPS | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 809 | 1 | 526.2922 | 129.61 | 2 | 38.5 | 29.2 | 0 | 1-11 | -.MQACGGGAAGR.R | Carbamidomethyl: 4;<br>Oxidation: 1 |
| 1958 | 1 | 745.7963 | -121.94 | 2 | 54.9 | 11.2 | 1 | 248-261 | R.DCGAAAEPFLLKAK.A | Carbamidomethyl: 2 |

# Detailed Protein Report

**Protein 224:** **PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X9 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578821730 | **Score:** | 40.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 423.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 2 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEKEETTREL | LLPNWQGSGS | HGLTIAQRDD | GVFVQEVTQN | SPAARTGVVK | EGDQIVGATI | YFDNLQSGEV | TQLLNTMGHH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TVGLKLHRKG | DRSPEPGQTW | TREVFSSCSS | EVVLSGDDEE | YQRIYTTKIK | PRLKSEDGVE | GDLGETQSRT | ITVTRRVTAY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TVDVTGREGA | KDIDISSPEF | KIKIPRHELT | EISNVDVETQ | SGKTVIRLPS | GSGAASPTGS | AVDIRAGAIS | ASGPELQGAG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HSKLQVTMPG | IKVGGSGVNV | NAKGLDLGGR | GGVQVPAVDI | SSSLGGRAVE | VQGPSLESGD | HGKIKFPTMK | VPKFGVSTGR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EGQTPKAGLR | VSAPEVSVGH | KGGKPGLTIQ | APQLEVSVPS | ANIEGLEGKL | KGPQITGPSL | EGDLGLKGAK | PQGHIGVDAS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| APQIGGSITG | PSVEVQAPDI | DVQGPGSKLN | VPKMKVPKFS | VSGAKGEETG | IDVTLPTGEV | TVPGVSGDVS | LPEIATGGLE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GKMKGTKVKT | PEMIIQKPKI | SMQDVDLSLG | SPKLKGDIKV | SAPGVQGDVK | GPQVALKGSR | VDIETPNLEG | TLTGPRLGSP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SGKTGTCRIS | MSEVDLNVAA | PKVKGGVDVT | LPRVEGKVKV | PEVDVRGPKV | DVSAPDVEAH | GPEWNLKMPK | MKMPTFSTPG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AKGEGPDVHM | TLPKGDISIS | GPKVNVEAPD | VNLEGLGGKL | KGPDVKLPDM | SVKTPKISMP | DVDLHVKGTK | VKGEYDVTVP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KLEGELKGPK | VDIDAPDVDV | HGPDWHLKMP | KMKMPKFSVP | GFKAEGPEVD | VNLPKADIDV | SGPKVDIEGP | DVNIEGPEGK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LKGPKFKMPE | MNIKAPKISM | PDIDLNLKGP | KVKGDVDVSL | PKVEGDLKGP | EVDIKGPKVD | IDAPDVDVHG | PDWHLKMPKI |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KMPKISMPGF | KGEGPDVDVN | LPKADIDVSG | PKVDVECPDV | NIEGPEGKWK | SPKFKMPEMH | FKTPKISMPD | IDLNLTGPKI |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KGDVDVTGPK | VEGDLKGPEV | DLKGPKVDID | VPDVNVQGPD | WHLKMPKMKM | PKFSMPGFKA | EGPEVDVNLP | KADVDVSGPK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VDVEGPDVNI | EGPEGKLKGP | KFKMPEMNIK | APKIPMPDFD | LHLKGPKVKG | DVDISLPKVE | GDLKGPEVDI | RGPQVDIDVP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DVGVQGPDWH | LKMPKVKMPK | FSMPGFKGEG | PDVDVNLPKA | DLDVSGPKVD | IDVPDVNIEG | PEGKLKGPKF | KMPEMNIKAP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KISMPDIDLN | LKGPKVKGDM | DVSLPKVEGD | MKVPDVDIKG | PKVDINAPDV | DVQGPDWHLK | MPKIKMPKIS | MPGFKGEGPE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VDVNLPKADL | DVSGPKVDVD | VPDVNIEGPD | AKLKGPKFKM | PEMNIKAPKI | SMPDLDLNLK | GPKMKGEVDV | SLANVEGDLK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| GPALDIKGPK | IDVDAPDIDI | HGPDAKLKGP | KLKMPDMHVN | MPKISMPEID | LNLKGSKLKG | DVDVSGPKLE | GDIKAPSLDI |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KGPEVDVSGP | KLNIEGKSKK | SRFKLPKFNF | SGSKVQTPEV | DVKGKKPDID | ITGPKVDINA | PDVEVQGKVK | GSKFKMPFLS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ISSPKVSMPD | VELNLKSPKV | KGDLDIAGPN | LEGDFKGPKV | DIKAPEVNLN | APDVDVHGPD | WNLKMPKMKM | PKFSVSGLKA |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| EGPDVAVDLP | KGDINIEGPS | MNIEGPDLNV | EGPEGGLKGP | KFKMPDMNIK | APKISMPDID | LNLKGPKVKG | DVDISLPKLE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| GDLKGPEVDI | KGPKVDINAP | DVDVHGPDWH | LKMPKVKMPK | FSMPGFKGEG | PEVDVTLPKA | DIDISGPNVD | VDVPDVNIEG |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| PDAKLKGPKF | KMPEMNIKAP | KISMPDFDLN | LKGPKMKGDV | VVSLPKVEGD | LKGPEVDIKG | PKVDIDTPDI | NIEGSEGKFK |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| GPKFKIPEMH | LKAPKISMPD | IDLNLKGPKV | KGDVDVSLPK | MEGDLKGPEV | DIKGPKVDIN | APDVDVQGPD | WHLKMPKVKM |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| PKFSMPGFKG | EGPDVDVNLP | KADLDVSGPK | VDIDVPDVNI | EGPEGKLKGP | KFKMPEMNIK | APKISMPDID | LNLKGPKVKG |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| DMDVSLPKVE | GDMQVPDLDI | KGPKVDINAP | DVDVRGPDWH | LKMPKIKMPK | ISMPGFKGEG | PEVDVNLPKA | DLDVSGPKVD |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| VDVPDVNIEG | PDAKLKGPKF | KMPEMNIKAP | KISMPDFDLH | LKGPKVKGDV | DVSLPKMEGD | LKAPEVDIKG | PKVDIDAPDV |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 92 | 1 | 726.3490 | -51.60 | 3 | 31.1 | 15.9 | 2 | 1041-1061 | K.VDVEGPDVNIEGPEGKLKGPK.F | |
| 1546 | 1 | 506.2878 | 21.02 | 2 | 47.6 | 11.8 | 1 | 2863-2872 | K.GPEADIKGPK.V | |

# Detailed Protein Report

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## Protein 225: catenin alpha-1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|55770844 | **Score:** | 40.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 100.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 3 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578810148 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: catenin alpha-1 isoform X4 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTAVHAGNIN | FKWDPKSLEI | RTLAVERLLE | PLVTQVTTLV | NTNSKGPSNK | KRGRSKKAHV | LAASVEQATE | NFLEKGDKIA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KESQFLKEEL | VAAVEDVRKQ | GDLMKAAAGE | FADDPCSSVK | RGNMVRAARA | LLSAVTRLLI | LADMADVYKL | LVQLKVVEDG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ILKLRNAGNE | QDLGIQYKAL | KPEVDKLNIM | AAKRQQELKD | VGHRDQMAAA | RGILQKNVPI | LYTASQACLQ | HPDVAAYKAN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RDLIYKQLQQ | AVTGISNAAQ | ATASDDASQH | QGGGGGELAY | ALNNFDKQII | VDPLSFSEER | FRPSLEERLE | SIISGAALMA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DSSCTRDDRR | ERIVAECNAV | RQALQDLLSE | YMGNAGRKER | SDALNSAIDK | MTKKTRDLRR | QLRKAVMDHV | SDSFLETNVP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LLVLIEAAKN | GNEKEVKEYA | QVFREHANKL | IEVANLACSI | SNNEEGVKLV | RMSASQLEAL | CPQVINAALA | LAAKPQSKLA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QENMDLFKEQ | WEKQVRVLTD | AVDDITSIDD | FLAVSENHIL | EDVNKCVIAL | QEKDVDGLDR | TAGAIRGRAA | RVIHVVTSEM |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DNYEPGVYTE | KVLEATKLLS | NTVMPRFTEQ | VEAAVEALSS | DPAQPMDENE | FIDASRLVYD | GIRDIRKAVL | MIRTPEELDD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SDFETEDFDV | RSRTSVQTED | DQLIAGQSAR | AIMAQLPQEQ | KAKIAEQVAS | FQEEKSKLDA | EVSKWDDSGN | DIIVLAKQMC |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| MIMMEMTDFT | RGKGPLKNTS | DVISAAKKIA | EAGSRMDKLG | RTIADHCPDS | ACKQDLLAYL | QRIALYCHQL | NICSKVKAEV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QNLGGELVVS | GVDSAMSLIQ | AAKNLMNAVV | QTVKASYVAS | TKYQKSQGMA | SLNLPAVSWK | MKAPEKKPLV | KREKQDETQT |
| 890 | 900 | 910 | | | | | |
| KIKRASQKKH | VNPVQALSEF | KAMDSI | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2291 | 2 | 682.7592 | -174.39 | 2 | 59.1 | 12.9 | 0 | 138-149 | R.LLILADMADVYK.L | |
| 2280 | 1 | 920.8411 | -26.04 | 2 | 58.9 | 13.1 | 0 | 718-731 | K.QMCMIMMEMTDFTR.G | Carbamidomethyl: 3;<br>Oxidation: 2 |
| 2652 | 3 | 659.3500 | 103.51 | 2 | 61.5 | 14.3 | 0 | 762-773 | R.TIADHCPDSACK.Q | Carbamidomethyl: 11 |

# Detailed Protein Report

## Protein 226: PREDICTED: diacylglycerol kinase alpha isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530399854 | **Score:** | 40.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530399856 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: diacylglycerol kinase alpha isoform X3 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVLRNRRGWG | ERLSPLGLNL | KEVDKIILQM | MRVAEYLDWD | VSELRPILQE | MMKEIDYDGS | GSVSQAEWVR | AGATTVPLLV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LLGLEMTLKD | DGQHMWRPKR | FPRPVYCNLC | ESSIGLGKQG | LSCNLCKYTV | HDQCAMKALP | CEVSTYAKSR | KDIGVQSHVW |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VRGGCESGRC | DRCQKKIRIY | HSLTGLHCVW | CHLEIHDDCL | QAVGHECDCG | LLRDHILPPS | SIYPSVLASG | PDRKNSKTSQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KTMDDLNLST | SEALRIDPVP | NTHPLLVFVN | PKSGGKQGQR | VLWKFQYILN | PRQVFNLLKD | GPEIGLRLFK | DVPDSRILVC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GGDGTVGWIL | ETIDKANLPV | LPPVAVLPLG | TGNDLARCLR | WGGGYEGQNL | AKILKDLEMS | KVVHMDRWSV | EVIPQQTEEK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SDPVPFQIIN | NYFSIGVDAS | IAHRFHIMRE | KYPEKFNSRM | KNKLWYFEFA | TSESIFSTCK | KLEESLTVEI | CGKPLDLSNL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SLEGIAVLNI | PSMHGGSNLW | GDTRRPHGDI | YGINQALGAT | AKVITDPDIL | KTCVPDLSDK | RLEVVGLEGA | IEMGQIYTKL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| KNAGRRLAKC | SEITFHTTKT | LPMQIDGEPW | MQTPCTIKIT | HKNQMPMLMG | PPPRSTNFFG | FLS | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1847 | 1 | 577.2815 | 93.89 | 2 | 52.9 | 16.5 | 1 | 163-172 | R.GGCESGRCDR.C | Carbamidomethyl: 3, 8 |

# Detailed Protein Report

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## Protein 227: PREDICTED: thyroglobulin isoform X9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530389281 | **Score:** | 40.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 232.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 2 |

### Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 0.32 | **CV:** 0.00 % | **No. of Peptides:** 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MALVLEIFTL | LASICWVSAN | IFEYQVDAQP | LRPCELQRET | AFLKQADYVP | QCAEDGSFQT | VQCQNDGRSC | WCVGANGSEV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LGSRQPGRPV | ACLSFCQLQK | QQILLSGYIN | STDTSYLPQC | QDSGDYAPVQ | CDVQQVQCWC | VDAEGMEVYG | TRQLGRPKRC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PRSCEIRNRR | LLHGVGDKSP | PQCSAEGEFM | PVQCKFVNTT | DMMIFDLVHS | YNRFPDAFVT | FSSFQRRFPE | VSGYCHCADS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QGRELAETGL | ELLLDEIYDT | IFAGLDLPST | FTETTLYRIL | QRRFLAVQSV | ISGRFRCPTK | CEVERFTATS | FGHPYVPSCR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RNGDYQAVQC | QTEGPCWCVD | AQGKEMHGTR | QQGEPPSCAE | GQSCASERQQ | ALSRLYFGTS | GYFSQHDLFS | SPEKRWASPR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VARFATSCPP | TIKELFVDSG | LLRPMVEGQS | QQFSVSENLL | KEAIRAIFPS | RGLARLALQF | TTNPKRLQQN | LFGGKFLVNV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GQFNLSGALG | TRGTFNFSQF | FQQLGLASFL | NGGRQEDLAK | PLSVGLDSNS | STGTPEAAKK | DGTMNKPTVG | SFGFEINLQE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NQNALKFLAS | LLELPEFLLF | LQHAISVPED | VARDLGDVME | TVLSSQTCEQ | TPERLFVPSC | TTEGSYEDVQ | CFSGECWCVN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SWGKELPGSR | VRGGQPRCPT | DCEKQRARMQ | SLMGSQPAGS | TLFVPACTSE | GHFLPVQCFN | SECYCVDAEG | QAIPGTRSAI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GKPKKCPTPC | QLQSEQAFLR | TVQALLSNSS | MLPTLSDTYI | PQCSTDGQWR | QVQCNGPPEQ | VFELYQRWEA | QNKGQDLTPA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KLLVKIMSYR | EAASGNFSLF | IQSLYEAGQQ | DVFPVLSQYP | SLQDVPLAAL | EGKRPQPREN | ILLEPYLFWQ | ILNGQLSQYP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GSYSDFSTPL | AHFDLRNCWC | VDEAGQELEG | MRSEPSKLPT | CPGSCEEAKL | RVLQFIRETE | EIVSASNSSR | FPLGESFLVA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KGIRLRNEDL | GLPPLFPPRE | AFAEQFLRGS | DYAIRLAAQS | TLSFYQRRRF | SPDDSAGASA | LLRSGPYMPQ | CDAFGSWEPV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QCHAGTGHCW | CVDEKGGFIP | GSLTARSLQI | PQCPTTCEKS | RTSGLLSSWK | QARSQENPSP | KDLFVPACLE | TGEYARLQAS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GAGTWCVDPA | SGEELRPGSS | SSAQCPSLCN | VLKSGVLSRR | VSPGYVPACR | AEDGGFSPVQ | CDQAQGSCWC | VMDSGEEVPG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TRVTGGQPAC | ESPRCPLPFN | ASEVVGGTIL | CETISGPTGS | AMQQCQLLCR | QGSWSVFPPG | PLICSLESGR | WESQLPQPRA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| CQRPQLWQTI | QTQGHFQLQL | PPGKMCSADY | ADLLQTFQVF | ILDELTARGF | CQIQVKTFGT | LVSIPVCNNS | SVQVGCLTRE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| RLGVNVTWKS | RLEDIPVASL | PDLHDIERAL | VGKDLLGRFT | DLIQSGSFQL | HLDSKTFPAE | TIRFLQGDHF | GTSPRTWFGC |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SEGFYQVLTS | EASQDGLGCV | KCPEGSYSQD | EECIPCPVGF | YQEQAGSLAC | VPCPVGRTTI | SAGAFSQTHC | VTDCQRNEAG |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| LQCDQNGQYR | ASQKDRGSGK | AFCVDGEGRR | LPWWETEAPL | EDSQCLMMQK | FEKVPESKVI | FDANAPVAVR | SKVPDSEFPV |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| MQCLTDCTED | EACSFFTVST | TEPEISCDFY | AWTSDNVACM | TSDQKRDALG | NSKATSFGSL | RCQVKVRSHG | QDSPAVYLKK |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| GQGSTTTLQK | RFEPTGFQNM | LSGLYNPIVF | SASGANLTDA | HLFCLLACDR | DLCCDGFVLT | QVQGGAIICG | LLSSPSVLLC |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| NVKDWMDPSE | AWANATCPGV | TYDQESHQVI | LRLGDQEFIK | SLTPLEGTQD | TFTNFQQVYL | WKDSDMGSRP | ESMGCRKDTV |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| PRPASPTEAG | LTTELFSPVD | LNQVIVNGNQ | SLSSQKHWLF | KHLFSAQQAN | LWCLSRCVQE | HSFCQLAEIT | ESASLYFTCT |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LYPEAQVCDD | IMESNAQGCR | LILPQMPKAL | FRKKVILEDK | VKNFYTRLPF | QKLMGISIRN | KVPMSEKSIS | NGFFECERRC |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| DADPCCTGFG | FLNVSQLKGG | EVTCLTLNSL | GIQMCSEENG | GAWRILDCGS | PDIEVHTYPF | GWYQKPIAQN | NAPSFCPLVV |
| 2090 | 2100 | 2110 | | | | | |
| LPSLTEKVFK | VREVRGTQLK | RME | | | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2716 | 3 | 645.8279 | 25.63 | 2 | 64.3 | 20.3 | 2 | 160-169 | R.CPRSCEIRNR.R | Carbamidomethyl: 1 | |
| 1580 | 1 | 502.6699 | -218.64 | 2 | 50.0 | 19.9 | 0 | 467-475 | R.LQQNLFGGK.F | | QU:MU 0.32 |

# Detailed Protein Report

## Protein 228: pleckstrin homology domain-containing family A member 4 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|238859653 | **Score:** | 40.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 64.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.7 |
| | | **Sequence Coverage [%]:** | 5.3 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.67 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.21 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEGSRPRSSL | SLASSASTIS | SLSSLSPKKP | TRAVNKIHAF | GKRGNALRRD | PNLPVHIRGW | LHKQDSSGLR | LWKRRWFVLS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GHCLFYYKDS | REESVLGSVL | LPSYNIRPDG | PGAPRGRRFT | FTAEHPGMRT | YVLAADTLED | LRGWLRALGR | ASRAEGDDYG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QPRSPARPQP | GEGPGGPGGP | PEVSRGEEGR | ISESPEVTRL | SRGRGRPRLL | TPSPTTDLHS | GLQMRRARSP | DLFTPLSRPP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SPLSLPRPRS | APARRPPAPS | GDTAPPARPH | TPLSRIDVRP | PLDWGPQRQT | LSRPPTPRRG | PPSEAGGGKP | PRSPQHWSQE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PRTQPGPPLE | STFHQSLETD | TLLTKLCGQD | RLLRRLQEEI | DQKQEEKEQL | EAALELTRQQ | LGQATREAGA | PGRAWGRQRL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LQDRLVSVRA | TLCHLTQERE | RVWDTYSGLE | QELGTLRETL | EYLLHLGSPQ | DRVSAQQQLW | MVEDTLAGLG | GPQKPPPHTE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PDSPSPVLQG | EESSERESLP | ESLELSSPRS | PETDWGRPPG | GDKDLASPHL | GLGSPRVSRA | SSPEGRHLPS | PQLGTKSKEH |
| 570 | 580 | 590 | | | | | |
| HPLLADFRRS | PGAGSQPLPS | PGY | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 489 | 3 | 603.8256 | 17.71 | 2 | 36.1 | 13.9 | 0 | 300-312 | R.GPPSEAGGGKPPR.S | | WUP:QUP 1.21<br>QU:MU 0.67 |
| 20 | 1 | 706.3988 | 42.59 | 2 | 29.2 | 15.0 | 2 | 387-399 | R.EAGAPGRAWGRQR.L | | |

# Detailed Protein Report

## Protein 229: PREDICTED: nipped-B-like protein isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530378766 | **Score:** | 40.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 257.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVSIDLHQAG | RVDSQASITQ | DSDSIKKPEE | IKQCNDAPVS | VLQEDIVGSL | KSTPENHPET | PKKKSDPELS | KSEMKQSESR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LAESKPNENR | LVETKSSENK | LETKVETQTE | ELKQNESRTT | ECKQNESTIV | EPKQNENRLS | DTKPNDNKQN | NGRSETTKSR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PETPKQKGES | RPETPKQKSD | GHPETPKQKG | DGRPETPKQK | GESRPETPKQ | KNEGRPETPK | HRHDNRRDSG | KPSTEKKPEV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SKHKQDTKSD | SPRLKSERAE | ALKQRPDGRS | VSESLRRDHD | NKQKSDDRGE | SERHRGDQSR | VRRPETLRSS | SRNEHGIKSD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SSKTDKLERK | HRHESGDSRE | RPSSGEQKSR | PDSPRVKQGD | SNKSRSDKLG | FKSPTSKDDK | RTEGNKSKVD | TNKAHPDNKA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EFPSYLLGGR | SGALKNFVIP | KIKRDKDGNV | TQETKKMEMK | GEPKDKVEKI | GLVEDLNKGA | KPVVVLQKLS | LDDVQKLIKD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| REDKSRSSLK | PIKNKPSKSN | KGSIDQSVLK | ELPPELLAEI | ESTMPLCERV | KMNKRKRSTV | NEKPKYAEIS | SDEDNDSDEA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FESSRKRHKK | DDDKAWEYEE | RDRRSSGDHR | RSGHSHEGRR | SSGGGRYRNR | SPSDSDMEDY | SPPPSLSEVA | RKMKKKEKQK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KRKAYEPKLT | PEEMMDSSTF | KRFTASIENI | LDNLEDMDFT | AFGDDDEIPQ | ELLLGKHQLN | ELGSESAKIK | AMGIMDKLST |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DKTVKVLNIL | EKNIQDGSKL | STLLNHNNDT | EEEERLWRDL | IMERVTKSAD | ACLTTINIMT | SPNMPKAVYI | EDVIERVIQY |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TKFHLQNTLY | PQYDPVYRLD | PHGGGLLSSK | AKRAKCSTHK | QRVIVMLYNK | VCDIVSSLSE | LLEIQLLTDT | TILQVSSMGI |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TPFFVENVSE | LQLCAIKLVT | AVFSRYEKHR | QLILEEIFTS | LARLPTSKRS | LRNFRLNSSD | MDGEPMYIQM | VTALVLQLIQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| CVVHLPSSEK | DSNAEEDSNK | KIDQDVVITN | SYETAMRTAQ | NFLSIFLKKC | GSKQGEEDYR | PLFENFVQDL | LSTVNKPEWP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AAELLLSLLG | RLLVHQFSNK | STEMALRVAS | LDYLGTVAAR | LRKDAVTSKM | DQGSIERILK | QVSGGEDEIQ | QLQKALLDYL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DENTETDPSL | VFSRKFYIAQ | WFRDTTLETE | KAMKSQKDEE | SSEGTHHAKE | IETTGQIMHR | AENRKKFLRS | IIKTTPSQFS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TLKMNSDTVD | YDDACLIVRY | LASMRPFAQS | FDIYLTQILR | VLGENAIAVR | TKAMKCLSEV | VAVDPSILAR | LDMQRGVHGR |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LMDNSTSVRE | AAVELLGRFV | LCRPQLAEQY | YDMLIERILD | TGISVRKRVI | KILRDICIEQ | PTFPKITEMC | VKMIRRVNDE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| EGIKKLVNET | FQKLWFTPTP | HNDKEAMTRK | ILNITDVVAA | CRDTGYDWFE | QLLQNLLKSE | EDSSYKPVKK | ACTQLVDNLV |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EHILKYEESL | ADSDNKGVNS | GRLVACITTL | FLFSKIRPQL | MVKHAMTMQP | YLTTKCSTQN | DFMVICNVAK | ILELVVPLME |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| HPSETFLATI | EEDLMKLIIK | YGMTVVQHCV | SCLGAVVNKV | TQNFKFVWAC | FNRYYGAISK | LKSQHQEDPN | NTSLLTNKPA |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LLRSLFTVGA | LCRHFDFDLE | DFKGNSKVNI | KDKVLELLMY | FTKHSDEEVQ | TKAIIGLGFA | FIQHPSLMFE | QEVKNLYNNI |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LSDKNSSVNL | KIQVLKNLQT | YLQEEDTRMQ | QADRDWKKVA | KQEDLKEMGD | VSSGMSSSIM | QLYLKQVLEA | FFHTQSSVRH |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| FALNVIALTL | NQGLIHPVQC | VPYLIAMGTD | PEPAMRNKAD | QQLVEIDKKY | AGFIHMKAVA | GMKMSYQVQQ | AINTCLKDPV |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| RGFRQDESSS | ALCSHLYSMI | RGNRQHRRAF | LISLLNLFDD | TAKTDVTMLL | YIADNLACFP | YQTQEEPLFI | MHHIDITLSV |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| SGSNLLQSFK | ESMVKDKRKE | RKSSPSKENE | SSDSEEEVSR | PRKSRKRVDS | DSDSDSEDDI | NSVMKCLPEN | SAPLIEFANV |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| SQGILLLLML | KQHLKNLCGF | SDSKIQKYSP | SESAKVYDKA | INRKTGVHFH | PKQTLDFLRS | DMANSKITEE | VKRSIVKQYL |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| DFKLLMEHLD | PDEEEEEGEV | SASTNARNKA | ITSLLGGGSP | KNNTAAETED | DESDGEDRGG | GTSGSLRRSK | RNSDSTELAA |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| QMNESVDVMD | VIAICCPKYK | DRPQIARVVQ | KTSSGFSVQW | MAGSYSGSWT | EAKRRDGRKL | VPWVDTIKES | DIIYKKIALT |
| 2250 | 2260 | 2270 | | | | | |
| SANKLTNKVV | QTLRSLYAAK | DGTSS | | | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2607 | 1 | 913.4633 | -59.64 | 2 | 62.6 | 12.0 | 1 | 909-923 | K.HRQLILEEIFTSLAR.L | |
| 425 | 1 | 946.2023 | 58.66 | 3 | 35.0 | 14.6 | 2 | 1692-1714 | K.IQVLKNLQTYLQEEDTRMQQADR.D | Oxidation: 18 |

# Detailed Protein Report

## **Protein 230:** ubiquitin carboxyl-terminal hydrolase 17 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|153792150 | **Score:** | 40.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 8.5 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.48 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.29 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEDDSLYLGG | EWQFNHFSKL | TSSRPDAAFA | EIQRTSLPEK | SPLSSEARVD | LCDDLAPVAR | QLAPRKKLPL | SSRRPAAVGA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GLQNMGNTCY | ENASLQCLTY | TPPLANYMLS | REHSQTCQRP | KCCMLCTMQA | HITWALHSPG | HVIQPSQALA | AGFHRGKQED |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AHEFLMFTVD | AMKKACLPGH | KQVDHHSKDT | TLIHQIFGGC | WRSQIKCLHC | HGISDTFDPY | LDIALDIQAA | QSVKQALEQL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VKPEELNGEN | AYHCGLCLQR | APASKTLTLH | TSAKVLILVL | KRFSDVTGNK | LAKNVQYPEC | LDMQPYMSQQ | NTGPLVYVLY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AVLVHAGWSC | HDGHYFSYVK | AQEGQWYKMD | DAKVTACSIT | SVLSQQAYVL | FYIQKSEWER | HSESVSRGRE | PRALGAEDTD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RRATQGELKR | DHPCLQAPEL | DERLVERATQ | ESTLDHWKFP | QEQNKTKPEF | NVRKVEGTLP | PNVLVIHQSK | YKCGMKNHHP |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| EQQSSLLNLS | STTRTDQESV | NTGTLASLQG | RTRRSKGKNK | HSKRALLVCQ | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1128 | 1 | 1019.1809 | 129.35 | 2 | 43.7 | 15.4 | 2 | 49-66 | R.VDLCDDLAPVARQLAPRK.K | Carbamidomethyl: 4 | |
| 184 | 1 | 424.2193 | 37.35 | 3 | 32.0 | 12.9 | 0 | 112-121 | R.EHSQTCQRPK.C | Carbamidomethyl: 6 | WUP:QUP 0.29<br>QU:MU 2.48 |

# Detailed Protein Report

## Protein 231: zinc finger protein 714 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|144953913 | **Score:** | 39.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 64.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.73 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 5.59 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MNVMLENYKN LVFLAGIAVS KQDPITSLEQ EKEPWNMKIC EMVDESPAMC SSFTRDLWPE QDIKDSFQQV ILRRHGKCEH
        90        100        110        120        130        140        150        160
ENLQLRKGSA NVVECKVYKK GYNELNQCLT TTQSKIFPCD KYIKVFHKIF NSNRHKTRHT GEKPFKCKKC DESFCMLLHL
       170        180        190        200        210        220        230        240
HQHKRIHIRE NSYQCEECDK VFKRFSTLTR HKRVHTGEKP FKCEECGKAF KHSSTLTTHK MIHTGEKPYR CEECGKAFYH
       250        260        270        280        290        300        310        320
SSHLTTHKVI HTGEKPFKCE ECGKAFNHPS ALTTHKFIHV KEKPYKCEEC DKAFNRFSYL TKHKIIHSGE KSYKCEQCGK
       330        340        350        360        370        380        390        400
GFNWSSTLTK HKRIHTGEKP YKCEECGKAF NVSSHLTTHK MIHTGEKPYK CEECGKAFNH SSKLTIHKII HTGEKPYKCE
       410        420        430        440        450        460        470        480
ECGKAFNQSS NLTKHKIIHT GEKLYKCEEC GKAFNRSSNL TTHKRIHTGE KPYKCEECGK AFNRSSNLTK HNIIHTGEKS
       490        500        510        520        530        540        550        560
YKCEECGKAF NQSSTLTKHR KIQQGMVAHA CNPNTLRGLG EQIARSGVQD QPGQHGKTPS LLKIQKFAGC GGRRL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2246 | 1 | 953.4417 | 47.81 | 2 | 58.5 | 14.9 | 0 | 39-55 | K.ICEMVDESPAMCSSFTR.D | | WUP:QUP | 5.59 |
| 2107 | 1 | 625.2545 | -125.14 | 2 | 54.7 | 10.4 | 2 | 544-554 | K.IQKFAGCGGRR.L | Carbamidomethyl: 7 | QU:MU | 1.73 |

# Detailed Protein Report

## Protein 232: von Willebrand factor preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|89191868 | **Score:** | 39.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 309.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.03 | **CV:** | 152.70 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 0.98 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MIPARFAGVL | LALALILPGT | LCAEGTRGRS | STARCSLFGS | DFVNTFDGSM | YSFAGYCSYL | LAGGCQKRSF | SIIGDFQNGK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RVSLSVYLGE | FFDIHLFVNG | TVTQGDQRVS | MPYASKGLYL | ETEAGYYKLS | GEAYGFVARI | DGSGNFQVLL | SDRYFNKTCG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LCGNFNIFAE | DDFMTQEGTL | TSDPYDFANS | WALSSGEQWC | ERASPPSSSC | NISSGEMQKG | LWEQCQLLKS | TSVFARCHPL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VDPEPFVALC | EKTLCECAGG | LECACPALLE | YARTCAQEGM | VLYGWTDHSA | CSPVCPAGME | YRQCVSPCAR | TCQSLHINEM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CQERCVDGCS | CPEGQLLDEG | LCVESTECPC | VHSGKRYPPG | TSLSRDCNTC | ICRNSQWICS | NEECPGECLV | TGQSHFKSFD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NRYFTFSGIC | QYLLARDCQD | HSFSIVIETV | QCADDRDAVC | TRSVTVRLPG | LHNSLVKLKH | GAGVAMDGQD | VQLPLLKGDL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RIQHTVTASV | RLSYGEDLQM | DWDGRGRLLV | KLSPVYAGKT | CGLCGNYNGN | QGDDFLTPSG | LAEPRVEDFG | NAWKLHGDCQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DLQKQHSDPC | ALNPRMTRFS | EEACAVLTSP | TFEACHRAVS | PLPYLRNCRY | DVCSCSDGRE | CLCGALASYA | AACAGRGVRV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AWREPGRCEL | NCPKGQVYLQ | CGTPCNLTCR | SLSYPDEECN | EACLEGCFCP | PGLYMDERGD | CVPKAQCPCY | YDGEIFQPED |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| IFSDHHTMCY | CEDGFMHCTM | SGVPGSLLPD | AVLSSPLSHR | SKRSLSCRPP | MVKLVCPADN | LRAEGLECTK | TCQNYDLECM |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SMGCVSGCLC | PPGMVRHENR | CVALERCPCF | HQGKEYAPGE | TVKIGCNTCV | CRDRKWNCTD | HVCDATCSTI | GMAHYLTFDG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LKYLFPGECQ | YVLVQDYCGS | NPGTFRILVG | NKGCSHPSVK | CKKRVTILVE | GGEIELFDGE | VNVKRPMKDE | THFEVVESGR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| YIILLLGKAL | SVVWDRHLSI | SVVLKQTYQE | KVCGLCGNFD | GIQNNDLTSS | NLQVEEDPVD | FGNSWKVSSQ | CADTRKVPLD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SSPATCHNNI | MKQTMVDSSC | RILTSDVFQD | CNKLVDPEPY | LDVCIYDTCS | CESIGDCACF | CDTIAAYAHV | CAQHGKVVTW |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RTATLCPQSC | EERNLRENGY | ECEWRYNSCA | PACQVTCQHP | EPLACPVQCV | EGCHAHCPPG | KILDELLQTC | VDPEDCPVCE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VAGRRFASGK | KVTLNPSDPE | HCQICHCDVV | NLTCEACQEP | GGLVVPPTDA | PVSPTTLYVE | DISEPPLHDF | YCSRLLDLVF |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LLDGSSRLSE | AEFEVLKAFV | VDMMERLRIS | QKWVRVAVVE | YHDGSHAYIG | LKDRKRPSEL | RRIASQVKYA | GSQVASTSEV |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LKYTLFQIFS | KIDRPEASRI | TLLLMASQEP | QRMSRNFVRY | VQGLKKKKVI | VIPVGIGPHA | NLKQIRLIEK | QAPENKAFVL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SSVDELEQQR | DEIVSYLCDL | APEAPPPTLP | PDMAQVTVGP | GLLGVSTLGP | KRNSMVLDVA | FVLEGSDKIG | EADFNRSKEF |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| MEEVIQRMDV | GQDSIHVTVL | QYSYMVTVEY | PFSEAQSKGD | ILQRVREIRY | QGGNRTNTGL | ALRYLSDHSF | LVSQGDREQA |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| PNLVYMVTGN | PASDEIKRLP | GDIQVVPIGV | GPNANVQELE | RIGWPNAPIL | IQDFETLPRE | APDLVLQRCC | SGEGLQIPTL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| SPAPDCSQPL | DVILLLDGSS | SFPASYFDEM | KSFAKAFISK | ANIGPRLTQV | SVLQYGSITT | IDVPWNVVPE | KAHLLSLVDV |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| MQREGGPSQI | GDALGFAVRY | LTSEMHGARP | GASKAVVILV | TDVSVDSVDA | AADAARSNRV | TVFPIGIGDR | YDAAQLRILA |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| GPAGDSNVVK | LQRIEDLPTM | VTLGNSFLHK | LCSGFVRICM | DEDGNEKRPG | DVWTLPDQCH | TVTCQPDGQT | LLKSHRVNCD |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| RGLRPSCPNS | QSPVKVEETC | GCRWTCPCVC | TGSSTRHIVT | FDGQNFKLTG | SCSYVLFQNK | EQDLEVILHN | GACSPGARQG |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| CMKSIEVKHS | ALSVELHSDM | EVTVNGRLVS | VPYVGGNMEV | NVYGAIMHEV | RFNHLGHIFT | FTPQNNEFQL | QLSPKTFASK |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| TYGLCGICDE | NGANDFMLRD | GTVTTDWKTL | VQEWTVQRPG | QTCQPILEEQ | CLVPDSSHCQ | VLLLPLFAEC | HKVLAPATFY |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1145 | 2 | 729.1568 | -199.23 | 2 | 42.6 | 14.5 | 0 | 1944-1956 | R.WTCPCVCTGSSTR.H | Carbamidomethyl: 5 | WUP:QUP 0.98<br>QU:MU 0.68 |
| 1133 | 2 | 729.1918 | -151.33 | 2 | 42.4 | 15.1 | 0 | 1944-1956 | R.WTCPCVCTGSSTR.H | Carbamidomethyl: 3 | |
| 99 | 1 | 845.3517 | -47.80 | 3 | 31.0 | 10.4 | 1 | 2289-2311 | K.VNCTTQPCPTAKAPTCGLCEVARL | Carbamidomethyl: 8, 16, 19 | QU:MU 6.08 |

# Detailed Protein Report

## Protein 233: PREDICTED: SPOC domain-containing protein 1 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578800076 | **Score:** | 39.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 100.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 4.4 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.73 | **CV:** | 12.14 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 0.59 | **CV:** | 55.09 % | **No. of Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSQAGDVEGP | STGDPVLSPQ | HNCELLQNME | GASSMPGLSP | DGPGASSGPG | VRAGSRRKIP | RKEALRGGSS | RAAGAAEVRP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GVLELLAVVQ | SRGSMLAPGL | HMQLPSVPTQ | GRALTSKRLQ | VSLCDILDDS | CPRKLCSRSA | GLPERALACR | ERLAGVEEVS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CLRPREARDG | GMSSPGCDRR | SPTLSKEEPP | GRPLTSSPDP | VPVRLGSGPV | IQLLGAISHG | QAGGQLPPKL | EVLEDLMEVS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SPSPAQRLRR | KKRPMVQGPA | GCQVFQPSPS | GGTAGDPGGL | SDPFYPPRSG | SLALGDPSSD | PACSQSGPME | AEEDSLPEQP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EDSAQLQQEK | PSLYIGVRGT | VVRSMQEVLW | TRLRELPDPV | LSEEVVEGIA | AGIEAALWDL | TQGTNGRYKT | KYRSLLFNLR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DPRNLDLFLK | VVHGDVTPYD | LVRMSSMQLA | PQELARWRDQ | EEKRGLNIIE | QQQKEPCRLP | ASKMTHKGEV | EIQRDMDQTL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TLEDLVGPQM | FMDCSPQALP | IASEDTTGQH | DHHFLDPNCH | ICKDWEPSNE | LLGSFEAAKS | CGDNIFQKAL | SQTPMPAPEM |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PKTRELSPTE | PQDRVPPSGL | HVPAAPTKAL | PCLPPWEGVL | DMFSIKRFRA | RAQLVSGHSC | RLVQALPTVI | RSAGCIPSNI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VWDLLASICP | AKAKDVCVVR | LCPHGARDTQ | NCRLLYSYLN | DRQRHGLASV | EHMGMVLLPL | PAFQPLPTRL | RPLGGPGLEV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| THSSLLLAVL | LPKEGLPDTA | GSSPWLGKVQ | KMVSFNSKVE | KRYYQPDDRR | PNVPLKGTPP | PGGAWQQSQG | RGSIAPRGIS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AWQRPPRGRG | RLWPEPENWQ | HPGRGQWPPE | PGLRQSQHPY | SVAPAGHGFG | RGQHFHRDSC | PHQALLRHLE | SLATMSHQLQ |
| 890 | 900 | 910 | 920 | 930 | 940 | | |
| ALLCPQTKSS | IPRPLQRLSS | ALAAPEPPGP | ARDSSLGPTD | EAGSECPFPR | KA | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 815 | 1 | 647.6499 | -180.41 | 2 | 38.6 | 10.3 | 1 | 169-180 | R.DGGMSSPGCDRR.S | Carbamidomethyl: 9 | QU:MU 2.42 |
| 1959 | 1 | 757.2595 | -164.75 | 2 | 54.9 | 16.2 | 2 | 455-467 | K.EPCRLPASKMTHK.G | Oxidation: 10 | WUP:QUP 0.99 |
| 78 | 1 | 877.8658 | -95.96 | 2 | 30.9 | 13.3 | 1 | 549-564 | K.ALSQTPMPAPEMPKTR.E | | QU:MU 3.08<br>WUP:QUP 0.35 |

# Detailed Protein Report

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## Protein 234: putative hexokinase HKDC1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|156151420 | **Score:** | 39.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 102.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.2 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

***WUP:QUP*** **Median:** 0.15 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFAVHLMAFY | FSKLKEDQIK | KVDRFLYHMR | LSDDTLLDIM | RRFRAEMEKG | LAKDTNPTAA | VKMLPTFVRA | IPDGSENGEF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LSLDLGGSKF | RVLKVQVAEE | GKRHVQMESQ | FYPTPNEIIR | GNGTELFEYV | ADCLADFMKT | KDLKHKKLPL | GLTFSFPCRQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TKLEEGVLLS | WTKKFKARGV | QDTDVVSRLT | KAMRRHKDMD | VDILALVNDT | VGTMMTCAYD | DPYCEVGVII | GTGTNACYME |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DMSNIDLVEG | DEGRMCINTE | WGAFGDDGAL | EDIRTEFDRE | LDLGSLNPGK | QLFEKMISGL | YLGELVRLIL | LKMAKAGLLF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GGEKSSALHT | KGKIETRHVA | AMEKYKEGLA | NTREILVDLG | LEPSEADCIA | VQHVCTIVSF | RSANLCAAAL | AAILTRLREN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KKVERLRTTV | GMDGTLYKIH | PQYPKRLHKV | VRKLVPSCDV | RFLLSESGST | KGAAMVTAVA | SRVQAQRKQI | DRVLALFQLT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| REQLVDVQAK | MRAELEYGLK | KKSHGLATVR | MLPTYVCGLP | DGTEKGKFLA | LDLGGTNFRV | LLVKIRSGRR | SVRMYNKIFA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IPLEIMQGTG | EELFDHIVQC | IADFLDYMGL | KGASLPLGFT | FSFPCRQMSI | DKGTLIGWTK | GFKATDCEGE | DVVDMLREAI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KRRNEFDLDI | VAVVNDTVGT | MMTCGYEDPN | CEIGLIAGTG | SNMCYMEDMR | NIEMVEGGEG | KMCINTEWGG | FGDNGCIDDI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RTRYDTEVDE | GSLNPGKQRY | EKMTSGMYLG | EIVRQILIDL | TKQGLLFRGQ | ISERLRTRGI | FETKFLSQIE | SDRLALLQVR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RILQQLGLDS | TCEDSIVVKE | VCGAVSRRAA | QLCGAGLAAI | VEKRREDQGL | EHLRITVGVD | GTLYKLHPHF | SRILQETVKE |
| 890 | 900 | 910 | 920 | | | | |
| LAPRCDVTFM | LSEDGSGKGA | ALITAVAKRL | QQAQKEN | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2718 | 2 | 648.3573 | 22.96 | 2 | 62.4 | 12.9 | 2 | 43-53 | R.FRAEMEKGLAK.D | Oxidation: 5 | |
| 1075 | 1 | 947.1189 | 99.83 | 2 | 43.5 | 13.9 | 2 | 147-162 | K.KLPLGLTFSFPCRQTK.L | Carbamidomethyl: 12 | |
| 2984 | 5 | 973.5068 | -23.83 | 2 | 66.1 | 13.0 | 2 | 313-331 | K.MAKAGLLFGGEKSSALHTK.G | | WUP:QUP 0.15 |

# Detailed Protein Report

## Protein 235: insulin receptor-related protein precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|31657140 | **Score:** | 39.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 143.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.52 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAVPSLWPWG | ACLPVIFLSL | GFGLDTVEVC | PSLDIRSEVA | ELRQLENCSV | VEGHLQILLM | FTATGEDFRG | LSFPRLTQVT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DYLLLFRVYG | LESLRDLFPN | LAVIRGTRLF | LGYALVIFEM | PHLRDVALPA | LGAVLRGAVR | VEKNQELCHL | STIDWGLLQP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| APGANHIVGN | KLGEECADVC | PGVLGAAGEP | CAKTTFSGHT | DYRCWTSSHC | QRVCPCPHGM | ACTARGECCH | TECLGGCSQP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EDPRACVACR | HLYFQGACLW | ACPPGTYQYE | SWRCVTAERC | ASLHSVPGRA | STFGIHQGSC | LAQCPSGFTR | NSSSIFCHKC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EGLCPKECKV | GTKTIDSIQA | AQDLVGCTHV | EGSLILNLRQ | GYNLEPQLQH | SLGLVETITG | FLKIKHSFAL | VSLGFFKNLK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LIRGDAMVDG | NYTLYVLDNQ | NLQQLGSWVA | AGLTIPVGKI | YFAFNPRLCL | EHIYRLEEVT | GTRGRQNKAE | INPRTNGDRA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ACQTRTLRFV | SNVTEADRIL | LRWERYEPLE | ARDLLSFIVY | YKESPFQNAT | EHVGPDACGT | QSWNLLDVEL | PLSRTQEPGV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TLASLKPWTQ | YAVFVRAITL | TTEEDSPHQG | AQSPIVYLRT | LPAAPTVPQD | VISTSNSSSH | LLVRWKPPTQ | RNGNLTYYLV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LWQRLAEDGD | LYLNDYCHRG | LRLPTSNNDP | RFDGEDGDPE | AEMESDCCPC | QHPPPGQVLP | PLEAQEASFQ | KKFENFLHNA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ITIPISPWKV | TSINKSPQRD | SGRHRRAAGP | LRLGGNSSDF | EIQEDKVPRE | RAVLSGLRHF | TEYRIDIHAC | NHAAHTVGCS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AATFVFARTM | PHREADGIPG | KVAWEASSKN | SVLLRWLEPP | DPNGLILKYE | IKYRRLGEEA | TVLCVSRLRY | AKFGGVHLAL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LPPGNYSARV | RATSLAGNGS | WTDSVAFYIL | GPEEEDAGGL | HVLLTATPVG | LTLLIVLAAL | GFFYGKKRNR | TLYASVNPEY |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FSASDMYVPD | EWEVPREQIS | IIRELGQGSF | GMVYEGLARG | LEAGEESTPV | ALKTVNELAS | PRECIEFLKE | ASVMKAFKCH |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| HVVRLLGVVS | QGQPTLVIME | LMTRGDLKSH | LRSLRPEAEN | NPGLPQPALG | EMIQMAGEIA | DGMAYLAANK | FVHRDLAARN |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| CMVSQDFTVK | IGDFGMTRDV | YETDYYRKGG | KGLLPVRWMA | PESLKDGIFT | THSDVWSFGV | VLWEIVTLAE | QPYQGLSNEQ |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VLKFVMDGGV | LEELEGCPLQ | LQELMSRCWQ | PNPRLRPSFT | HILDSIQEEL | RPSFRLLSFY | YSPECRGARG | SLPTTDAEPD |
| 1290 | 1300 | | | | | | |
| SSPTPRDCSP | QNGGPGH | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 608 | 1 | 730.3714 | 88.53 | 2 | 37.6 | 15.3 | 0 | 213-225 | R.VCPCPHGMACTAR.G | Carbamidomethyl: 2, 4 | QU:MU | 1.52 |

# Detailed Protein Report

**Protein 236:** **PREDICTED: zinc finger protein 197 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578805510 | **Score:** | 39.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 96.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 3 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MALMLLTAQP | QELVMFEEVS | VCFTSEEWAC | LGPIQRALYW | DVMLENYGNV | TSLEWETMTE | NEEVTSKPSS | SQRADSHKGT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SKRLQGSVPQ | VLDFEEECEW | QVLASQWGNE | TDERADTVKK | VSLCERDKKK | RTPPEKQGQK | WKELGDSLTF | GSAISESLIG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TEGKKFYKCD | MCCKHFNKIS | HLINHRRIHT | GEKPHKCKEC | GKGFIQRSSL | LMHLRNHSGE | KPYKCNECGK | AFSQSAYLLN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HQRIHTGEKP | YKCKECGKGF | YRHSGLIIHL | RRHSGERPYK | CNECGKVFSQ | NAYLIDHQRL | HKGEEPYKCN | KCQKAFILKK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SLILHQRIHS | GEKPYKCDEC | GKTFAQTTYL | IDHQRLHSAE | NPYKCKECGK | VFIRSKSLLL | HQRVHTEKKT | FGCKKCGKIF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SSKSNFIDHK | RMHSREKPYK | CTECGKAFTQ | SAYLFDHQRL | HNGEKPYECN | ECGKVFILKK | SLILHQRFHT | GENLYECKDC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GKVFGSNRNL | IDHERLHNGE | KPYECRECGK | TFIMSKSFMV | HQKLHTQEKA | YKCEDCGKAF | SYNSSLLVHR | RIHTGEKPFE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| CSECGRAFSS | NRNLIEHKRI | HSGEKPYECD | ECGKCFILKK | SLIGHQRIHT | REKSYKCNDC | GKVFSYRSNL | IAHQRIHTGE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KPYACSECGK | GFTYNRNLIE | HQRIHSGEKT | YECHVCRKVL | TSSRNLMVHQ | RIHTGEKPYK | CNECGKDFSQ | NKNLVVHQRM |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HTGEKPYECD | KCRKSFTSKR | NLVGHQRIHT | GEKPYGCNDC | SKVFRQRKNL | TVHQKIHTDE | KPCECDVSEK | EFSQTSNLHL |
| 810 | 820 | 830 | | | | | |
| QQKIHTIEEF | SWLQNTNESK | IEIQKI | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1461 | 1 | 671.4129 | 203.04 | 2 | 46.6 | 14.0 | 2 | 165-174 | K.KFYKCDMCCK.H | Carbamidomethyl: 8;<br>Oxidation: 7 |
| 926 | 1 | 539.7356 | -166.84 | 2 | 41.1 | 10.3 | 2 | 312-320 | K.CQKAFILKK.S | |
| 2133 | 1 | 797.3986 | -7.50 | 2 | 57.0 | 15.4 | 0 | 343-355 | K.TFAQTTYLIDHQR.L | |

# Detailed Protein Report

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## Protein 237: putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|255982614 | **Score:** | 39.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 119.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MATPAGLERW | VQDELHSVLG | LSERHVAQFL | IGTAQRCTSA | EEFVQRLRDT | DTLDLSGPAR | DFALRLWNKV | PRKAVVEKPA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RAAEREARAL | LEKNRSYRLL | EDSEESSEET | VSRAGSSLQK | KRKKRKHLRK | KREEEEEEEA | SEKGKKKTGG | SKQQTEKPES |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EDEWERTERE | RLQDLEERDA | FAERVRQRDK | DRTRNVLERS | DKKAYEEAQK | RLKMAEEDRK | AMVPELRKKS | RREYLAKRER |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EKLEDLEAEL | ADEEFLFGDV | ELSRHERQEL | KYKRRVRDLA | REYRAAGEQE | KLEATNRYHM | PKETRGQPAR | AVDLVEEESG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| APGEEQRRWE | EARLGAASLK | FGARDAASQE | PKYQLVLEEE | ETIEFVRATQ | LQGDEEPSAP | PTSTQAQQKE | SIQAVRRSLP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VFPFREELLA | AIANHQVLII | EGETGSGKTT | QIPQYLFEEG | YTNKGMKIAC | TQPRRVAAMS | VAARVAREMG | VKLGNEVGYS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IRFEDCTSER | TVLRYMTDGM | LLREFLSEPD | LASYSVVMVD | EAHERTLHTD | ILFGLIKDVA | RFRPELKVLV | ASATMDTARF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| STFFDDAPVF | RIPGRRFPVD | IFYTKAPEAD | YLEACVVSVL | QIHVTQPPGD | ILVFLTGQEE | IEAACEMLQD | RCRRLGSKIR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ELLVLPIYAN | LPSDMQARIF | QPTPPGARKV | VVATNIAETS | LTIEGIIYVL | DPGFCKQKSY | NPRTGMESLT | VTPCSKASAN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QRAGRAGRVA | AGKCFRLYTA | WAYQHELEET | TVPEIQRTSL | GNVVLLLKSL | GIHDLMHFDF | LDPPPYETLL | LALEQLYALG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ALNHLGELTT | SGRKMAELPV | DPMLSKMILA | SEKYSCSEEI | LTVAAMLSVN | NSIFYRPKDK | VVHADNARVN | FFLPGGDHLV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LLNVYTQWAE | SGYSSQWCYE | NFVQFRSMRR | ARDVREQLEG | LLERVEVGLS | SCQGDYIRVR | KAITAGYFYH | TARLTRSGYR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TVKQQQTVFI | HPNSSLFEQQ | PRWLLYHELV | LTTKEFMRQV | LEIESSWLLE | VAPHYYKAKE | LEDPHAKKMP | KKIGKTREEL |
| 1050 | | | | | | | |
| G | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1748 | 1 | 1044.9652 | -43.04 | 2 | 51.7 | 25.1 | 2 | 285-302 | R.AAGEQEKLEATNRYHMPK.E | Oxidation: 16 |

# Detailed Protein Report

## Protein 238: PREDICTED: zinc finger protein 41 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530421580 | **Score:** | 39.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 79.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.2 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.98 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.01 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578838101 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 41 isoform X15 [Homo sapiens] |
| gi\|530421582 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 41 isoform X6 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MLEGEAPHQS CSGEAIGKMQ QQGIPGGIFF HCERFDQPIG EDSLCSILEE LWQDNDQLEQ RQENQNNLLS HVKVLIKERG
        90        100        110        120        130        140        150        160
YEHKNIEKII HVTTKLVPSI KRLHNCDTIL KHTLNSHNHN RNSATKNLGK IFGNGNNFPH SPSSTKNENA KTGANSCEHD
       170        180        190        200        210        220        230        240
HYEKHLSHKQ APTHHQKIHP EEKLYVCTEC VMGFTQKSHL FEHQRIHAGE KSRECDKSNK VFPQKPQVDV HPSVYTGEKP
       250        260        270        280        290        300        310        320
YLCTQCGKVF TLKSNLITHQ KIHTGQKPYK CSECGKAFFQ RSDLFRHLRI HTGEKPYECS ECGKGFSQNS DLSIHQKTHT
       330        340        350        360        370        380        390        400
GEKHYECNEC GKAFTRKSAL RMHQRIHTGE KPYVCADCGK AFIQKSHFNT HQRIHTGEKP YECSDCGKSF TKKSQLHVHQ
       410        420        430        440        450        460        470        480
RIHTGEKPYI CTECGKVFTH RTNLTTHQKT HTGEKPYMCA ECGKAFTDQS NLIKHQKTHT GEKPYKCNGC GKAFIWKSRL
       490        500        510        520        530        540        550        560
KIHQKSHIGE RHYECKDCGK AFIQKSTLSV HQRIHTGEKP YVCPECGKAF IQKSHFIAHH RIHTGEKPYE CSDCGKCFTK
       570        580        590        600        610        620        630        640
KSQLRVHQKI HTGEKPNICA ECGKAFTDRS NLITHQKIHT REKPYECGDC GKTFTWKSRL NIHQKSHTGE RHYECSKCGK
       650        660        670        680        690        700
AFIQKATLSM HQIIHTGKKP YACTECQKAF TDRSNLIKHQ KMHSGEKRYK ASD
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1222 | 1 | 955.6757 | 154.26 | 2 | 44.9 | 10.3 | 2 | 80-95 | R.GYEHKNIEKIIHVTTK.L | | |
| 2726 | 1 | 884.9432 | 75.73 | 2 | 64.4 | 16.1 | 0 | 430-444 | K.THTGEKPYMCAECGK.A | Carbamidomethyl: 10, 13 | |
| 1481 | 1 | 727.3860 | 6.97 | 2 | 48.7 | 13.2 | 1 | 455-466 | K.HQKTHTGEKPYK.C | | QU:MU 1.98<br>WUP:QUP 1.01 |

# Detailed Protein Report

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## Protein 239: putative uncharacterized zinc finger protein 814 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|222418585 | **Score:** | 39.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 97.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.7 |
|  |  | **No. of unique Peptides:** | 2 |

## Quantitation

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.80 | **CV:** | 23.03 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 1.94 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAAATLRLS | AQGTVTFEDV | AVNFTWEEWN | LLSEAQRCLY | RDVTLENLAL | ISSLGCWCGV | EDEAAPSKQS | IYIQRETQVR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TPMAGVSPKK | AHPCEMCGPI | LGDILHVADH | QGTHHKQKLH | RCEAWGNKLY | DSGNFHQHQN | EHIGEKPYRG | SVEEALFAKR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CKLHVSGESS | VFSESGKDFL | PRSGLLQQEA | SHTGEKSNSK | TECVSPIQCG | GAHYSCGESM | KHFSTKHILS | QHQRLLTREE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CYVCCECGKS | FSKYASLSNH | QRVHTEKKHE | CGECGKSFSK | YVSFSNHQRV | HTEKKHECGE | CGKSFSKYVS | FSNHQRVHTG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KRPYECGECG | KSFSKYASFS | NHQRVHTEKK | HYECGECGKS | FSKYVSFSNH | QRVHTGKRPY | ECGECGKSFS | KYASFSNHQR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VHTDKKHYEC | GECGKSFSQK | SSLIQHQRFH | TGEKPYGCEE | CGKSFSSEGH | LRSHQRVHAG | ERPFKCGECV | KSFSHKRSLV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HHQRVHSGER | PYQCGECGKS | FSQKGNLVLH | QRVHTGARPY | ECGECGKSFS | SKGHLRNHQQ | IHTGDRLYEC | GECGKSFSHK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GTLILHQRVH | PRERSYGCGE | CGKSFSSIGH | LRSHQRVHTG | ERPYECGECG | KSFSHKRSLV | HHQRMHTGER | PYKCGDCGKS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FNEKGHLRNH | QRVHTTERPF | KCGECGKCFS | HKGNLILHQH | GHTGERPYVC | RECGKLFKKK | SHLLVHQRIH | NGEKPYACEA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CQKFFRNKYQ | LIAHQRVHTG | ERPYECNDCG | KSFTHSSTFC | VHKRIHTGEK | PYECSECGKS | FAESSSFTKH | KRVHTGEKPY |
| 810 | 820 | 830 | 840 | 850 | 860 |  |  |
| ECSECGKSFA | ESSSLTKHKR | VHTGEKPYKC | EKCGKLFNKK | SHLLVHQSSH | WRKAI |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2009 | 1 | 766.2777 | -53.66 | 2 | 55.5 | 17.9 | 1 | 351-363 | K.HYECGECGKSFSK.Y | Carbamidomethyl: 7 | QU:MU 0.64 |
| 417 | 1 | 564.5160 | -156.98 | 3 | 35.2 | 11.2 | 1 | 653-667 | R.VHTTERPFKCGECGK.C |  | WUP:QUP 1.94<br>QU:MU 1.00 |

# Detailed Protein Report

## Protein 240: PREDICTED: uncharacterized protein LOC101928409 [Homo sapiens]

**Accession:** gi|530358441
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl, Oxidation

**Score:** 39.6
**MW [kDa]:** 60.4
**pI:** 11.3
**Sequence Coverage [%]:** 7.0
**No. of unique Peptides:** 3

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.04 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.35 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLGTVASPRP | GSLFSPPLAV | IKPGYEQGFK | SSLPHPQVYR | AAPELSDMLR | CGGQRRGGGI | ALCSLGVKSN | MNVKYCGKTE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SFQSRQRGPS | AGGPGRPESL | LPRVRLPEAL | LLAEDCRGNV | GEGEMDGGSR | AYKSDKYAHT | LTVTASHHAP | PPPTHMEGFE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LFHLPELCSP | SQDAQTTGRT | QMKPDHSPRP | SHRGRWVPKR | LLRLHPSSRV | VVRLVAEGAD | GARFGNTPHC | ILFHFTSTKE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ESRIGGRPPS | CFLMQITQHS | NRKSKLQGLL | LRGALEKEER | VVRARAGASE | AKSHSRGGWD | AWGLKANARG | RDGVGSGGRS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ALQSRPLPPA | SLEGGSGTCA | RSLSPGLCAS | AWRLPGKNLI | YFLPSRVSSL | PPRAAPFRRP | EPAPGPRGCS | GERGLGMSGG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VRAPPHPRAL | LGGDIQELKE | IPQEEVETSE | RRGNRLFCKK | TERRLEGLRK | AADGSQDNSV | RPVLQGNFNP | TRTQAKTIYI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YIYELTQNRA | TLVPTPPQVG | RHIQVALSED | GTWRLAGVAL | WRSRSPVSSY | EVSLLLQSSL | QRGDLATSLP | LGFPVNPL |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1973 | 1 | 902.8715 | -113.53 | 2 | 55.1 | 11.5 | 1 | 57-74 | R.GGGIALCSLGVKSNMNVK.Y | Carbamidomethyl: 7 | WUP:QUP 1.35<br>QU:MU 1.04 |
| 1325 | 1 | 640.6479 | -178.43 | 2 | 46.2 | 14.4 | 0 | 118-130 | R.GNVGEGEMDGGSR.A | Oxidation: 8 | |
| 2625 | 1 | 885.4475 | -93.73 | 1 | 62.9 | 13.6 | 0 | 515-522 | R.LAGVALWR.S | | |

# Detailed Protein Report

## Protein 241: E3 ubiquitin-protein ligase TRIP12 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|10863903 | **Score:** | 39.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 220.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 2 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSNRPNNNPG | GSLRRSQRNT | AGAQPQDDSI | GGRSCSSSSA | VIVPQPEDPD | RANTSERQKT | GQVPKKDNSR | GVKRSASPDY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NRTNSPSSAK | KPKALQHTES | PSETNKPHSK | SKKRHLDQEQ | QLKSAQSPST | SKAHTRKSGA | TGGSRSQKRK | RTESSCVKSG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SGSESTGAEE | RSAKPTKLAS | KSATSAKAGC | STITDSSSAA | STSSSSSAVA | SASSTVPPGA | RVKQGKDQNK | ARRSRSASSP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SPRRSSREKE | QSKTGGSSKF | DWAARFSPKV | SLPKTKLSLP | GSSKSETSKP | GPSGLQAKLA | SLRKSTKKRS | ESPPAELPSL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RRSTRQKTTG | SCASTSRRGS | GLGKRGAAEA | RRQEKMADPE | SNQEAVNSSA | ARTDEAPQGA | AGAVGMTTSG | ESESDDSEMG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RLQALLEARG | LPPHLFGPLG | PRMSQLFHRT | IGSGASSKAQ | QLLQGLQASD | ESQQLQAVIE | MCQLLVMGNE | ETLGGFPVKS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VVPALITLLQ | MEHNFDIMNH | ACRALTYMME | ALPRSSAVVV | DAIPVFLEKL | QVIQCIDVAE | QALTALEMLS | RRHSKAILQA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GGLADCLLYL | EFFSINAQRN | ALAIAANCCQ | SITPDEFHFV | ADSLPLLTQR | LTHQDKKSVE | STCLCFARLV | DNFQHEENLL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QQVASKDLLT | NVQQLLVVTP | PILSSGMFIM | VVRMFSLMCS | NCPTLAVQLM | KQNIAETLHF | LLCGASNGSC | QEQIDLVPRS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PQELYELTSL | ICELMPCLPK | EGIFAVDTML | KKGNAQNTDG | AIWQWRDDRG | LWHPYNRIDS | RIIEQINEDT | GTARAIQRKP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NPLANSNTSG | YSESKKDDAR | AQLMKEDPEL | AKSFIKTLFG | VLYEVYSSSA | GPAVRHKCLR | AILRIIYFAD | AELLKDVLKN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| HAVSSHIASM | LSSQDLKIVV | GALQMAEILM | QKLPDIFSVY | FRREGVMHQV | KHLAESESLL | TSPPKACTNG | SGSMGSTTSV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SSGTATAATH | AAADLGSPSL | QHSRDDSLDL | SPQGRLSDVL | KRKRLPKRGP | RRPKYSPPRD | DDKVDNQAKS | PTTTQSPKSS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| FLASLNPKTW | GRLSTQSNSN | NIEPARTAGG | SGLARAASKD | TISNNREKIK | GWIKEQAHKF | VERYFSSENM | DGSNPALNVL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QRLCAATEQL | NLQVDGGAEC | LVEIRSIVSE | SDVSSFEIQH | SGFVKQLLLY | LTSKSEKDAV | SREIRLKRFL | HVFFSSPLPG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EEPIGRVEPV | GNAPLLALVH | KMNNCLSQME | QFPVKVHDFP | SGNGTGGSFS | LNRGSQALKF | FNTHQLKCQL | QRHPDCANVK |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| QWKGGPVKID | PLALVQAIER | YLVVRGYGRV | REDDEDSDDD | GSDEEIDESL | AAQFLNSGNV | RHRLQFYIGE | HLLPYNMTVY |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| QAVRQFSIQA | EDERESTDDE | SNPLGRAGIW | TKTHTIWYKP | VREDEESNKD | CVGGKRGRAQ | TAPTKTSPRN | AKKHDELWHD |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GVCPSVSNPL | EVYLIPTPPE | NITFEDPSLD | VILLLRVLHA | ISRYWYYLYD | NAMCKEIIPT | SEFINSKLTA | KANRQLQDPL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| VIMTGNIPTW | LTELGKTCPF | FFPFDTRQML | FYVTAFDRDR | AMQRLLDTNP | EINQSDSQDS | RVAPRLDRKK | RTVNREELLK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QAESVMQDLG | SSRAMLEIQY | ENEVGTGLGP | TLEFYALVSQ | ELQRADLGLW | RGEEVTLSNP | KGSQEGTKYI | QNLQGLFALP |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| FGRTAKPAHI | AKVKMKFRFL | GKLMAKAIMD | FRLVDLPLGL | PFYKWMLRQE | TSLTSHDLFD | IDPVVARSVY | HLEDIVRQKK |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| RLEQDKSQTK | ESLQYALETL | TMNGCSVEDL | GLDFTLPGFP | NIELKKGGKD | IPVTIHNLEE | YLRLVIFWAL | NEGVSRQFDS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| FRDGFESVFP | LSHLQYFYPE | ELDQLLCGSK | ADTWDAKTLM | ECCRPDHGYT | HDSRAVKFLF | EILSSFDNEQ | QRLFLQFVTG |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| SPRLPVGGFR | SLNPPLTIVR | KTFESTENPD | DFLPSVMTCV | NYLKLPDYSS | IEIMREKLLI | AAREGQQSFH | LS |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1453 | 1 | 929.4464 | 3.04 | 2 | 46.5 | 10.5 | 1 | 16-33 | R.SQRNTAGAQPQDDSIGGR.S | |
| 1915 | 1 | 643.3072 | -50.38 | 2 | 54.3 | 12.5 | 2 | 133-145 | K.AHTRKSGATGGSR.S | |

# Detailed Protein Report

**Protein 242:** **PREDICTED: histone-lysine N-methyltransferase ASH1L isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530365070 | **Score:** | 39.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 296.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDPRNTAMLG | LGSDSEGFSR | KSPSAISTGT | LVSKREVELE | KNTKEEEDLR | KRNRERNIEA | GKDDGLTDAQ | QQFSVKETNF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SEGNLKLKIG | LQAKRTKKPP | KNLENYVCRP | AIKTTIKHPR | KALKSGKMTD | EKNEHCPSKR | DPSKLYKKAD | DVAAIECQSE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EVIRLHSQGE | NNPLSKKLSP | VHSEMADYIN | ATPSTLLGSR | DPDLKDRALL | NGGTSVTEKL | AQLIATCPPS | KSSKTKPKKL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GTGTTAGLVS | KDLIRKAGVG | SVAGIIHKDL | IKKPTISTAV | GLVTKDPGKK | PVFNAAVGLV | NKDSVKKLGT | GTTAVFINKN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LGKKPGTITT | VGLLSKDSGK | KLGIGIVPGL | VHKESGKKLG | LGTVVGLVNK | DLGKKLGSTV | GLVAKDCAKK | IVASSAMGLV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NKDIGKKLMS | CPLAGLISKD | AINLKAEALL | PTQEPLKASC | STNINNQESQ | ELSESLKDSA | TSKTFEKNVV | RQNKESILEK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FSVRKEIINL | EKEMFNEGTC | IQQDSFSSSE | KGSYETSKHE | KQPPVYCTSP | DFKMGGASDV | STAKSPFSAV | GESNLPSPSP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TVSVNPLTRS | PPETSSQLAP | NPLLLSSTTE | LIEEISESVG | KNQFTSESTH | LNVGHRSVGH | SISIECKGID | KEVNDSKTTH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IDIPRISSSL | GKKPSLTSES | SIHTITPSVV | NFTSLFSNKP | FLKLGAVSAS | DKHCQVAESL | STSLQSKPLK | KRKGRKPRWT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KVVARSTCRS | PKGLELERSE | LFKNVSCSSL | SNSNSEPAKF | MKNIGPPSFV | DHDFLKRRLP | KLSKSTAPSL | ALLADSEKPS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| HKSFATHKLS | SSMCVSSDLL | SDIYKPKRGR | PKSKEMPQLE | GPPKRTLKIP | ASKVFSLQSK | EEQEPPILQP | EIEIPSFKQG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LSVSPFPKKR | GRPKRQMRSP | VKMKPPVLSV | APFVATESPS | KLESESDNHR | SSSDFFESED | QLQDPDDLDD | SHRPSVCSMS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DLEMEPDKKI | TKRNNGQLMK | TIIRKINKMK | TLKRKKLLNQ | ILSSSVESSN | KGKVQSKLHN | TVSSLAATFG | SKLGQQINVS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KKGTIYIGKR | RGRKPKTVLN | GILSGSPTSL | AVLEQTAQQA | AGSALGQILP | PLLPSSASSS | EILPSPICSQ | SSGTSGGQSP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| VSSDAGFVEP | SSVPYLHLHS | RQGSMIQTLA | MKKASKGRRR | LSPPTLLPNS | PSHLSELTSL | KEATPSPISE | SHSDETIPSD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SGIGTDNNST | SDRAEKFCGQ | KKRRHSFEHV | SLIPPETSTV | LSSLKEKHKH | KCKRRNHDYL | SYDKMKRQKR | KRKKKYPQLR |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| NRQDPDFIAE | LEELISRLSE | IRITHRSHHF | IPRDLLPTIF | RINFNSFYTH | PSFPLDPLHY | IRKPDLKKKR | GRPPKMREAM |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| AEMPFMHSLS | FPLSSTGFYP | SYGMPYSPSP | LTAAPIGLGY | YGRYPPTLYP | PPPSPSFTTP | LPPPSYMHAG | HLLLNPAKYH |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KKKHKLLRQE | AFLTTSRTPL | LSMSTYPSVP | PEMAYGWMVE | HKHRHRHKHR | EHRSSEQPQV | SMDTGSSRSV | LESLKRYRFG |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| KDAVGERYKH | KEKHRCHMSC | PHLSPSKSLI | NREEQWVHRE | PSESSPLALG | LQTPLQIDCS | ESSPSLSLGG | FTPNSEPASS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| DEHTNLFTSA | IGSCRVSNPN | SSGRKKLTDS | PGLFSAQDTS | LNRLHRKESL | PSNERAVQTL | AGSQPTSDKP | SQRPSESTNC |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| SPTRKRSSSE | STSSTVNGVP | SRSPRLVASG | DDSVDSLLQR | MVQNEDQEPM | EKSIDAVIAT | ASAPPSSSPG | RSHSKDRTLG |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| KPDSLLVPAV | TSDSCNNSIS | LLSEKLTSSC | SPHHIKRSVV | EAMQRQARKM | CNYDKILATK | KNLDHVNKIL | KAKKLQRQAR |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| TGNNFVKRRP | GRPRKCPLQA | VVSMQAFQAA | QFVNPELNRD | EEGAALHLSP | DTVTDVIEAV | VQSVNLNPEH | KKGLKRKGWL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LEEQTRKKQK | PLPEEEEQEN | NKSFNEAPVE | IPSPSETPAK | PSEPESTLQP | VLSLIPREKK | PPRPPKKKYQ | KAGLYSDVYK |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| TTDPKSRLIQ | LKKEKLEYTP | GEHEYGLFPA | PIHVGKYLRQ | KRIDFQLPYD | ILWQWKHNQL | YKKPDVPLYK | KIRSNVYVDV |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| KPLSGYEATT | CNCKKPDDDT | RKGCVDDCLN | RMIFAECSPN | TCPCGEQCCN | QRIQRHEWVQ | CLERFRAEEK | GWGIRTKEPL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1736 | 1 | 853.3885 | -153.79 | 2 | 50.1 | 10.2 | 2 | 256-272 | R.KAGVGSVAGIIHKDLIK.K | |
| 1687 | 1 | 696.2420 | -115.78 | 3 | 49.4 | 11.7 | 1 | 744-762 | K.NVSCSSLSNSNSEPAKFMK.N | Carbamidomethyl: 4 |
| 1905 | 1 | 673.3043 | -162.57 | 2 | 54.2 | 17.5 | 0 | 2460-2472 | R.QALAAPLLNLPPK.K | |

# Detailed Protein Report

## Protein 243: probable exonuclease mut-7 homolog isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|145279204 | **Score:** | 39.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 96.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDPGDPAGDP | AAGERHRMGR | DPLLLLQALQ | TLWSTRERKQ | LREEAWRGFA | ALDDPLAGLL | DMLESCRGQR | GEGPSLAAWI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SHQLQCWLQA | QPCPSLAQHS | LRLKQLQARA | VKVLTESPPS | LAAPLASIFQ | LQDADRSCLL | AHVHRLHHEG | RFREAATLGA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TLKLQSELGV | EKMSIPLLLQ | DKVALVERYV | AGFPDLQRRL | LVLMDSWCQP | GFDIKDVARR | YPEVTSLSLE | KLSPKALSRQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VLRLQERYGV | APALCPNAAI | QQRLAALRHL | CHKRFVEKSL | SQENWTDHVQ | GLVGQSPWLQ | EQLSQLLVSH | SDPVTAAQCA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MELLLPEERL | PAAVAVELRR | FRLQGRATEA | DSRLEVKDMK | DRYYQLPIPR | ENVHLLASWE | DLTRHEGALL | QCHQVVGVDV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EWTPVFVAGG | RPRPSLLQVA | VEGHVFLLDV | LALSQPPTGQ | GAQAFSRLVA | QLLSDPSITK | LGYGMVGDLQ | KLGTSCPALA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HVEKQILGGM | DLLLVHRQMR | VASVPAPAVD | RARELRGLSL | LVQQVLGTAL | DKTQQLSNWD | RRPLCEEQVI | YAAADAYCLL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EVHQALCREP | ARFHLSEDLA | GSRRPRHRER | PGARKPPGLQ | KASAPAAPRQ | VPVAVAVSEG | AAPQIPARAF | RVVCDNMLQG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LARSLRCLGV | DARMLGNGED | HRRAAEVARQ | EGRIILTSGQ | PFHKLRAQVG | AGRCLSVDCS | LKAQQQAKAV | LKHFNVRVTH |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ADIFSRCQAC | NCDQYLKVSR | DMMKQLMWLS | SHQEGPRSSG | DEATQSQAVQ | EPGPAPDAAP | EGCTYDRPCR | WLQMADLRAE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TPDMLADGTR | LQLAGVPVGV | LRTPGLRCFY | CCTGCGKVFW | DGSHLGRVAT | HFRDMLESAP | SPCEPSPAPS | PASSPF |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1319 | 1 | 571.1608 | -69.20 | 2 | 46.1 | 14.7 | 0 | 828-837 | R.CFYCCTGCGK.V | Carbamidomethyl: 5 |

# Detailed Protein Report

## Protein 244: vitamin D3 receptor isoform VDRA [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4507883 | **Score:** | 39.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 48.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578824200 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: vitamin D3 receptor isoform X1 [Homo sapiens] |
| gi\|63054845 | refseq_human (refseq_human_20140103.fasta) | vitamin D3 receptor isoform VDRA [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MEAMAASTSL PDPGDFDRNV PRICGVCGDR ATGFHFNAMT CEGCKGFFRR SMKRKALFTC PFNGDCRITK DNRRHCQACR
        90        100        110        120        130        140        150        160
LKRCVDIGMM KEFILTDEEV QRKREMILKR KEEEALKDSL RPKLSEEQQR IIAILLDAHH KTYDPTYSDF CQFRPPVRVN
       170        180        190        200        210        220        230        240
DGGGSHPSRP NSRHTPSFSG DSSSSCSDHC ITSSDMMDSS SFSNLDLSEE DSDDPSVTLE LSQLSMLPHL ADLVSYSIQK
       250        260        270        280        290        300        310        320
VIGFAKMIPG FRDLTSEDQI VLLKSSAIEV IMLRSNESFT MDDMSWTCGN QDYKYRVSDV TKAGHSLELI EPLIKFQVGL
       330        340        350        360        370        380        390        400
KKLNLHEEEH VLLMAICIVS PDRPGVQDAA LIEAIQDRLS NTLQTYIRCR HPPPGSHLLY AKMIQKLADL RSLNEEHSKQ
       410        420        430
YRCLSFQPEC SMKLTPLVLE VFGNEIS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2332 | 3 | 665.1572 | -192.83 | 2 | 59.6 | 12.9 | 0 | 403-413 | R.CLSFQPECSMK.L | Carbamidomethyl: 1 |
| 2538 | 1 | 673.3328 | 74.17 | 2 | 61.7 | 14.1 | 0 | 403-413 | R.CLSFQPECSMK.L | Carbamidomethyl: 8; Oxidation: 10 |

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# Detailed Protein Report

**Protein 245:** **PREDICTED: arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 3 isoform X7 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578810904 | **Score:** | 39.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 149.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| | | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDPGCLYYGV | QPVGTPGAPD | RRESRGVCQG | RAEHRLSRQD | LEAREDAGYA | SLELPGDSTL | LSPTLETEET | SDDLISPYAS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FSFTADRLTP | LLSGWLDKLS | PQGNYVFQRR | FVQFNGRSLM | YFGSDKDPFP | KGVIPLTAIE | MTRSSKDNKF | QVITGQRVFV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FRTESEAQRD | MWCSTLQSCL | KEQRLLGHPR | PPQPPRPLRT | GMLELRGHKA | KVFAALSPGE | LALYKSEQAF | SLGIGICFIE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LQGCSVRETK | SRSFDLLTPH | RCFSFTAESG | GARQSWAAAL | QEAVTETLSD | YEVAEKIWSN | RANRQCADCG | SSRPDWAAVN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LGVVICKQCA | GQHRALGSGI | SKVQSLKLDT | SVWSNEIVQL | FIVLGNDRAN | RFWAGTLPPG | EGLHPDATPG | PRGEFISRKY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RLGLFRKPHP | QYPDHSQLLQ | ALCAAVARPN | LLKNMTQLLC | VEAFEGEEPW | FPPAPDGSCP | GLLPSDPSPG | VYNEVVVRAT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YSGFLYCSPV | SNKAGPSPPR | RGRDAPPRLW | CVLGAALEMF | ASENSPEPLS | LIQPQDIVCL | GVSPPPTDPG | DRFPFSFELI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LAGGRIQHFG | TDGADSLEAW | TSAVGKWFSP | LSCHQLLGPG | LLRLGRLWLR | SPSHTAPAPG | LWLSGFGLLR | GDHLFLCSAP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GPGPPAPEDM | VHLRRLQEIS | VVSAADTPDK | KEHLVLVETG | RTLYLQGEGR | LDFTAWNAAI | GGAAGGGGTG | LQEQQMSRGD |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| IPIIVDACIS | FVTQHGLRLE | GVYRKGGARA | RSLRLLAEFR | RDARSVKLRP | GEHFVEDVTD | TLKRFFRELD | DPVTSARLLP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RWREAAELPQ | KNQRLEKYKD | VIGCLPRVNR | RTLATLIGHL | YRVQKCAALN | QMCTRNLALL | FAPSVFQTDG | RGEHEVRVLQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ELIDGYISVF | DIDSDQVAQI | DLEVSLITTW | KDVQLSQAGD | LIMEVYIEQQ | LPDNCVTLKV | SPTLTAEELT | NQVLEMRGTA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| AGMDLWVTFE | IREHGELERP | LHPKEKVLEQ | ALQWCQLPEP | CSASLLLKKV | PLAQAGCLFT | GIRRESPRVG | LLRCREEPPR |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LLGSRFQERF | FLLRGRCLLL | LKEKKSSKPE | REWPLEGAKV | YLGIRKKLKP | PTPWGFTLIL | EKMHLYLSCT | DEDEMWDWTT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SILKAQHDDQ | QPVVLRRHSS | SDLARQKFGT | MPLLPIRGDD | SGATLLSANQ | TLRRLHNRRT | LSMFFPMKSS | QGSVEEQEEL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EEPVYEEPVY | EEVGAFPELI | QDTSTSFSTT | REWTVKPENP | LTSQKSLDQP | FLSKSSTLGQ | EERPPEPPPG | PPSKSSPQAR |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | |
| GSLEEQLLQE | LSSLILRKGE | TTAGLGSPSQ | PSSPQSPSPT | GLPTQTPGFP | TQPPCTSSPP | SSQPLT | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1500 | 1 | 850.8827 | -87.14 | 2 | 48.9 | 14.3 | 1 | 656-671 | R.LQEISVVSAADTPDKK.E | |

# Detailed Protein Report

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**Protein 246:** **PREDICTED: coiled-coil domain-containing protein 136 isoform X4 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530386309 | **Score:** | 38.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 131.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.5 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEAGAGAGAG | AAGWSCPGPG | PTVTTLGSYE | ASEGCERKKG | QRWGSLERRG | MQAMEGEVLL | PALYEEEEEE | EEEEEEVEEE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EEQVQKGGSV | GSLSVNKHRG | LSLTETELEE | LRAQVLQLVA | ELEETRELAG | QHEDDSLELQ | GLLEDERLAS | AQQAEVFTKQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IQQLQGELRS | LREEISLLEH | EKESELKEIE | QELHLAQAEI | QSLRQAAEDS | ATEHESDIAS | LQEDLCRMQN | ELEDMERIRG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DYEMEIASLR | AEMEMKSSEP | SGSLGLSDYS | GLQEELQELR | ERYHFLNEEY | RALQESNSSL | TGQLADLESE | RTQRATERWL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QSQTLSMTSA | ESQTSEMDFL | EPDPEMQLLR | QQLRDAEEQM | HGMKNKCQEL | CCELEELQHH | RQVSEEEQRR | LQRELKCAQN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EVLRFQTSHS | VTQNEELKSR | LCTLQKKYDT | SQDEQNELLK | MQLQLQTELR | QLKVMKSTLV | ENQSEKELLC | RLQKLHLQHQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NVTCEKEKLL | ERQQQLQEEL | QCHEAELQHL | RDTVASFKES | NEKDTETHAQ | LQEMKQLYQA | SKDELERQKH | MYDQLEQDLL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LCQLELKELK | ASHPIPEDKG | KCANKSQELL | TKLEDLCELQ | LLYQGMQEEQ | KKLIQNQDCV | LKEQLEIHEE | LRRFKESHFQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EVLENPDDSK | LAKSSKCNRN | KQSKLLMEQM | QALQVMYDAG | QAKQELLQQE | QGRLLEERKR | LQADLQLCLE | EMQLLQVQSP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SIKMSLESYG | KSYGSMVPSN | ENCRKTYDTT | VDDNESYYKS | YTSTQTSSKS | FLKSYDSSTS | ASEAYGKSYC | TTSNSSITYK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KSYGSTSSSD | TCQKSFVSSC | TDEEPAEPED | MERFEEMVVK | VLIKLQAVQA | MYQISQEEHS | QLQEQMEKLL | AKQKDLKEEL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DACEREFKEC | MECLEKPMAP | QNDKNEIKEL | QTKLRELQLQ | YQASMDEQGR | LLVVQEQLEG | QLQCCQEELR | QLREKRPSVV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KEARGKNANK | NMNKNANGVK | MKKVTKPCSD | TSESDLETRK | SLEVVLYYKA | SQRKLDGLAK | EEEKKEEMEE | EKKQVKEEAK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EQCGDELVAE | PADPEEAKST | EDQEENEEDK | EEEEKEEDSE | EEEDDADSSL | ESPEENNPLR | LSESKKNMFG | LWKPMVFLAI |
| 1130 | 1140 | 1150 | | | | | |
| AAVALYVLPN | MRQQESEFCL | ME | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 488 | 1 | 686.3221 | -115.45 | 2 | 36.1 | 10.5 | 2 | 905-915 | K.NEIKELQTKLR.E | |

# Detailed Protein Report

## **Protein 247:** tripartite motif-containing protein 66 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|209977097 | **Score:** | 38.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 134.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.8 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MARNCSECKE | KRAAHILCTY | CNRWLCSSCT | EEHRHSPVPG | GPFFPRAQKG | SPGVNGGPGD | FTLYCPLHTQ | EVLKLFCETC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DMLTCHSCLV | VEHKEHRCRH | VEEVLQNQRM | LLEGVTTQVA | HKKSSLQTSA | KQIEDRIFEV | KHQHRKVENQ | IKMAKMVLMN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ELNKQANGLI | EELEGITNER | KRKLEQQLQS | IMVLNRQFEH | VQNFINWAVC | SKTSVPFLFS | KELIVFQMQR | LLETSCNTDP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GSPWSIRFTW | EPNFWTKQLA | SLGCITTEGG | QMSRADAPAY | GGLQGSSPFY | QSHQSPVAQQ | EALSHPSHKF | QSPAVCSSSV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CCSHCSPVSP | SLKGQVPPPS | IHPAHSFRQP | PEMVPQQLGS | LQCSALLPRE | KELACSPHPP | KLLQPWLETQ | PPVEQESTSQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RLGQQLTSQP | VCIVPPQDVQ | QGAHAQPTLQ | TPSIQVQFGH | HQKLKLSHFQ | QQPQQQLPPP | PPPLPHPPPP | LPPPPQQPHP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PLPPSQHLAS | SQHESPPGPA | CSQNMDIMHH | KFELEEMQKD | LELLLQAQQP | SLQLSQTKSP | QHLQQTIVGQ | INYIVRQPAP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VQSQSQEETL | QATDEPPASQ | GSKPALPLDK | NTAAALPQAS | GEETPLSVPP | VDSTIQHSSP | NVVRKHSTSL | SIMGFSNTLE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| MELSSTRLER | PLEPQIQSVS | NLTAGAPQAV | PSLLSAPPKM | VSSLTSVQNQ | AMPSLTTSHL | QTVPSLVHST | FQSMPNLISD |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SPQAMASLAS | DHPQAGPSLM | SGHTQAVPSL | ATCPLQSIPP | VSDMQPETGS | SSSSGRTSGS | LCPRDGADPS | LENALCKVKL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EEPINLSVKK | PPLAPVVSTS | TALQQYQNPK | ECENFEQGAL | ELDAKENQSI | RAFNSEHKIP | YVRLERLKIC | AASSGEMPVF |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KLKPQKNDQD | GSFLLIIECG | TESSSMSIKV | SQDRLSEATQ | APGLEGRKVT | VTSLAGQRPP | EVEGTSPEEH | RLIPRTPGAK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KGPPAPIENE | DFCAVCLNGG | ELLCCDRCPK | VFHLSCHVPA | LLSFPGGEWV | CTLCRSLTQP | EMEYDCENAC | YNQPGMRASP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GLSMYDQKKC | EKLVLSLCCN | NLSLPFHEPV | SPLARHYYQI | IKRPMDLSII | RRKLQKKDPA | HYTTPEEVVS | DVRLMFWNCA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KFNYPDSEVA | EAGRCLEVFF | EGWLKEIYPE | KRFAQPRQED | SDSEEVSSES | GCSTPQGFPW | PPYMQEGIQP | KRRRRHMENE |
| 1210 | 1220 | | | | | | |
| RAKRMSFRLA | NSISQV | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1060 | 1 | 540.7960 | -96.21 | 2 | 41.5 | 11.4 | 2 | 952-961 | R.LIPRTPGAKK.G | |
| 862 | 1 | 942.1586 | 54.56 | 3 | 40.3 | 12.8 | 1 | 1098-1121 | K.DPAHYTTPEEVVSDVRLMFWNCAK.F | Oxidation: 18 |
| 2820 | 1 | 676.8699 | 24.74 | 2 | 63.9 | 14.6 | 1 | 1205-1216 | R.MSFRLANSISQV.- | |

# Detailed Protein Report

**Protein 248:** **frizzled-10 precursor [Homo sapiens]**

**Accession:** gi|6005762
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl, Oxidation

**Score:** 38.7
**MW [kDa]:** 65.3
**pI:** 9.9
**Sequence Coverage [%]:** 6.4
**No. of unique Peptides:** 2

```
        10         20         30         40         50         60         70         80
MQRPGPRLWL VLQVMGSCAA ISSMDMERPG DGKCQPIEIP MCKDIGYNMT RMPNLMGHEN QREAAIQLHE FAPLVEYGCH
        90        100        110        120        130        140        150        160
GHLRFFLCSL YAPMCTEQVS TPIPACRVMC EQARLKCSPI MEQFNFKWPD SLDCRKLPNK NDPNYLCMEA PNNGSDEPTR
       170        180        190        200        210        220        230        240
GSGLFPPLFR PQRPHSAQEH PLKDGGPGRG GCDNPGKFHH VEKSASCAPL CTPGVDVYWS REDKRFAVVW LAIWAVLCFF
       250        260        270        280        290        300        310        320
SSAFTVLTFL IDPARFRYPE RPIIFLSMCY CVYSVGYLIR LFAGAESIAC DRDSGQLYVI QEGLESTGCT LVFLVLYYFG
       330        340        350        360        370        380        390        400
MASSLWWVVL TLTWFLAAGK KWGHEAIEAN SSYFHLAAWA IPAVKTILIL VMRRVAGDEL TGVCYVGSMD VNALTGFVLI
       410        420        430        440        450        460        470        480
PLACYLVIGT SFILSGFVAL FHIRRVMKTG GENTDKLEKL MVRIGLFSVL YTVPATCVIA CYFYERLNMD YWKILAAQHK
       490        500        510        520        530        540        550        560
CKMNNQTKTL DCLMAASIPA VEIFMVKIFM LLVVGITSGM WIWTSKTLQS WQQVCSRRLK KKSRRKPASV ITSGGIYKKA
       570        580        590
QHPQKTHHGK YEIPAQSPTC V
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1958 | 1 | 655.2730 | -62.48 | 2 | 52.8 | 10.4 | 0 | 281-292 | R.LFAGAESIACDR.D | Carbamidomethyl: 10 |
| 2186 | 1 | 928.7350 | -68.15 | 3 | 55.7 | 17.1 | 1 | 483-507 | K.MNNQTKTLDCLMAASIPAVEIFMVK.I | Oxidation: 23 |

# Detailed Protein Report

## Protein 249: PREDICTED: otoferlin isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530368284 | **Score:** | 38.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 225.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.81 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.12 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MALLIHLKTV | SELRGRGDRI | AKVTFRGQSF | YSRVLENCED | VADFDETFRW | PVASSIDRNE | MLEIQVFNYS | KVFSNKLIGT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FRMVLQKVVE | ESHVEVTDTL | IDDNNAIIKT | SLCVEVRYQA | TDGTVGSWDD | GDFLGDESLQ | EEEKDSQETD | GLLPGSRPSS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RPPGEKSFRS | KGREKTKGGR | DDEHKAGRSV | FSAMKLGKNR | SHKEEPQRPD | EPAVLEMEDL | DHLAIRLGDG | LDPDSVSLAS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VTALTTNVSN | KRSKPDIKME | PSAGRPMDYQ | VSITVIEARQ | LVGLNMDPVV | CVEVGDDKKY | TSMKESTNCP | YYNEYFVFDF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HVSPDVMFDK | IIKISVIHSK | NLLRSGTLVG | SFKMDVGTVY | SQPEHQFHHK | WAILSDPDDI | SSGLKGYVKC | DVAVVGKGDN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IKTPHKANET | DEDDIEGNLL | LPEGVPPERQ | WARFYVKIYR | AEGLPRMNTS | LMANVKKAFI | GENKDLVDPY | VQVFFAGQKG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KTSVQKSSYE | PLWNEQVVFT | DLFPPLCKRM | KVQIRDSDKV | NDVAIGTHFI | DLRKISNDGD | KGFLPTLGPA | WVNMYGSTRN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YTLLDEHQDL | NEGLGEGVSF | RARLLLGLAV | EIVDTSNPEL | TSSTEVQVEQ | ATPISESCAG | KMEEFFLFGA | FLEASMIDRR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NGDKPITFEV | TIGNYGNEVD | GLSRPQRPRP | RKEPGDEEEV | DLIQNASDDE | AGDAGDLASV | SSTPPMRPQV | TDRNYFHLPY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LERKPCIYIK | SWWPDQRRRL | YNANIMDHIA | DKLEEGLNDI | QEMIKTEKSY | PERRLRGVLE | ELSCGCCRFL | SLADKDQGHS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SRTRLDRERL | KSCMRELENM | GQQARMLRAQ | VKRHTVRDKL | RLCQNFLQKL | RFLADEPQHS | IPDIFIWMMS | NNKRVAYARV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PSKDLLFSIV | EEETGKDCAK | VKTLFLKLPG | KRGFGSAGWT | VQAKVELYLW | LGLSKQRKEF | LCGLPCGFQE | VKAAQGLGLH |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| AFPPVSLVYT | KKQAFQLRAH | MYQARSLFAA | DSSGLSDPFA | RVFFINQSQC | TEVLNETLCP | TWDQMLVFDN | LELYGEAHEL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RDDPPIIVIE | IYDQDSMGKA | DFMGRTFAKP | LVKMADEAYC | PPRFPPQLEY | YQIYRGNATA | GDLLAAFELL | QIGPAGKADL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PPINGPVDVD | RGPIMPVPMG | IRPVLSKYRV | EVLFWGLRDL | KRVNLAQVDR | PRVDIECAGK | GVQSSLIHNY | KKNPNFNTLV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KWFEVDLPEN | ELLHPPLNIR | VVDCRAFGRY | TLVGSHAVSS | LRRFIYRPPD | RSAPSWNTTG | EVVVTMEPEV | PIKKLETMVK |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LDATSEAVVK | VDVAEEEKEK | KKKKKGTAEE | PEEEEPDESM | LDWWSKYFAS | IDTMKEQLRQ | QEPSGIDLEE | KEEVDNTEGL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KGSMKGKEKA | RAAKEEKKKK | TQSSGSGQGS | EAPEKKKPKI | DELKVYPKEL | ESEFDNFEDW | LHTFNLLRGK | TGDDEDGSTE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EERIVGRFKG | SLCVYKVPLP | EDVSREAGYD | STYGMFQGIP | SNDPINVLVR | VYVVRATDLH | PADINGKADP | YIAIRLGKTD |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| IRDKENYISK | QLNPVFGKSF | DIEASFPMES | MLTVAVYDWD | LVGTDDLIGE | TKIDLENRFY | SKHRATCGIA | QTYSTHGYNI |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| WRDPMKPSQI | LTRLCKDGKV | DGPHFGPPGR | VKVANRVFTG | PSEIEDENGQ | RKPTDEHVAL | LALRHWEDIP | RAGCRLVPEH |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| VETRPLLNPD | KPGIEQGRLE | LWVDMFPMDM | PAPGTPLDIS | PRKPKKYELR | VIIWNTDEVV | LEDDDFFTGE | KSSDIFVRGW |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| LKGQQEDKQD | TDVHYHSLTG | EGNFNWRYLF | PFDYLAAEEK | IVISKKESMF | SWDETEYKIP | ARLTLQIWDA | DHFSADDFLG |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| AIELDLNRFP | RGAKTAKQCT | MEMATGEVDV | PLVSIFKQKR | VKGWWPLLAR | NENDEFELTG | KVEAELHLLT | AEEAEKNPVG |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LARNEPDPLE | KPNRPDTAFV | WFLNPLKSIK | YLICTRYKWL | IIKIVLALLG | LLMLGLFLYS | LPGYMVKKLL | GA |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1211 | 2 | 839.3736 | -36.62 | 2 | 45.3 | 13.7 | 2 | 181-195 | R.DDEHKAGRSVFSAMK.L | | WUP:QUP 1.12<br>QU:MU 0.81 |
| 1207 | 1 | 984.1444 | 151.03 | 2 | 43.4 | 10.7 | 0 | 542-559 | K.GFLPTLGPAWVNMYGSTR.N | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2705 | 1 | 558.6699 | 91.00 | 3 | 64.9 | 14.3 | 1 | 739-752 | R.RLYNANIMDHIADK.L | | |

# Detailed Protein Report

**Protein 250:** **vasopressin-neurophysin 2-copeptin preproprotein [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|13259533 | **Score:** | 38.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 17.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 11.0 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MPDTMLPACF LGLLAFSSAC YFQNCPRGGK RAMSDLELRQ CLPCGPGGKG RCFGPSICCA DELGCFVGTA EALRCQEENY
        90        100        110        120        130        140        150        160
LPSPCQSGQK ACGSGGRCAA FGVCCNDESC VTEPECREGF HRRARASDRS NATQLDGPAG ALLLRLVQLA GAPEPFEPAQ
       170
PDAY
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2048 | 2 | 945.8202 | -134.22 | 2 | 56.0 | 14.9 | 1 | 32-49 | R.AMSDLELRQCLPCGPGGK.G | Oxidation: 2 |

# Detailed Protein Report

## Protein 251: rho GTPase-activating protein 11A isoform 3 [Homo sapiens]

**Accession:** gi|557128992
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 38.5
**MW [kDa]:** 92.6
**pI:** 9.9
**Sequence Coverage [%]:** 5.8
**No. of unique Peptides:** 3

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578827655 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: rho GTPase-activating protein 11A isoform X3 [Homo sapiens] |
| gi\|557129007 | refseq_human (refseq_human_20140103.fasta) | rho GTPase-activating protein 11A isoform 3 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MDSSNLAVIF APNLLQTSEG HEKMSSNTEK KLRLQAAVVQ TLIDYASDIG RVPDFILEKI PAMLGIDGLC ATPSLEGFEE
        90        100        110        120        130        140        150        160
GEYETPGEYK RKRRQSVGDF VSGALNKFKP NRTPSITPQE ERIAQLSESP VILTPNAKRT LPVDSSHGFS SKKRKSIKHN
       170        180        190        200        210        220        230        240
FNFELLPSNL FNSSSTPVSV HIDTSSEGSS QSSLSPVLIG GNHLITAGVP RRSKRIAGKK VCRVESGKAG CFSPKISHKE
       250        260        270        280        290        300        310        320
KVRRSLRLKF NLGKNGREVN GCSGVNRYES VGWRLANQQS LKNRIESVKT GLLFSPDVDE KLPKKGSEKI SKSEETLLTP
       330        340        350        360        370        380        390        400
ERLVGTNYRM SWTGPNNSSF QEVDANEASS MVENLEVENS LEPDIMVEKS PATSCELTPS NLNNKHNSNI TSSPLSGDEN
       410        420        430        440        450        460        470        480
NMTKETLVKV QKAFSESGSN LHALMNQRQS SVTNVGKVKL TEPSYLEDSP EENLFETNDL TIVESKEKYE HHTGKGEKCF
       490        500        510        520        530        540        550        560
SERDFSPLQT QTFNRETTIK CYSTQMKMEH EKDIHSNMPK DYLSKQEFSS DEEIKKQQSP KDKLNNKLKE NENMMEGNLP
       570        580        590        600        610        620        630        640
KCAAHSKDEA RSSFSQQSTC VVTNLSKPRP MRIAKQQSLE TCEKTVSESS QMTEHRKVSD HIQWFNKLSL NEPNRIKVKS
       650        660        670        680        690        700        710        720
PLKFQRTPVR QSVRRINSLL EYSRQPTGHK LASLGDTASP LVKSVSCDGA LSSCIESASK DSSVSCIKSG PKEQKSMSCE
       730        740        750        760        770        780        790        800
ESNIGAISKS SMELPSKSFL KMRKHPDSVN ASLRSTTVYK QKILSDGQVK VPLDDLTNHD IVKPVVNNNM GISSGINNRV
       810        820        830        840
LRRPSERGRA WYKGSPKHPI GKTQLLPTSK PVDL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1727 | 3 | 682.5948 | -72.91 | 3 | 51.9 | 11.1 | 0 | 386-404 | K.HNSNITSSPLSGDENNMTK.E | |
| 2120 | 2 | 703.2439 | -91.13 | 2 | 54.9 | 13.2 | 0 | 550-561 | K.ENENMMEGNLPK.C | |
| 2613 | 2 | 822.4595 | 113.47 | 2 | 63.4 | 14.2 | 0 | 684-700 | K.SVSCDGALSSCIESASK.D | |

# Detailed Protein Report

## Protein 252: PREDICTED: tetratricopeptide repeat protein 18 isoform X8 [Homo sapiens]

**Accession:** gi|530392981
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 38.4
**MW [kDa]:** 105.0
**pI:** 5.6
**Sequence Coverage [%]:** 4.3
**No. of unique Peptides:** 2

## Quantitation

***QU:MU*** **Median:** 0.36 **CV:** 0.00 % **No. of Peptides:** 1
***WUP:QUP*** **Median:** 2.95 **CV:** 0.00 % **No. of Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578818878 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: tetratricopeptide repeat protein 18 isoform X16 [Homo sapiens] |
| gi\|578818876 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: tetratricopeptide repeat protein 18 isoform X15 [Homo sapiens] |
| gi\|578818874 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: tetratricopeptide repeat protein 18 isoform X14 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVGLQVPSLG | EKDYPILFKN | GTLKLGGERE | PVPRPKKWPI | ANILAPGANN | IPDAFIVGGP | YEEEEGELNH | PEDSEFRNQA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ECIKKRIIWD | LESRCYLDPS | AVVSFQKRIA | DCRLWPVEIT | RVPLVTIPKG | KAGKTEKTDE | EAQLSFHGVA | YVNMVPLLYP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GVKRIRGAFH | VYPYLDSVVH | EKTKCLLSLF | RDIGHHLIHN | NKIGGINSLL | SKQAVSKNLK | EDKPVKEKDI | DGRPRPGDVQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| APSIKSQSSD | TPLEGEPPLS | HNPEGQQYVE | AGTYIVLEIQ | LDKALVPKRM | PEELARRVKE | MIPPRPPLTR | RTGGAQKAVS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DYHIQIKNIS | RAILDEYYRM | FGKQVAKLES | DMDSETLEEQ | KCQLSYELNC | SGKYFAFKEQ | LKHAVVKIVR | DKYLKTTSFE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SQEELQTFIS | ELYVFLVDQM | HVALNQTMPD | DVQGTVATIY | TSSEQLQLFA | FEAEVNENFE | MAAAYYKERL | VREPQNLDHW |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LDYGAFCLLT | EDNIKAQECF | QKALSLNQSH | IHSLLLCGVL | AVLLENYEQA | EIFFEDATCL | EPTNVVAWTL | LGLYYEIQNN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DIRMEMAFHE | ASKQLQARML | QAQVTKQKST | GVEDTEERGK | RESSLGPWGI | TNGSATAIKV | EAPAGPGAAL | SILDKFLEES |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SKLQSDSQEP | ILTTQTWDPS | ISQKPSNTFI | KEIPTKKEAS | KCQDSSALLH | PGLHYGVSQT | TTIFMETIHF | LMKVKAVQYV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HRVLAHELLC | PQGGPSCEYY | LVLAQTHILK | KNFAKAEEYL | QQAAQMDYLN | PNVWGLKGHL | YFLSGNHSEA | KACYERTISF |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VVDASEMHFI | FLRLGLIYLE | EKEYEKAKKT | YMQACKRSPS | CLTWLGLGIA | CYRLEELTEA | EDALSEANAL | NNYNAEVWAY |
| 890 | 900 | 910 | 920 | 930 | | | |
| LALVCLKVGR | QLEAEQAYKY | MIKLKLKDEA | LLAEIHTLQE | TVGFGNPSF | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1779 | 1 | 516.2947 | 29.06 | 2 | 50.6 | 10.7 | 0 | 87-94 | R.IIWDLESR.C | | WUP:QUP 2.95<br>QU:MU 0.36 |
| 81 | 1 | 1120.1328 | 99.73 | 2 | 30.9 | 12.9 | 1 | 778-796 | K.GHLYFLSGNHSEAKACYER.T | Carbamidomethyl: 16 | |

# Detailed Protein Report

## Protein 253: PREDICTED: serine-protein kinase ATM isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578822211 | **Score:** | 38.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 310.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MADICHQVFN | EDTRSLEISQ | SYTTTQRESS | DYSVPCKRKK | IELGWEVIKD | HLQKSQNDFD | LVPWLQIATQ | LISKYPASLP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NCELSPLLMI | LSQLLPQQRH | GERTPYVLRC | LTEVALCQDK | RSNLESSQKS | DLLKLWNKIW | CITFRGISSE | QIQAENFGLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GAIIQGSLVE | VDREFWKLFT | GSACRPSCPA | VCCLTLALTT | SIVPGTVKMG | IEQNMCEVNR | SFSLKESIMK | WLLFYQLEGD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LENSTEVPPI | LHSNFPHLVL | EKILVSLTMK | NCKAAMNFFQ | SVPECEHHQK | DKEELSFSEV | EELFLQTTFD | KMDFLTIVRE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CGIEKHQSSI | GFSVHQNLKE | SLDRCLLGLS | EQLLNNYSSE | ITNSETLVRC | SRLLVGVLGC | YCYMGVIAEE | EAYKSELFQK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AKSLMQCAGE | SITLFKNKTN | EEFRIGSLRN | MMQLCTRCLS | NCTKKSPNKI | ASGFFLRLLT | SKLMNDIADI | CKSLASFIKK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PFDRGEVESM | EDDTNGNLME | VEDQSSMNLF | NDYPDSSVSD | ANEPGESQST | IGAINPLAEE | YLSKQDLLFL | DMLKFLCLCV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TTAQTNTVSF | RAADIRRKLL | MLIDSSTLEP | TKSLHLHMYL | MLLKELPGEE | YPLPMEDVLE | LLKPLSNVCS | LYRRDQDVCK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TILNHVLHVV | KNLGQSNMDS | ENTRDAQGQF | LTVIGAFWHL | TKERKYIFSV | RMALVNCLKT | LLEADPYSKW | AILNVMGKDF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PVNEVFTQFL | ADNHHQVRML | AAESINRLFQ | DTKGDSSRLL | KALPLKLQQT | AFENAYLKAQ | EGMREMSHSA | ENPETLDEIY |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NRKSVLLTLI | AVVLSCSPIC | EKQALFALCK | SVKENGLEPH | LVKKVLEKVS | ETFGYRRLED | FMASHLDYLV | LEWLNLQDTE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| YNLSSFPFIL | LNYTNIEDFY | RSCYKVLIPH | LVIRSHFDEV | KSIANQIQED | WKSLLTDCFP | KILVNILPYF | AYEGTRDSGM |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| AQQRETATKV | YDMLKSENLL | GKQIDHLFIS | NLPEIVVELL | MTLHEPANSS | ASQSTDLCDF | SGDLDPAPNP | PHFPSHVIKA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TFAYISNCHK | TKLKSILEIL | SKSPDSYQKI | LLAICEQAAE | TNNVYKKHRI | LKIYHLFVSL | LLKDIKSGLG | GAWAFVLRDV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| IYTLIHYINQ | RPSCIMDVSL | RSFSLCCDLL | SQVCQTAVTY | CKDALENHLH | VIVGTLIPLV | YEQVEVQKQV | LDLLKYLVID |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| NKDNENLYIT | IKLLDPFPDH | VVFKDLRITQ | QKIKYSRGPF | SLLEEINHFL | SVSVYDALPL | TRLEGLKDLR | RQLELHKDQM |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VDIMRASQDN | PQDGIMVKLV | VNLLQLSKMA | INHTGEKEVL | EAVGSCLGEV | GPIDFSTIAI | QHSKDASYTK | ALKLFEDKEL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| QWTFIMLTYL | NNTLVEDCVK | VRSAAVTCLK | NILATKTGHS | FWEIYKMTTD | PMLAYLQPFR | TSRKKFLEVP | RFDKENPFEG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LDDINLWIPL | SENHDIWIKT | LTCAFLDSGG | TKCEILQLLK | PMCEVKTDFC | QTVLPYLIHD | ILLQDTNESW | RNLLSTHVQG |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| FFTSCLRHFS | QTSRSTTPAN | LDSESEHFFR | CCLDKKSQRT | MLAVVDYMRR | QKRPSSGTIF | NDAFWLDLNY | LEVAKVAQSC |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| AAHFTALLYA | EIYADKKSMD | DQEKRSLAFE | EGSQSTTISS | LSEKSKEETG | ISLQDLLLEI | YRSIGEPDSL | YGCGGGKMLQ |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| PITRLRTYEH | EAMWGKALVT | YDLETAIPSS | TRQAGIIQAL | QNLGLCHILS | VYLKGLDYEN | KDWCPELEEL | HYQAAWRNMQ |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| WDHCTSVSKE | VEGTSYHESL | YNALQSLRDR | EFSTFYESLK | YARVKEVEEM | CKRSLESVYS | LYPTLSRLQA | IGELESIGEL |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| FSRSVTHRQL | SEVYIKWQKH | SQLLKDSDFS | FQEPIMALRT | VILEILMEKE | MDNSQRECIK | DILTKHLVEL | SILARTFKNT |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| QLPERAIFQI | KQYNSVSCGV | SEWQLEEAQV | FWAKKEQSLA | LSILKQMIKK | LDASCAANNP | SLKLTYTECL | RVCGNWLAET |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| CLENPAVIMQ | TYLEKAVEVA | GNYDGESSDE | LRNGKMKAFL | SLARFSDTQY | QRIENYMKSS | EFENKQALLK | RAKEEVGLLR |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| EHKIQTNRYT | VKVQRELELD | ELALRALKED | RKRFLCKAVE | NYINCLLSGE | EHDMWVFRLC | SLWLENSGVS | EVNGMMKRDG |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| MKIPTYKFLP | LMYQLAARMG | TKMMGGLGFH | EVLNNLISRI | SMDHPHHTLF | IILALANANR | DEFLTKPEVA | RRSRITKNVP |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| KQSSQLDEDR | TEAANRIICT | IRSRRPQMVR | SVEALCDAYI | ILANLDATQW | KTQRKGINIP | ADQPITKLKN | LEDVVVPTME |
| 2330 | 2340 | 2350 | 2360 | 2370 | 2380 | 2390 | 2400 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2544 | 1 | 885.4222 | -31.19 | 2 | 61.8 | 14.9 | 1 | 403-418 | K.SLMQCAGESITLFKNK.T | |

# Detailed Protein Report

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**Protein 254:** **protein FAM104A isoform 3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|574956994 | **Score:** | 38.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 9.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.7 |
| | | **Sequence Coverage [%]:** | 40.8 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MGGRGADAGS SGGTGPTEGY SPPAASTRAA ARAKARGGGR GGRRNTTPSV PSLRGAAPRS FHPPAAMSER LRPSLQAVTV
        90        100        110
VGAAAAAAAA SIARTGPAGR KAA
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2165 | 4 | 974.4048 | -53.21 | 3 | 55.4 | 21.1 | 2 | 1-32 | -.MGGRGADAGSSGGTGPTEGYSPPAASTRAAAR.A | |

# Detailed Protein Report

## Protein 255: ATP-dependent DNA helicase Q1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|14591902 | **Score:** | 38.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 73.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 5.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578823000 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: ATP-dependent DNA helicase Q1 isoform X5 [Homo sapiens] |
| gi\|530399347 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: ATP-dependent DNA helicase Q1 isoform X4 [Homo sapiens] |
| gi\|530399345 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: ATP-dependent DNA helicase Q1 isoform X3 [Homo sapiens] |
| gi\|530399343 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: ATP-dependent DNA helicase Q1 isoform X2 [Homo sapiens] |
| gi\|530399341 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: ATP-dependent DNA helicase Q1 isoform X1 [Homo sapiens] |
| gi\|14591904 | refseq_human (refseq_human_20140103.fasta) | ATP-dependent DNA helicase Q1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASVSALTEE | LDSITSELHA | VEIQIQELTE | RQQELIQKKK | VLTKKIKQCL | EDSDAGASNE | YDSSPAAWNK | EDFPWSGKVK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DILQNVFKLE | KFRPLQLETI | NVTMAGKEVF | LVMPTGGGKS | LCYQLPALCS | DGFTLVICPL | ISLMEDQLMV | LKQLGISATM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LNASSSKEHV | KWVHAEMVNK | NSELKLIYVT | PEKIAKSKMF | MSRLEKAYEA | RRFTRIAVDE | VHCCSQWGHD | FRPDYKALGI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LKRQFPNASL | IGLTATATNH | VLTDAQKILC | IEKCFTFTAS | FNRPNLYYEV | RQKPSNTEDF | IEDIVKLING | RYKGQSGIIY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CFSQKDSEQV | TVSLQNLGIH | AGAYHANLEP | EDKTTVHRKW | SANEIQVVVA | TVAFGMGIDK | PDVRFVIHHS | MSKSMENYYQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ESGRAGRDDM | KADCILYYGF | GDIFRISSMV | VMENVGQQKL | YEMVSYCQNI | SKCRRVLMAQ | HFDEVWNSEA | CNKMCDNCCK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DSAFERKNIT | EYCRDLIKIL | KQAEELNEKL | TPLKLIDSWM | GKGAAKLRVA | GVVAPTLPRE | DLEKIIAHFL | IQQYLKEDYS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FTAYATISYL | KIGPKANLLN | NEAHAITMQV | TKSTQNSFRA | ESSQTCHSEQ | GDKKMEEKNS | GNFQKKAANM | LQQSGSKNTG |
| 650 | | | | | | | |
| AKKRKIDDA | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2269 | 1 | 701.1276 | 94.64 | 3 | 58.2 | 13.1 | 1 | 540-556 | R.EDLEKIIAHFLIQQYLK.E | |

# Detailed Protein Report

## Protein 256: uncharacterized protein LOC284677 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|197116396 | **Score:** | 38.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 25.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.6 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 8.1 |
| | | **No. of unique Peptides:** | 2 |

```
         10         20         30         40         50         60         70         80
MGMLAPGPLQ GRRPRKGHKG QEDAVAPGCK ASGRGSRVTH LLGYPTQNVS RSLRRKYAPP PCGGPEDVAL APCTAAAACE
         90        100        110        120        130        140        150        160
AGPSPVYVKV KSAEPADCAE GPVQCKNGLL VSSPHCEEPC AHSCAHPGLP PHLVHKLPLS YLQTQDTDAA SRRINAPLAA
        170        180        190        200        210        220        230        240
GWSWLRLWLV TLASGVDFPQ VSAWMRALPS PDCPGLRTTG EQMQKLLLKE NKVKTRKSKR RSGEGSHLTT SILEQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2182 | 1 | 682.2713 | -87.72 | 3 | 57.7 | 10.9 | 1 | 187-205 | R.ALPSPDCPGLRTTGEQMQK.L | Oxidation: 17 |
| 2206 | 2 | 701.3221 | -23.13 | 3 | 57.5 | 27.4 | 1 | 187-205 | R.ALPSPDCPGLRTTGEQMQK.L | Carbamidomethyl: 7;<br>Oxidation: 17 |

# Detailed Protein Report

## Protein 257: neuroblastoma breakpoint family member 6 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|221136848 | **Score:** | 38.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 72.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MVVSADPLSS | ERAEMNILEI | NQELRSQLAE | SNQQFRDLKE | KFLITQATAY | SLANQLKKYK | CEEYKDIIDS | VLRDELQSME |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KLAEKLRQAE | ELRQYKALVH | SQAKELTQLR | EKLREGRDAS | RWLNKHLKTL | LTPDDPDKSQ | GQDLREQLAE | GHRLAEHLVH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KLSPENDEDE | DEDEDDKDEE | VEKVQESPAP | REVQKTEEKE | VPQDSLEECA | VTCSNSHNPS | NSNQPHRSTK | ITFKEHEVDS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ALVVESEHPH | DEEEEALNIP | PENQNDHEEE | EGKAPVPPRH | HDKSNSYRHR | EVSFLALDEQ | KVCSAQDVAR | DYSNPKWDET |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SLGFLEKQSD | LEEVKGQETV | APRLSRGPLR | VDKHEIPQES | LDGCCLTPSI | LPDLTPSYHP | YWSTLYSFED | KQVSLALVDK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IKKDQEEIED | QSPPCPRLSQ | ELPEVKEQEV | PEDSVNEVYL | TPSVHHDVSD | CHQPYSSTLS | SLEDQLACSA | LDVASPTEAA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CPQGTWSGDL | SHHRSEVQIS | QAQLEPSTLV | PSCLRLQLDQ | GFHCGNGLAQ | RGLSSTTCSF | SANADSGNQW | PFQELVLEPS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LGMKNPPQLE | DDALEGSASN | TQGRQVTGRI | RASLVLILKT | IRRRLPFSKW | RLAFRFAGPH | AESAEIPNTA | ERMQRMIG |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1180 | 1 | 384.1589 | -56.37 | 2 | 44.9 | 12.5 | 1 | 633-638 | R.MQRMIG.- | Oxidation: 1, 4 |

# Detailed Protein Report

## Protein 258: cadherin EGF LAG seven-pass G-type receptor 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|7656967 | **Score:** | 38.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 329.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAPPPPPVLP | VLLLLAAAAA | LPAMGLRAAA | WEPRVPGGTR | AFALRPGCTY | AVGAACTPRA | PRELLDVGRD | GRLAGRRRVS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GAGRPLPLQV | RLVARSAPTA | LSRRLRARTH | LPGCGARARL | CGTGARLCGA | LCFPVPGGCA | AAQHSALAAP | TTLPACRCPP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RPRPRCPGRP | ICLPPGGSVR | LRLLCALRRA | AGAVRVGLAL | EAATAGTPSA | SPSPSPPLPP | NLPEARAGPA | RRARRGTSGR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GSLKFPMPNY | QVALFENEPA | GTLILQLHAH | YTIEGEEERV | SYYMEGLFDE | RSRGYFRIDS | ATGAVSTDSV | LDRETKETHV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LRVKAVDYST | PPRSATTYIT | VLVKDTNDHS | PVFEQSEYRE | RVRENLEVGY | EVLTIRASDR | DSPINANLRY | RVLGGAWDVF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QLNESSGVVS | TRAVLDREEA | AEYQLLVEAN | DQGRNPGPLS | ATATVYIEVE | DENDNYPQFS | EQNYVVQVPE | DVGLNTAVLR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VQATDRDQGQ | NAAIHYSILS | GNVAGQFYLH | SLSGILDVIN | PLDFEDVQKY | SLSIKAQDGG | RPPLINSSGV | VSVQVLDVND |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NEPIFVSSPF | QATVLENVPL | GYPVVHIQAV | DADSGENARL | HYRLVDTAST | FLGGGSAGPK | NPAPTPDFPF | QIHNSSGWIT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VCAELDREEV | EHYSFGVEAV | DHGSPPMSSS | TSVSITVLDV | NDNDPVFTQP | TYELRLNEDA | AVGSSVLTLQ | ARDRDANSVI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TYQLTGGNTR | NRFALSSQRG | GGLITLALPL | DYKQEQQYVL | AVTASDGTRS | HTAHVLINVT | DANTHRPVFQ | SSHYTVSVSE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DRPVGTSIAT | LSANDEDTGE | NARITYVIQD | PVPQFRIDPD | SGTMYTMMEL | DYENQVAYTL | TIMAQDNGIP | QKSDTTTLEI |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LILDANDNAP | QFLWDFYQGS | IFEDAPPSTS | ILQVSATDRD | SGPNGRLLYT | FQGGDDGDGD | FYIEPTSGVI | RTQRRLDREN |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VAVYNLWALA | VDRGSPTPLS | ASVEIQVTIL | DINDNAPMFE | KDELELFVEE | NNPVGSVVAK | IRANDPDEGP | NAQIMYQIVE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GDMRHFFQLD | LLNGDLRAMV | ELDFEVRREY | VLVVQATSAP | LVSRATVHIL | LVDQNDNPPV | LPDFQILFNN | YVTNKSNSFP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TGVIGCIPAH | DPDVSDSLNY | TFVQGNELRL | LLLDPATGEL | QLSRDLDNNR | PLEALMEVSV | SDGIHSVTAF | CTLRVTIITD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DMLTNSITVR | LENMSQEKFL | SPLLALFVEG | VAAVLSTTKD | DVFVFNVQND | TDVSSNILNV | TFSALLPGGV | RGQFFPSEDL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| QEQIYLNRTL | LTTISTQRVL | PFDDNICLRE | PCENYMKCVS | VLRFDSSAPF | LSSTTVLFRP | IHPINGLRCR | CPPGFTGDYC |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ETEIDLCYSD | PCGANGRCRS | REGGYTCECF | EDFTGEHCEV | DARSGRCANG | VCKNGGTCVN | LLIGGFHCVC | PPGEYERPYC |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EVTTRSFPPQ | SFVTFRGLRQ | RFHFTISLTF | ATQERNGLLL | YNGRFNEKHD | FIALEIVDEQ | VQLTFSAGET | TTTVAPKVPS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| GVSDGRWHSV | QVQYYNKPNI | GHLGLPHGPS | GEKMAVVTVD | DCDTTMAVRF | GKDIGNYSCA | AQGTQTGSKK | SLDLTGPLLL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| GGVPNLPEDF | PVHNRQFVGC | MRNLSVDGKN | VDMAGFIANN | GTREGCAARR | NFCDGRRCQN | GGTCVNRWNM | YLCECPLRFG |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| GKNCEQAMPH | PQLFSGESVV | SWSDLNIIIS | VPWYLGLMFR | TRKEDSVLME | ATSGGPTSFR | LQILNNYLQF | EVSHGPSDVE |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SVMLSGLRVT | DGEWHHLLIE | LKNVKEDSEM | KHLVTMTLDY | GMDQNKADIG | GMLPGLTVRS | VVVGGASEDK | VSVRRGFRGC |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| MQGVRMGGTP | TNVATLNMNN | ALKVRVKDGC | DVDDPCTSSP | CPPNSRCHDA | WEDYSCVCDK | GYLGINCVDA | CHLNPCENMG |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| ACVRSPGSPQ | GYVCECGPSH | YGPYCENKLD | LPCPRGWWGN | PVCGPCHCAV | SKGFDPDCNK | TNGQCQCKEN | YYKLLAQDTC |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| LPCDCFPHGS | HSRTCDMATG | QCACKPGVIG | RQCNRCDNPF | AEVTTLGCEV | IYNGCPKAFE | AGIWWPQTKF | GQPAAVPCPK |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| GSVGNAVRHC | SGEKGWLPPE | LFNCTTISFV | DLRAMNEKLS | RNETQVDGAR | ALQLVRALRS | ATQHTGTLFG | NDVRTAYQLL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 155 | 1 | 855.3273 | -115.70 | 2 | 31.7 | 12.6 | 0 | 715-730 | R.DANSVITYQLTGGNTR.N | |

# Detailed Protein Report

## Protein 259: coiled-coil domain-containing protein 33 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|117168273 | **Score:** | 38.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 84.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| | | **Sequence Coverage [%]:** | 5.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGLKNKKNTE | DPEEPLIASQ | STEPEIGHLS | PSKKETIMVT | LHGATNLPAC | KDGSEPWPYV | VVKSTSEEKN | NQSSKAVTSV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TSEPTRAPIW | GDTVNVEIQA | EDAGQEDVIL | KVVDNRKKQE | LLSYKIPIKY | LRVFHPYHFE | LVKPTESGKA | DEATAKTQLY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ATVVRKSSFI | PRYIGCNHMA | LEIFLRGVNE | PLANNPNPIV | VIARVVPNYK | EFKVSQANRD | LASVGLPITP | LSFPIPSMMN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FDVPRVSQNG | CPQLSKPGGP | PEQPLWNQSF | LFQGRDGATS | FSEDTALVLE | YYSSTSMKGS | QPWTLNQPLG | ISVLPLKSRL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YQKMLTGKGL | DGLHVERLPI | MDTSLKTIND | EAPTVALSFQ | LLSSERPENF | LTPNNSKALP | TLDPKILDKK | LRTIQESWSK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DTVSSTMDLS | TSTPREAEEE | PLVPEMSHDT | EMNNYRRAMQ | KMAEDILSLR | RQASILEGEN | RILRSRLAQQ | EEEEGQGKAS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EAQNTVSMKQ | KLLLSELDMK | KLRDRVQHLQ | NELIRKNDRE | KELLLLYQAQ | QPQAALLKQY | QGKLQKMKAL | EETVRHQEKV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IEKMERVLED | RLQDRSKPPP | LNRQQGKPYT | GFPMLSASGL | PLGSMGENLP | VELYSVLLAE | NAKLRTELDK | NRHQQAPIIL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QQQALPDLLS | GTSDKFNLLA | KLEHAQSRIL | SLESQLEDSA | RRWGREKQDL | ATRLQEQEKG | FRHPSNSIII | EQPSALTHSM |
| 730 | 740 | 750 | 760 | | | | |
| DLKQPSELEP | LLPSSDSKLN | KPLSPQKETA | NSQQT | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1293 | 1 | 679.7520 | 127.71 | 3 | 46.3 | 12.9 | 1 | 52-69 | K.DGSEPWPYVVVKSTSEEK.N | |

# Detailed Protein Report

## Protein 260: PREDICTED: CLIP-associating protein 1 isoform X9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578803955 | **Score:** | 38.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 162.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEPRMESCLA | QVLQKDVGKR | LQVGQELIDY | FSDKQKSADL | EHDQTMLDKL | VDGLATSWVN | SSNYKVVLLG | MDILSALVTR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LQDRFKAQIG | TVLPSLIDRL | GDAKDSVREQ | DQTLLLKIMD | QAANPQYVWD | RMLGGFKHKN | FRTREGICLC | LIATLNASGA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QTLTLSKIVP | HICNLLGDPN | SQVRDAAINS | LVEIYRHVGE | RVRADLSKKG | LPQSRLNVIF | TKFDEVQKSG | NMIQSANDKN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FDDEDSVDGN | RPSSASSTSS | KAPPSSRRNV | GMGTTRRLGS | STLGSKSSAA | KEGAGAVDEE | DFIKAFDDVP | VVQIYSSRDL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EESINKIREI | LSDDKHDWEQ | RVNALKKIRS | LLLAGAAEYD | NFFQHLRLLD | GAFKLSAKDL | RSQVVREACI | TLGHLSSVLG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NKFDHGAEAI | MPTIFNLIPN | SAKIMATSGV | VAVRLIIRHT | HIPRLIPVIT | SNCTSKSVAV | RRRCFEFLDL | LLQEWQTHSL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ERHISVLAET | IKKGIHDADS | EARIEARKCY | WGFHSHFSRE | AEHLYHTLES | SYQKALQSHL | KNSDSIVSLP | QSDRSSSSSQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ESLNRPLSAK | RSPTGSTTSR | ASTVSTKSVS | TTGSLQRSRS | DIDVNAAASA | KSKVSSSSGT | TPFSSAAALP | PGSYASLESR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HMREDMEYIG | LDSGRIRTRR | QSSGSATNVA | STPDNRGRSR | AKVVSQSQPG | SRSSSPGKLL | GSGYGGLTGG | SSRGPPVTPS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SEKRSKIPRS | QGCSRETSPN | RIGLDRFGLG | QPGRIPGSVN | AMRVLSTSTD | LEAAVADALK | KPVRRRYEPY | GMYSDDDANS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DASSVCSERS | YGSRNGGIPH | YLRQTEDVAE | VLNHCASSNW | SERKEGLLGL | QNLLKSQRTL | SRVELKRLCE | IFTRMFADPH |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SKRVFSMFLE | TLVDFIIIHK | DDLQDWLFVL | LTQLLKKMGA | DLLGSVQAKV | QKALDVTRDS | FPFDQQFNIL | MRFIVDQTQT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PNLKVKVAIL | KYIESLARQM | DPTDFVNSSE | TRLAVSRIIT | WTTEPKSSDV | RKAAQIVLIS | LFELNTPEFT | MLLGALPKTF |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QDGATKLLHN | HLKNSSNTSV | GSPSNTIGRT | PSRHTSSRTS | PLTSPTNCSH | GGLSPSMLDY | DTENLNSEEI | YSSLRGVTEA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| IEKFSFRSQE | DLNEPIKRDG | KKECDIVSRD | GGAASPATEG | RGGSEVEGGR | TALDNKTSLL | NTQPPRAFPG | PRARDYNPYP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| YSDAINTYDK | TALKEAVFDD | DMEQLRDVPI | DHSDLVADLL | KELSNHNERV | EERKGALLEL | LKITREDSLG | VWEEHFKTIL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LLLLETLGDK | DHSIRALALR | VLREILRNQP | ARFKNYAELT | IMKTLEAHKD | SHKEVVRAAE | EAASTLASSI | HPEQCIKVLC |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PIIQTADYPI | NLAAIKMQTK | VVERIAKESL | LQLLVDIIPG | LLQGYDNTES | SVRKASVFCL | VAIYSVIGED | LKPHLAQLTG |
| 1450 | 1460 | 1470 | 1480 | | | | |
| SKMKLLNLYI | KRAQTTNSNS | SSSSDVSTHS | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2270 | 1 | 614.2104 | -96.89 | 3 | 58.8 | 10.1 | 1 | 641-655 | R.HMREDMEYIGLDSGR.I | Oxidation: 2, 6 |
| 1389 | 1 | 816.1017 | 171.47 | 2 | 47.0 | 10.2 | 1 | 953-966 | R.FIVDQTQTPNLKVK.V | |

# Detailed Protein Report

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## Protein 261: uncharacterized protein LOC100132994 [Homo sapiens]

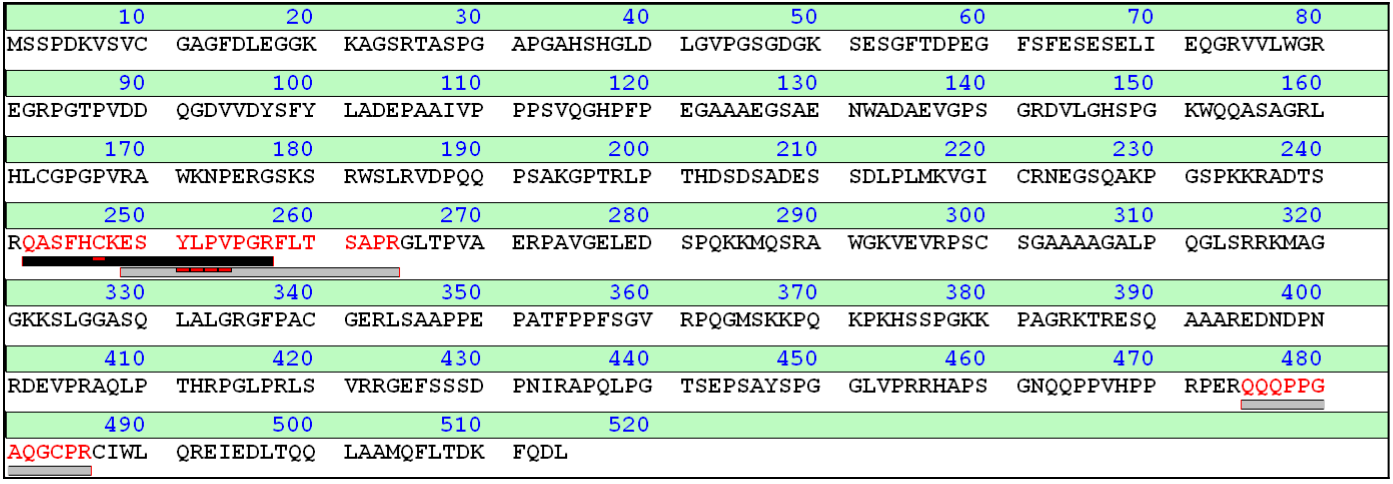
| | | | |
|---|---|---|---|
| **Accession:** | gi\|223468690 | **Score:** | 38.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.8 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.52 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.31 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|223468693 | refseq_human (refseq_human_20140103.fasta) | putative uncharacterized protein CXorf49 [Homo sapiens] |



```
        10         20         30         40         50         60         70         80
MSSPDKVSVC GAGFDLEGGK KAGSRTASPG APGAHSHGLD LGVPGSGDGK SESGFTDPEG FSFESESELI EQGRVVLWGR
        90        100        110        120        130        140        150        160
EGRPGTPVDD QGDVVDYSFY LADEPAAIVP PPSVQGHPFP EGAAAEGSAE NWADAEVGPS GRDVLGHSPG KWQQASAGRL
       170        180        190        200        210        220        230        240
HLCGPGPVRA WKNPERGSKS RWSLRVDPQQ PSAKGPTRLP THDSDSADES SDLPLMKVGI CRNEGSQAKP GSPKKRADTS
       250        260        270        280        290        300        310        320
RQASFHCKES YLPVPGRFLT SAPRGLTPVA ERPAVGELED SPQKKMQSRA WGKVEVRPSC SGAAAAGALP QGLSRRKMAG
       330        340        350        360        370        380        390        400
GKKSLGGASQ LALGRGFPAC GERLSAAPPE PATFPPFSGV RPQGMSKKPQ KPKHSSPGKK PAGRKTRESQ AAAREDNDPN
       410        420        430        440        450        460        470        480
RDEVPRAQLP THRPGLPRLS VRRGEFSSSD PNIRAPQLPG TSEPSAYSPG GLVPRRHAPS GNQQPPVHPP RPERQQQPPG
       490        500        510        520
AQGCPRCIWL QREIEDLTQQ LAAMQFLTDK FQDL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 198 | 1 | 938.4465 | -16.72 | 2 | 31.3 | 13.1 | 1 | 242-257 | R.QASFHCKESYLPVPGR.F | Carbamidomethyl: 6 | WUP:QUP 1.31<br>QU:MU 0.52 |
| 1392 | 1 | 895.6264 | 159.72 | 2 | 47.0 | 14.8 | 1 | 249-264 | K.ESYLPVPGRFLTSAPR.G | | |
| 1182 | 1 | 662.2009 | -171.93 | 2 | 44.9 | 10.2 | 0 | 475-486 | R.QQQPPGAQGCPR.C | Carbamidomethyl: 10 | |

# Detailed Protein Report

## Protein 262: PREDICTED: ryanodine receptor 1 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578834746 | **Score:** | 38.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 563.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 3 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGDAEGEDEV | QFLRTDDEVV | LQCSATVLKE | QLKLCLAAEG | FGNRLCFLEP | TSNAQNVPPD | LAICCFVLEQ | SLSVRALQEM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LANTVEAGVE | SSQGGGHRTL | LYGHAILLRH | AHSRMYLSCL | TTSRSMTDKL | AFDVGLQEDA | TGEACWWTMH | PASKQRSEGE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KVRVGDDIIL | VSVSSERYLH | LSTASGELQV | DASFMQTLWN | MNPICSRCEE | GFVTGGHVLR | LFHGHMDECL | TISPADSDDQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RRLVYYEGGA | VCTHARSLWR | LEPLRISWSG | SHLRWGQPLR | VRHVTTGQYL | ALTEDQGLVV | VDASKAHTKA | TSFCFRISKE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KLDVAPKRDV | EGMGPPEIKY | GESLCFVQHV | ASGLWLTYAA | PDPKALRLGV | LKKKAMLHQE | GHMDDALSLT | RCQQEESQAA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RMIHSTNGLY | NQFIKSLDSF | SGKPRGSGPP | AGTALPIEGV | ILSLQDLIIY | FEPPSEDLQH | EEKQSKLRSL | RNRQSLFQEE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GMLSMVLNCI | DRLNVYTTAA | HFAEFAGEEA | AESWKEIVNL | LYELLASLIR | GNRSNCALFS | TNLDWLVSKL | DRLEASSGIL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EVLYCVLIES | PEVLNIIQEN | HIKSIISLLD | KHGRNHKVLD | VLCSLCVCNG | VAVRSNQDLI | TENLLPGREL | LLQTNLINYV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TSIRPNIFVG | RAEGTTQYSK | WYFEVMVDEV | TPFLTAQATH | LRVGWALTEG | YTPYPGAGEG | WGGNGVGDDL | YSYGFDGLHL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| WTGHVARPVT | SPGQHLLAPE | DVISCCLDLS | VPSISFRING | CPVQGVFESF | NLDGLFFPVV | SFSAGVKVRF | LLGGRHGEFK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FLPPPGYAPC | HEAVLPRERL | HLEPIKEYRR | EGPRGPHLVG | PSRCLSHTDF | VPCPVDTVQI | VLPPHLERIR | EKLAENIHEL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| WALTRIEQGW | TYGPVRDDNK | RLHPCLVDFH | SLPEPERNYN | LQMSGETLKT | LLALGCHVGM | ADEKAEDNLK | KTKLPKTYMM |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SNGYKPAPLD | LSHVRLTPAQ | TTLVDRLAEN | GHNVWARDRV | GQGWSYSAVQ | DIPARRNPRL | VPYRLLDEAT | KRSNRDSLCQ |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AVRTLLGYGY | NIEPPDQEPS | QVENQSRCDR | VRIFRAEKSY | TVQSGRWYFE | FEAVTTGEMR | VGWARPELRP | DVELGADELA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| YVFNGHRGQR | WHLGSEPFGR | PWQPGDVVGC | MIDLTENTII | FTLNGEVLMS | DSGSETAFRE | IEIGDGFLPV | CSLGPGQVGH |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LNLGQDVSSL | RFFAICGLQE | GFEPFAINMQ | RPVTTWFSKG | LPQFEPVPLE | HPHYEVSRVD | GTVDTPPCLR | LTHRTWGSQN |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SLVEMLFLRL | SLPVQFHQHF | RCTAGATPLA | PPGLQPPAED | EARAAEPDPD | YENLRRSAGG | WSEAENGKEG | TAKEGAPGGT |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PQAGGEAQPA | RAENEKDATT | EKNKKRGFLF | KAKKVAMMTQ | PPATPTLPRL | PHDVVPADNR | DDPEIILNTT | TYYYSVRVFA |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GQEPSCVWAG | WVTPDYHQHD | MSFDLSKVRV | VTVTMGDEQG | NVHSSLKCSN | CYMVWGGDFV | SPGQQGRISH | TDLVIGCLVD |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| LATGLMTFTA | NGKESNTFFQ | VEPNTKLFPA | VFVLPTHQNV | IQFELGKQKN | IMPLSAAMFQ | SERKNPAPQC | PPRLEMQMLM |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| PVSWSRMPNH | FLQVETRRAG | ERLGWAVQCQ | EPLTMMALHI | PEENRCMDIL | ELSERLDLQR | FHSHTLRLYR | AVCALGNNRV |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| AHALCSHVDQ | AQLLHALEDA | HLPGPLRAGY | YDLLISIHLE | SACRSRRSML | SEYIVPLTPE | TRAITLFPPG | RSTENGHPRH |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| GLPGVGVTTS | LRPPHHFSPP | CFVAALPAAG | AAEAPARLSP | AIPLEALRDK | ALRMLGEAVR | DGGQHARDPV | GGSVEFQFVP |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| VLKLVSTLLV | MGIFGDEDVK | QILKMIEPEV | FTEEEEEEDE | EEEGEEEDEE | EKEEDEEETA | QEKEDEEKEE | EEAAEGEKEE |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| GLEEGLLQMK | LPESVKLQMC | HLLEYFCDQE | LQHRVESLAA | FAERYVDKLQ | ANQRSRYGLL | IKAFSMTAAE | TARRTREFRS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| PPQEQINMLL | QFKDGTDEED | CPLPEEIRQD | LLDFHQDLLA | HCGIQLDGEE | EEPEEETTLG | SRLMSLLEKV | RLVKKKEEKP |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| EEERSAEESK | PRSLQELVSH | MVVRWAQEDF | VQSPELVRAM | FSLLHRQYDG | LGELLRALPR | AYTISPSSVE | DTMSLLECLG |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2169 | 2 | 714.6084 | -134.05 | 3 | 57.5 | 14.8 | 1 | 595-614 | R.NHKVLDVLCSLCVCNGVAVR.S | |
| 1512 | 1 | 727.4065 | 108.16 | 2 | 49.1 | 11.1 | 0 | 2601-2612 | R.DVIEDCLMSLCR.Y | Carbamidomethyl: 11 |
| 2682 | 1 | 705.8622 | 37.53 | 2 | 64.6 | 12.1 | 2 | 3478-3490 | K.MAKSGGSDQERTK.K | Oxidation: 1 |

# Detailed Protein Report

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**Protein 263:** **symplekin [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|124028529 | **Score:** | 37.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 141.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530417312 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: symplekin isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MASGSGDSVT | RRSVASQFFT | QEEGPGIDGM | TTSERVVDLL | NQAALITNDS | KITVLKQVQE | LIINKDPTLL | DNFLDEIIAF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QADKSIEVRK | FVIGFIEEAC | KRDIELLLKL | IANLNMLLRD | ENVNVVKKAI | LTMTQLYKVA | LQWMVKSRVI | SELQEACWDM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VSAMAGDIIL | LLDSDNDGIR | THAIKFVEGL | IVTLSPRMAD | SEIPRRQEHD | ISLDRIPRDH | PYIQYNVLWE | EGKAALEQLL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KFMVHPAISS | INLTTALGSL | ANIARQRPMF | MSEVIQAYET | LHANLPPTLA | KSQVSSVRKN | LKLHLLSVLK | HPASLEFQAQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ITTLLVDLGT | PQAEIARNMP | SSKDTRKRPR | DDSDSTLKKM | KLEPNLGEDD | EDKDLEPGPS | GTSKASAQIS | GQSDTDITAE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FLQPLLTPDN | VANLVLISMV | YLPEAMPASF | QAIYTPVESA | GTEAQIKHLA | RLMATQMTAA | GLGPGVEQTK | QCKEEPKEEK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VVKTESVLIK | RRLSAQGQAI | SVVGSLSSMS | PLEEEAPQAK | RRPEPIIPVT | QPRLAGAGGR | KKIFRLSDVL | KPLTDAQVEA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MKLGAVKRIL | RAEKAVACSG | AAQVRIKILA | SLVTQFNSGL | KAEVLSFILE | DVRARLDLAF | AWLYQEYNAY | LAAGASGSLD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KYEDCLIRLL | SGLQEKPDQK | DGIFTKVVLE | APLITESALE | VVRKYCEDES | RTYLGMSTLR | DLIFKRPSRQ | FQYLHVLLDL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SSHEKDKVRS | QALLFIKRMY | EKEQLREYVE | KFALNYLQLL | VHPNPPSVLF | GADKDTEVAA | PWTEETVKQC | LYLYLALLPQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NHKLIHELAA | VYTEAIADIK | RTVLRVIEQP | IRGMGMNSPE | LLLLVENCPK | GAETLVTRCL | HSLTDKVPPS | PELVKRVRDL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| YHKRLPDVRF | LIPVLNGLEK | KEVIQALPKL | IKLNPIVVKE | VFNRLLGTQH | GEGNSALSPL | NPGELLIALH | NIDSVKCDMK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SIIKATNLCF | AERNVYTSEV | LAVVMQQLME | QSPLPMLLMR | TVIQSLTMYP | RLGGFVMNIL | SRLIMKQVWK | YPKVWEGFIK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| CCQRTKPQSF | QVILQLPPQQ | LGAVFDKCPE | LREPLLAHVR | SFTPHQQAHI | PNSIMTILEA | SGKQEPEAKE | APAGPLEEDD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LEPLTLAPAP | APRPPQDLIG | LRLAQEKALK | RQLEEEQKLK | PGGVGAPSSS | SPSPSPSARP | GPPPSEEAMD | FREEGPECET |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PGIFISMDDD | SGLTEAALLD | SSLEGPLPKE | TAAGGLTLKE | ERSPQTLAPV | GEDAMKTPSP | AAEDAREPEA | KGNS |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2866 | 1 | 655.3693 | -17.94 | 2 | 66.3 | 14.3 | 1 | 128-138 | K.KAILTMTQLYK.V | |

**Protein 264:** **PREDICTED: probable ATP-dependent RNA helicase DDX60-like isoform X6 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578809622 | **Score:** | 37.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 193.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 2.50 | **CV:** 44.93 % | **No. of Peptides:** 2 |

```
        10         20         30         40         50         60         70         80
MGSKDHAVFF REMTQLILNE MPKAGYSSIL NDFVESNFFV IDGDSLLVTC LGVKSFKWGQ NLHFFYLVEC YLVDLLSNGG
        90        100        110        120        130        140        150        160
QFTIVFFKDA EYAYFDFPEL LSLRTALILH LQHNTNIDVQ TEFSGCLSQD WKLFLEQHYP YFLIVSEEGL SDLQTYLFNF
       170        180        190        200        210        220        230        240
LIIHSWGMKV NVVLSSGHES DTLRFYAYTM ESTDRNQTFS KENETVIQSA YKSLIQHLEE IRVLVLATHF EHLKWNDMME
       250        260        270        280        290        300        310        320
EAYQTLFLLQ HLWSEGSDIQ RVLCVTSCSL SLRMYHRVLV HSNCLSLQEV EDFCRLRCLC VAFQLHLPLS QRACSRVITC
       330        340        350        360        370        380        390        400
SWIRNSDSFL KMNKWCEYFI LSNLNVFGCW NLNLNHVSDL YDEQLLKNIA FYYEFESTQE PHLNLGDSIR RDYEDLWNVV
       410        420        430        440        450        460        470        480
SHLVKEFNVG KSFPLRTTRR HFLRQEKSVI QEISLEKMPS VGFIPMTSAV IDEFVGDMMK DLPILKSDDP VVPSLFKQKT
       490        500        510        520        530        540        550        560
SDELLHWHAQ RLLSDDYDRI KCHVDEQSRD PHVLDFLKKI QDYQQFYGKS LESISTKVIV TQTTRPKEDS SGASGEILQN
       570        580        590        600        610        620        630        640
TKPHQITKKS KKKSFLKEDQ NKAQQNDDLL FSIEEEMKNN LHSGIRKLED YLTSCASNSV KFGVEMLGLI ACFKAWKKHC
       650        660        670        680        690        700        710        720
RGEGKISKDL SIAVQMMKRI HSLLERYPEI LEAEHHQYIA KCLKYLGFND LANSLDPTLI GDDKNKKKYS IDIGPARFQL
       730        740        750        760        770        780        790        800
QYMGHYLIRD ERKDRDPRVQ DFIPNAWQQE LLDVVDKNES AVIVAPTSSG KTYASYYCME KVLRESDVGV VVYVAPAKSL
       810        820        830        840        850        860        870        880
VGQVAATVEN RFTKTLPAGR TLCGAFTRDY CHNVLNCQVL ITVPECFEIL LLAPHRQKWV ERIRYVIFDE VHYLGREVGA
       890        900        910        920        930        940        950        960
KFWELLLVII RCPFLVLSAT INNPNLLTKW LQSVKQYWKQ ADKIMEEKCI SEKQADKCLN FLQDHSYKNQ SYEVRLVLCG
       970        980        990       1000       1010       1020       1030       1040
ERYNDLEKHI CSVKHDDVYF DHFHPCAALT TDIIEKYGFP PDLTLTPQES IQLYDTMAQV WETWPRAQEL CPEEFILFKN
      1050       1060       1070       1080       1090       1100       1110       1120
KIVIKKLDAR KYEENLKAEL TNWIKNGQVK KVKRVLKNLS PDSLSSSKDM VKMFPLLVEK LRQMDKLPAI FFLFKNDDVG
      1130       1140       1150       1160       1170       1180       1190       1200
KRAGSVCTFL EKTETKSHPH TECHSYVFAI DEVLEKVRKT QKRISTKKNP KKAEKLERKK VYRAEYINFL ENLKILEISE
      1210       1220       1230       1240       1250       1260       1270       1280
DCTYADVKAL HTEITRNKDS TLERVLPRVR FTRHGKELKA LAQRGIGYHH SSMYFKEKEF VEILFVKGLI RVVTATETLA
      1290       1300       1310       1320       1330       1340       1350       1360
LGIHMPCKSV VFAQDSVYLD ALNYRQMSGR AGRRGQDLLG NVYFFDIPLP KIKRLLASSV PELRGQFPLS ITLVLRLMLL
      1370       1380       1390       1400       1410       1420       1430       1440
ASKGDDPEDA KAKDYLNKKG NPKKFAGLAS YLHGHEPSNL VFVNFLKRGL FHNLCKPAWK GSQQFSQDVM EKLVLVLANL
      1450       1460       1470       1480       1490       1500       1510       1520
FGRKYIPAKF QNANLSFSQS KVILAELPED FKAALYEYNL AVMKDFASFL LIASKSVNMK KEHQLPLSRI KFTGKECEDS
      1530       1540       1550       1560       1570       1580       1590       1600
QLVSHLMSCK KGRVAISPFV CLSGNTDNDL LRPETINQVI LRTVGVSGTQ APLLWPWKLD NRGRRMPLNA YVLNFYKHNC
      1610       1620       1630       1640       1650       1660       1670       1680
LTRLDQKNGM RMGQLLKCLK DFAFNIQAIS DSLSELCENK RDNVVLAFKQ LSQTFYEKLQ EMQIQMSQNH LE
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|

| | | | [ppm] | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1058 | 1 | 586.1731 | -222.69 | 2 | 42.8 | 12.2 | 2 | 639-648 | K.HCRGEGKISK.D | Carbamidomethyl: 2 | QU:MU 3.85 |
| 225 | 1 | 641.7812 | -36.28 | 2 | 32.5 | 12.3 | 1 | 924-933 | K.IMEEKCISEK.Q | Carbamidomethyl: 6;<br>Oxidation: 2 | |
| 1639 | 1 | 926.8312 | -90.99 | 2 | 50.2 | 13.2 | 1 | 1516-1531 | K.ECEDSQLVSHLMSCKK.G | Oxidation: 12 | QU:MU 1.63 |

**BRUKER**

# Detailed Protein Report

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## Protein 265: tyrosine-protein kinase SYK isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|205277435 | **Score:** | 37.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 6.9 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|293332611 | refseq_human<br>(refseq_human_20140103.fasta) | tyrosine-protein kinase SYK isoform 2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASSGMADSA | NHLPFFFGNI | TREEAEDYLV | QGGMSDGLYL | LRQSRNYLGG | FALSVAHGRK | AHHYTIEREL | NGTYAIAGGR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| THASPADLCH | YHSQESDGLV | CLLKKPFNRP | QGVQPKTGPF | EDLKENLIRE | YVKQTWNLQG | QALEQAIISQ | KPQLEKLIAT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TAHEKMPWFH | GKISREESEQ | IVLIGSKTNG | KFLIRARDNN | GSYALCLLHE | GKVLHYRIDK | DKTGKLSIPE | GKKFDTLWQL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VEHYSYKADG | LLRVLTVPCQ | KIGTQGNVNF | GGRPQLPGSH | PASSPAQGNR | QESTVSFNPY | EPELAPWAAD | KGPQREALPM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DTEVYESPYA | DPEEIRPKEV | YLDRKLLTLE | DKELGSGNFG | TVKKGYYQMK | KVVKTVAVKI | LKNEANDPAL | KDELLAEANV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MQQLDNPYIV | RMIGICEAES | WMLVMEMAEL | GPLNKYLQQN | RHVKDKNIIE | LVHQVSMGMK | YLEESNFVHR | DLAARNVLLV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TQHYAKISDF | GLSKALRADE | NYYKAQTHGK | WPVKWYAPEC | INYYKFSSKS | DVWSFGVLMW | EAFSYGQKPY | RGMKGSEVTA |
| 570 | 580 | 590 | 600 | 610 | 620 | | |
| MLEKGERMGC | PAGCPREMYD | LMNLCWTYDV | ENRPGFAAVE | LRLRNYYYDV | VN | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2468 | 2 | 1044.5140 | -52.13 | 2 | 61.4 | 15.4 | 2 | 173-191 | K.ISREESEQIVLIGSKTNGK.F | |
| 1105 | 1 | 653.6417 | -205.60 | 2 | 42.1 | 10.9 | 1 | 565-576 | K.GERMGCPAGCPR.E | Carbamidomethyl: 10;<br>Oxidation: 4 |

# Detailed Protein Report

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## Protein 266: eosinophil peroxidase preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4503595 | **Score:** | 37.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 81.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | |
|---|---|---|---|---|---|
| ***WUP:QUP*** | **Median:** 0.65 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578831504 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: eosinophil peroxidase isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MHLLPALAGV | LATLVLAQPC | EGTDPASPGA | VETSVLRDCI | AEAKLLVDAA | YNWTQKSIKQ | RLRSGSASPM | DLLSYFKQPV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AATRTVVRAA | DYMHVALGLL | EEKLQPQRSG | PFNVTDVLTE | PQLRLLSQAS | GCALRDQAER | CSDKYRTITG | RCNNKRRPLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GASNQALARW | LPAEYEDGLS | LPFGWTPSRR | RNGFLLPLVR | AVSNQIVRFP | NERLTSDRGR | ALMFMQWGQF | IDHDLDFSPE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SPARVAFTAG | VDCERTCAQL | PPCFPIKIPP | NDPRIKNQRD | CIPFFRSAPS | CPQNKNRVRN | QINALTSFVD | ASMVYGSEVS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LSLRLRNRTN | YLGLLAINQR | FQDNGRALLP | FDNLHDDPCL | LTNRSARIPC | FLAGDTRSTE | TPKLAAMHTL | FMREHNRLAT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ELRRLNPRWN | GDKLYNEARK | IMGAMVQIIT | YRDFLPLVLG | KARARRTLGH | YRGYCSNVDP | RVANVFTLAF | RFGHTMLQPF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| MFRLDSQYRA | SAPNSHVPLS | SAFFASWRIV | YEGGIDPILR | GLMATPAKLN | RQDAMLVDEL | RDRLFRQVRR | IGLDLAALNM |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QRSRDHGLPG | YNAWRRFCGL | SQPRNLAQLS | RVLKNQDLAR | KFLNLYGTPD | NIDIWIGAIA | EPLLPGARVG | PLLACLFENQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FRRARDGDRF | WWQKRGVFTK | RQRKALSRIS | LSRIICDNTG | ITTVSRDIFR | ANIYPRGFVN | CSRIPRLNLS | AWRGT |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 873 | 1 | 575.3008 | 19.33 | 2 | 40.5 | 19.5 | 0 | 368-377 | R.IPCFLAGDTR.S | Carbamidomethyl: 3 | WUP:QUP 0.65 |
| 2217 | 1 | 927.3936 | -145.10 | 2 | 56.1 | 18.0 | 2 | 547-562 | R.QVRRIGLDLAALNMQR.S | | |

# Detailed Protein Report

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## Protein 267: vacuolar protein sorting-associated protein 13B isoform 5 [Homo sapiens]

**Accession:** gi|35493713
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl, Oxidation

**Score:** 37.5
**MW [kDa]:** 448.4
**pI:** 6.0
**Sequence Coverage [%]:** 1.4
**No. of unique Peptides:** 3

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530388780 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: vacuolar protein sorting-associated protein 13B isoform X2 [Homo sapiens] |
| gi\|530388778 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: vacuolar protein sorting-associated protein 13B isoform X1 [Homo sapiens] |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLESYVTPIL | MSYVNRYIKN | LKPSDLQLSL | WGGDVVLSKL | ELKLDVLEQE | LKLPFTFLSG | HIHELRIHVP | WTKLGSEPVV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ITINTMECIL | KLKDGIQDDH | ESCGSNSTNR | STAESTKSSI | KPRRMQQAAP | TDPDLPPGYV | QSLIRRVVNN | VNIVINNLIL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KYVEDDIVLS | VNITSAECYT | VGELWDRAFM | DISATDLVLR | KVINFSDCTV | CLDKRNASGK | IEFYQDPLLY | KCSFRTRLHF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TYENLNSKMP | SVIKIHTLVE | SLKLSITDQQ | LPMFIRIMQL | GIALYYGEIG | NFKEGEIEDL | TCHNKDMLGN | ITGSEDETRI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DMQYPAQHKG | QELYSQQDEE | QPQGWVSWAW | SFVPAIVSYD | DGEEDFVGND | PASTMHQQKA | QTLKDPIVSI | GFYCTKATVT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FKLTEMQVES | SYYSPQKVKS | KEVLCWEQEG | TTVEALMMGE | PFFDCQIGFV | GCRAMCLKGI | MGVKDFEENM | NRSETEACFF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ICGDNLSTKG | FTYLTNSLFD | YRSPENNGTR | AEFILDSTHH | KETYTEIAGM | QRFGAFYMDY | LYTMENTSGK | GSTNQQDFSS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GKSEDLGTVQ | EKSTKSLVIG | PLDFRLDSSA | VHRILKMIVC | ALEHEYEPYS | RLKSDIKDEN | ETILNPEEVA | LLEEYIPTRH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TSVTLLKCTC | TISMAEFNLL | DHLLPVIMGE | KNSSNFMNTT | NFQSLRPLPS | IRILVDKINL | EHSVPMYAEQ | LVHVVSSLTQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PSDNLLHYCY | VHCYLKIFGF | QAGLTSLDCS | GSYCLPVPVI | PSFSTALYGK | LLKLPTCWTK | RSQIAITEGI | FELPNLTIQA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TRAQTLLLQA | IYQSWSHLGN | VSSSAVIEAL | INEIFLSIGV | KSKNPLPTLE | GSIQNVELKY | CSTSLVKCAS | GTMGSIKICA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KAPVDSGKEK | LIPLLQGPSD | TKDLHSTKWL | NESRKPESLL | APDLMAFTIQ | VPQYIDYCHN | SGAVLLCSIQ | GLAVNIDPIL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| YTWLIYQPQK | RTSRHMQQQP | VVAVPLVMPV | CRRKEDEVSI | GSAPLAKQQS | YQASEYASSP | VKTKTVTESR | PLSVPVKAML |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| NISESCRSPE | ERMKEFIGIV | WNAVKHLTLQ | LEVQSCCVFI | PNDSLPSPST | IVSGDIPGTV | RSWYHGQTSM | PGTLVLCLPQ |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| IKIISAGHKY | MEPLQEIPFV | IPRPILEEGD | AFPWTISLHN | FSIYTLLGKQ | VTLCLVEPMG | CTSTLAVTSQ | KLLATGPDTR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| HSFVVCLHVD | LESLEIKCSN | PQVQLFYELT | DIMNKVWNKI | QKRGNLNLSP | TSPETMAGPV | PTSPVRSSIG | TAPPDTSTCS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PSADIGTTTE | GDSIQAGEES | PFSDSVTLEQ | TTSNIGGTSG | RVSLWMQWVL | PKITIKLFAP | DPENKGTEVC | MVSELEDLSA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| SIDVQDVYTK | VKCKIESFNI | DHYRSSLGEE | CWSLGQCGGV | FLSCTDKLNR | RTLLVRPISK | QDPFSNCSGF | FPSTTTKLLD |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GTHQQHGFLS | LTYTKAVTKN | VRHKLTSRNE | RRSFHKLSEG | LMDGSPHFLH | EILLSAQAFD | IVLYFPLLNA | IASIFQAKLP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| KTQKEKRKSP | GQPMRTHTLT | SRNLPLIYVN | TSVIRIFIPK | TEEMQPTVEA | NQAAKEDTVV | LKIGSVAMAP | QADNPLGRSV |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LRKDIYQRAL | NLGILRDPGS | EIEDRQYQID | LQSINIGTAQ | WHQLKPEKES | VSGGVVTETE | RNSQNPALEW | NMASSIRRHQ |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| ERRAILTPVL | TDFSVRITGA | PAVIFTKVVS | PENLHTEEIL | VCGHSLEVNI | TTNLDFFLSV | AQVQLLHQLI | VANMTGLEPS |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| NKAAEISKQE | QKKVDIFDGG | MAETSSRYSG | AQDSGIGSDS | VKIRIVQIEQ | HSGASQHRIA | RPSRQSSIVK | NLNFIPFDIF |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| ITASRISLMT | YSCMALSKSK | SQEQKNNEKT | DKSSLNLPEV | DSDVAKPNQA | CISTVTAEDL | LRSSISFPSG | KKIGVLSLES |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LHASTRSSAR | QALGITIVRQ | PGRRGTGDLQ | LEPFLYFIVS | QPSLLLSCHH | RKQRVEVSIF | DAVLKGVASD | YKCIDPGKTL |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| PEALDYCTVW | LQTVPGEIDS | KSGIPPSFIT | LQIKDFLNGP | ADVNLDISKP | LKANLSFTKL | DQINLFLKKI | KNAHSLAHSE |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| ETSAMSNTMV | NKDDLPVSKY | YRGKLSKPKI | HGDGVQKISA | QENMWRAVSC | FQKISVQTTQ | IVISMETVPH | TSKPCLLASL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1794 | 2 | 1023.9088 | -120.39 | 2 | 52.3 | 12.4 | 1 | 385-402 | K.DPIVSIGFYCTKATVTFK.L | Carbamidomethyl: 10 |
| 1639 | 1 | 911.3413 | -106.88 | 2 | 50.8 | 14.4 | 1 | 2218-2233 | K.WCKHSGNPGPEQSIPK.I | Carbamidomethyl: 2 |
| 1842 | 1 | 1273.5438 | -34.83 | 2 | 51.4 | 10.7 | 1 | 3135-3157 | K.EYFRVPDSATFSICPGGEQPAMK.S | Oxidation: 22 |

# Detailed Protein Report

## Protein 268: triosephosphate isomerase isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|384475517 | **Score:** | 37.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 17.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 7.8 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MIKDCGATWV VLGHSERRHV FGESDELIGQ KVAHALAEGL GVIACIGEKL DEREAGITEK VVFEQTKVIA DNVKDWSKVV
        90        100        110        120        130        140        150        160
LAYEPVWAIG TGKTATPQQA QEVHEKLRGW LKSNVSDAVA QSTRIIYGGS VTGATCKELA SQPDVDGFLV GGASLKPEFV
       170
DIINAKQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 219 | 1 | 663.8152 | -36.93 | 2 | 32.7 | 37.4 | 0 | 125-137 | R.IIYGGSVTGATCK.E | Carbamidomethyl: 12 |

# Detailed Protein Report

## Protein 269: sortilin isoform 2 [Homo sapiens]

**Accession:** gi|327315343
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 37.3
**MW [kDa]:** 77.3
**pI:** 5.1
**Sequence Coverage [%]:** 3.9
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTFGQSKLYR | SEDYGKNFKD | ITDLINNTFI | RTEFGMAIGP | ENSGKVVLTA | EVSGGSRGGR | IFRSSDFAKN | FVQTDLPFHP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LTQMMYSPQN | SDYLLALSTE | NGLWVSKNFG | GKWEEIHKAV | CLAKWGSDNT | IFFTTYANGS | CTDLGALELW | RTSDLGKSFK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TIGVKIYSFG | LGGRFLFASV | MADKDTTRRI | HVSTDQGDTW | SMAQLPSVGQ | EQFYSILAAN | DDMVFMHVDE | PGDTGFGTIF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TSDDRGIVYS | KSLDRHLYTT | TGGETDFTNV | TSLRGVYITS | VLSEDNSIQT | MITFDQGGRW | THLRKPENSE | CDATAKNKNE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CSLHIHASYS | ISQKLNVPMA | PLSEPNAVGI | VIAHGSVGDA | ISVMVPDVYI | SDDGGYSWTK | MLEGPHYYTI | LDSGGIIVAI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EHSSRPINVI | KFSTDEGQCW | QTYTFTRDPI | YFTGLASEPG | ARSMNISIWG | FTESFLTSQW | VSYTIDFKDI | LERNCEEKDY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TIWLAHSTDP | EDYEDGCILG | YKEQFLRLRK | SSVCQNGRDY | VVTKQPSICL | CSLEDFLCDF | GYYRPENDSK | CVEQPELKGH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DLEFCLYGRE | EHLTTNGYRK | IPGDKCQGGV | NPVREVKDLK | KKCTSNFLSP | EKQNSKSNSV | PIILAIVGLM | LVTVVAGVLI |
| 650 | 660 | 670 | 680 | 690 | 700 | | |
| VKKYVCGGRF | LVHRYSVLQQ | HAEANGVDGV | DALDTASHTN | KSGYHDDSDE | DLLE | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1682 | 1 | 1058.4833 | -30.52 | 2 | 51.3 | 12.7 | 1 | 317-334 | K.NKNECSLHIHASYSISQK.L | Carbamidomethyl: 5 |

# Detailed Protein Report

## Protein 270: zinc finger protein 573 isoform 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|289577063 | **Score:** | 37.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 77.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.0 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MFPVLEPHQV GLIRSYNSKT MTCELVTFRD VAIDFSRQEW EYLDPNQRDL YRDVMLENYR NLVSLGGHSI SKPVVVDLLE
        90        100        110        120        130        140        150        160
RGKEPWMILR EETQFTDLDL QCEIISYIEV PTYETDISST QLQSIYKREK LYECKKCQKK FSSGYQLILH HRFHVIERPY
       170        180        190        200        210        220        230        240
ECKECGKNFR SGYQLTLHQR FHTGEKPYEC TECGKNFRSG YQLTVHQRFH TGEKTYECRQ CGKAFIYASH IVQHERIHTG
       250        260        270        280        290        300        310        320
GKPYECQECG RAFSQGGHLR IHQRVHTGEK PYKCKECGKT FSRRSNLVEH GQFHTDEKPY ICEKCGKAFR RGHQLTVHQR
       330        340        350        360        370        380        390        400
VHTGKKPYEC KECGKGYTTA SYFLLHQRIH KGGKPYECKE CKKTFTLYRN LTRHQNIHTG EKLFECKQCG KTYTTGSKLF
       410        420        430        440        450        460        470        480
QHQKTHTGEK PYECKECGKA FSLYGYLKQH QKIHTGMKHF ECKECKKTFT LYRNLTRHQN IHTGKKLFEC QECGKAYSTG
       490        500        510        520        530        540        550        560
SNLIQHRKTH TGEKPYKCKE CGKTFSLHGY LNQHQKIHTG MKPYECKVCR KTFTFYRNLT LHQSIHTDEK PFECKECGKT
       570        580        590        600        610        620        630        640
FRRSSHLTAH QSIHADKKPY ECKECGKAFK MYGYLTQHQK IHTGGKPYEC KECGKAFSRA SNLVQHERIH TGEKPYVCKQ
       650        660        670
CGKTFRYGSA LKAHQRIHRS IKV
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2167 | 1 | 900.3438 | -97.52 | 3 | 55.5 | 11.8 | 2 | 15-37 | R.SYNSKTMTCELVTFRDVAIDFSR.Q | Oxidation: 7 |

# Detailed Protein Report

## Protein 271: PERQ amino acid-rich with GYF domain-containing protein 2 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|156766047 | **Score:** | 37.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 149.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAETQTLNF | GPEWLRALSS | GGSITSPPLS | PALPKYKLAD | YRYGREEMLA | LFLKDNKIPS | DLLDKEFLPI | LQEEPLPPLA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LVPFTEEEQR | NFSMSVNSAA | VLRLTGRGGG | GTVVGAPRGR | SSSRGRGRGR | GECGFYQRSF | DEVEGVFGRG | GGREMHRSQS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WEERGDRRFE | KPGRKDVGRP | NFEEGGPTSV | GRKHEFIRSE | SENWRIFREE | QNGEDEDGGW | RLAGSRRDGE | RWRPHSPGWR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EHMERRRRFE | FDFRDRDDER | GYRRVRSGSG | SIDDDRDSLP | EWCLEDAEEE | MGTFDSSGAF | LSLKKVQKEP | IPEEQEMDFR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PVDEGEECSD | SEGSHNEEAK | EPDKTNKKEG | EKTDRVGVEA | SEETPQTSSS | SARPGTPSDH | QSQEASQFER | KDEPKTEQTE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KAEEETRMEN | SLPAKVPSRG | DEMVADVQQP | LSQIPSDTAS | PLLILPPPVP | NPSPTLRPVE | TPVVGAPGMG | SVSTEPDDEE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GLKHLEQQAE | KMVAYLQDSA | LDDERLASKL | QEHRAKGVSI | PLMHEAMQKW | YYKDPQGEIQ | GPFNNQEMAE | WFQAGYFTMS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LLVKRACDES | FQPLGDIMKM | WGRVPFSPGP | APPPHMGELD | QERLTRQQEL | TALYQMQHLQ | YQQFLIQQQY | AQVLAQQQKA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ALSSQQQQQL | ALLLQQFQTL | KMRISDQNII | PSVTRSVSVP | DTGSIWELQP | TASQPTVWEG | GSVWDLPLDT | TTPGPALEQL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QQLEKAKAAK | LEQERREAEM | RAKREEEERK | RQEELRRQQE | EILRRQQEEE | RKRREEEELA | RRKQEEALRR | QREQEIALRR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QREEEERQQQ | EEALRRLEER | RREEEERRKQ | EELLRKQEEE | AAKWAREEEE | AQRRLEENRL | RMEEEAARLR | HEEEERKRKE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LEVQRQKELM | RQRQQQQEAL | RRLQQQQQQQ | QLAQMKLPSS | STWGQQSNTT | ACQSQATLSL | AEIQKLEEER | ERQLREEQRR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QQRELMKALQ | QQQQQQQQKL | SGWGNVSKPS | GTTKSLLEIQ | QEEARQMQKQ | QQQQQQHQQP | NRARNNTHSN | LHTSIGNSVW |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GSINTGPPNQ | WASDLVSSIW | SNADTKNSNM | GFWDDAVKEV | GPRNSTNKNK | NNASLSKSVG | VSNRQNKKVE | EEEKLLKLFQ |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GVNKAQDGFT | QWCEQMLHAL | NTANNLDVPT | FVSFLKEVES | PYEVHDYIRA | YLGDTSEAKE | FAKQFLERRA | KQKANQQRQQ |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| QQLPQQQQQQ | PPQQPPQQPQ | QQDSVWGMNH | STLHSVFQTN | QSNNQQSNFE | AVQSGKKKKK | QKMVRADPSL | LGFSVNASSE |
| 1290 | 1300 | | | | | | |
| RLNMGEIETL | DDY | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1750 | 1 | 863.3936 | -7.87 | 2 | 51.7 | 13.5 | 1 | 565-579 | K.RACDESFQPLGDIMK.M | Oxidation: 14 |

# Detailed Protein Report

## Protein 272: probable global transcription activator SNF2L2 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|574957245 | **Score:** | 37.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 172.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSTPTDPGAM | PHPGPSPGPG | PSPGPILGPS | PGPGPSPGSV | HSMMGPSPGP | PSVSHPMPTM | GSTDFPQEGM | HQMHKPIDGI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HDKGIVEDIH | CGSMKGTGMR | PPHPGMGPPQ | SPMDQHSQGY | MSPHPSPLGA | PEHVSSPMSG | GGPTPPQMPP | SQPGALIPGD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PQAMSQPNRG | PSPFSPVQLH | QLRAQILAYK | MLARGQPLPE | TLQLAVQGKR | TLPGLQQQQQ | QQQQQQQQQQ | QQQQQQQQPQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QQPPQPQTQQ | QQQPALVNYN | RPSGPGPELS | GPSTPQKLPV | PAPGGRPSPA | PPAAAQPPAA | AVPGPSVPQP | APGQPSPVLQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LQQKQSRISP | IQKPQGLDPV | EILQEREYRL | QARIAHRIQE | LENLPGSLPP | DLRTKATVEL | KALRLLNFQR | QLRQEVVACM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RRDTTLETAL | NSKAYKRSKR | QTLREARMTE | KLEKQQKIEQ | ERKRRQKHQE | YLNSILQHAK | DFKEYHRSVA | GKIQKLSKAV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ATWHANTERE | QKKETERIEK | ERMRRLMAED | EEGYRKLIDQ | KKDRRLAYLL | QQTDEYVANL | TNLVWEHKQA | QAAKEKKKRR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RRKKKAEENA | EGGESALGPD | GEPIDESSQM | SDLPVKVTHT | ETGKVLFGPE | APKASQLDAW | LEMNPGYEVA | PRSDSEESDS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DYEEEDEEEE | SSRQETEEKI | LLDPNSEEVS | EKDAKQIIET | AKQDVDDEYS | MQYSARGSQS | YYTVAHAISE | RVEKQSALLI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NGTLKHYQLQ | GLEWMVSLYN | NNLNGILADE | MGLGKTIQTI | ALITYLMEHK | RLNGPYLIIV | PLSTLSNWTY | EFDKWAPSVV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KISYKGTPAM | RRSLVPQLRS | GKFNVLLTTY | EYIIKDKHIL | AKIRWKYMIV | DEGHRMKNHH | CKLTQVDLNE | EETILIIRRL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| HKVLRPFLLR | RLKKEVESQL | PEKVEYVIKC | DMSALQKILY | RHMQAKGILL | TDGSEKDKKG | KGGAKTLMNT | IMQLRKICNH |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PYMFQHIEES | FAEHLGYSNG | VINGAELYRA | SGKFELLDRI | LPKLRATNHR | VLLFCQMTSL | MTIMEDYFAF | RNFLYLRLDG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TTKSEDRAAL | LKKFNEPGSQ | YFIFLLSTRA | GGLGLNLQAA | DTVVIFDSDW | NPHQDLQAQD | RAHRIGQQNE | VRVLRLCTVN |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SVEEKILAAA | KYKLNVDQKV | IQAGMFDQKS | SSHERRAFLQ | AILEHEEENE | EEDEVPDDET | LNQMIARREE | EFDLFMRMDM |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DRRREDARNP | KRKPRLMEED | ELPSWIIKDD | AEVERLTCEE | EEEKIFGRGS | RQRRDVDYSD | ALTEKQWLRA | IEDGNLEEME |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| EEVRLKKRKR | RRNVDKDPAK | EDVEKAKKRR | GRPPAEKLSP | NPPKLTKQMN | AIIDTVINYK | DSSGRQLSEV | FIQLPSRKEL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PEYYELIRKP | VDFKKIKERI | RNHKYRSLGD | LEKDVMLLCH | NAQTFNLEGS | QIYEDSIVLQ | SVFKSARQKI | AKEEESEDES |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| NEEEEEEDEE | ESESEAKSVK | VKIKLNKKDD | KGRDKGKGKK | RPNRGKAKPV | VSDFDSDEEQ | DEREQSEGSG | TDDE |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2593 | 1 | 648.3609 | 19.71 | 2 | 62.4 | 10.6 | 2 | 802-812 | K.ISYKGTPAMRR.S | Oxidation: 9 |
| 2825 | 2 | 1024.0347 | -1.30 | 2 | 65.7 | 15.7 | 1 | 1053-1069 | K.KFNEPGSQYFIFLLSTR.A | |

# Detailed Protein Report

**Protein 273:** **polycystic kidney disease and receptor for egg jelly-related protein precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5174633 | **Score:** | 37.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 255.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 2 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRPGPALLLL | GVGLSLSVGR | LPLPPVPRGA | QAAVSGAPGG | LLRGAPGLGV | RGGRALLSLR | PSAVRAGGAV | LSGRGSLCFP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HGGTGRRWYC | LDLRVLLSAQ | RLPWPAAPAL | ALVDLQLSAR | GGRLSLTWSV | RLPRSPGRLA | WAFRLRLLGP | GAARPASPAA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RVSPRSAAPG | PRPQQGFVAR | TECPTDGPAR | VMLQAVNSSS | HRAVESSVSC | QINACVIQRV | RINTDQKGAP | VRLSMQAEAT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| INASVQLDCP | AARAIAQYWQ | VFSVPAVGQA | PDWTQPLDLP | QLEIRNSPLF | IHIPNNSLQW | GVYVFNFTVS | ITTGNPKMPE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VKDSDAVYVW | IVRSSLQAVM | LGDANITANF | TEQLILDGST | SSDPDADSPL | QGLQFFWYCT | TDPRNYGGDR | IILGSKEVCH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PEQANLKWPW | ASGPVLTLLP | ETLKGDHVYF | FRMVIRKDSR | TAFSDKRVHV | LQGPKAIAHI | TCIENCERNF | IVSDRFSLFL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NCTNCASRDF | YKWSILSSSG | GEMLFDWMGE | TVTGRNGAYL | SIKAFAFRHF | LEAEFSISLY | LACWSGVTSV | FRHSFIINHG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PQIGECKINP | AKGIALITKF | VVQCSNFRDK | HVPLTYKIIV | SDLHSVGEIS | SVKENTLGTI | LYLGPQSTVP | PSFLPVGMLA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SQYGLKIYAQ | VYDSLGAFSQ | VTLHATAQAP | TDKNSSKTVL | NQLLSFTVGP | SSLLSTLIQK | KDFLPAGYLL | YIVASVLNNM |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KTELPLRDDR | VNLRKHLIDQ | SFLLPVSTLV | EIGQVVMTIT | KLTQKPSEFT | WDAQKRATMR | VWQANQALQE | YQQKDKRFRS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EQIEIVSTGI | LMSLSNILKM | TSPHQVVKDP | FYVIESLSDT | ILANKVPGNK | TTSMRTPNFN | MYVKKVEKWG | INQLFRNEKH |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| CRNCFYPTLN | VSSVPGLSAN | GPISTMFCDF | TNDLFPWLND | QENTSVEVSG | FRMTGVADNG | SVLEITPDVA | EVYLVRKNLT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FAAFNLTVGP | NSEVDGSLKK | TTGGFSFQVD | STVLREVLVH | IVTEVMVLFT | VLVYTGSQIT | PTALVATFLV | PHDIPPFASQ |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SALFDPACTV | KKARVVCLPV | SLLQLIAQHS | HSPHCTVSIV | LQAPRFVMKL | NDKLVRISIF | SVQCLDMYGI | QSEWREGYCI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LGEKTSWYEV | HCICKNVVRA | RRQLGTIGLT | GIHLHTHYVM | AKVIVIPNPV | DLRLNIIKSL | HQNPVTLFTV | LFIILLYVGL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| AFWALYRDEM | DQHLRGHVIV | LPDNDPYDNL | CYLVTIFTGS | RWGSGTRANV | FVQLRGTVST | SDVHCLSHPH | FTTLYRGSIN |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TFLLTTKSDL | GDIHSIRVWH | NNEGRSPSWY | LSRIKVENLF | SRHIWLFICQ | KWLSVDTTLD | RTFHVTHPDE | RLTRKDFFFI |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| DVSSNLRKNH | MWFSIFASVV | AKTFNRLQRL | SCCLAMLLSS | LLCNIMFFNL | NRQEQTESRE | RKYMRSMMIG | IESVLITIPV |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| QLLITFLFTC | SQRKPQADLK | EVSPQKHPLM | SEASEHWEEY | LRKWHAYETA | KVHPREVAKP | ASKGKPRLPK | ASPKATSKPK |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| HRHRKAQIKT | PETLGPNTNS | NNNIEDDQDV | HSEQHPSQKD | LQQLKKKPRI | VLPWWCVYVA | WFLVFATSSI | SSFFIVFYGL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| TYGYDKSIEW | LFASFCSFCQ | SVLLVQPSKI | ILLSGFRTNK | PKYCKNLSWS | TKYKYTEIRL | DGMRMHPEEM | QRIHDQIVRI |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| RGTRMYQPLT | EDEIRIFKRK | KRIKRRALLF | LSYILTHFIF | LALLLILIVL | LRHTDCFYYN | QFIRDRFSMD | LATVTKLEDI |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| YRWLNSVLLP | LLHNDLNPTF | LPESSSKILG | LPLMRQVRAK | SSEKMCLPAE | KFVQNSIRRE | IHCHPKYGID | PEDTKNYSGF |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| WNEVDKQAID | ESTNGFTYKP | QGTQWLYYSY | GLLHTYGSGG | YALYFFPEQQ | RFNSTLRLKE | LQESNWLDEK | TWAVVLELTT |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| FNPDINLFCS | ISVIFEVSQL | GVVNTSISLH | SFSLADFDRK | ASAEIYLYVA | ILIFFLAYVV | DEGCIIMQER | ASYVRSVYNL |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| LNFALKCIFT | VLIVLFLRKH | FLATGIIRFY | LSNPEDFIPF | HAVSQVDHIM | RIILGFLLFL | TILKTLRYSR | FFYDVRLAQR |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| AIQAALPGIC | HMAFVVSVYF | FVYMAFGYLV | FGQHEWNYSN | LIHSTQTVFS | YCVSAFQNTE | FSNNRILGVL | FLSSFMLVMI |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2763 | 1 | 741.8475 | 25.09 | 2 | 64.9 | 12.5 | 0 | 1125-1135 | K.TSWYEVHCICK.N | Carbamidomethyl: 8, 10 |
| 2608 | 1 | 648.3616 | -63.29 | 2 | 62.6 | 12.8 | 1 | 1788-1798 | K.ILGLPLMRQVR.A | |

# Detailed Protein Report

## Protein 274: PREDICTED: F-box/WD repeat-containing protein 11 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530380941 | **Score:** | 36.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 9.7 |
| | | **No. of unique Peptides:** | 3 |

```
        10          20          30          40          50          60          70          80
MISNGTSSVI  VSRKRPSEGN  YQKEKDLCIK  YFDQWSESDQ  VEFVEHLISR  MCHYQHGHIN  SYLKPMLQRD  FITALPEQGL

        90         100         110         120         130         140         150         160
DHIAENILSY  LDARSLCAAE  LVCKEWQRVI  SEGMLWKKLI  ERMVRTDPLW  KGLSERRGWD  QYLFKNRPTD  GPPNSFYRSL

       170         180         190         200         210         220         230         240
YPKIIQDIET  IESNWRCGRH  NLQRIQCRSE  NSKGVYCLQY  DDEKIISGLR  DNSIKIWDKT  SLECLKVLTG  HTGSVLCLQY

       250         260         270         280         290         300         310         320
DERVIVTGSS  DSTVRVWDVN  TGEVLNTLIH  HNEAVLHLRF  SNGLMVTCSK  DRSIAVWDMA  SATDITLRRV  LVGHRAAVNV

       330         340         350         360         370         380         390         400
VDFDDKYIVS  ASGDRTIKVW  STSTCEFVRT  LNGHKRGIAC  LQYRDRLVVS  GSSDNTIRLW  DIECGACLRV  LEGHEELVRC

       410         420         430         440         450         460         470         480
IRFDNKRIVS  GAYDGKIKVW  DLQAALDPRA  PASTLCLRTL  VEHSGRVFRL  QFDEFQIISS  SHDDTILIWD  FLNVPPSAQN

       490         500
ETRSPSRTYT  YISR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 891 | 1 | 630.9500 | -54.02 | 3 | 39.5 | 12.1 | 0 | 227-243 | K.VLTGHTGSVLCLQYDER.V | |
| 2270 | 3 | 596.7864 | -15.83 | 2 | 56.7 | 13.1 | 0 | 316-326 | R.AAVNVVDFDDK.Y | |
| 1138 | 1 | 751.8302 | 130.90 | 3 | 42.5 | 11.7 | 1 | 419-438 | K.VWDLQAALDPRAPASTLCLR.T | Carbamidomethyl: 18 |

# Detailed Protein Report

## Protein 275: metallothionein-4 [Homo sapiens]

**Accession:** gi|14269578

**Database:** refseq_human(refseq_human_20140103.fasta)

**Database Date:** 2015-11-30

**Modification(s):** Carbamidomethyl

**Score:** 36.8

**MW [kDa]:** 6.4

**pI:** 10.8

**Sequence Coverage [%]:** 53.2

**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70
MDPRECVCMS GGICMCGDNC KCTTCNCKTC RKSCCPCCPP GCAKCARGCI CKGGSDKCSC CP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1709 | 1 | 892.3390 | 4.69 | 2 | 51.7 | 11.6 | 1 | 33-47 | K.SCCPCCPPGCAKCAR.G | Carbamidomethyl: 2, 3, 6, 10, 13 |

# Detailed Protein Report

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## Protein 276: tripartite motif-containing protein 65 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|371122551 | **Score:** | 36.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 8.1 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAAQLLEEKL | TCAICLGLYQ | DPVTLPCGHN | FCGACIRDWW | DRCGKACPEC | REPFPDGAEL | RRNVALSGVL | EVVRAGPARD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PGPDPGPGPD | PAARCPRHGR | PLELFCRTEG | RCVCSVCTVR | ECRLHERALL | DAERLKREAQ | LRASLEVTQQ | QATQAEGQLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ELRKQSSQIQ | NSACILASWV | SGKFSSLLQA | LEIQHTTALR | SIEVAKTQAL | AQARDEEQRL | RVHLEAVARH | GCRIRELLEQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VDEQTFLQES | QLLQPPGPLG | PLTPLQWDED | QQLGDLKQLL | SRLCGLLLEE | GSHPGAPAKP | VDLAPVDYRN | LTFDPVSANR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HFYLSRQDQQ | VKHCRQSRGP | GGPGSFELWQ | VQCAQSFQAG | HHYWEVRASD | HSVTLGVSYP | QLPRCRLGPH | TDNIGRGPCS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| WGLCVQEDSL | QAWHNGEAQR | LPGVSGRLLG | MDLDLASGCL | TFYSLEPQTQ | PLYTFHALFN | QPLTPVFWLL | EGRTLTLCHQ |
| 490 | 500 | | | | | | |
| PGAVFPLGPQ | EEVLS | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 347 | 1 | 764.8773 | 64.49 | 2 | 34.3 | 12.1 | 1 | 112-123 | R.CVCSVCTVRECR.L | Carbamidomethyl: 1, 3, 6 |
| 40 | 1 | 661.7546 | -162.80 | 2 | 30.3 | 10.4 | 1 | 124-134 | R.LHERALLDAER.L | |

# Detailed Protein Report

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## Protein 277: PREDICTED: mucin-5AC [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578821001 | **Score:** | 36.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 520.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSVGRRKLAL | LWALALALAC | TRHTGHAQDG | SSESSYKHHP | ALSPIARGPS | GVPLRGATVF | PSLRTIPVVR | ASNPAHNGRV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CSTWGSFHYK | TFDGDVFRFP | GLCNYVFSEH | CGAAYEDFNI | QLRRSQESAA | PTLSRVLMKV | DGVVIQLTKG | SVLVNGHPVL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LPFSQSGVLI | QQSSSYTKVE | ARLGLVLMWN | HDDSLLLELD | TKYANKTCGL | CGDFNGMPVV | SELLSHNTKL | TPMEFGNLQK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MDDPTDQCQD | PVPEPPRNCS | TGFGICEELL | HGQLFSGCVA | LVDVGSYLEA | CRQDLCFCED | TDLLSCVCHT | LAEYSRQCTH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AGGLPQDWRG | PDFCPQKCPN | NMQYHECRSP | CADTCSNQEH | SRACEDHCVA | GCFCPEGTVL | DDIGQTGCVP | VSKCACVYNG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AAYAPGATYS | TDCTNCTCSG | GRWSCQEVPC | PGTCSVLGGA | HFSTFDGKQY | TVHGDCSYVL | TKPCDSSAFT | VLAELRRCGL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TDSETCLKSV | TLSLDGAQTV | VVIKASGEVF | LNQIYTQLPI | SAANVTIFRP | STFFIIAQTS | LGLQLNLQLV | PTMQLFMQLA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PKLRGQTCGL | CGNFNSIQAD | DFRTLSGVVE | ATAAAFFNTF | KTQAACPNIR | NSFEDPCSLS | VENEKYAQHW | CSQLTDADGP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FGRCHAAVKP | GTYYSNCMFD | TCNCERSEDC | LCAALSSYVH | ACAAKGVQLG | GWRDGVCTKP | MTTCPKSMTY | HYHVSTCQPT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CRSLSEGDIT | CSVGFIPVDG | CICPKGTFLD | DTGKCVQASN | CPCYHRGSMI | PNGESVHDSG | AICTCTHGKL | SCIGGQAPAP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VCAAPMVFFD | CRNATPGDTG | AGCQKSCHTL | DMTCYSPQCV | PGCVCPDGLV | ADGEGGCITA | EDCPCVHNEA | SYRAGQTIRV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GCNTCTCDSR | MWRCTDDPCL | ATCAVYGDGH | YLTFDGQSYS | FNGDCEYTLV | QNHCGGKDST | QDSFRVVTEN | VPCGTTGTTC |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SKAIKIFLGG | FELKLSHGKV | EVIGTDESQE | VPYTIRQMGI | YLVVDTDIGL | VLLWDKKTSI | FINLSPEFKG | RVCGLCGNFD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| DIAVNDFATR | SRSVVGDVLE | FGNSWKLSPS | CPDALAPKDP | CTANPFRKSW | AQKQCSILHG | PTFAACHAHV | EPARYYEACV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| NDACACDSGG | DCECFCTAVA | AYAQACHEVG | LCVSWRTPSI | CPLFCDYYNP | EGQCEWHYQP | CGVPCLRTCR | NPRGDCLRDV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| RGLEGCYPKC | PPEAPIFDED | KMQCVATCPT | PPLPPRCHVH | GKSYRPGAVV | PSDKNCQSCL | CTERGVECTY | KAEACVCTYN |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| GQRFHPGDVI | YHTTDGTGGC | ISARCGANGT | IERRVYPCSP | TTPVPPTTFS | FSTPPLVVSS | THTPSNGPSS | AHTGPPSSAW |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PTTAGTSPRT | RLPTASASLP | PVCGEKCLWS | PWMDVSRPGR | GTDSGDFDTL | ENLRAHGYRV | CESPRSVECR | AEDAPGVPLR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ALGQRVQCSP | DVGLTCRNRE | QASGLCYNYQ | IRVQCCTPLP | CSTSSSPAQT | TPPTTSKTTE | TRASGSSAPS | STPGTVSLST |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ARTTPAPGTA | TSVKKTFSTP | SPPPVPATST | SSMSTTAPGT | SVVSSKPTPT | EPSTSSCLQE | LCTWTEWIDG | SYPAPGINGG |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| DFDTFQNLRD | EGYTFCESPR | SVQCRAESFP | NTPLADLGQD | VICSHTEGLI | CLNKNQLPPI | CYNYEIRIQC | CETVNVCRDI |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| TRLPKTVATT | RPTPHPTGAQ | TQTTFTTHMP | SASTEQPTAT | SRGGPTATSV | TQGTHTTLVT | RNCHPRCTWT | KWFDVDFPSP |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| GPHGGDKETY | NNIIRSGEKI | CRRPEEITRL | QCRAKSHPEV | SIEHLGQVVQ | CSREEGLVCR | NQDQQGPFKM | CLNYEVRVLC |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| CETPRGCHMT | STPGSTSSSP | AQTTPSTTSK | TTETQASGSS | APSSTPGTVS | LSTARTTPAP | GTATSVKKTF | STPSPPPVPA |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| TSTSSMSTTA | PGTSVVSSKP | TPTEPSTSSC | LQELCTWTEW | IDGSYPAPGI | NGGDFDTFQN | LRDEGYTFCE | SPRSVQCRAE |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| SFPNTPLADL | GQDVICSHTE | GLICLNKNQL | PPICYNYEIR | IQCCETVNVC | RDITRPPKTV | ATTRPTPHPT | GAQTQTTFTT |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| HMPSASTEQP | TATSRGGPTA | TSVTQGTHTT | PVTRNCHPRC | TWTTWFDVDF | PSPGPHGGDK | ETYNNIIRSG | EKICRRPEEI |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1356 | 1 | 863.9173 | -123.12 | 2 | 46.6 | 12.1 | 1 | 7-22 | R.KLALLWALALALACTR.H | |
| 2649 | 2 | 734.8562 | 20.51 | 2 | 63.2 | 12.1 | 0 | 317-329 | R.QCTHAGGLPQDWR.G | |
| 2548 | 1 | 1044.5297 | 54.57 | 2 | 61.8 | 12.6 | 1 | 2203-2218 | K.MCLNYEVRVLCCETPK.G | Carbamidomethyl: 2, 11, 12; Oxidation: 1 |

# Detailed Protein Report

## Protein 278: NF-X1-type zinc finger protein NFXL1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|89363020 | **Score:** | 36.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 101.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.2 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|520261838 | refseq_human (refseq_human_20140103.fasta) | NF-X1-type zinc finger protein NFXL1 [Homo sapiens] |
| gi\|520261712 | refseq_human (refseq_human_20140103.fasta) | NF-X1-type zinc finger protein NFXL1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEASWRQVAG | GRGRSRGRAT | AAPSGNGVHL | RGAGGGREKG | SVGAVPSGTS | PGGVATTAAA | GSRHSPAGSQ | ALQTTAASEL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MSQKKFEEIK | KANQAAARKL | VEEQFSSSSE | EGDEDFEGKQ | GKILANTFIT | YTTQTDGDTR | ELERTKQYVN | EAFQAGAMTC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LICIASVKRN | QAVWSCSGCF | CIFHMPCIQK | WAKDSQFLVS | SVTDDDFGKK | DCPWPCPKCR | FEYKRSETPS | RYYCYCGKVE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DPPLDPWLVP | HSCGQVCERE | FKPPCGHKCL | LLCHPGPCPP | CPKMVTTTCY | CKKAKPIPRR | CSAKEWSCQL | PCGQKLLCGQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HKCENPCHAG | SCQPCPRVSR | QKCVCGKKVA | ERSCASPLWH | CDQVCGKTLP | CGNHTCEQVC | HVGACGECPR | SGKRFCPCQK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SKFSLPCTED | VPTCGDSCDK | VLECGIHRCS | QRCHRGPCET | CRQEVEKHCR | CGKHTKRMPC | HKPYLCETKC | VKMRDCQKHQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CRRKCCPGNC | PPCDQNCGRT | LGCRNHKCPS | VCHRGSCYPC | PETVDVKCNC | GNTKVTVPCG | RERTTRPPKC | KEQCSRPPTC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HHTSQEKHRC | HFGSCPPCHQ | PCQKVLEKCG | HLCPAPCHDQ | ALIKQTGRHQ | PTGPWEQPSE | PAFIQTALPC | PPCQVPIPME |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CLGKHEVSPL | PCHAVGPYSC | KRVCGRILDC | QNHTCMKECH | KVTKTDGCTG | KNKAGPECLH | CEEGCSKSRP | LGCLHPCILR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CHPGECPPCV | QMLRIKCHCK | ITSLYVECRK | ITTADVNEKN | LLSCCKNQCP | KELPCGHRCK | EMCHPGECPF | NCNQKVKLRC |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PCKRIKKELQ | CNKVRENQVS | IECDTTCKEM | KRKASEIKEA | EAKAALEEEK | RRQQAELEAF | ENRLKGRRKK | NRKRDEVAVE |
| 890 | 900 | 910 | 920 | | | | |
| LSLWQKHKYY | LISVCGVVVV | VFAWYITHDV | N | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2093 | 1 | 732.3366 | -79.70 | 2 | 56.6 | 10.4 | 1 | 17-31 | R.GRATAAPSGNGVHLR.G | |
| 1824 | 1 | 916.3237 | -87.07 | 2 | 53.1 | 10.4 | 2 | 433-447 | R.CHRGPCETCRQEVEK.H | Carbamidomethyl: 6 |

# Detailed Protein Report

## Protein 279: protein TANC1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|225543463 | **Score:** | 36.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 152.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLKAVLKKSR | EGGKGGKKEA | GSDFGPETSP | VLHLDHSADS | PVSSLPTAED | TYRVSLAKGV | SMSLPSSPLL | PRQSHLVQSR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VNKKSPGPVR | KPKYVESPRV | PGDAVIMPFR | EVAKPTEPDE | HAKADNEPSC | SPAAQELLTR | LGFLLGEGIP | SATHITIEDK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NETMCTALSQ | GISPCSTLTS | STASPSTDSP | CSTLNSCVSK | TAANKSPCET | ISSPSSTLES | KDSGIIATIT | SSSENDDRSG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SSLEWNKDGN | LRLGVQKGVL | HDRRADNCSP | VAEEETTGSA | ESTLPKAESS | AGDGPVPYSQ | GSSSLIMPRP | NSVAATSSTK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LEDLSYLDGQ | RNAPLRTSIR | LPWHNTAGAR | FAPYKPQDIL | LKPLLFEVPS | ITTDSVFVGR | DWLFHQIEEN | LRNTELAENR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GAVVVGNVGF | GKTAIISKLV | ALSCHGSRMR | QIASNSPGSS | PKTSDPTQDL | HFTPLLSPSS | STSASSTAKT | PLGSISAENQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RPREDAVKYL | ASKVVAYHYC | QADNTYTCLV | PEFVHSIAAL | LCRSHQLAAY | RDLLIKEPQL | QSMLSLRSCV | QDPVAAFKRG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VLEPLTNLRN | EQKIPEEEYI | ILIDGLNEAE | FHKPDYGDTL | SSFITKIISK | FPAWLKLIVT | VRANFQEIIS | ALPFVKLSLD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DFPDNKDIHS | DLHAYVQHRV | HSSQDILSNI | SLNGKADATL | IGKVSSHLVL | RSLGSYLYLK | LTLDLFQRGH | LVIKSASYKV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VPVSLSELYL | LQCNMKFMTQ | SAFERALPIL | NVALASLHPM | TDEQIFQAIN | AGHIQGEQGW | EDFQQRMDAL | SCFLIKRRDK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TRMFCHPSFR | EWLVWRADGE | NTAFLCEPRN | GHALLAFMFS | RQEGKLNRQQ | TMELGHHILK | AHIFKGLSKK | TGISSSHLQA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LWIGYSTEGL | SAALASLRNL | YTPNVKVSRL | LILGGANVNY | RTEVLNNAPI | LCVQSHLGHE | EVVTLLLEFG | ACLDGTSENG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| MTALCYAAAA | GHMKLVCLLT | KKGVRVDHLD | KKGQCALVHS | ALRGHGDILQ | YLLTCEWSPG | PPQPGTLRKS | HALQQALTAA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ASMGHSSVVQ | CLLGMEKEHE | VEVNGTDTLW | GETALTAAAG | RGKLEVCELL | LGHGAAVSRT | NRRGVPPLFC | AARQGHWQIV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RLLLERGCDV | NLSDKQGRTP | LMVAACEGHL | STVEFLLSKG | AALSSLDKEG | LSALSWACLK | GHRAVVQYLV | EEGAAIDQTD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KNGRTPLDLA | AFYGDAETVL | YLVEKGAVIE | HVDHSGMRPL | DRAIGCRNTS | VVVALLRKGA | KLGNAAWAMA | TSKPDILIIL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LQKLMEEGNV | MYKKGKMKEA | AQRYQYALRK | FPREGFGEDM | RPFNELRVSL | YLNLSRCRRK | TNDFGMAEEF | ASKALELKPK |
| 1370 | 1380 | 1390 | 1400 | | | | |
| SYEAFYARAR | AKRNSRYRNS | WQLWLTCKRL | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2703 | 5 | 673.3636 | 27.60 | 2 | 64.1 | 17.2 | 1 | 419-430 | K.LVALSCHGSRMR.Q | Oxidation: 11 |
| 2221 | 1 | 953.0764 | 108.03 | 2 | 58.2 | 19.2 | 0 | 1226-1242 | K.GAVIEHVDHSGMRPLDR.A | Oxidation: 12 |

# Detailed Protein Report

## Protein 280: PREDICTED: afadin isoform X15 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578812779 | **Score:** | 36.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 185.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 3.14 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.05 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSAGGRDEER | RKLADIIHHW | NANRLDLFEI | SQPTEDLEFH | GVMRFYFQDK | AAGNFATKCI | RVSSTATTQD | VIETLAEKFR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PDMRMLSSPK | YSLYEVHVSG | EERRLDIDEK | PLVVQLNWNK | DDREGRFVLK | NENDAIPPKK | AQSNGPEKQE | KEGVIQNFKR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TLSKKEKKEK | KKREKEALRQ | ASDKDDRPFQ | GEDVENSRLA | AEVYKDMPET | SFTRTISNPE | VVMKRRRQQK | LEKRMQEFRS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SDGRPDSGGT | LRIYADSLKP | NIPYKTILLS | TTDPADFAVA | EALEKYGLEK | ENPKDYCIAR | VMLPPGAQHS | DEKGAKEIIL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DDDECPLQIF | REWPSDKGIL | VFQLKRRPPD | HIPKKTKKHL | EGKTPKGKER | ADGSGYGSTL | PPEKLPYLVE | LSPGRRNHFA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YYNYHTYEDG | SDSRDKPKLY | RLQLSVTEVG | TEKLDDNSIQ | LFGPGIQPHH | CDLTNMDGVV | TVTPRSMDAE | TYVEGQRISE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TTMLQSGMKV | QFGASHVFKF | VDPSQDHALA | KRSVDGGLMV | KGPRHKPGIV | QETTFDLGGD | IHSGTALPTS | KSTTRLDSDR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VSSASSTAER | GMVKPMIRVE | QQPDYRRQES | RTQDASGPEL | ILPASIEFRE | SSEDSFLSAI | INYTNSSTVH | FKLSPTYVLY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| MACRYVLSNQ | YRPDISPTER | THKVIAVVNK | MVSMMEGVIQ | EVDQVDQKQK | NIAGALAFWM | ANASELLNFI | KQDRDLSRIT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LDAQDVLAHL | VQMAFKYLVH | CLQSELNNYM | PAFLDDPEEN | SLQRPKIDDV | LHTLTGAMSL | LRRCRVNAAL | TIQLFSQLFH |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FINMWLFNRL | VTDPDSGLCS | HYWGAIIRQQ | LGHIEAWAEK | QGLELAADCH | LSRIVQATTL | LTMDKYAPDD | IPNINSTCFK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LNSLQLQALL | QNYHCAPDEP | FIPTDLIENV | VTVAENTADE | LARSDGREVQ | LEEDPDLQLP | FLLPEDGYSC | DVVRNIPNGL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QEFLDPLCQR | GFCRLIPHTR | SPGTWTIYFE | GADYESHLLR | ENTELAQPLR | KEPEIITVTL | KKQNGMGLSI | VAAKGAGQDK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LGIYVKSVVK | GGAADVDGRL | AAGDQLLSVD | GRSLVGLSQE | RAAELMTRTS | SVVTLEVAKQ | GAIYHGLATL | LNQPSPMMQR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ISDRRGSGKP | RPKSEGFELY | NNSTQNGSPE | SPQLPWAEYS | EPKKLPGDDR | LMKNRADHRS | SPNVANQPPS | PGGKSAYASG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TTAKITSVST | GNLCTEEQTP | PPRPEAYPIP | TQTYTREYFT | FPASKSQDRM | APPQNQWPNY | EEKPHMHTDS | NHSSIAIQRV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TRSQEELRED | KAYQLERHRI | EAAMDRKSDS | DMWINQSSSL | DSSTSSQEHL | NHSSKSVTPA | STLTKSGPGR | WKTPAAIPAT |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PVAVSQPIRT | DLPPPPPPPP | VHYAGDFDGM | SMDLPLPPPP | SANQIGLPSA | QVAAAERRKR | EEHQRWYEKE | KARLEEERER |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KRREQERKLG | QMRTQSLNPA | PFSPLTAQQM | KPEKPSTLQR | PQETVIRELQ | PQQQPRTIER | RDLQYITVSK | EELSSGDSLS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PDPWKRDAKE | KLEKQQQMHI | VDMLSKEIQE | LQSKPDRSAE | ESDRLRKLML | EWQFQKRLQE | SKQKDEDDEE | EEDDDVDTML |
| 1610 | 1620 | 1630 | 1640 | | | | |
| IMQRLEAERR | ARQTAMPAIS | VLDLVCSCFF | PFGTFFLS | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1199 | 1 | 533.6590 | -250.21 | 2 | 44.6 | 12.3 | 0 | 1502-1510 | R.DLQYITVSK.E |  | WUP:QUP 0.05<br>QU:MU 3.14 |

# Detailed Protein Report

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**Protein 281:** **PREDICTED: conserved oligomeric Golgi complex subunit 4 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578828932 | **Score:** | 36.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 73.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| | | **Sequence Coverage [%]:** | 9.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.74 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDGVQTALRS | EDYEQAAAHT | HRYLCLDKSV | IELSRQGKEG | SMIDANLKLL | QEAEQRLKAI | VAEKFAIATK | EGDLPQVERF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FKIFPLLGLH | EEGLRKFSEY | LCKQVASKAE | ENLLMVLGTD | MSDRRAAVIF | ADTLTLLFEG | IARIVETHQP | IVETYYGPGR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LYTLIKYLQV | ECDRQVEKVV | DKFIKQRDYH | QQFRHVQNNL | MRNSTTEKIE | PRELDPILTE | VTLMNARSEL | YLRFLKKRIS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SDFEVGDSMA | SEEVKQEHQK | CLDKLLNNCL | LSCTMQELIG | LYVTMEEYFM | RETVNKAVAL | DTYEKGQLTS | SMVDDVFYIV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KKCIGRALSS | SSIDCLCAMI | NLATTELESD | FRDVLCNKLR | MGFPATTFQD | IQRGVTSAVN | IMHSSLQQGK | FDTKGIESTD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EAKMSFLVTL | NNVEVCSENI | STLKKTLESD | CTKLFSQGIG | GEQAQAKFDS | CLSDLAAVSN | KFRDLLQEGL | TELNSTAIKP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QVQPWINSFF | SVSHNIEEEE | FNDYEANDPW | VQQFILNLEQ | QMAEFKASLS | PVIYDSLTGL | MTSLVAVELE | KVVLKSTFNR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LGGLQFDKEL | RSLIAYLTTV | TTWTIRDKFA | RLSQMATILN | LERVTEILDY | WGPNSGPLTW | RLTPAEVRQV | LALRIDFRSE |
| 650 | | | | | | | |
| DIKRLRL | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1637 | 1 | 993.4172 | -42.79 | 2 | 50.7 | 12.5 | 1 | 238-255 | K.RISSDFEVGDSMASEEVK.Q | | QU:MU | 0.74 |

# Detailed Protein Report

## Protein 282: zinc finger protein castor homolog 1 isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|119709834 | **Score:** | 36.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 189.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578799307 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein castor homolog 1 isoform X2 [Homo sapiens] |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDLGTAEGTR | CTDPPAGKPA | MAPKRKGGLK | LNAICAKLSR | QVVVEKRADA | GSHTEGSPSQ | PRDQERSGPE | SGAARAPRSE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EDKRRAVIEK | WVNGEYSEEP | APTPVLGRIA | REGLELPPEG | VYMVQPQGCS | DEEDHAEEPS | KDGGALEEKD | SDGAASKEDS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GPSTRQASGE | ASSLRDYAAS | TMTEFLGMFG | YDDQNTRDEL | ARKISFEKLH | AGSTPEAATS | SMLPTSEDTL | SKRARFSKYE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EYIRKLKAGE | QLSWPAPSTK | TEERVGKEVV | GTLPGLRLPS | STAHLETKAT | ILPLPSHSSV | QMQNLVARAS | KYDFFIQKLK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TGENLRPQNG | STYKKPSKYD | LENVKYLHLF | KPGEGSPDMG | GAIAFKTGKV | GRPSKYDVRG | IQKPGPAKVP | PTPSLAPAPL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ASVPSAPSAP | GPGPEPPASL | SFNTPEYLKS | TFSKTDSITT | GTVSTVKNGL | PTDKPAVTED | VNIYQKYIAR | FSGSQHCGHI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HCAYQYREHY | HCLDPECNYQ | RFTSKQDVIR | HYNMHKKRDN | SLQHGFMRFS | PLDDCSVYYH | GCHLNGKSTH | YHCMQVGCNK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VYTSTSDVMT | HENFHKKNTQ | LINDGFQRFR | ATEDCGTADC | QFYGQKTTHF | HCRRPGCTFT | FKNKCDIEKH | KSYHIKDDAY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AKDGFKKFYK | YEECKYEGCV | YSKATNHFHC | IRAGCGFTFT | STSQMTSHKR | KHERRHIRSS | GALGLPPSLL | GAKDTEHEES |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SNDDLVDFSA | LSSKNSSLSA | SPTSQQSSAS | LAAATAATEA | GPSATKPPNS | KISGLLPQGL | PGSIPLALAL | SNSGLPTPTP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| YFPILAGRGS | TSLPVGTPSL | LGAVSSGSAA | SATPDTPTLV | ASGAGDSAPV | AAASVPAPPA | SIMERISASK | GLISPMMARL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| AAAALKPSAT | FDPGSGQQVT | PARFPPAQVK | PEPGESTGAP | GPHEASQDRS | LDLTVKEPSN | ESNGHAVPAN | SSLLSSLMNK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| MSQGNPGLGS | LLNIKAEAEG | SPAAEPSPFL | GKAVKALVQE | KLAEPWKVYL | RRFGTKDFCD | GQCDFLHKAH | FHCVVEECGA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LFSTLDGAIK | HANFHFRTEG | GAAKGNTEAA | FPASAAETKP | PMAPSSPPVP | PVTTATVSSL | EGPAPSPASV | PSTPTLLAWK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QLASTIPQMP | QIPASVPHLP | ASPLATTSLE | NAKPQVKPGF | LQFQENDPCL | ATDCKYANKF | HFHCLFGNCK | YVCKTSGKAE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SHCLDHINPN | NNLVNVRDQF | AYYSLQCLCP | NQHCEFRMRG | HYHCLRTGCY | FVTNITTKLP | WHIKKHEKAE | RRAANGFKYF |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TKREECGRLG | CKYNQVNSHF | HCIREGCQFS | FLLKHQMTSH | ARKHMRRMLG | KNFDRVPPSQ | GPPGLMDAET | DECMDYTGCS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PGAMSSESST | MDRSCSSTPV | GNESTAAGNT | ISMPTASGAK | KRFWIIEDMS | PFGKRRKTAS | SRKMLDEGMM | LEGFRRFDLY |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EDCKDAACQF | SLKVTHYHCT | RENCGYKFCG | RTHMYKHAQH | HDRVDNLVLD | DFKRFKASLS | CHFADCPFSG | TSTHFHCLRC |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| RFRCTDSTKV | TAHRKHHGKQ | DVISAAGFCQ | FSSSADCAVP | DCKYKLKCSH | FHCTFPGCRH | TVVGMSQMDS | HKRKHEKQER |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| GEPAAEGPAP | GPPISLDGSL | SLGAEPGSLL | FLQSAAAGLG | LALGDAGDPG | PPDAAAPGPR | EGAAAAAAAA | GESSQEDEEE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| ELELPEEEAE | DDEDEDDDED | DDDEDDDEDD | DDEDLRTDSE | ESLPEAAAEA | AGAGARTPAL | AALAALGAPG | PAPTAASSP |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1857 | 1 | 604.2655 | -35.90 | 2 | 53.6 | 12.3 | 2 | 1283-1292 | K.REECGRLGCK.Y | Carbamidomethyl: 9 |

# Detailed Protein Report

## Protein 283: PREDICTED: calcyphosin-like protein isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578809847 | **Score:** | 36.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 23.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 18.1 |
| | | **No. of unique Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MQETASIVSV RSNWWQKMAG TARHDREMAI QAKKKLTTAT DPIERLRLQC LARGSAGIKG LGRVFRIMDD DNNRTLDFKE
        90        100        110        120        130        140        150        160
FMKGLNDYAV VMEKEEVEEL FRRFDKDGNG TIDFNEFLLT LRPPMSRARK EVIMQAFRKL DKTGDGVITI EDLREVYNAK
       170        180        190        200
HHPKYQNGEW SEEQVFRKFL DNFDSPYDKD GLVHKVGAH
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2813 | 1 | 895.4559 | 30.47 | 2 | 63.8 | 12.6 | 1 | 80-94 | K.EFMKGLNDYAVVMEK.E | Oxidation: 3 |
| 19 | 3 | 1205.0501 | -38.96 | 2 | 29.8 | 23.5 | 0 | 107-127 | K.DGNGTIDFNEFLLTLRPPMSR.A | Oxidation: 19 |

# Detailed Protein Report

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**Protein 284:** **inhibitor of nuclear factor kappa-B kinase subunit alpha [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|62241001 | **Score:** | 36.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 84.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.11 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.16 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MERPPGLRPG | AGGPWEMRER | LGTGGFGNVC | LYQHRELDLK | IAIKSCRLEL | STKNRERWCH | EIQIMKKLNH | ANVVKACDVP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EELNILIHDV | PLLAMEYCSG | GDLRKLLNKP | ENCCGLKESQ | ILSLLSDIGS | GIRYLHENKI | IHRDLKPENI | VLQDVGGKII |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HKIIDLGYAK | DVDQGSLCTS | FVGTLQYLAP | ELFENKPYTA | TVDYWSFGTM | VFECIAGYRP | FLHHLQPFTW | HEKIKKKDPK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CIFACEEMSG | EVRFSSHLPQ | PNSLCSLVVE | PMENWLQLML | NWDPQQRGGP | VDLTLKQPRC | FVLMDHILNL | KIVHILNMTS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AKIISFLLPP | DESLHSLQSR | IERETGINTG | SQELLSETGI | SLDPRKPASQ | CVLDGVRGCD | SYMVYLFDKS | KTVYEGPFAS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RSLSDCVNYI | VQDSKIQLPI | IQLRKVWAEA | VHYVSGLKED | YSRLFQGQRA | AMLSLLRYNA | NLTKMKNTLI | SASQQLKAKL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EFFHKSIQLD | LERYSEQMTY | GISSEKMLKA | WKEMEEKAIH | YAEVGVIGYL | EDQIMSLHAE | IMELQKSPYG | RRQGDLMESL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EQRAIDLYKQ | LKHRPSDHSY | SDSTEMVKII | VHTVQSQDRV | LKELFGHLSK | LLGCKQKIID | LLPKVEVALS | NIKEADNTVM |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FMQGKRQKEI | WHLLKIACTQ | SSARSLVGSS | LEGAVTPQTS | AWLPPTSAEH | DHSLSCVVTP | QDGETSAQMI | EENLNCLGHL |
| 730 | 740 | 750 | | | | | |
| STIIHEANEE | QGNSMMNLDW | SWLTE | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2406 | 1 | 665.3146 | -54.38 | 2 | 60.5 | 21.5 | 0 | 366-377 | R.KPASQCVLDGVR.G | Carbamidomethyl: 6 | |
| 1405 | 1 | 533.6158 | -246.47 | 2 | 45.9 | 14.5 | 1 | 510-517 | K.AWKEMEEK.A | Oxidation: 5 | QU:MU 1.11<br>WUP:QUP 1.16 |

# Detailed Protein Report

## Protein 285: thymidine phosphorylase isoform 1 proprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4503445 | **Score:** | 36.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 9.5 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|384229049 | refseq_human (refseq_human_20140103.fasta) | thymidine phosphorylase isoform 1 proprotein [Homo sapiens] |
| gi\|166158925 | refseq_human (refseq_human_20140103.fasta) | thymidine phosphorylase isoform 1 proprotein [Homo sapiens] |
| gi\|166158922 | refseq_human (refseq_human_20140103.fasta) | thymidine phosphorylase isoform 1 proprotein [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAALMTPGTG | APPAPGDFSG | EGSQGLPDPS | PEPKQLPELI | RMKRDGGRLS | EADIRGFVAA | VVNGSAQGAQ | IGAMLMAIRL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RGMDLEETSV | LTQALAQSGQ | QLEWPEAWRQ | QLVDKHSTGG | VGDKVSLVLA | PALAACGCKV | PMISGRGLGH | TGGTLDKLES |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IPGFNVIQSP | EQMQVLLDQA | GCCIVGQSEQ | LVPADGILYA | ARDVTATVDS | LPLITASILS | KKLVEGLSAL | VVDVKFGGAA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VFPNQEQARE | LAKTLVGVGA | SLGLRVAAAL | TAMDKPLGRC | VGHALEVEEA | LLCMDGAGPP | DLRDLVTTLG | GALLWLSGHA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GTQAQGAARV | AAALDDGSAL | GRFERMLAAQ | GVDPGLARAL | CSGSPAERRQ | LLPRAREQEE | LLAPADGTVE | LVRALPLALV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LHELGAGRSR | AGEPLRLGVG | AELLVDVGQR | LRRGTPWLRV | HRDGPALSGP | QSRALQEALV | LSDRAPFAAP | SPFAELVLPP |
| 490 | | | | | | | |
| QQ | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 41 | 1 | 906.3675 | -118.89 | 2 | 29.5 | 10.9 | 1 | 140-157 | K.VPMISGRGLGHTGGTLDK.L | Oxidation: 3 |
| 1488 | 1 | 671.3911 | -17.76 | 2 | 47.0 | 12.0 | 0 | 223-235 | K.LVEGLSALVVDVK.F | |

# Detailed Protein Report

## Protein 286: PREDICTED: centriolar coiled-coil protein of 110 kDa isoform X4 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|578828704 | **Score:** | 35.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 109.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.2 |
|  |  | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MEEYEKFCEK SLARIQEASL STESFLPAQS ESISLIRFHG VAILSPLLNI EKRKEMQQEK QKALDVEARK QVNRKKALLT
        90        100        110        120        130        140        150        160
RVQEILDNVQ VRKAPNASDF DQWEMETVYS NSEVRNLNVP ATFPNSFPSH TEHSTAAKLD KIAGILPLDN EDQCKTDGID
       170        180        190        200        210        220        230        240
LARDSEGFNS PKQCDSSNIS HVENEAFPKT SSATPQETLI SDGPFSVNEQ QDLPLLAEVI PDPYVMSLQN LMKKSKEYIE
       250        260        270        280        290        300        310        320
REQSRRSLRG SINRIVNESH LDKEHDAVEV ADCVKEKGQL TGKHCVSVIP DKPSLNKSNV LLQGASTQAS SMSMPVLASF
       330        340        350        360        370        380        390        400
SKVDIPIRTG HPTVLESNSD FKVIPTFVTE NNVIKSLTGS YAKLPSPEPS MSPKMHRRRS RTSSACHILI NNPINACELS
       410        420        430        440        450        460        470        480
PKGKEQAMDL IIQDTDENTN VPEIMPKLPT DLAGVCSSKV YVGKNTSEVK EDVVLGKSNQ VCQSSGNHLE NKVTHGLVTV
       490        500        510        520        530        540        550        560
EGQLTSDERG AHIMNSTCAA MPKLHEPYAS SQCIASPNFG TVSGLKPASM LEKNCSLQTE LNKSYDVKNP SPLLMQNQNT
       570        580        590        600        610        620        630        640
RQQMDTPMVS CGNEQFLDNS FEKVKRRLDL DIDGLQKENC PYVITSGITE QERQHLPEKR YPKGSGFVNK NKMLGTSSKE
       650        660        670        680        690        700        710        720
SEELLKSKML AFEEMRKRLE EQHAQQLSLL IAEQEREQER LQKEIEEQEK MLKEKKAMTA EASELDINNA VELEWRKISD
       730        740        750        760        770        780        790        800
SSLLETMLSQ ADSLHTSNSN SSGFTNSAMQ YSFVSANEAP FYLWGSSTSG LTKLSVTRPF GRAKTRWSQV FSLEIQAKFN
       810        820        830        840        850        860        870        880
KITAVAKGFL TRRLMQTDKL KQLRQTVKDT MEFIRSFQSE APLKRGIVSA QDASLQERVL AQLRAALYGI HDIFFVMDAA
       890        900        910        920        930        940        950        960
ERMSILHHDR EVRKEKMLRQ MDKMKSPRVA LSAATQKSLD RKKYMKAAEM GMPNKKFLVK QNPSETRSIC RKNPKKAAKC
       970        980
CDNLRRQHSL G
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2559 | 1 | 693.6709 | -206.81 | 2 | 60.3 | 11.2 | 1 | 924-935 | K.YMKAAEMGMPNK.K | Oxidation: 7 |

# Detailed Protein Report

## Protein 287: PREDICTED: multiple PDZ domain protein isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530390235 | **Score:** | 35.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 213.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.8 |
| | | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 3 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLEAIDKNRA | LHAAERLQTK | LRERGDVANE | DKLSLLKSVL | QSPLFSQILS | LQTSVQQLKD | QVNIATSATS | NIEYAHVPHL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SPAVIPTLQN | ESFLLSPNNG | NLEALTGPGI | PHINGKPACD | EFDQLIKNMA | QGRHVEVFEL | LKPPSGGLGF | SVVGLRSENR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GELGIFVQEI | QEGSVAHRDG | RLKETDQILA | INGQALDQTI | THQQAISILQ | KAKDTVQLVI | ARGSLPQLVS | PIVSRSPSAA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| STISAHSNPV | HWQHMETIEL | VNDGSGLGFG | IIGGKATGVI | VKTILPGGVA | DQHGRLCSGD | HILKIGDTDL | AGMSSEQVAQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VLRQCGNRVK | LMIARGAIEE | RTAPTALGIT | LSSSPTSTPE | LRVDASTQKG | EESETFDVEL | TKNVQGLGIT | IAGYIGDKKL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EPSGIFVKSI | TKSSAVEHDG | RIQIGDQIIA | VDGTNLQGFT | NQQAVEVLRH | TGQTVLLTLM | RRGMKQEAEL | MSREDVTKDA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DLSPVNASII | KENYEKDEDF | LSSTRNTNIL | PTEEEGYPLL | SAEIEEIEDA | QKQEAALLTK | WQRIMGINYE | IVVAHVSKFS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ENSGLGISLE | ATVGHHFIRS | VLPEGPVGHS | GKLFSGDELL | EVNGITLLGE | NHQDVVNILK | ELPIEVTMVC | CRRTVPPTTQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SELDSLDLCD | IELTEKPHVD | LGEFIGSSET | EDPVLAMTDA | GQSTEEVQAP | LAMWEAGIQH | IELEKGSKGL | GFSILDYQDP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| IDPASTVIII | RSLVPGGIAE | KDGRLLPGDR | LMFVNDVNLE | NSSLEEAVEA | LKGAPSGTVR | IGVAKPLPLS | PEEGYVSAKE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DSFLYPPHSC | EEAGLADKPL | FRADLALVGT | NDADLVDEST | FESPYSPEND | SIYSTQASIL | SLHGSSCGDG | LNYGSSLPSS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PPKDVIENSC | DPVLDLHMSL | EELYTQNLLQ | RQDENTPSVD | ISMGPASGFT | INDYTPANAI | EQQYECENTI | VWTESHLPSE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VISSAELPSV | LPDSAGKGSE | YLLEQSSLAC | NAECVMLQNV | SKESFERTIN | IAKGNSSLGM | TVSANKDGLG | MIVRSIIHGG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AISRDGRIAI | GDCILSINEE | STISVTNAQA | RAMLRRHSLI | GPDIKITYVP | AEHLEEFKIS | LGQQSGRVMA | LDIFSSYTGR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DIPELPEREE | GEGEESELQN | TAYSNWNQPR | RVELWREPSK | SLGISIVGGR | GMGSRLSNGE | VMRGIFIKHV | LEDSPAGKNG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TLKPGDRIVE | APSQSESEPE | KAPLCSVPPP | PPSAFAEMGS | DHTQSSASKI | SQDVDKEDEF | GYSWKNIRER | YGTLTGELHM |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| IELEKGHSGL | GLSLAGNKDR | SRMSVFIVGI | DPNGAAGKDG | RLQIADELLE | INGQILYGRS | HQNASSIIKC | APSKVKIIFI |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| RNKDAVNQMA | VCPGNAVEPL | PSNSENLQNK | ETEPTVTTSD | AAVDLSSFKN | VQHLELPKDQ | GGLGIAISEE | DTLSGVIIKS |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LTEHGVAATD | GRLKVGDQIL | AVDDEIVVGY | PIEKFISLLK | TAKMTVKLTI | HAENPDSQAV | PSAAGAASGE | KKNSSQSLMV |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PQSGSPEPES | IRNTSRSSTP | AIFASDPATC | PIIPGCETTI | EISKGRTGLG | LSIVGGSDTL | LGAIIIHEVY | EEGAACKDGR |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LWAGDQILEV | NGIDLRKATH | DEAINVLRQT | PQRVRLTLYR | DEAPYKEEEV | CDTLTIELQK | KPGKGLGLSI | VGKRNDTGVF |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| VSDIVKGGIA | DADGRLMQGD | QILMVNGEDV | RNATQEAVAA | LLKCSLGTVT | LEVGRIKAGP | FHSERRPSQS | SQVSEGSLSS |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| FTFPLSGSST | SESLESSSKK | NALASEIQGL | RTVEMKKGPT | DSLGISIAGG | VGSPLGDVPI | FIAMMHPTGV | AAQTQKLRVG |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| DRIVTICGTS | TEGMTHTQAV | NLLKNASGSI | EMQVVAGGDV | SVVTGHQQEP | ASSSLSFTGL | TSSSIFQDDL | GPPQCKSITL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| ERGPDGLGFS | IVGGYGSPHG | DLPIYVKTVF | AKGAASEDGR | LKRGDQIIAV | NGQSLEGVTH | EEAVAILKRT | KGTVTLMVLS |
| 2010 | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2017 | 1 | 788.3019 | -141.73 | 2 | 55.1 | 14.1 | 0 | 1303-1318 | R.MSVFIVGIDPNGAAGK.D | |
| 2930 | 1 | 899.4860 | 0.41 | 2 | 65.4 | 11.6 | 2 | 1340-1356 | R.SHQNASSIIKCAPSKVK.I | |
| 1435 | 1 | 627.2993 | -161.59 | 2 | 47.6 | 10.2 | 1 | 1661-1673 | K.KPGKGLGLSIVGK.R | |

# Detailed Protein Report

## Protein 288: myosin light chain kinase, smooth muscle isoform 3B [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|116008190 | **Score:** | 35.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 197.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.66 | **CV:** | 43.99 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 0.51 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGDVKLVASS | HISKTSLSVD | PSRVDSMPLT | EAPAFILPPR | NLCIKEGATA | KFEGRVRGYP | EPQVTWHRNG | QPITSGGRFL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LDCGIRGTFS | LVIHAVHEED | RGKYTCEATN | GSGARQVTVE | LTVEGSFAKQ | LGQPVVSKTL | GDRFSAPAVE | TRPSIWGECP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PKFATKLGRV | VVKEGQMGRF | SCKITGRPQP | QVTWLKGNVP | LQPSARVSVS | EKNGMQVLEI | HGVNQDDVGV | YTCLVVNGSG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KASMSAELSI | QGLDSANRSF | VRETKATNSD | VRKEVTNVIS | KESKLDSLEA | AAKSKNCSSP | QRGGSPPWAA | NSQPQPPRES |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KLESCKDSPR | TAPQTPVLQK | TSSSITLQAA | RVQPEPRAPG | LGVLSPSGEE | RKRPAPPRPA | TFPTRQPGLG | SQDVVSKAAN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RRIPMEGQRD | SAFPKFESKP | QSQEVKENQT | VKFRCEGLAV | MEVAPSFSSV | LKDCAVIEGQ | DFVLQCSVRG | TPVPRITWLL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NGQPIQYARS | TCEAGVAELH | IQDALPEDHG | TYTCLAENAL | GQVSCSAWVT | VHEKKSSRKS | EYLLPVAPSK | PTAPIFLQGL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SDLKVMDGSQ | VTMTVQVSGN | PPPEVIWLHN | GNEIQESEDF | HFEQRGTQHS | LCIQEVFPED | TGTYTCEAWN | SAGEVRTQAV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LTVQEPHDGT | QPWFISKPRS | VTASLGQSVL | ISCAIAGDPF | PTVHWLRDGK | ALCKDTGHFE | VLQNEDVFTL | VLKKVQPWHA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GQYEILLKNR | VGECSCQVSL | MLQNSSARAL | PRGREPASCE | DLCGGGVGAD | GGGSDRYGSL | RPGWPARGQG | WLEEEDGEDV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RGVLKRRVET | RQHTEEAIRQ | QEVEQLDFRD | LLGKKVSTKT | LSEDDLKEIP | AEQMDFRANL | QRQVKPKTVS | EEERKVHSPQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QVDFRSVLAK | KGTSKTPVPE | KVPPPKPATP | DFRSVLGGKK | KLPAENGSSS | AETLNAKAVE | SSKPLSNAQP | SGPLKPVGNA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KPAETLKPMG | NAKPAETLKP | MGNAKPDENL | KSASKEELKK | DVKNDVNCKR | GHAGTTDNEK | RSESQGTAPA | FKQKLQDVHV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AEGKKLLLQC | QVSSDPPATI | IWTLNGKTLK | TTKFIILSQE | GSLCSVSIEK | ALPEDRGLYK | CVAKNDAGQA | ECSCQVTVDD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| APASENTKAP | EMKSRRPKSS | LPPVLGTESD | ATVKKKPAPK | TPPKAAMPPQ | IIQFPEDQKV | RAGESVELFG | KVTGTQPITC |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TWMKFRKQIQ | ESEHMKVENS | ENGSKLTILA | ARQEHCGCYT | LLVENKLGSR | QAQVNLTVVD | KPDPPAGTPC | ASDIRSSSLT |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LSWYGSSYDG | GSAVQSYSIE | IWDSANKTWK | ELATCRSTSF | NVQDLLPDHE | YKFRVRAINV | YGTSEPSQES | ELTTVGEKPE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| EPKDEVEVSD | DDEKEPEVDY | RTVTINTEQK | VSDFYDIEER | LGSGKFGQVF | RLVEKKTRKV | WAGKFFKAYS | AKEKENIRQE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ISIMNCLHHP | KLVQCVDAFE | EKANIVMVLE | IVSGGELFER | IIDEDFELTE | RECIKYMRQI | SEGVEYIHKQ | GIVHLDLKPE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| NIMCVNKTGT | RIKLIDFGLA | RRLENAGSLK | VLFGTPEFVA | PEVINYEPIG | YATDMWSIGV | ICYILNRLDC | TQCLQHPWLM |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KDTKNMEAKK | LSKDRMKKYM | ARRKWQKTGN | AVRAIGRLSS | MAMISGLSGR | KSSTGSPTSP | LNAEKLESEE | DVSQAFLEAV |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| AEEKPHVKPY | FSKTIRDLEV | VEGSAARFDC | KIEGYPDPEV | VWFKDDQSIR | ESRHFQIDYD | EDGNCSLIIS | DVCGDDDAKY |
| 1770 | 1780 | 1790 | 1800 | | | | |
| TCKAVNSLGE | ATCTAELIVE | TMEEGEGEGE | EEEE | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 678 | 1 | 670.8078 | -108.06 | 2 | 38.5 | 14.1 | 1 | 2-14 | M.GDVKLVASSHISK.T | | QU:MU 1.09 |
| 2055 | 1 | 643.7814 | 9.77 | 2 | 54.1 | 11.7 | 0 | 104-115 | K.YTCEATNGSGAR.Q | Carbamidomethyl: 3 | |
| 2643 | 1 | 995.0088 | -31.93 | 2 | 63.9 | 10.1 | 1 | 180-196 | R.FSCKITGRPQPQVTWLK.G | | WUP:QUP 0.51<br>QU:MU 2.52 |

# Detailed Protein Report

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## Protein 289: PREDICTED: rho guanine nucleotide exchange factor 12 isoform X3 [Homo sapiens]

**Accession:** gi|530397943
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 35.8
**MW [kDa]:** 161.8
**pI:** 5.3
**Sequence Coverage [%]:** 2.3
**No. of unique Peptides:** 2

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRAGVQTGDR | IIKVNGTLVT | HSNHLEVVKL | IKSGSYVALT | VQGRPPGSPQ | IPLADSEVEP | SVIGHMSPIM | TSPHSPGASG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NMERITSPVL | MGEENNVVHN | QKVEILRKML | QKEQERLQLL | QEDYNRTPAQ | RLLKEIQEAK | KHIPQLQEQL | SKATGSAQDG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AVVTPSRPLG | DTLTVSEAET | DPGDVLGRTD | CSSGDASRPS | SDNADSPKSG | PKERIYLEEN | PEKSETIQDT | DTQSLVGSPS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TRIAPHIIGA | EDDDFGTEHE | QINGQCSCFQ | SIELLKSRPA | HLAVFLHHVV | SQFDPATLLC | YLYSDLYKHT | NSKETRRIFL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EFHQFFLDRS | AHLKVSVPDE | MSADLEKRRP | ELIPEDLHRH | YIQTMQERVH | PEVQRHLEDF | RQKRSMGLTL | AESELTKLDA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ERDKDRLTLE | KERTCAEQIV | AKIEEVLMTA | QAVEEDKSST | MQYVILMYMK | HLGVKVKEPR | NLEHKRGRIG | FLPKIKQSMK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KDKEGEEKGK | RRGFPSILGP | PRRPSRHDNS | AIGRAMELQK | ARHPKHLSTP | SSVSPEPQDS | AKLRQSGLAN | EGTDAGYLPA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NSMSSVASGA | SFSQEGGKEN | DTGSKQVGET | SAPGDTLDGT | PRTLNTVFDF | PPPPLDQVQE | EECEVERVTE | HGTPKPFRKF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DSVAFGESQS | EDEQFENDLE | TDPPNWQQLV | SREVLLGLKP | CEIKRQEVIN | ELFYTERAHV | RTLKVLDQVF | YQRVSREGIL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SPSELRKIFS | NLEDILQLHI | GLNEQMKAVR | KRNETSVIDQ | IGEDLLTWFS | GPGEEKLKHA | AATFCSNQPF | ALEMIKSRQK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KDSRFQTFVQ | DAESNPLCRR | LQLKDIIPTQ | MQRLTKYPLL | LDNIAKYTEW | PTEREKVKKA | ADHCRQILNY | VNQAVKEAEN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KQRLEDYQRR | LDTSSLKLSE | YPNVEELRNL | DLTKRKMIHE | GPLVWKVNRD | KTIDLYTLLL | EDILVLLQKQ | DDRLVLRCHS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KILASTADSK | HTFSPVIKLS | TVLVRQVATD | NKALFVISMS | DNGAQIYELV | AQTVSEKTVW | QDLICRMAAS | VKEQSTKPIP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LPQSTPGEGD | NDEEDPSKLK | EEQHGISVTG | LQSPDRDLGL | ESTLISSKPQ | SHSLSTSGKS | EVRDLFVAER | QFAKEQHTDG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TLKEVGEDYQ | IAIPDSHLPV | SEERWALDAL | RNLGLLKQLL | VQQLGLTEKS | VQEDWQHFPR | YRTASQGPQT | DSVIQNSENI |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KAYHSGEGHM | PFRTGTGDIA | TCYSPRTSTE | SFAPRDSVGL | APQDSQASNI | LVMDHMIMTP | EMPTMEPEGG | LDDSGEHFFD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| AREAHSDENP | SEGDGAVNKE | EKDVNLRISG | NYLILDGYDP | VQESSTDEEV | ASSLTLQPMT | GIPAVESTHQ | QQHSPQNTHS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| DGAISPFTPE | FLVQQRWGAM | EYSCFEIQSP | SSCADSQSQI | MEYIHKIEAD | LEHLKKVEES | YTILCQRLAG | SALTDKHSDK |
| 1450 | | | | | | | |
| S | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 85 | 1 | 710.2749 | -87.79 | 2 | 30.8 | 12.0 | 0 | 335-347 | K.VSVPDEMSADLEK.R | |
| 1443 | 1 | 1022.6499 | 109.61 | 1 | 47.7 | 10.9 | 1 | 458-465 | K.EPRNLEHK.R | |

# Detailed Protein Report

## Protein 290: protein LAP2 isoform 7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|55770895 | **Score:** | 35.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 146.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| | | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTTKRSLFVR | LVPCRCLRGE | EETVTTLDYS | HCSLEQVPKE | IFTFEKTLEE | LYLDANQIEE | LPKQLFNCQS | LHKLSLPDND |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LTTLPASIAN | LINLRELDVS | KNGIQEFPEN | IKNCKVLTIV | EASVNPISKL | PDGFSQLLNL | TQLYLNDAFL | EFLPANFGRL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TKLQILELRE | NQLKMLPKTM | NRLTQLERLD | LGSNEFTEVP | EVLEQLSGLK | EFWMDANRLT | FIPGFIGSLK | QLTYLDVSKN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NIEMVEEGIS | TCENLQDLLL | SSNSLQQLPE | TIGSLKNITT | LKIDENQLMY | LPDSIGGLIS | VEELDCSFNE | VEALPSSIGQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LTNLRTFAAD | HNYLQQLPPE | IGSWKNITVL | FLHSNKLETL | PEEMGDMQKL | KVINLSDNRL | KNLPFSFTKL | QQLTAMWLSD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NQSKPLIPLQ | KETDSETQKM | VLTNYMFPQQ | PRTEDVMFIS | DNESFNPSLW | EEQRKQRAQV | AFECDEDKDE | REAPPREGNL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KRYPTPYPDE | LKNMVKTVQT | IVHRLKDEET | NEDSGRDLKP | HEDQQDINKD | VGVKTSESTT | TVKSKVDERE | KYMIGNSVQK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ISEPEAEISP | GSLPVTANMK | ASENLKHIVN | HDDVFEESEE | LSSDEEMKMA | EMRPPLIETS | INQPKVVALS | NNKKDDTKET |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DSLSDEVTHN | SNQNNSNCSS | PSRMSDSVSL | NTDSSQDTSL | CSPVKQTHID | INSKIRQEDE | NFNSLLQNGD | ILNSSTEEKF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KAHDKKDFNL | PEYDLNVEER | LVLIEKSVDS | TATADDTHKL | DHINMNLNKL | ITNDTFQPEI | MERSKTQDIV | LGTSFLSINS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KEETEHLENG | NKYPNLESVN | KVNGHSEETS | QSPNRTEPHD | SDCSVDLGIS | KSTEDLSPQK | SGPVGSVVKS | HSITNMEIGG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LKIYDILSDN | GPQQPSTTVK | ITSAVDGKNI | VRSKSATLLY | DQPLQVFTGS | SSSSDLISGT | KAIFKFDSNH | NPEEPNIIRG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PTSGPQSAPQ | IYGPPQYNIQ | YSSSAAVKDT | LWHSKQNPQI | DHASFPPQLL | PRSESTENQS | YAKHSANMNF | SNHNNVRANT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AYHLHQRLGP | ARHGEMWAIS | PNDRLIPAVT | RSTIQRQSSV | SSTASVNLGD | PGSTRRAQIP | EGDYLSYREF | HSAGRTPPMM |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PGSQRPLSAR | TYSIDGPNAS | RPQSARPSIN | EIPERTMSVS | DFNYSRTSPS | KRPNARVGSE | HSLLDPPGKS | KVPRDWREQV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LRHIEAKKLE | KIRVRVEKDP | ELGFSISGGV | GGRGNPFRPD | DDGIFVTRVQ | PEGPASKLLQ | PGDKIIQANG | YSFINIEHGQ |
| 1290 | 1300 | 1310 | | | | | |
| AVSLLKTFQN | TVELIIVREV | SS | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 486 | 1 | 668.2076 | -211.28 | 2 | 34.5 | 10.8 | 0 | 1177-1189 | R.VGSEHSLLDPPGK.S | |
| 2597 | 1 | 913.4719 | -133.82 | 1 | 63.1 | 13.2 | 2 | 1209-1215 | K.LEKIRVR.V | |

# Detailed Protein Report

## Protein 291: EP300-interacting inhibitor of differentiation 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|56605998 | **Score:** | 35.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 14.7 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| ***WUP:QUP*** | **Median:** 0.51 | **CV:** 0.00 % | **No. of Peptides:** 1 |
|---|---|---|---|

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKMDVSVRAA | GCSDDLSSGE | ADVDPKLLEL | TADEEKCRSI | RRQYRQLMYC | VRQNREDIVS | SANNSLTEAL | EEANVLFDGV |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| SRTREAALDA | RFLVMASDLG | KEKAKQLNSD | MNFFNQLAFC | DFLFLFVGLN | WMEGDPDKLS | DCDDSIALSF | WKAIEKEATS |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| WMVKAETFHF | VFGSFKLERS | APKPRLEHQK | KVRKMEENGN | MPTKLQKLDL | SSYPEATEKN | VERILGLLQT | YFRKYPDTPV |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| SYFEFVIDPN | SFSRTVENIF | YVSFIVRDGF | ARIRLDEDRL | PILEPMNVNQ | MGEGNDSSCH | GRKQGVISLT | LQEWKNIVAA |
| **330** | **340** | | | | | | |
| FEISEAMITY | SSY | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2097 | 1 | 900.3873 | -17.91 | 3 | 54.6 | 12.2 | 2 | 1-26 | -. MKMDVSVRAAGCSDDLSSGEAD L | Oxidation: 1 | |
| 936 | 1 | 647.6555 | -210.59 | 2 | 41.8 | 10.9 | 1 | 194-204 | R.KMEENGNMPTK.L | Oxidation: 8 | WUP:QUP 0.51 |
| 399 | 1 | 701.3413 | -70.15 | 2 | 35.0 | 12.6 | 0 | 304-315 | K.QGVISLTLQEWK.N | | |

# Detailed Protein Report

## Protein 292: PREDICTED: pecanex-like protein 3 isoform X4 [Homo sapiens]

**Accession:** gi|530396772
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 35.7
**MW [kDa]:** 115.4
**pI:** 6.0
**Sequence Coverage [%]:** 4.0
**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MGSQVLQILR QGVWASLTGG WFFDPHQSTF SNCFHLYVWI FLLIFPFLLY MVLPPSLMVA GVYCLVVAVI FATIKTVNYR

        90        100        110        120        130        140        150        160
LHAMFDQGEI VEKRSSTMGE LEEEPAQGDS NPPRDPGVEM TVFRKVSSTP PVRCSSQHSV FGFNQVSELL PRMEDSGPLR

       170        180        190        200        210        220        230        240
DIKELVREQG SNNVIVTSAD REMLKLSSQE KLIGDLPQTP PGAVPDPSLA STDSSEPSPL AGDGAPWSGS SMADTPMSPL

       250        260        270        280        290        300        310        320
LKGSLSQELS KSFLTLTQPD RALVRTSSRR EQRRGAGGYQ PLDRRGSGEP TPQKAGSSDS CFSGTDRETL SSFKSEKTNS

       330        340        350        360        370        380        390        400
THLDSPPGGP APEGSDTDPP SEAELPASPD AGVPSDDTLR SFDTVIGAGT PPGLAEPLLV VRPKDLALLR PSKRQPPLRR

       410        420        430        440        450        460        470        480
HSPPGRAPRR PLLEGGGFFE DEDTSEGSEL SPASSLRSQR RYSTDSSSST SCYSPESSRG AAGGPRKRRA PHGAEEGTAV

       490        500        510        520        530        540        550        560
PPKRPYGTQR TPSTASAKTH ARVLSMDGAG GDVLRPPLAG CKAELEAQVG VEQAASEPVV LPAEARRGPA ANQPGWRGEL

       570        580        590        600        610        620        630        640
QEEGAVGGAA EETGRRDRSS SVRRTQAIRR RHNAGSNPTP PASVMGSPPS SLQEAQRGRA ASHSRALTLP SALHFASSLL

       650        660        670        680        690        700        710        720
LTRAGANVHE ACTFDDTSEG AVHYFYDESG VRRSYTFGLA GGGYENPVGQ QGEQTANGAW DRHSHSSSFH SADVPEATGG

       730        740        750        760        770        780        790        800
LNLLQPRPVV LQGMQVRRVP LEIPEFDLLD QDSLHESQEQ TLMEEAPPRA QHSYKYWLLP GRWTSVRYER LALLALLDRT

       810        820        830        840        850        860        870        880
RGVLENIFGV GLSSLVAFLG YLLLLKGFFT DIWVFQFCLV IASCQYSLLK SVQPDAASPM HGHNWVIAYS RPVYFCICCL

       890        900        910        920        930        940        950        960
LIWLLDALGS AQPFPPVSLY GLTLFSASFF FCARDVATVF TLCFPFVFLL GLLPQVNTCL MYLLEQIDMH GFGGTAATSP

       970        980        990       1000       1010       1020       1030       1040
LTAVFSLSRS LLAAALLYGF CLGAIKTPWP EQHVPVLFSV FCGLLVALSY HLSRQSSDPT VLWSLIRSKL FPELEERSLE

      1050       1060       1070
TARAEPPDPL PDKMRQSVLN VSPGPAA
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2754 | 1 | 1086.0034 | 31.79 | 2 | 64.8 | 11.5 | 1 | 286-307 | R.GSGEPTPQKAGSSDSCFSGTDR.E | |

# Detailed Protein Report

## Protein 293: neurogenic locus notch homolog protein 1 preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|148833508 | **Score:** | 35.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 272.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.8 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.27 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.88 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPPLLAPLLC | LALLPALAAR | GPRCSQPGET | CLNGGKCEAA | NGTEACVCGG | AFVGPRCQDP | NPCLSTPCKN | AGTCHVVDRR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GVADYACSCA | LGFSGPLCLT | PLDNACLTNP | CRNGGTCDLL | TLTEYKCRCP | PGWSGKSCQQ | ADPCASNPCA | NGGQCLPFEA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SYICHCPPSF | HGPTCRQDVN | ECGQKPGLCR | HGGTCHNEVG | SYRCVCRATH | TGPNCERPYV | PCSPSPCQNG | GTCRPTGDVT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HECACLPGFT | GQNCEENIDD | CPGNNCKNGG | ACVDGVNTYN | CRCPPEWTGQ | YCTEDVDECQ | LMPNACQNGG | TCHNTHGGYN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CVCVNGWTGE | DCSENIDDCA | SAACFHGATC | HDRVASFYCE | CPHGRTGLLC | HLNDACISNP | CNEGSNCDTN | PVNGKAICTC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PSGYTGPACS | QDVDECSLGA | NPCEHAGKCI | NTLGSFECQC | LQGYTGPRCE | IDVNECVSNP | CQNDATCLDQ | IGEFQCICMP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GYEGVHCEVN | TDECASSPCL | HNGRCLDKIN | EFQCECPTGF | TGHLCQYDVD | ECASTPCKNG | AKCLDGPNTY | TCVCTEGYTG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| THCEVDIDEC | DPDPCHYGSC | KDGVATFTCL | CRPGYTGHHC | ETNINECSSQ | PCRHGGTCQD | RDNAYLCFCL | KGTTGPNCEI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NLDDCASSPC | DSGTCLDKID | GYECACEPGY | TGSMCNINID | ECAGNPCHNG | GTCEDGINGF | TCRCPEGYHD | PTCLSEVNEC |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NSNPCVHGAC | RDSLNGYKCD | CDPGWSGTNC | DINNNECESN | PCVNGGTCKD | MTSGYVCTCR | EGFSGPNCQT | NINECASNPC |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LNQGTCIDDV | AGYKCNCLLP | YTGATCEVVL | APCAPSPCRN | GGECRQSEDY | ESFSCVCPTG | WQGQTCEVDI | NECVLSPCRH |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GASCQNTHGG | YRCHCQAGYS | GRNCETDIDD | CRPNPCHNGG | SCTDGINTAF | CDCLPGFRGT | FCEEDINECA | SDPCRNGANC |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TDCVDSYTCT | CPAGFSGIHC | ENNTPDCTES | SCFNGGTCVD | GINSFTCLCP | PGFTGSYCQH | DVNECDSQPC | LHGGTCQDGC |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GSYRCTCPQG | YTGPNCQNLV | HWCDSSPCKN | GGKCWQTHTQ | YRCECPSGWT | GLYCDVPSVS | CEVAAQRQGV | DVARLCQHGG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LCVDAGNTHH | CRCQAGYTGS | YCEDLVDECS | PSPCQNGATC | TDYLGGYSCK | CVAGYHGVNC | SEEIDECLSH | PCQNGGTCLD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LPNTYKCSCP | RGTQGVHCEI | NVDDCNPPVD | PVSRSPKCFN | NGTCVDQVGG | YSCTCPPGFV | GERCEGDVNE | CLSNPCDARG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TQNCVQRVND | FHCECRAGHT | GRRCESVING | CKGKPCKNGG | TCAVASNTAR | GFICKCPAGF | EGATCENDAR | TCGSLRCLNG |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| GTCISGPRSP | TCLCLGPFTG | PECQFPASSP | CLGGNPCYNQ | GTCEPTSESP | FYRCLCPAKF | NGLLCHILDY | SFGGGAGRDI |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| PPPLIEEACE | LPECQEDAGN | KVCSLQCNNH | ACGWDGGDCS | LNFNDPWKNC | TQSLQCWKYF | SDGHCDSQCN | SAGCLFDGFD |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| CQRAEGQCNP | LYDQYCKDHF | SDGHCDQGCN | SAECEWDGLD | CAEHVPERLA | AGTLVVVVLM | PPEQLRNSSF | HFLRELSRVL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| HTNVVFKRDA | HGQQMIFPYY | GREEELRKHP | IKRAAEGWAA | PDALLGQVKA | SLLPGGSEGG | RRRRELDPMD | VRGSIVYLEI |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| DNRQCVQASS | QCFQSATDVA | AFLGALASLG | SLNIPYKIEA | VQSETVEPPP | PAQLHFMYVA | AAFVLLFFV | GCGVLLSRKR |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| RRQHGQLWFP | EGFKVSEASK | KKRREPLGED | SVGLKPLKNA | SDGALMDDNQ | NEWGDEDLET | KKFRFEEPVV | LPDLDDQTDH |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| RQWTQQHLDA | ADLRMSAMAP | TPPQGEVDAD | CMDVNVRGPD | GFTPLMIASC | SGGGLETGNS | EEEEDAPAVI | SDFIYQGASL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| HNQTDRTGET | ALHLAARYSR | SDAAKRLLEA | SADANIQDNM | GRTPLHAAVS | ADAQGVFQIL | IRNRATDLDA | RMHDGTTPLI |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| LAARLAVEGM | LEDLINSHAD | VNAVDDLGKS | ALHWAAAVNN | VDAAVVLLKN | GANKDMQNNR | EETPLFLAAR | EGSYETAKVL |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| LDHFANRDIT | DHMDRLPRDI | AQERMHHDIV | RLLDEYNLVR | SPQLHGAPLG | GTPTLSPPLC | SPNGYLGSLK | PGVQGKKVRK |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| PSSKGLACGS | KEAKDLKARR | KKSQDGKGCL | LDSSGMLSPV | DSLESPHGYL | SDVASPPLLP | SPFQQSPSVP | LNHLPGMPDT |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| HLGIGHLNVA | AKPEMAALGG | GGRLAFETGP | PRLSHLPVAS | GTSTVLGSSS | GGALNFTVGG | STSLNGQCEW | LSRLQSGMVP |
| 2330 | 2340 | 2350 | 2360 | 2370 | 2380 | 2390 | 2400 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2073 | 4 | 698.2445 | -185.84 | 2 | 55.8 | 21.5 | 0 | 1992-2004 | R.MHDGTTPLILAAR.L |  | WUP:QUP 0.88<br>QU:MU 2.27 |

# Detailed Protein Report

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**Protein 294:** **PREDICTED: proteasome-associated protein ECM29 homolog isoform X5 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530390837 | **Score:** | 35.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 203.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.40 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 3.27 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| METGSDSDQL | ERVFLRLGHA | ETDEQLQNII | SKFLPPVLLK | LSSTQEGVRK | KVMELLVHLN | KRIKSRPKIQ | LPVETLLVQY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QDPAAVSFVT | NFTIIYVKMG | YPRLPVEKQC | ELAPTLLTAM | EGKPQPQQDS | LMHLLIPTLF | HMKYPVESSK | SASPFNLAEK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PKTVQLLLDF | MLDVLLMPYG | YVLNESQSRQ | NSSSAQGSSS | NSGGGSGIPQ | PPPGMSFYAA | KRVIGDNPWT | PEQLEQCKLG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IVKFIEAEQV | PELEAVLHLV | IASSDTRHSV | ATAADLELKS | KQSLIDWNNP | AIINKMYKVY | LGDIPLKTKE | GAVLKPELKR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DPVSTRVKLK | IVPHLLRSRQ | AAETFPANIQ | VVYDGLFGTN | TNSKLRTLSL | QFVHHICITC | PEIKIKPLGP | MLLNGLTKLI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NEYKEDPKLL | SMAYSAVGKL | SSRMPHLFTK | DIALVQQLFE | ALCKEEPETR | LAIQEALSMM | VGAYSTLEGA | QRTLMEALVA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SYLIKPEVQV | RQVAVKFAST | VFPSDHIPSR | YLLLLAAGDP | REEVHGEAQR | VLRCLPGRNR | KESTSEQMPS | FPEMVYYIQE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KASHRMKTPV | KYMTGTTVLP | FNPAAFGEIV | LYLRMCLAHS | AGVVPTSQSL | ADMQDHAPAI | GRYIRTLMSS | GQMAPSSSNK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SGETNPVQIY | IGLLQQLLAG | VGGLPVMYCL | LEAVSVYPEK | LATKFVDKTE | WIKSLMNNSK | EEMRELAALF | YSVVVSTVSG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NELKSMIEQL | IKTTKDNHSP | EIQHGSLLAL | GFTVGRYLAK | KKMRMSEQQD | LERNADTLPD | QEELIQSATE | TIGSFLDSTS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PLLAIAACTA | LGEIGRNGPL | PIPSEGSGFT | KLHLVESLLS | RIPSSKETNK | MKERAIQTLG | YFPVGDGDFP | HQKLLLQGLM |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DSVEAKQIEL | QFTIGEAITS | AAIGTSSVAA | RDAWQMTEEE | YTPPAGAKVN | DVVPWVLDVI | LNKHIISPNP | HVRQAACIWL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LSLVRKLSTH | KEVKSHLKEI | QSAFVSVLSE | NDELSQDVAS | KGLGLVYELG | NEQDQQELVS | TLVETLMTGK | RVKHEVSGET |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VVFQGGALGK | TPDGQGLSTY | KELCSLASDL | SQPDLVYKFM | NLANHHAMWN | SRKGAAFGFN | VIATRAGEQL | APFLPQLVPR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LYRYQFDPNL | GIRQAMTSIW | NALVTDKSMV | DKYLKEILQD | LVKNLTSNMW | RVRESSCLAL | NDLLRGRPLD | DIIDKLPEIW |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ETLFRVQDDI | KESVRKAAEL | ALKTLSKVCV | KMCDPAKGAA | GQRTIAALLP | CLLDKGMMST | VTEVRALSIN | TLVKISKSAG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| AMLKPHAPKL | IPALLESLSV | LEPQVLNYLS | LRATEQEKAA | MDSARLSAAK | SSPMMETINM | CLQYLDVSVL | GELVPRLCEL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| IRSGVGLGTK | GGCASVIVSL | TTQCPQDLTP | YSGKLMSALL | SGLTDRNSVI | QKSCAFAMGH | LVRTSRDSST | EKLLQKLNGW |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| YMEKEEPIYK | TSCALTIHAI | GRYSPDVLKN | HAKEVLPLAF | LGMHEIADEE | KSEKEECNLW | TEVWQENVPG | SFGGIRLYLQ |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ELITITQKAL | QSQSWKMKAQ | GAIAMASIAK | QTSSLVPPYL | GMILTALLQG | LAGRTWAGKE | ELLKAIACVV | TACSAELEKS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| VPNQPSTNEI | LQAVLKECSK | ENVKYKIVAI | SCAADILKAT | KEDRFQEFSN | IVIPLIKKNS | LESSGVRTTK | NEEENEKEKE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LQLEYLLGAF | ESLGKAWPRN | AETQRCYRQE | LCKLMCERLK | LSTWKVQLGV | LQSMNAFFQG | LMLLEEEHAD | PEALAEILLE |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| TCKSITYSLE | NKTYSSVRTE | ALSVIELLLK | KLEESKQWEC | LTSECRVLLI | ESLATMEPDS | RPELQEKAAL | LKKTLENLE |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 681 | 1 | 625.0022 | 62.66 | 3 | 38.5 | 10.4 | 1 | 1079-1093 | K.FMNLANHHAMWNSRK.G | Oxidation: 2 | QU:MU 0.40<br>WUP:QUP 3.27 |
| 2061 | 1 | 703.7752 | -146.50 | 2 | 54.1 | 12.0 | 1 | 1537-1550 | K.MKAQGAIAMASIAK.Q | Oxidation: 1 | |

# Detailed Protein Report

## Protein 295: PREDICTED: histone-lysine N-methyltransferase 2B isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578835223 | **Score:** | 35.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 212.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| | | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MPPLEKARIA GVGSLPLSGV EEKMFSLLKR AKVQLFKIDQ QQQQKVAASM PLSPGGQMEE VAGAVKQISD RGPVRSEDES
        90        100        110        120        130        140        150        160
VEAKRERPSG PESPVQGPRI KHVCRHAAVA LGQARAMVPE DVPRLSALPL RDRQDLATED TSSASETESV PSRSRRGKVE
       170        180        190        200        210        220        230        240
AAGPGGESEP TGSGGTLAHT PRRSLPSHHG KKMRMARCGH CRGCLRVQDC GSCVNCLDKP KFGGPNTKKQ CCVYRKCDKI
       250        260        270        280        290        300        310        320
EARKMERLAK KGRTIVKTLL PWDSDESPEA SPGPPGPRRG AGAGGPREEV VAHPGPEEQD SLLQRKSARR CVKQRPSYDI
       330        340        350        360        370        380        390        400
FEDSDDSEPG GPPAPRRRTP RENELPLPEP EEQSRPRKPT LQPVLQLKAR RRLDKDALAP GPFASFPNGW TGKQKSPDGV
       410        420        430        440        450        460        470        480
HRVRVDFKED CDLENVWLMG GLSVLTSVPG GPPMVCLLCA SKGLHELVFC QVCCDPFHPF CLEEAERPLP QHHDTWCCRR
       490        500        510        520        530        540        550        560
CKFCHVCGRK GRGSKHLLEC ERCRHAYHPA CLGPSYPTRA TRKRRHWVRD EICSACVRCK SCGATPGKNW DVEWSGDYSL
       570        580        590        600        610        620        630        640
CPRCTQLYEK GNYCPICTRC YEDNDYESKM MQCAQCDHWV HAKCEGLSDE DYEILSGLPD SVLYTCGPCA GAAQPRWREA
       650        660        670        680        690        700        710        720
LSGALQGGLR QVLQGLLSSK VVGPLLLCTQ CGPDGKQLHP GPCGLQAVSQ RFEDGHYKSV HSFMEDMVGI LMRHSEEGET
       730        740        750        760        770        780        790        800
PDRRAGGQMK GLLLKLLESA FGWFDAHDPK YWRRSTRLPN GVLPNAVLPP SLDHVYAQWR QQEPETPESG QPPGDPSAAF
       810        820        830        840        850        860        870        880
QGKDPAAFSH LEDPRQCALC LKYGDADSKE AGRLLYIGQN EWTHVNCAIW SAEVFEENDG SLKNVHAAVA RGRQMRCELC
       890        900        910        920        930        940        950        960
LKPGATVGCC LSSCLSNFHF MCARASYCIF QDDKKVFCQK HTDLLDGKEI VNPDGFDVLR RVYVDFEGIN FKRKFLTGLE
       970        980        990       1000       1010       1020       1030       1040
PDAINVLIGS IRIDSLGTLS DLSDCEGRLF PIGYQCSRLY WSTVDARRRC WYRCRILEYR PWGPREEPAH LEAAEENQTI
      1050       1060       1070       1080       1090       1100       1110       1120
VHSPAPSSEP PGGEDPPLDT DVLVPGAPER HSPIQNLDPP LRPDSGSAPP PAPRSFSGAR IKVPNYSPSR RPLGGVSFGP
      1130       1140       1150       1160       1170       1180       1190       1200
LPSPGSPSSL THHIPTVGDP DFPAPPRRSR RPSPLAPRPP PSRWASPPLK TSPQLRVPPP TSVVTALTPT SGELAPPGPA
      1210       1220       1230       1240       1250       1260       1270       1280
PSPPPPEDLG PDFEDMEVVS GLSAADLDFA ASLLGTEPFQ EEIVAAGAMG SSHGGPGDSS EEESSPTSRY IHFPVTVVSA
      1290       1300       1310       1320       1330       1340       1350       1360
PGLAPSATPG APRIEQLDGV DDGTDSEAEA VQQPRGQGTP PSGPGVVRAG VLGAAGDRAR PPEDLPSEIV DFVLKNLGGP
      1370       1380       1390       1400       1410       1420       1430       1440
GDGGAGPREE SLPPAPPLAN GSQPSQGLTA SPADPTRTFA WLPGAPGVRV LSLGPAPEPP KPATSKIILV NKLGQVFVKM
      1450       1460       1470       1480       1490       1500       1510       1520
AGEGEPVPPP VKQPPLPPTI SPTAPTSWTL PPGPLLGVLP VVGVVRPAPP PPPPPLTLVL SSGPASPPRQ AIRVKRVSTF
      1530       1540       1550       1560       1570       1580       1590       1600
SGRSPPAPPP YKAPRLDEDG EASEDTPQVP GLGSGGFSRV RMKTPTVRGV LDLDRPGEPA GEESPGPLQE RSPLLPLPED
      1610       1620       1630       1640       1650       1660       1670       1680
GPPQVPDGPP DLLLESQWHH YSGEASSSEE EPPSPDDKEN QAPKRTGPHL RFEISSEDGF SVEAESLEGA WRTLIEKVQE
      1690       1700       1710       1720       1730       1740       1750       1760
ARGHARLRHL SFSGMSGARL LGIHHDAVIF LAEQLPGAQR CQHYKFRYHQ QGEGQEEPPL NPHGAARAEV YLRKCTFDMF
      1770       1780       1790       1800       1810       1820       1830       1840
NFLASQHRVL PEGATCDEEE DEVQLRSTRR ATSLELPMAM RFRHLKKTSK EAVGVYRSAI HGRGLFCKRN IDAGEMVIEY
      1850       1860       1870       1880       1890       1900       1910       1920
SGIVIRSVLT DKREKFYDGK GIGCYMFRMD DFDVVDATMH GNAARFINHS CEPNCFSRVI HVEGQKHIVI FALRRILRGE
      1930       1940       1950       1960
ELTYDYKFPI EDASNKLPCN CGAKRCRRFL N
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2760 | 1 | 841.9053 | -83.22 | 2 | 63.0 | 12.2 | 1 | 7-23 | K.ARIAGVGSLPLSGVEEK.M | |

# Detailed Protein Report

**Protein 296:** **PREDICTED: maestro heat-like repeat-containing protein family member 2A isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578804228 | **Score:** | 35.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 189.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTEAITEAAV | ASSEEVSEER | DDLGPLELHD | SGTFQQVVNL | LDIIDSESAK | TDTTGAGLDM | RKTLASVIIM | EKATTEPSVV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| INTLIRCLQV | PEISTQRKVN | IYNILQDIIQ | QEGELEEQCV | QRLVAIASKE | MREIPEMEGY | MKAEVASDTL | VALSRNHFSL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VMYELQHHLK | PLNLTDEFVI | ITLAKLANGN | VFEFMPYMGI | TLATIFTMLR | LANEAKIRQA | ICSAMETFCE | TVQFYLKHLE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ESVYPVMTEE | EFALKVFPMY | RYFVTVWLRH | YNPEVKLGVI | KSLKPMLGLL | LPNDDLREQV | YDYIPLLLAE | YQGSLEVLFV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TQVLRQILEL | SVTTNTPVPQ | MQLHTIFTEL | HVQVCNKAPA | QHQYSSQNLM | EMVHCFVALA | RSYPKELMKF | FFSQMETNKE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AVRVGTLNLI | RAIVSADEPR | MSIRAIYLAI | RVVKNTISDT | RSKVRMAILH | IIGQLALCGY | QERIKGWGLK | YLSVQLTLST |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YKLTNRREKF | YQRDLEERMV | HKVTMDTVKI | ITSSVSGMTT | EFWVRLLCYI | METDYVEALT | PICISLTNLA | EHQLHGQDVD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VSVAGKSRQV | DLPAPQKLLA | RLLVLMSSPY | KGEGRGIAML | NLLRTLSQSI | APSMADMWEL | EIALLVRYLE | EHTEFTWDQK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AWEDKLIQFL | RNSLKKTRGS | SWSLRLSKEL | NNQIASFDSP | SLEKGFLYRA | LGFTLATGLE | ASKVEVLLLE | LLYKTDYSND |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| FDSEGVIMCF | GLCARGQVKT | VLNVLHDFEE | RIQESEQSWQ | ISAWRKDHPW | RRETVKSALM | VMYSCVASYC | HPQLLLNLVD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SPITAKIIHH | YVSSCQDICL | KMAFMKSVVQ | VTKAINNIKD | LEDFHFAQKT | TLTSIIVAVI | KAEPTDNLVS | PVRALAMEAL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SHLSKLKPFY | STEENSELMD | ISIHSVISLQ | LPGEDNESIK | TLYANALSSL | EQLMESLLQR | QLDPKGLQEM | VQLLEKWILS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| EKEWEREKAV | SLHLYLMWIY | VHSTAVCIHL | KLGQFGTMVG | LIAPCTCDAH | QRTRMASMNV | LSSLLDLHAS | QTCSLWGPSK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QKELEKCKGD | LQSTDVEKIF | CASSRIAKVV | CMEFSCDEVV | SLIQKLCENT | GAMNLQHDKA | SVTWIAFFLQ | MRAKELEDKV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| AEILSAILVH | LPVVDHPEVR | RLLIDGILLL | AHHHQETILT | SLLRQPLPME | SHLAEVWLAV | SENVPFARTM | LHSLMGRLQS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| RLSPRISATS | KADIWRLAAV | DPLMTLCTIH | LLIQKLDEND | KLPDFLPDLI | YTLLLQLGSS | HRPEAAPPVL | KMWKLVHTTP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LPEEMNLQRV | TIKSMQLLFK | RVKSQHLAHT | LDEQAVWDLL | QDGGTFLEGV | SLLARLCMQH | VEGHRQRLAE | LVLRGMDSEV |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LSCRISSTAV | CFMSGPVLYQ | EKLLKPAALL | LEKGADQEED | EALRVLSLRA | LGNMALGAPK | KVKQYRKVLL | EKCLGPLREP |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| VSNSVTAEGM | EALTKILAEL | REGDVGSSFD | AMSEQCRIFF | DNESELLRLK | AFILFGKLAR | VVGMSKKHFF | KGEVKKAWIP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| LMLHSQDPCS | NAAQACMATM | FQCVHFWGWK | SLEHPSGPSD | TATDDKMTVF | QTTMCSILTR | KKPAVLYRFL | LETMAYVKNN |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LSRIRIAACN | LAGIIMKQMS | THYLKKLDFP | ALRNSLQELQ | LDPDPGVRRA | ALETLTVLDS | CSQHGFLASP | QGMS |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1832 | 2 | 577.2623 | 1.72 | 2 | 52.7 | 13.5 | 0 | 51-61 | K.TDTTGAGLDMR.K | Oxidation: 10 |
| 2646 | 1 | 616.8461 | -35.09 | 2 | 61.4 | 11.5 | 1 | 62-72 | R.KTLASVIIMEK.A | |
| 288 | 1 | 636.2301 | -155.37 | 3 | 32.3 | 10.6 | 1 | 1348- | R.LAELVLRGMDSEVLSCR.I | Oxidation: 9 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
|  |  |  |  |  |  |  |  | 1364 |  |  |

# Detailed Protein Report

## Protein 297: PREDICTED: coiled-coil domain-containing protein 74B isoform X9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578805131 | **Score:** | 35.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 36.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 14.5 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSGAGVAAGT | RPPSSPTPGS | RRRRQRPSVG | VQSLRPQSPQ | LRQSDPQKRN | LDLEKSLQFL | QQQHSEMLAK | LHEEIEHLKR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ENKGEPARGP | RPALPPQAHS | TLPLPQHRNT | AINSSTRLGS | GGTQDDLRYK | LIMNQTSQKK | DGPSGNHLSR | ASAPLGARWV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CINGVWVEPG | GPSPARLKEG | SSRTHRPGGK | HGRLAGGSAD | TVRSPADSLS | TSSFQSVKSI | SNSANSQGKA | RPQPGSFNKQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DSKADVPQKA | DLEEEPLLHN | SKLDKVPGVQ | GQASPPHLGS | AKCSSASCGI | PTSCRPKSCS | TSSPSWKGAR | GPRQSRRKLA |
| 330 | 340 | 350 | | | | | |
| FPGTKKPRIS | PRSPPRASPR | NACF | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2681 | 1 | 945.9624 | -37.93 | 2 | 61.9 | 11.2 | 2 | 140-158 | K.KDGPSGNHLSRASAPLGAR.W | |
| 1874 | 1 | 860.9002 | -14.63 | 2 | 51.8 | 11.4 | 2 | 298-313 | K.SCSTSSPSWKGARGPR.Q | Carbamidomethyl: 2 |

# Detailed Protein Report

## **Protein 298:** protein FAM117B [Homo sapiens]

| | | | | |
|---|---|---|---|---|
| **Accession:** | gi\|254910983 | | **Score:** | 35.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | | **MW [kDa]:** | 61.9 |
| **Database Date:** | 2015-11-30 | | **pI:** | 10.8 |
| **Modification(s):** | Carbamidomethyl | | **Sequence Coverage [%]:** | 7.1 |
| | | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSQRVRRNGS | PTPAGSLGGG | AVATAGGPGS | RLQPMRATVP | FQLKQQQQQQ | HGSPTRSGGG | GGGNNNGGCC | GGASGPAGGG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GGGGPRTASR | STSPTRGGGN | AAARTSPTVA | TQTGASATST | RGTSPTRSAA | PGARGSPPRP | PPPPPLLGTV | SSPSSSPTHL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WTGEVSAAPP | PARVRHRRRS | PEQSRSSPEK | RSPSAPVCKA | GDKTRQPSSS | PSSIIRRTSS | LDTLAAPYLA | GHWPRDSHGQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AAPCMRDKAT | QTESAWAEEY | SEKKKGSHKR | SASWGSTDQL | KEIAKLRQQL | QRSKHSSRHH | RDKERQSPFH | GNHAAINQCQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| APVPKSALIP | VIPITKSTGS | RFRNSVEGLN | QEIEIIIKET | GEKEEQLIPQ | DIPDGHRAPP | PLVQRSSSTR | SIDTQTPGGA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DRGSNNSSRS | QSVSPTSFLT | ISNEGSEESP | CSADDLLVDP | RDKENGNNSP | LPKYATSPKP | NNSYMFKREP | PEGCERVKVF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EECSPKQLHE | IPAFYCPDKN | KVNFIPKSGS | AFCLVSILKP | LLPTPDLTLK | GSGHSLTVTT | GMTTTLLQPI | AVASLSTNTE |
| 570 | 580 | 590 | | | | | |
| QDRVSRGTST | VMPSASLLPP | PEPIEEAEG | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2079 | 1 | 772.9176 | -77.41 | 3 | 55.9 | 13.4 | 0 | 57-86 | R.SGGGGGGNNNGGCCGGASGPAGGGGGGGPR.T | Carbamidomethyl: 14 |

# Detailed Protein Report

## Protein 299: SKI family transcriptional corepressor 1 [Homo sapiens]

**Accession:** gi|384407369
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 35.6
**MW [kDa]:** 93.7
**pI:** 8.5
**Sequence Coverage [%]:** 6.2
**No. of unique Peptides:** 2

## Quantitation

***WUP:QUP*** **Median:** 0.37 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MIPKSLVQAA | ETQRGLCEPG | GKGREGRSGG | KGETRPRGVG | TQEGKGTIPG | SPREKRGERG | EGDPALLPAE | DLWRLPGSKD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RLRSSLLPPP | GPPSSDSGPG | PPSSHSGKTA | QGPRTLNWAR | KQSARTSSNL | CAWSLAMATK | MAEIPSSPYE | PGQRGMKDTQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RGDAPQRGSP | EPRILQLARV | GNVYLKEESS | RSGRLEAKKW | IPTKFLENLS | VPHVDLGGNQ | LWSGGMEALT | TQLGPGREGS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SSPNSKQELQ | PYSGSSALKP | NQVGETSLYG | VPIVSLVIDG | QERLCLAQIS | NTLLKNYSYN | EIHNRRVALG | ITCVQCTPVQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LEILRRAGAM | PISSRRCGMI | TKREAERLCK | SFLGEHKPPK | LPENFAFDVV | HECAWGSRGS | FIPARYNSSR | AKCIKCGYCS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MYFSPNKFIF | HSHRTPDAKY | TQPDAANFNS | WRRHLKLSDK | SATDELSHAW | EDRGLGLATG | ASGPAGPGGP | GGGAGVRSYP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VIPVPSKGFG | LLQKLPPPLF | PHPYGFPTAF | GLCPKKDDPV | LGAGEPKGGS | YVSAFRPVVK | DTESIAKLYG | SAREAYGAGP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ARGPGPGAGS | GGYVSPDFLS | EGSSSYNSAS | PDVDTADEPE | VDVESNRFPD | DEDAQEETEP | SAPSAGGGPD | AGRPAFGDLA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AEDLVRRPER | SPPSGGGGYE | LREPCGPLGG | PAPAKVFAPE | RDEHVKSAAV | ALGPAASYVC | TPEAHEPDKE | DNHSPADDLE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TRKSYPDQRS | ISQPSPANTD | RGEDGLTLDV | TGTHLVEKDI | ENLAREELQK | LLLEQMELRK | KLEREFQSLK | DNFQDQMKRE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | |
| LAYREEMVQQ | LQIVRDTLCN | ELDQERKARY | AIQQKLKEAH | DALHHFSCKM | LTPRHCTGNC | SFKPPLLP | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1961 | 1 | 599.9124 | -123.71 | 3 | 52.9 | 10.6 | 2 | 38-55 | R.GVGTQEGKGTIPGSPREK.R | | |
| 2760 | 1 | 729.3797 | -5.05 | 2 | 65.6 | 13.2 | 1 | 759-770 | K.DIENLAREELQK.L | | WUP:QUP 0.37 |

# Detailed Protein Report

## Protein 300: ectoderm-neural cortex protein 1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|375268727 | **Score:** | 35.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.8 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***WUP:QUP*** **Median:** 1.61 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MFSGGLKESQ DSEVNFDNSI HPEVLELLLD YAYSSRVIIN EENAESLLEA GDMLEFQDIR DACAEFLEKN LHPTNCLGML
        90        100        110        120        130        140        150        160
LLSDAHQCTK LYELSWRMCL SNFQTIRKNE DFLQLPQDMV VQLLSSEELE TEDERLVYES AINWISYDLK KRYCYLPELL
       170        180        190        200        210        220        230        240
QTVRLALLPA IYLMENVAME ELITKQRKSK EIVEEAIRCK LKILQNDGVV TSLCARPRKT GHALFLLGGQ TFMCDKLYLV
       250        260        270        280        290        300        310        320
DQKAKEIIPK ADIPSPRKEF SACAIGCKVY ITGGRGSENG VSKDVWVYDT LHEEWSKAAP MLVARFGHGS AELKHCLYVV
       330        340        350        360        370        380        390        400
GGHTAATGCL PASPSVSLKQ VEHYDPTINK WTMVAPLREG VSNAAVVSAK LKLFAFGGTS VSHDKLPKVQ CYDQCENRWT
       410        420        430        440        450        460        470        480
VPATCPQPWR YTAAAVLGNQ IFIMGGDTEF SACSAYKFNS ETYQWTKVGD VTAKRMSCHA VASGNKLYVV GGYFGIQRCK
       490        500        510        520
TLDCYDPTLD VWNSITTVPY SLIPTAFVST WKHLPS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1599 | 1 | 948.4653 | 4.77 | 2 | 50.2 | 12.3 | 0 | 220-236 | K.TGHALFLLGGQTFMCDK.L | Carbamidomethyl: 15 | WUP:QUP 1.61 |
| 1786 | 1 | 916.3119 | -145.37 | 2 | 52.7 | 10.3 | 1 | 259-275 | K.EFSACAIGCKVYITGGR.G | Carbamidomethyl: 5 | |

# Detailed Protein Report

## Protein 301: tenascin-N precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|62988324 | **Score:** | 35.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 143.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***QU:MU*** **Median:** 2.27 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSLQEMFRFP | MGLLLGSVLL | VASAPATLEP | PGCSNKEQQV | TVSHTYKIDV | PKSALVQVDA | DPQPLSDDGA | SLLALGEARE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EQNIIFRHNI | RLQTPQKDCE | LAGSVQDLLA | RVKKLEEEMV | EMKEQCSAQR | CCQGVTDLSR | HCSGHGTFSL | ETCSCHCEEG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| REGPACERLA | CPGACSGHGR | CVDGRCLCHE | PYVGADCGYP | ACPENCSGHG | ECVRGVCQCH | EDFMSEDCSE | KRCPGDCSGH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GFCDTGECYC | EEGFTGLDCA | QVVTPQGLQL | LKNTEDSLLV | SWEPSSQVDH | YLLSYYPLGK | ELSGKQIQVP | KEQHSYEILG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LLPGTKYIVT | LRNVKNEVSS | SPQHLLATTD | LAVLGTAWVT | DETENSLDVE | WENPSTEVDY | YKLRYGPMTG | QEVAEVTVPK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SSDPKSRYDI | TGLHPGTEYK | ITVVPMRGEL | EGKPILLNGR | TEIDSPTNVV | TDRVTEDTAT | VSWDPVQAVI | DKYVVRYTSA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DGDTKEMAVH | KDESSTVLTG | LKPGEAYKVY | VWAERGNQGS | KKADTNALTE | IDSPANLVTD | RVTENTATIS | WDPVQATIDK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YVVRYTSADD | QETREVLVGK | EQSSTVLTGL | RPGVEYTVHV | WAQKGDRESK | KADTNAPTDI | DSPKNLVTDR | VTENMATVSW |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DPVQAAIDKY | VVRYTSAGGE | TREVPVGKEQ | SSTVLTGLRP | GMEYMVHVWA | QKGDQESKKA | DTKAQTDIDS | PQNLVTDRVT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ENMATVSWDP | VRATIDRYVV | RYTSAKDGET | REVPVGKEQS | STVLTGLRPG | VEYTVHVWAQ | KGAQESKKAD | TKAQTDIDSP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QNLVTDWVTE | NTATVSWDPV | QATIDRYVVH | YTSANGETRE | VPVGKEQSST | VLTGLRPGME | YTVHVWAQKG | NQESKKADTK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| AQTEIDGPKN | LVTDWVTENM | ATVSWDPVQA | TIDKYMVRYT | SADGETREVP | VGKEHSSTVL | TGLRPGMEYM | VHVWAQKGAQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ESKKADTKAQ | TELDPPRNLR | PSAVTQSGGI | LTWTPPSAQI | HGYILTYQFP | DGTVKEMQLG | REDQRFALQG | LEQGATYPVS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LVAFKGGRRS | RNVSTTLSTV | GARFPHPSDC | SQVQQNSNAA | SGLYTIYLHG | DASRPLQVYC | DMETDGGGWI | VFQRRNTGQL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DFFKRWRSYV | EGFGDPMKEF | WLGLDKLHNL | TTGTPARYEV | RVDLQTANES | AYAIYDFFQV | ASSKERYKLT | VGKYRGTAGD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ALTYHNGWKF | TTFDRDNDIA | LSNCALTHHG | GWWYKNCHLA | NPNGRYGETK | HSEGVNWEPW | KGHEFSIPYV | ELKIRPHGYS |
| 1290 | 1300 | | | | | | |
| REPVLGRKKR | TLRGRLRTF | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2128 | 9 | 698.2808 | -172.59 | 2 | 55.0 | 24.0 | 0 | 428-440 | R.GELEGKPILLNGR.T | | QU:MU 2.27 |
| 2573 | 1 | 590.4386 | 252.94 | 1 | 62.8 | 11.4 | 0 | 516-521 | R.GNQGSK.K | | |

# Detailed Protein Report

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## Protein 302: GH3 domain-containing protein isoform 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|217330592 | **Score:** | 35.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 53.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 6.5 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.70 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLLWPLLLLL | LLLPTLALLR | QQRSQDARLS | WLAGLQHRVA | WGALVWAATW | QRRRLEQSTL | HVHQSQQQAL | RWCLQGAQRP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HCSLRRSTDI | STFRNHLPLT | KAYPEVLAQG | RTARVTLTSP | WPRPLPWPGN | TLGQVGTPGT | KDPRALLLDA | LRSPGLRALE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AGTAVELLDV | FLGLETDGEE | LAGAIAAGNP | GAPLRERAAE | LREALEQGPR | GLALRLWPKL | QVVVTLDAGG | QAEAVAALGA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LWCQGLAFFS | PAYAASGGVL | GLNLQPEQPH | GLYLLPPGAP | FIELLPVKEG | TQEEAASTLL | LAEAQQGKEY | ELVLTDRASL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TRCRLGDVVR | VVGAYNQCPV | VRFICRLDQT | LSVRGEDIGE | DLFSEALGRA | VGQWAGAKLL | DHGCVESSIL | DSSAGSAPHY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EVFVALRGLR | NLSEENRDKL | DHCLQEASPR | YKSLRFWGSV | GPARVHLVGQ | GAFRALRAAL | AACPSSPFPP | AMPRVLRHRH |
| 490 | 500 | | | | | | |
| LAQCLQERVV | S | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 273 | 1 | 442.6382 | -324.42 | 2 | 32.1 | 14.2 | 0 | 145-152 | R.ALLLDALR.S | | |
| 2063 | 1 | 634.7944 | -18.66 | 2 | 54.2 | 10.9 | 0 | 420-430 | K.LDHCLQEASPR.Y | | |
| 734 | 1 | 712.3429 | -104.91 | 2 | 39.2 | 10.3 | 1 | 445-457 | R.VHLVGQGAFRALR.A | | QU:MU 0.70 |

# Detailed Protein Report

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**Protein 303:** **PREDICTED: plasma membrane calcium-transporting ATPase 2 isoform X9 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578806173 | **Score:** | 35.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 129.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGDMTNSDFY | SKNQRNESSH | GGEFGCTMEE | LRSLMELRGT | EAVVKIKETY | GDTEAICRRL | KTSPVEGLPG | TAPDLEKRKQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IFGQNFIPPK | KPKTFLQLVW | EALQDVTLII | LEIAAIISLG | LSFYHPPGEG | NEGCATAQGG | AEDEGEAEAG | WIEGAAILLS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VICVVLVTAF | NDWSKEKQFR | GLQSRIEQEQ | KFTVVRAGQV | VQIPVAEIVV | GDIAQVKYGD | LLPADGLFIQ | GNDLKIDESS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LTGESDQVRK | SVDKDPMLLS | GTHVMEGSGR | MLVTAVGVNS | QTGIIFTLLG | AGGEEEEKKD | KKGKMQDGNV | DASQSKAKQQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DGAAAMEMQP | LKSAEGGDAD | DRKKASMHKK | EKSVLQGKLT | KLAVQIGKAG | LVMSAITVII | LVLYFTVDTF | VVNKKPWLPE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CTPVYVQYFV | KFFIIGVTVL | VVAVPEGLPL | AVTISLAYSV | KKMMKDNNLV | RHLDACETMG | NATAICSDKT | GTLTTNRMTV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VQAYVGDVHY | KEIPDPSSIN | TKTMELLINA | IAINSAYTTK | ILPPEKEGAL | PRQVGNKTEC | GLLGFVLDLK | QDYEPVRSQM |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PEEKLYKVYT | FNSVRKSMST | VIKLPDESFR | MYSKGASEIV | LKKCCKILNG | AGEPRVFRPR | DRDEMVKKVI | EPMACDGLRT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ICVAYRDFPS | SPEPDWDNEN | DILNELTCIC | VVGIEDPVRP | EVPEAIRKCQ | RAGITVRMVT | GDNINTARAI | AIKCGIIHPG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EDFLCLEGKE | FNRRIRNEKG | EIEQERIDKI | WPKLRVLARS | SPTDKHTLVK | GIIDSTHTEQ | RQVVAVTGDG | TNDGPALKKA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DVGFAMGIAG | TDVAKEASDI | ILTDDNFSSI | VKAVMWGRNV | YDSISKFLQF | QLTVNVVAVI | VAFTGACITQ | DSPLKAVQML |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| WVNLIMDTFA | SLALATEPPT | ETLLLRKPYG | RNKPLISRTM | MKNILGHAVY | QLALIFTLLF | VGEKMFQIDS | GRNAPLHSPP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SEHYTIIFNT | FVMMQLFNEI | NARKIHGERN | VFDGIFRNPI | FCTIVLGTFA | IQIVIVQFGG | KPFSCSPLQL | DQWMWCIFIG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LGELVWGQVI | ATIPTSRLKF | LKEAGRLTQK | EEIPEEELNE | DVEEIDHAER | ELRRGQILWF | RGLNRIQTQI | EVVNTFKSGA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | | |
| SFQGALRRQS | SVTSQSQDVA | NLSSPSRVSL | SNALSSPTSL | PPAAAGHPRR | EGVP | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 336 | 1 | 625.9844 | -32.51 | 3 | 34.2 | 10.9 | 2 | 568-583 | K.VYTFNSVRKSMSTVIK.L | Oxidation: 11 |

# Detailed Protein Report

## Protein 304: A disintegrin and metalloproteinase with thrombospondin motifs 6 preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|64276808 | **Score:** | 35.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 125.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 6.5 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

***QU:MU*** **Median:** 1.34 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEILWKTLTW | ILSLIMASSE | FHSDHRLSYS | SQEEFLTYLE | HYQLTIPIRV | DQNGAFLSFT | VKNDKHSRRR | RSMDPIDPQQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AVSKLFFKLS | AYGKHFHLNL | TLNTDFVSKH | FTVEYWGKDG | PQWKHDFLDN | CHYTGYLQDQ | RSTTKVALSN | CVGLHGVIAT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EDEEYFIEPL | KNTTEDSKHF | SYENGHPHVI | YKKSALQQRH | LYDHSHCGVS | DFTRSGKPWW | LNDTSTVSYS | LPINNTHIHH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RQKRSVSIER | FVETLVVADK | MMVGYHGRKD | IEHYILSVMN | IVAKLYRDSS | LGNVVNIIVA | RLIVLTEDQP | NLEINHHADK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SLDSFCKWQK | SILSHQSDGN | TIPENGIAHH | DNAVLITRYD | ICTYKNKPCG | TLGLASVAGM | CEPERSCSIN | EDIGLGSAFT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IAHEIGHNFG | MNHDGIGNSC | GTKGHEAAKL | MAAHITANTN | PFSWSACSRD | YITSFLDSGR | GTCLDNEPPK | RDFLYPAVAP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GQVYDADEQC | RFQYGATSRQ | CKYGEVCREL | WCLSKSNRCV | TNSIPAAEGT | LCQTGNIEKG | WCYQGDCVPF | GTWPQSIDGG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| WGPWSLWGEC | SRTCGGGVSS | SLRHCDSPAP | SGGGKYCLGE | RKKRYRSCNTD | PCPLGSRDFR | EKQCADFDNM | PFRGKYYNWK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PYTGGGVKPC | ALNCLAEGYN | FYTERAPAVI | DGTQCNADSL | DICINGECKH | VGCDNILGSD | AREDRCRVCG | GDGSTCDAIE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GFFNDSLPRG | GYMEVVQIPR | GSVHIEVREV | AMSKNYIALK | SEGDDYYING | AWTIDWPRKF | DVAGTAFHYK | RPTDEPESLE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ALGPTSENLI | VMVLLQEQNL | GIRYKFNVPI | TRTGSGDNEV | GFTWNHQPWS | ECSATCAGGV | QRQEVVCKRL | DDNSIVQNNY |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| CDPDSKPPEN | QRACNTEPCP | PEWFIGDWLE | CSKTCDGGMR | TRAVLCIRKI | GPSEEETLDY | SGCLTHRPVE | KEPCNNQSCP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PQWVALDWSE | CTPKCGPGFK | HRIVLCKSSD | LSKTFPAAQC | PEESKPPVRI | RCSLGRCPPP | RWVTGDWGQC | SAQCGLGQQM |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RTVQCLSYTG | QASSDCLETV | RPPSMQQCES | KCDSTPISNT | EECKDVNKVA | YCPLVLKFKF | CSRAYFRQMC | CKTCQGH |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 885 | 1 | 649.9950 | 65.11 | 3 | 39.5 | 10.1 | 1 | 584-601 | R.HCDSPAPSGGGKYCLGER.K | Carbamidomethyl: 2, 14 | |
| 1669 | 1 | 1061.1845 | 59.73 | 3 | 50.6 | 11.4 | 0 | 833-862 | R. TGSGDNEVGFTWNHQPWSECSA Q | | |
| 2995 | 1 | 964.4577 | 34.33 | 3 | 66.2 | 13.8 | 1 | 1017-1041 | R. CPPPRWVTGDWGQCSAQCGLG T | Carbamidomethyl: 14, 18; Oxidation: 24 | QU:MU 1.34 |

# Detailed Protein Report

## Protein 305: protein-methionine sulfoxide oxidase MICAL3 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|209862789 | **Score:** | 35.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 224.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 0.39 | **CV:** 0.00 % | **No. of Peptides:** 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530426255 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein-methionine sulfoxide oxidase MICAL3 isoform X6 [Homo sapiens] |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEERKHETMN | PAHVLFDRFV | QATTCKGTLK | AFQELCDHLE | LKPKDYRSFY | HKLKSKLNYW | KAKALWAKLD | KRGSHKDYKK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GKACTNTKCL | IIGAGPCGLR | TAIDLSLLGA | KVVVIEKRDA | FSRNNVLHLW | PFTIHDLRGL | GAKKFYGKFC | AGAIDHISIR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QLQLILLKVA | LILGIEIHVN | VEFQGLIQPP | EDQENERIGW | RALVHPKTHP | VSEYEFEVII | GGDGRRNTLE | GFRRKEFRGK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LAIAITANFI | NRNTTAEAKV | EEISGVAFIF | NQKFFQELRE | ATGIDLENIV | YYKDDTHYFV | MTAKKQSLLD | KGVILHDYAD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TELLLSRENV | DQEALLSYAR | EAADFSTQQQ | LPSLDFAINH | YGQPDVAMFD | FTCMYASENA | ALVREQNGHQ | LLVALVGDSL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LEPFWPMGTG | IARGFLAAMD | SAWMVRSWSL | GTSPLEVLAE | RESIYRLLPQ | TTPENVSKNF | SQYSIDPVTR | YPNINVNFLR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PSQVRHLYDT | GETKDIHLEM | ESLVNSRTTP | KLTRNESVAR | SSKLLGWCQR | QTDGYAGVNV | TDLTMSWKSG | LALCAIIHRY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RPDLIDFDSL | DEQNVEKNNQ | LAFDIAEKEL | GISPIMTGKE | MASVGEPDKL | SMVMYLTQFY | EMFKDSLPSS | DTLDLNAEEK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AVLIASTRSP | ISFLSKLGQT | ISRKRSPKDK | KEKDLDGAGK | RRKTSQSEEE | EAPRGHRGER | PTLVSTLTDR | RMDVAVGNQN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KVKYMATQLL | AKFEENAPAQ | SIGIRRQGSM | KKEFPQNLGG | SDTCYFCQKR | VYVMERLSAE | GKFFHRSCFK | CEYCATTLRL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SAYAYDIEDG | KFYCKPHYCY | RLSGYAQRKR | PAVAPLSGKE | AKGPLQDGAT | TDANGRANAV | ASSTERTPGS | GVNGLEEPSI |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| AKRLRGTPER | IELENYRLSL | RQAEALQEVP | EETQAEHNLS | SVLDTGAEED | VASSSSESEM | EEEGEEEEEE | PRLPPSDLGG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VPWKEAVRIH | ALLKGKSEEE | LEASKSFGPG | NEEEEEEEEE | YEEEEEEDYD | EEEEESSEAG | NQRLQQVMHA | ADPLEIQADV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| HWTHIREREE | EERMAPASES | SASGAPLDEN | DLEEDVDSEP | AEIEGEAAED | GDPGDTGAEL | DDDQHWSDSP | SDADRELRLP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| CPAEGEAELE | LRVSEDEEKL | PASPKHQERG | PSQATSPIRS | PQESALLFIP | VHSPSTEGPQ | LPPVPAATQE | KSPEERLFPE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PLLPKEKPKA | DAPSDLKAVH | SPIRSQPVTL | PEARTPVSPG | SPQPQPPVAA | STPPPSPLPI | CSQPQPSTEA | TVPSPTQSPI |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| RFQPAPAKTS | TPLAPLPVQS | QSDTKDRLGS | PLAVDEALRR | SDLVEEFWMK | SAEIRRSLGL | TPVDRSKGPE | PSFPTPAFRP |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VSLKSYSVEK | SPQDEGLHLL | KPLSIPKRLG | LPKPEGEPLS | LPTPRSPSDR | ELRSAQEERR | ELSSSSGLGL | HGSSSNMKTL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GSQSFNTSDS | AMLTPPSSPP | PPPPPGEEPA | TLRRKLREAE | PNASVVPPPL | PATWMRPPRE | PAQPPREEVR | KSFVESVEEI |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PFADDVEDTY | DDKTEDSSLQ | EKFFTPPSCW | PRPEKPRHPP | LAKENGRLPA | LEGTLQPQKR | GLPLVSAEAK | ELAEERMRAR |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| EKSVKSQALR | DAMARQLSRM | QQMELASGAP | RPRKASSAPS | QGKERRPDSP | TRPTLRGSEE | PTLKHEATSE | EVLSPPSDSG |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| GPDGSFTSSE | GSSGKSKKRS | SLFSPRRNKK | EKKSKGEGRP | PEKPSSNLLE | EAAAKPKSLW | KSVFSGYKKD | KKKKADDKSC |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| PSTPSSGATV | DSGKHRVLPV | VRAELQLRRQ | LSFSEDSDLS | SDDVLEKSSQ | KSRREPRTYT | EEELNAKLTR | RVQKAARRQA |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| KQEELKRLHR | AQIIQRQLQQ | VEERQRRLEE | RGVAVEKALR | GEAGMGKKDD | PKLMQEWFKL | VQEKNAMVRY | ESELMIFARE |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LELEDRQSRL | QQELRERMAV | EDHLKTEEEL | SEEKQILNEM | LEVVEQRDSL | VALLEEQRLR | EREEDKDLEA | AMLSKGFSLN |
| 2010 | | | | | | | |
| WS | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1700 | 1 | 538.2445 | -35.71 | 2 | 51.5 | 12.2 | 0 | 712-721 | R.MDVAVGNQNK.V | | QU:MU 0.39 |

# Detailed Protein Report

**Protein 306:** **NACHT, LRR and PYD domains-containing protein 2 isoform 3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|291463280 | **Score:** | 35.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 117.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVSSAQMGFN | LQALLEQLSQ | DELSKFKYLI | TTFSLAHELQ | KIPHKEMASL | QVFEKMHRMD | LSERAKDEVR | EAALKSFNKR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KPLSLGITRK | ERPPLDVDEM | LERFKTEAQA | FTETKGNVIC | LGKEVFKGKK | PDKDNRCRYI | LKTKFREMWK | SWPGDSKEVQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VMAERYKMLI | PFSNPRVLPG | PFSYTVVLYG | PAGLGKTTLA | QKLMLDWAED | NLIHKFKYAF | YLSCRELSRL | GPCSFAELVF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RDWPELQDDI | PHILAQARKI | LFVIDGFDEL | GAAPGALIED | ICGDWEKKKP | VPVLLGSLLN | RVMLPKAALL | VTTRPRALRD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LRILAEEPIY | IRVEGFLEED | RRAYFLRHFG | DEDQAMRAFE | LMRSNAALFQ | LGSAPAVCWI | VCTTLKLQME | KGEDPVPTCL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TRTGLFLRFL | CSRFPQGAQL | RGALRTLSLL | AAQGLWAQTS | VLHREDLERL | GVQESDLRLF | LDGDILRQDR | VSKGCYSFIH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LSFQQFLTAL | FYTLEKEEEE | DRDGHTWDIG | DVQKLLSGVE | RLRNPDLIQA | GYYSFGLANE | KRAKELEATF | GCRMSPDIKQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ELLRCDISCK | GGHSTVTDLQ | ELLGCLYESQ | EEELVKEVMA | QFKEISLHLN | AVDVVPSSFC | VKHCRNLQKM | SLQVIKENLP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ENVTASESDA | EVERSQDDQH | MLPFWTDLCS | IFGSNKDLMG | LAINDSFLSA | SLVRILCEQI | ASDTCHLQRV | VFKNISPADA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HRNLCLALRG | HKTVTYLTLQ | GNDQDDMFPA | LCEVLRHPEC | NLRYLGLVSC | SATTQQWADL | SLALEVNQSL | TCVNLSDNEL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LDEGAKLLYT | TLRHPKCFLQ | RLSLENCHLT | EANCKDLAAV | LVVSRELTHL | CLAKNPIGNT | GVKFLCEGLR | YPECKLQTLV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LWNCDITSDG | CCDLTKLLQE | KSSLLCLDLG | LNHIGVKGMK | FLCEALRKPL | CNLRCLWLWG | CSIPPFSCED | LCSALSCNQS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LVTLDLGQNP | LGSSGVKMLF | ETLTCSSGTL | RTLRLKIDDF | NDELNKLLEE | IEEKNPQLII | DTEKHHPWAE | RPSSHDFMI |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1922 | 1 | 893.8122 | -134.43 | 2 | 53.9 | 11.2 | 0 | 695-709 | R.ILCEQIASDTCHLQR.V | Carbamidomethyl: 3 |
| 223 | 1 | 636.6401 | -68.84 | 3 | 32.8 | 23.9 | 1 | 846-863 | R.ELTHLCLAKNPIGNTGVK.F | |

# Detailed Protein Report

| | | | |
|---|---|---|---|
| **Protein 307:** | **PREDICTED: bromodomain and WD repeat-containing protein 1 isoform X1 [Homo sapiens]** | | |
| **Accession:** | gi\|530418950 | **Score:** | 35.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 253.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.10 | **CV:** | 0.00 % | **No. of Peptides:** | 1 | |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MAEPSSARRP VPLIESELYF LIARYLSAGP CRRAAQVLVQ ELEQYQLLPK RLDWEGNEHN RSYEELVLSN KHVAPDHLLQ
        90        100        110        120        130        140        150        160
ICQRIGPMLD KEIPPSISRV TSLLGAGRQS LLRTAKDCRH TVWKGSAFAA LHRGRPPEMP VNYGSPPNLV EIHRGKQLTG
       170        180        190        200        210        220        230        240
CSTFSTAFPG TMYQHIKMHR RILGHLSAVY CVAFDRTGHR IFTGSDDCLV KIWSTHNGRL LSTLRGHSAE ISDMAVNYEN
       250        260        270        280        290        300        310        320
TMIAAGSCDK IIRVWCLRTC APVAVLQGHT GSITSLQFSP MAKGSQRYMV STGADGTVCF WQWDLESLKF SPRPLKFTEK
       330        340        350        360        370        380        390        400
PRPGVQMLCS SFSVGGMFLA TGSTDHVIRM YFLGFEAPEK IAELESHTDK VDSIQFCNNG DRFLSGSRDG TARIWRFEQL
       410        420        430        440        450        460        470        480
EWRSILLDMA TRISGDLSSE EERFMKPKVT MIAWNQNDSI VVTAVNDHVL KVWNSYTGQL LHNLMGHADE VFVLETHPFD
       490        500        510        520        530        540        550        560
SRIMLSAGHD GSIFIWDITK GTKMKHYFNM IEGQGHGAVF DCKFSQDGQH FACTDSHGHL LIFGFGCSKP YEKIPDQMFF
       570        580        590        600        610        620        630        640
HTDYRPLIRD SNNYVLDEQT QQAPHLMPPP FLVDVDGNPH PTKYQRLVPG RENSADEHLI PQLGYVATSD GEVIEQIISL
       650        660        670        680        690        700        710        720
QTNDNDERSP ESSILDGMIR QLQQQQDQRM GADQDTIPRG LSNGEETPRR GFRRLSLDIQ SPPNIGLRRS GQVEGVRQMH
       730        740        750        760        770        780        790        800
QNAPRSQIAT ERDLQAWKRR VVVPEVPLGI FRKLEDFRLE KGEEERNLYI IGRKRKTLQL SHKSDSVVLV SQSRQRTCRR
       810        820        830        840        850        860        870        880
KYPNYGRRNR SWRELSSGNE SSSSVRHETS CDQSEGSGSS EEDEWRSDRK SESYSESSSD SSSRYSDWTA DAGINLQPPL
       890        900        910        920        930        940        950        960
RTSCRRRITR FCSSSEDEIS TENLSPPKRR RKRKKENKPK KEDQELVKIV GIRYEVGPPT LCCLKLAFID PATGKLMDKS
       970        980        990       1000       1010       1020       1030       1040
FSIRYHDMPD VIDFLVLRQF YDEARQRNWQ SCDRFRSIID DAWWFGTVLS QEPYQPQYPD SHFQCYIVRW DNTEIEKLSP
      1050       1060       1070       1080       1090       1100       1110       1120
WDMEPIPDNV DPPEELGASI SVTTDELEKL LYKPQAGEWG QKSRDEECDR IISGIDQLLN LDIAAAFAGP VDLCTYPKYC
      1130       1140       1150       1160       1170       1180       1190       1200
TVVAYPTDLY TIRMRLVNRF YRRLSALVWE VRYIEHNART FNEPESVIAR SAKKITDQLL KFIKNQHCTN ISELSNTSEN
      1210       1220       1230       1240       1250       1260       1270       1280
DEQNAEDLDD SDLPKTSSGR RRVHDGKKSI RATNYVESNW KKQCKELVNL IFQCEDSEPF RQPVDLVEYP DYRDIIDTPM
      1290       1300       1310       1320       1330       1340       1350       1360
DFGTVRETLD AGNYDSPLEF CKDIRLIFSN AKAYTPNKRS KIYSMTLRLS ALFEEKMKKI SSDFKIGQKF NEKLRRSQRF
      1370       1380       1390       1400       1410       1420       1430       1440
KQRQNCKGDS QPNKSIRNLK PKRLKSQTKI IPELVGSPTQ STSSRTAYLG THKTSAGISS GVTSGDSSDS AESSERRKRN
      1450       1460       1470       1480       1490       1500       1510       1520
RPITNGSTLS ESEVEDSLAT SLSSSASSSS EESKESSRAR ESSSRSGLSR SSNLRVTRTR AAQRKTGPVS LANGCGRKAT
      1530       1540       1550       1560       1570       1580       1590       1600
RKRVYLSDSD NNSLETGEIL KARAGNNRKV LRKCAAVAAN KIKLMSDVEE NSSSESVCSG RKLPHRNASA VARKKLLHNS
      1610       1620       1630       1640       1650       1660       1670       1680
EDEQSLKSEI EEEELKDENQ LLPVSSSHTA QSNVDESENR DSESESDLRV ARKNWHANGY KSHTPAPSKT KFLKIESSEE
      1690       1700       1710       1720       1730       1740       1750       1760
DSKSHDSDHA CNRTAGPSTS VQKLKAESIS EEADSEPGRS GGRKYNTFHK NASFFKKTKI LSDSEDSESE EQDREDGKCH
      1770       1780       1790       1800       1810       1820       1830       1840
KMEMNPISGN LNCDPIAMSQ CSSDHGCETD LDSDDDKIEK PNNFMKDSAS QDNGLSRKIS RKRVCSSDSD SSLQVVKKSS
      1850       1860       1870       1880       1890       1900       1910       1920
KARTGLLRIT RRCAATAANK IKLMSDVEDV SLENVHTRSK NGRKKPLHLA CTTAKKKLSD CEGSVHCEVP SEQYACEGKP
      1930       1940       1950       1960       1970       1980       1990       2000
PDPDSEGSTK VLSQALNGDS DSEDMLNSEH KHRHTNIHKI DAPSKRKSSS VTSSGEDSKS HIPGSETDRT FSSESTLAQK
      2010       2020       2030       2040       2050       2060       2070       2080
ATAENNFEVE LNYGLRRWNG RRLRTYGKAP FSKTKVIHDS QETAEKEVKR KRSHPELENV KISETTGNSK FRPDTSSKSS
      2090       2100       2110       2120       2130       2140       2150       2160
DLGSVTESDI DCTDNTKTKR RKTKGKAKVV RKEFVPRDRE PNTKVRTCMH NQKDAVQMPS ETLKAKMVPE KVPRRCATVA
      2170       2180       2190       2200       2210       2220       2230       2240
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 127 | 1 | 724.8357 | -58.74 | 2 | 31.3 | 12.0 | 1 | 762-773 | K.GEEERNLYIIGR.K |  | QU:MU 2.10 |

# Detailed Protein Report

## Protein 308: TMF-regulated nuclear protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|61966741 | **Score:** | 35.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 23.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 14.1 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPGCRISACG | PGAQEGTAEQ | RSPPPPRDPM | PSSQPPPPTP | TLTPTPTPGQ | SPPLPDAAGA | SAGAAEDQEL | QRWRQGASGI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AGLAGPGGGS | GAAAGAGGRA | LELAEARRRL | LEVEGRRRLV | SELESRVLQL | HRVFLAAELR | LAHRAESLSR | LSGGVAQAEL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | |
| YLAAHGSRLK | KGPRRGRRGR | PPALLASALG | LGGCVPWGAG | RLRRGHGPEP | DSPFRRSPPR | GPASPQR | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1625 | 2 | 682.3281 | 20.05 | 3 | 50.6 | 17.4 | 1 | 2-21 | M.PGCRISACGPGAQEGTAEQR.S | Carbamidomethyl: 8 |
| 1148 | 1 | 676.2570 | -106.06 | 2 | 44.5 | 17.6 | 1 | 205-216 | R.GHGPEPDSPFRR.S | |

# Detailed Protein Report

---

**Protein 309:** **PREDICTED: GAS2-like protein 2 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578830659 | **Score:** | 35.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 92.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 4.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSQPAGGRRK | PRTLGPPVCS | IRPFKSSEQY | LEAMKEDLAE | WLRDLYGLDI | DAANFLQVLE | TGLVLCQHAN | VVTDAALAFL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AEAPAQAQKI | PMPRVGVSCN | GAAQPGTFQA | RDNVSNFIQW | CRKEMGIQEV | LMFETEDLVL | RKNVKNVVLC | LLELGRRAWR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FGVAAPTLVQ | LEEEIEEEVR | RELALPPPDP | SPPAPPRRQP | CHFRNLDQMI | LRNHVMVRVG | GGWDTLGHYL | DKHDPCRCTS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LSHKPGSFLK | PPAPPVQHEV | RVQDGPSQTQ | PTMTISRSQS | PPPPVDWKTY | TSSDRRLRPP | TPSSPRPRRE | RGAGTGASRE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MAPFLRCQER | SLIPSWRQPT | AGDSPPSPQS | SSTQKGRDPQ | CTSSGKREER | YPPELPRGRI | PTSWVHEETD | SWGTDAGNPT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PQRLRAIEAT | TKGISARGPS | PLPRSFGPAE | CLGLRLPLRD | EAKGAFFQFR | EPESVRSPTP | VQGLTKIPIR | LPPARPPTPG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RSFPGATSGS | PRTELGRDPI | PLRAVTVDLA | GSTHGDCSVE | VRQEDQQLDI | QVMAEARESW | DLGLQEQEGR | YTPLPLGGNK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EQAIYCSLEE | EILGNMKLLE | VRSACPQGTR | SGVIPRSGVY | IPRLAGQWPE | PGGPYDKAIQ | ELAQGSPSLL | KVDLEAWKAA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PTGSPKPAVT | PGPGSLKGKL | GARQSGPRTK | ASLSAKGTHM | RKVPPQGGQD | CSASTVSASP | EAPTPSPLDP | NSDKAKACLS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KGRRTLRKPK | RVPSIYKLKL | RPRIRPRRDH | RPEKQPSRIP | RPLAYVFLGP | ARQPPKDRLL | RAVLGSKGGE | ASRVDGASVG |
| 810 | 820 | 830 | 840 | 850 | | | |
| EEEEEGKEEK | EPAAPLESSP | QPPEGLQPHW | LNQAPLPPEE | ESWV | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1978 | 1 | 643.7875 | -102.56 | 2 | 54.6 | 14.5 | 2 | 671-682 | K.ASLSAKGTHMRK.V | |

# Detailed Protein Report

## Protein 310: PREDICTED: putative uncharacterized protein CXorf49-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|410170282 | **Score:** | 34.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 53.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| | | **Sequence Coverage [%]:** | 7.0 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.68 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.35 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSSTDEVSVC RAGLGPEGGE QAGAHTASPG APRGDGHGRD LNFGGQRSGK GKGKGESGFT DPESFSFESE SELIEQGRVV
        90        100        110        120        130        140        150        160
LWGQEGRPGT PVDDQAGGGD YSFYLADEPA TIMPPSSVQG HPSPEGATAK GSTDIWADLE VGPSWRGALS PSPGEWQQAS
       170        180        190        200        210        220        230        240
AGPLHLSVPG PGPAWENPER GSKSRLSFQV DPQQPSAEGP AGLNTDDSDS ADESSDLPVI RVIISTKEGS QAKPGSPKKP
       250        260        270        280        290        300        310        320
GDTCGRRSFH RRESYLQVQG PLLISPPRRL TPVVERPAVG ELDVPSLKKM QSMVWGKRGV RPSCSGAAVR GPLPRGTLGR
       330        340        350        360        370        380        390        400
KVAQEKKSLE GAPELALRGA FPAWGQRLSA VPPDPASFPP VSGVGLLGKS VRPKEPKHSS PGKKPAGRKT RESQAAARED
       410        420        430        440        450        460        470        480
NDPNRDEVPR AQLPTQKPEL ISLSVRRGEY SSGDPNIRAP QVLGTSQPSA FTLRRLVPRC HASSGDWQPP VHPPRPERQQ
       490        500        510
QPPGAQGCPR VMLCVAPRNR GPH
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 674 | 1 | 512.2810 | -49.78 | 2 | 38.0 | 12.2 | 1 | 311-320 | R.GPLPRGTLGR.K | | WUP:QUP 2.35<br>QU:MU 1.68 |

# Detailed Protein Report

## Protein 311: PREDICTED: tau-tubulin kinase 2 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578826647 | **Score:** | 34.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 129.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLPGKDHVCR | FIGCGRNDRF | NYVVMQLQGR | NLADLRRSQS | RGTFTISTTL | RLGRQILESI | ESIHSVGFLH | RDIKPSNFAM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GRFPSTCRKC | YMLDFGLARQ | FTNSCGDVRP | PRAVAGFRGT | VRYASINAHR | NREMGRHDDL | WSLFYMLVEF | VVGQLPWRKI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KDKEQVGSIK | ERYDHRLMLK | HLPPEFSIFL | DHISSLDYFT | KPDYQLLTSV | FDNSIKTFGV | IESDPFDWEK | TGNDGSLTTT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TTSTTPQLHT | RLTPAAIGIA | NATPIPGDLL | RENTDEVFPD | EQLSDGENGI | PVGVSPDKLP | GSLGHPRPQE | KDVWEEMDAN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KNKIKLGICK | AATEEENSHG | QANGLLNAPS | LGSPIRVRSE | ITQPDRDIPL | VRKLRSIHSF | ELEKRLTLEP | KPDTDKFLET |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CLEKMQKDTS | AGKESILPAL | LHKPCVPAVS | RTDHIWHYDE | EYLPDASKPA | SANTPEQADG | GGSNGFIAVN | LSSCKQEIDS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KEWVIVDKEQ | DLQDFRTNEA | VGHKTTGSPS | DEEPEVLQVL | EASPQDEKLQ | LGPWAENDHL | KKETSGVVLA | LSAEGPPTAA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SEQYTDRLEL | QPGAASQFIA | ATPTSLMEAQ | AEGPLTAITI | PRPSVASTQS | TSGSFHCGQQ | PEKKDLQPME | PTVELYSPRE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NFSGLVVTEG | EPPSGGSRTD | LGLQIDHIGH | DMLPNIRESN | KSQDLGPKEL | PDHNRLVVRE | FENLPGETEE | KSILLESDNE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DEKLSRGQHC | IEISSLPGDL | VIVEKDHSAT | TEPLDVTKTQ | TFSVVPNQDK | NNEIMKLLTV | GTSEISSRDI | DPHVEGQIGQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VAEMQKNKIS | KDDDIMSEDL | PGHQGDLSTF | LHQEGKREKI | TPRNGELFHC | VSENEHGAPT | RKDMVRSSFV | TRHSRIPVLA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QEIDSTLESS | SPVSAKEKLL | QKKAYQPDLV | KLLVEKRQFK | SFLGDLSSAS | DKLLEEKLAT | VPAPFCEEEV | LTPFSRLTVD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SHLSRSAEDS | FLSPIISQSR | KSKIPRPVSW | VNTDQVNSST | SSQFFPRPPP | GKPPTRPGVE | ARLRRYKVLG | SSNSDSDLFS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RLAQILQNGS | QKPRSTTQCK | SPGSPHNPKT | PPKSPVVPRR | SPSASPRSSS | LPRTSSSSPS | RAGRPHHDQR | SSSPHLGRSK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | | |
| SPPSHSGSSS | SRRSCQQEHC | KPSKNGLKGS | GSLHHHSAST | KTPQGKSKPA | SKLSR | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1491 | 1 | 626.6231 | -220.31 | 2 | 48.3 | 12.6 | 0 | 312-321 | K.DVWEEMDANK.N | Oxidation: 6 |
| 2024 | 1 | 694.3465 | 21.44 | 2 | 55.7 | 10.8 | 1 | 1119-1132 | R.SKSPPSHSGSSSSR.R | |

# Detailed Protein Report

**Protein 312:** **myeloperoxidase precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4557759 | **Score:** | 34.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 83.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

```
        10          20          30          40          50          60          70          80
MGVPFFSSLR  CMVDLGPCWA  GGLTAEMKLL  LALAGLLAIL  ATPQPSEGAA  PAVLGEVDTS  LVLSSMEEAK  QLVDKAYKER

        90         100         110         120         130         140         150         160
RESIKQRLRS  GSASPMELLS  YFKQPVAATR  TAVRAADYLH  VALDLLERKL  RSLWRRPFNV  TDVLTPAQLN  VLSKSSGCAY

       170         180         190         200         210         220         230         240
QDVGVTCPEQ  DKYRTITGMC  NNRRSPTLGA  SNRAFVRWLP  AEYEDGFSLP  YGWTPGVKRN  GFPVALARAV  SNEIVRFPTD

       250         260         270         280         290         300         310         320
QLTPDQERSL  MFMQWGQLLD  HDLDFTPEPA  ARASFVTGVN  CETSCVQQPP  CFPLKIPPND  PRIKNQADCI  PFFRSCPACP

       330         340         350         360         370         380         390         400
GSNITIRNQI  NALTSFVDAS  MVYGSEEPLA  RNLRNMSNQL  GLLAVNQRFQ  DNGRALLPFD  NLHDDPCLLT  NRSARIPCFL

       410         420         430         440         450         460         470         480
AGDTRSSEMP  ELTSMHTLLL  REHNRLATEL  KSLNPRWDGE  RLYQEARKIV  GAMVQIITYR  DYLPLVLGPT  AMRKYLPTYR

       490         500         510         520         530         540         550         560
SYNDSVDPRI  ANVFTNAFRY  GHTLIQPFMF  RLDNRYQPME  PNPRVPLSRV  FFASWRVVLE  GGIDPILRGL  MATPAKLNRQ

       570         580         590         600         610         620         630         640
NQIAVDEIRE  RLFEQVMRIG  LDLPALNMQR  SRDHGLPGYN  AWRRFCGLPQ  PETVGQLGTV  LRNLKLARKL  MEQYGTPNNI

       650         660         670         680         690         700         710         720
DIWMGGVSEP  LKRKGRVGPL  LACIIGTQFR  KLRDGDRFWW  ENEGVFSMQQ  RQALAQISLP  RIICDNTGIT  TVSKNNIFMS

       730         740         750
NSYPRDFVNC  STLPALNLAS  WREAS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1893 | 1 | 640.7817 | -156.88 | 2 | 54.0 | 15.3 | 0 | 537-548 | R.VVLEGGIDPILR.G | |

# Detailed Protein Report

## Protein 313: serine protease 58 precursor [Homo sapiens]

**Accession:** gi|48255915
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl, Oxidation

**Score:** 34.9
**MW [kDa]:** 27.1
**pI:** 6.4
**Sequence Coverage [%]:** 20.7
**No. of unique Peptides:** 2

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKFILLWALL | NLTVALAFNP | DYTVSSTPPY | LVYLKSDYLP | CAGVLIHPLW | VITAAHCNLP | KLRVILGVTI | PADSNEKHLQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VIGYEKMIHH | PHFSVTSIDH | DIMLIKLKTE | AELNDYVKLA | NLPYQTISEN | TMCSVSTWSY | NVCDIYKEPD | SLQTVNISVI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SKPQCRDAYK | TYNITENMLC | VGIVPGRRQP | CKEVSAAPAI | CNGMLQGILS | FADGCVLRAD | VGIYAKIFYY | IPWIENVIQN |
| 250 | | | | | | | |
| N | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1245 | 1 | 1072.1826 | -52.32 | 3 | 43.9 | 19.6 | 1 | 36-63 | K.SDYLPCAGVLIHPLWVITAAHCNLPKLR.V | Carbamidomethyl: 6, 22 |
| 2776 | 1 | 862.7428 | -25.62 | 3 | 65.9 | 15.2 | 2 | 167-188 | R.DAYKTYNITENMLCVGIVPGRR.Q | Carbamidomethyl: 14;<br>Oxidation: 12 |

# Detailed Protein Report

**Protein 314:** **PREDICTED: receptor-type tyrosine-protein phosphatase mu isoform X4 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578832170 | **Score:** | 34.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 161.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MPSGSFMLVN ASGRPEGQRA HLLLPQLKEN DTHCIDFHYF VSSKSNSPPG LLNVYVKVNN GPLGNPIWNI SGDPTRTWNR
        90        100        110        120        130        140        150        160
AELAISTFWP NFYQVIFEVI TSGHQGYLAI DEVKVLGHPC TRTPHFLRIQ NVEVNAGQFA TFQCSAIGRT VAGDRLWLQG
       170        180        190        200        210        220        230        240
IDVRDAPLKE IKVTSSRRFI ASFNVVNTTK RDAGKYRCMI RTEGGVGISN YAELVVKEPP VPIAPPQLAS VGATYLWIQL
       250        260        270        280        290        300        310        320
NANSINGDGP IVAREVEYCT ASGSWNDRQP VDSTSYKIGH LDPDTEYEIS VLLTRPGEGG TGSPGPALRT RTKCADPMRG
       330        340        350        360        370        380        390        400
PRKLEVVEVK SRQITIRWEP FGYNVTRCHS YNLTVHYCYQ VGGQEQVREE VSWDTENSHP QHTITNLSPY TNVSVKLILM
       410        420        430        440        450        460        470        480
NPEGRKESQE LIVQTDEDLP GAVPTESIQG STFEEKIFLQ WREPTQTYGV ITLYEITYKA VSSFDPEIDL SNQSGRVSKL
       490        500        510        520        530        540        550        560
GNETHFLFFG LYPGTTYSFT IRASTAKGFG PPATNQFTTK ISAPSMPAYE LETPLNQTDN TVTVMLKPAH SRGAPVSVYQ
       570        580        590        600        610        620        630        640
IVVEEERPRR TKKTTEILKC YPVPIHFQNA SLLNSQYYFA AEFPADSLQA AQPFTIGDNK TYNGYWNTPL LPYKSYRIYF
       650        660        670        680        690        700        710        720
QAASRANGET KIDCVQVATK AAIIVTQLTT PYIRIAPAAG DGQLTGAATP KPVPEPEKQT DHTVKIAGVI AGILLFVIIF
       730        740        750        760        770        780        790        800
LGVVLVMKKR KLAKKRKETM SSTRQEMTVM VNSMDKSYAE QGTNCDEAFS FMDTHNLNGR SVSSPSSFTM KTNTLSTSVP
       810        820        830        840        850        860        870        880
NSYYPDETHT MASDTSSLVQ SHTYKKREPA DVPYQTGQLH PAIRVADLLQ HITQMKCAEG YGFKEEYESF FEGQSAPWDS
       890        900        910        920        930        940        950        960
AKKDENRMKN RYGNIIAYDH SRVRLQTIEG DTNSDYINGN YIDGYHRPNH YIATQGPMQE TIYDFWRMVW HENTASIIMV
       970        980        990       1000       1010       1020       1030       1040
TNLVEVGRVK CCKYWPDDTE IYKDIKVTLI ETELLAEYVI RTFAVEKGGA GGEANCSPSR EVSQRGVHEI REIRQFHFTG
      1050       1060       1070       1080       1090       1100       1110       1120
WPDHGVPYHA TGLLGFVRQV KSKSPPSAGP LVVHCSAGAG RTGCFIVIDI MLDMAEREGV VDIYNCVREL RSRRVNMVQT
      1130       1140       1150       1160       1170       1180       1190       1200
EEQYVFIHDA ILEACLCGDT SVPASQVRSL YYDMNKLDPQ TNSSQIKEEF RTLNMVTPTL RVEDCSIALL PRNHEKNRCM
      1210       1220       1230       1240       1250       1260       1270       1280
DILPPDRCLP FLITIDGESS NYINAALMDS YKQPSAFIVT QHPLPNTVKD FWRLVLDYHC TSVVMLNDVD PAQLCPQYWP
      1290       1300       1310       1320       1330       1340       1350       1360
ENGVHRHGPI QVEFVSADLE EDIISRIFRI YNAARPQDGY RMVQQFQFLG WPMYRDTPVS KRSFLKLIRQ VDKWQEEYNG
      1370       1380       1390       1400       1410       1420       1430       1440
GEGRTVVHCL NGGGRSGTFC AISIVCEMLR HQRTVDVFHA VKTLRNNKPN MVDLLDQYKF CYEVALEYLN SG
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1436 | 1 | 927.4440 | -10.35 | 3 | 47.6 | 22.6 | 1 | 1365-1390 | R.TVVHCLNGGGRSGTFCAISIVCEMLR.H | Carbamidomethyl: 22 |

# Detailed Protein Report

## Protein 315: uncharacterized protein KIAA0408 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|59806363 | **Score:** | 34.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 79.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.78 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.50 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MDLHKQWENT ETNWHKEKME LLDQFDNERK EWESQWKIMQ KKIEELCREV KLWRKININE SAKIIDLYHE KTIPEKVIES
        90        100        110        120        130        140        150        160
SPNYPDLGQS EFIRTNHKDG LRKENKREQS LVSGGNQMCK EQKATKKSKV GFLDPLATDN QKECEAWPDL RTSEEDSKSC
       170        180        190        200        210        220        230        240
SGALSTALEE LAKVSEELCS FQEEIRKRSN HRRMKSDSFL QEMPNVTNIP HGDPMINNDQ CILPISLEKE KQKNRKNLSC
       250        260        270        280        290        300        310        320
TNVLQSNSTK KCGIDTIDLK RNETPPVPPP RSTSRNFPSS DSEQAYERWK ERLDHNSWVP HEGRSKRNYN PHFPLRQQEM
       330        340        350        360        370        380        390        400
SMLYPNEGKT SKDGIIFSSL VPEVKIDSKP PSNEDVGLSM WSCDIGIGAK RSPSTSWFQK TCSTPSNPKY EMVIPDHPAK
       410        420        430        440        450        460        470        480
SHPDLHVSND CSSSVAESSS PLRNFSCGFE RTTRNEKLAA KTDEFNRTVF RTDRNCQAIQ QNHSCSKSSE DLKPCDTSST
       490        500        510        520        530        540        550        560
HTGSISQSND VSGIWKTNAH MPVPMENVPD NPTKKSTTGL VRQMQGHLSP RSYRNMLHEH DWRPSNLSGR PRSADPRSNY
       570        580        590        600        610        620        630        640
GVVEKLLKTY ETATESALQN SKCFQDNWTK CNSDVSGGAT LSQHLEMLQM EQQFQQKTAV WGGQEVKQGI DPKKITEESM
       650        660        670        680        690        700
SVNASHGKGF SRPARPANRR LPSRWASRSP SAPPALRRTT HNYTISLRSE ALMV
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2738 | 3 | 841.8972 | 10.76 | 2 | 62.7 | 13.5 | 1 | 17-29 | K.EKMELLDQFDNER.K | Oxidation: 3 | WUP:QUP 0.50<br>QU:MU 1.78 |
| 1324 | 1 | 727.1757 | -204.08 | 2 | 46.2 | 10.1 | 0 | 108-120 | R.EQSLVSGGNQMCK.E | Carbamidomethyl: 12;<br>Oxidation: 11 | |

# Detailed Protein Report

## Protein 316: PREDICTED: zinc finger protein 554 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578832959 | **Score:** | 34.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 43.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 5.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 2.44 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTVLRNQDST | YKKVALQEEP | ASGINMIKLI | REDGGWKQLE | DSHEDPQGLL | SQKASLHVVA | VPQEKATAWH | GFGENGNLSP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ALVLSQGSSK | GNHLCGSELD | ITSLASDSVL | NHHQLGYADR | RPCESNECGN | AIRQNSHFIQ | HGGKMFVYLE | NGQSLNHGMA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LTIHNKINTA | EKPFECHQCG | KVFNRRHSLS | EHQRIHTGEK | PYECQECGRA | FTHSSTLTRH | LRTHTGEKPY | GCGECGKAFN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RISSLTQHQR | IHTGEKPYKC | EDCGKSFCQS | SYLILHKRTH | TGEKPYECSE | CGKAFSDRSS | LNQHERTHTG | ENPYECKQCG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| RAFSQRSSLV | RHERTHTGEK | PYRCQECGKA | FSQSSSLVTH | QKTHSSQKTY | KIIDCGKAFY | QNRHLIGY | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1743 | 1 | 560.7234 | -120.44 | 2 | 52.1 | 14.2 | 0 | 210-219 | R.AFTHSSTLTR.H | | WUP:QUP 2.44 |

# Detailed Protein Report

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## Protein 317: procollagen galactosyltransferase 1 precursor [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|31377697 | **Score:** | 34.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 71.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.0 |
|  |  | **Sequence Coverage [%]:** | 4.2 |
|  |  | **No. of unique Peptides:** | 1 |

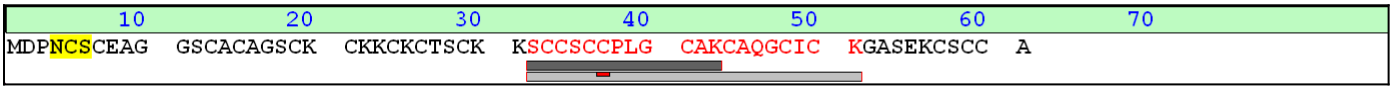
|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAAPRAGRR | RGQPLLALLL | LLLAPLPPGA | PPGADAYFPE | ERWSPESPLQ | APRVLIALLA | RNAAHALPTT | LGALERLRHP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RERTALWVAT | DHNMDNTSTV | LREWLVAVKS | LYHSVEWRPA | EEPRSYPDEE | GPKHWSDSRY | EHVMKLRQAA | LKSARDMWAD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YILFVDADNL | ILNPDTLSLL | IAENKTVVAP | MLDSRAAYSN | FWCGMTSQGY | YKRTPAYIPI | RKRDRRGCFA | VPMVHSTFLI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DLRKAASRNL | AFYPPHPDYT | WSFDDIIVFA | FSCKQAEVQM | YVCNKEEYGF | LPVPLRAHST | LQDEAESFMH | VQLEVMVKHP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PAEPSRFISA | PTKTPDKMGF | DEVFMINLRR | RQDRRERMLR | ALQAQEIECR | LVEAVDGKAM | NTSQVEALGI | QMLPGYRDPY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HGRPLTKGEL | GCFLSHYNIW | KEVVDRGLQK | SLVFEDDLRF | EIFFKRRLMN | LMRDVEREGL | DWDLIYVGRK | RMQVEHPEKA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VPRVRNLVEA | DYSYWTLAYV | ISLQGARKLL | AAEPLSKMLP | VDEFLPVMFD | KHPVSEYKAH | FSLRNLHAFS | VEPLLIYPTH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 |  |
| YTGDDGYVSD | TETSVVWNNE | HVKTDWDRAK | SQKMREQQAL | SREAKNSDVL | QSPLDSAARD | EL |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 718 | 2 | 450.6336 | -247.78 | 2 | 37.4 | 13.7 | 1 | 1-9 | -.MAAAPRAGR.R |  |

# Detailed Protein Report

## Protein 318: metallothionein-1H [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|10835085 | **Score:** | 34.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 6.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 49.2 |
| | | **No. of unique Peptides:** | 2 |



```
         10         20         30         40         50         60         70
MDPNCSCEAG GSCACAGSCK CKKCKCTSCK KSCCSCCPLG CAKCAQGCIC KGASEKCSCC A
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2498 | 1 | 673.3379 | 138.11 | 2 | 61.8 | 10.5 | 0 | 32-43 | K.SCCSCCPLGCAK.C | Carbamidomethyl: 5, 6, 10 |
| 1117 | 1 | 1019.4619 | 75.11 | 2 | 43.5 | 10.7 | 1 | 32-51 | K.SCCSCCPLGCAKCAQGCICK.G | Carbamidomethyl: 2 |

# Detailed Protein Report

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**Protein 319:** **PREDICTED: zinc finger SWIM domain-containing protein 3 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578835782 | **Score:** | 34.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 78.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.9 |
| | | **Sequence Coverage [%]:** | 4.5 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKTRLERQAE | TTSGHPSLAS | LYYWTAPALP | GPELEMAPPP | HCAHNRYVQV | KFVCIRTQSN | RKRTREADMC | PAYLLLRYNE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RLDRLFISEL | NTQHIHGDSK | VASPGGDTTG | KSQKTMCLQR | LQPVQPTTKK | DLDTAEKSLV | EPSFCLDKVQ | VSSKPEQEGI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TPSDLAKIAK | VMKNFLKVDE | GSMASFSVGD | SQHLDRLSFQ | SSKMTDLFIR | FPENLLLHRV | ENTQGHILYA | FLVENKERES |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RVVHFAVLKA | ETVTSVAKML | SIFTEFNSDW | PKVKVVFVDP | SFHYRAILQE | IFPAARILLS | IYHTTRLLEK | KLHRSSANPS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FKRLMKEALR | EAVFVTSEAS | LKNLCQMSQA | VLDEDLFNFL | QAHWFTCELL | WYMHVRKGLL | ACNTYMDSLD | IVTSKVSSLF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| REQQSLLDCI | LCFVDYIDFF | NTKGLKNLPT | PPPKLKRARP | ASMPLKSKKA | FGICGESLTS | LPAEETKPDA | QQVQVQQQSQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VPPSQVGMLD | TLHQSGSELA | YKLCHNEWEV | VQNSTHLVDM | AGSSVDVQLL | EDSHQVSKDG | CSCSCSFQQW | YHLPCRHILA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LLHTSQQPVG | EAMVCRRWQK | KYQYLLGPNG | ELQDRGMVPN | TGQPEKQGRN | DMIQDLSREL | ANLLMQTEGP | ELEERYSTLR |
| 650 | 660 | 670 | 680 | 690 | 700 | | |
| KIVDIWAGPS | QPSELFQQPG | DFKDVGRLPF | LWGKQEEGEG | FPPATAVMHY | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2524 | 1 | 1044.0930 | 32.96 | 2 | 62.2 | 15.4 | 2 | 112-129 | K.SQKTMCLQRLQPVQPTTK.K | |
| 2543 | 2 | 701.8414 | -144.22 | 2 | 61.8 | 19.2 | 2 | 424-436 | K.GLKNLPTPPPKLK.R | |

# Detailed Protein Report

## Protein 320: splicing factor, proline- and glutamine-rich [Homo sapiens]

**Accession:** gi|4826998
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 34.5
**MW [kDa]:** 76.1
**pI:** 9.9
**Sequence Coverage [%]:** 6.9
**No. of unique Peptides:** 3

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.43 | **CV:** | 42.02 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 0.84 | **CV:** | 25.78 % | **No. of Peptides:** | 2 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530363144 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: splicing factor, proline- and glutamine-rich isoform X3 [Homo sapiens] |
| gi\|530363142 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: splicing factor, proline- and glutamine-rich isoform X2 [Homo sapiens] |
| gi\|530363140 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: splicing factor, proline- and glutamine-rich isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSRDRFRSRG | GGGGGFHRRG | GGGGRGGLHD | FRSPPPGMGL | NQNRGPMGPG | PGQSGPKPPI | PPPPPHQQQQ | QPPPQQPPPQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QPPPHQPPPH | PQPHQQQQPP | PPPQDSSKPV | VAQGPGPAPG | VGSAPPASSS | APPATPPTSG | APPGSGPGPT | PTPPPAVTSA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PPGAPPPTPP | SSGVPTTPPQ | AGGPPPPPAA | VPGPGPGPKQ | GPGPGGPKGG | KMPGGPKPGG | GPGLSTPGGH | PKPPHRGGGE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PRGGRQHHPP | YHQQHHQGPP | PGGPGGRSEE | KISDSEGFKA | NLSLLRRPGE | KTYTQRCRLF | VGNLPADITE | DEFKRLFAKY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GEPGEVFINK | GKGFGFIKLE | SRALAEIAKA | ELDDTPMRGR | QLRVRFATHA | AALSVRNLSP | YVSNELLEEA | FSQFGPIERA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VVIVDDRGRS | TGKGIVEFAS | KPAARKAFER | CSEGVFLLTT | TPRPVIVEPL | EQLDDEDGLP | EKLAQKNPMY | QKERETPPRF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AQHGTFEYEY | SQRWKSLDEM | EKQQREQVEK | NMKDAKDKLE | SEMEDAYHEH | QANLLRQDLM | RRQEELRRME | ELHNQEMQKR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KEMQLRQEEE | RRRREEEMMI | RQREMEEQMR | RQREESYSRM | GYMDPRERDM | RMGGGGAMNM | GDPYGSGGQK | FPPLGGGGGI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | |
| GYEANPGVPP | ATMSGSMMGS | DMRTERFGQG | GAGPVGGQGP | RGMGPGTPAG | YGRGREEYEG | PNKKPRF | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 406 | 1 | 678.2016 | -174.41 | 2 | 34.7 | 11.5 | 1 | 268-279 | R.SEEKISDSEGFK.A | | WUP:QUP 1.08<br>QU:MU 0.96 |
| 6 | 1 | 736.0027 | 52.34 | 3 | 29.0 | 13.0 | 1 | 609-630 | R. DMRMGGGGAMNMGDPYGSGGQ F | Oxidation: 4, 12 | |
| 284 | 1 | 671.3405 | 5.90 | 2 | 33.5 | 10.1 | 0 | 667-681 | R.FGQGGAGPVGGQGPR.G | | WUP:QUP 0.65<br>QU:MU 2.15 |

# Detailed Protein Report

## Protein 321: zinc finger protein 189 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|37574608 | **Score:** | 34.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 68.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 4.8 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578817874 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 189 isoform X2 [Homo sapiens] |
| gi\|578817872 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 189 isoform X1 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MMENYGNLVS LDVLNRDKDE EPTVKQEIEE IEEEVEPQGV IVTRIKSEID QDPMGRETFE LVGRLDKQRG IFLWEIPRES
        90        100        110        120        130        140        150        160
LTQEQRMFRE NTNIIRKRPN SEEKCHKCEE CGKGFVRKAH FIQHQRVHTG EKPFQCNECG KSFSRSSFVI EHQRIHTGER
       170        180        190        200        210        220        230        240
PYECNYCGKT FSVSSTLIRH QRIHTGERPY QCNQCKQSFS QRRSLVKHQR IHTGEKPHKC SDCGKAFSWK SHLIEHQRTH
       250        260        270        280        290        300        310        320
TGEKPYHCTK CKKSFSRNSL LVEHQRIHTG ERPHKCGECG KAFRLSTYLI QHQKIHTGEK PFLCIECGKS FSRSSFLIEH
       330        340        350        360        370        380        390        400
QRIHTGERPY QCKECGKSFS QLCNLTRHQR IHTGDKPHKC EECGKAFSRS SGLIQHQRIH TREKTYPYNE TKESFDPNCS
       410        420        430        440        450        460        470        480
LVIQQEVYPK EKSYKCDECG KTFSVSAHLV QHQRIHTGEK PYLCTVCGKS FSRSSFLIEH QRIHTGERPY LCRQCGKSFS
       490        500        510        520        530        540        550        560
QLCNLIRHQG VHTGNKPHKC DECGKAFSRN SGLIQHQRIH TGEKPYKCEK CDKSFSQQRS LVNHQKIHAE VKTQETHECD
       570        580        590
ACGEAFNCRI SLIQHQKLHT AWMQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1729 | 1 | 1051.5453 | -9.31 | 2 | 51.4 | 14.5 | 1 | 70-86 | R.GIFLWEIPRESLTQEQR.M | |

# Detailed Protein Report

## Protein 322: G patch domain and KOW motifs-containing protein [Homo sapiens]

**Accession:** gi|15811782
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 34.5
**MW [kDa]:** 52.2
**pI:** 5.8
**Sequence Coverage [%]:** 6.1
**No. of unique Peptides:** 1

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.76 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.52 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MADSKEGVLP LTAASTAPIS FGFTRTSARR RLADSGDGAG PSPEEKDFLK TVEGRELQSV KPQEAPKELV IPLIQNGHRR
        90        100        110        120        130        140        150        160
QPPARPPGPS TDTGALADGV VSQAVKELIA ESKKSLEERE NAGVDPTLAI PMIQKGCTPS GEGADSEPRA ETVPEEANYE
       170        180        190        200        210        220        230        240
AVPVEAYGLA MLRGMGWKPG EGIGRTFNQV VKPRVNSLRP KGLGLGANLT EAQALTPTGP SRMPRPDEEQ EKDKEDQPQG
       250        260        270        280        290        300        310        320
LVPGGAVVVL SGPHRGLYGK VEGLDPDNVR AMVRLAVGSR VVTVSEYYLR PVSQQEFDKN TLDLRQQNGT ASSRKTLWNQ
       330        340        350        360        370        380        390        400
ELYIQQDNSE RKRKHLPDRQ DGPAAKSEKA APRSQHWLHR DLRVRFVDNM YKGGQYYNTK MIIEDVLSPD TCVCRTDEGR
       410        420        430        440        450        460        470        480
VLEGLREDML ETLVPKAEGD RVMVVLGPQT GRVGHLLSRD RARSRALVQL PRENQVVELH YDAICQYMGP SDTDDD
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1518 | 1 | 816.3814 | -50.98 | 2 | 49.2 | 16.7 | 1 | 256-270 | R.GLYGKVEGLDPDNVR.A | | QU:MU 0.76<br>WUP:QUP 1.52 |

# Detailed Protein Report

## Protein 323: PREDICTED: ankyrin repeat domain-containing protein 30B isoform X1 [Homo sapiens]

**Accession:** gi|578832133
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 34.4
**MW [kDa]:** 171.3
**pI:** 5.9
**Sequence Coverage [%]:** 2.1
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKRLLAAAGK | GVRGPEPPNP | FSERVYTEKD | YGTIYFGDLG | KIHTAASRGQ | VQKLEKMTVG | KKPVNLNKRD | MKKRTALHWA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CVNGHAEVVT | FLVDRKCQLN | VLDGEGRTPL | MKALQCEREA | CANILIDAGA | DLNYVDVYGN | TALHYAVYSE | NLLMVATLLS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YGAVIEVQNK | ASLTPLLLAI | QKRSKQTVEF | LLTKNANANA | FNESKCTALM | LAICEGSSEI | VGMLLQQNVD | VFAEDIHGIT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AERYAAACGV | NYIHQQLLEH | IRKLPKNPQN | TNPEGTSTGT | PDEAAPLAER | TPDTAESLLE | KTPDEAARLV | EGTSAKIQCL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GKATSGKFEQ | STEETPRKIL | RPTKETSEKF | SWPAKERSRK | ITWEEKETSV | KTECVAGVTP | NKTEVLEKGT | SNMIACPTKE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TSTKASTNVD | VSSVEPIFSL | FGTRTIENSQ | CTKVEEDFNL | ATKIISKSAA | QNYTCLPDAT | YQKDIKTINH | KIEDQMFPSE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SKREEDEEYS | WDSGSLFESS | AKTQVCIPES | MYQKVMEINR | EVEELPEKPS | AFKPAVEMQK | TVPNKAFELK | NEQTLRAAQM |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FPSESKQKDD | EENSWDSESP | CETVSQKDVY | LPKATHQKEF | DTLSGKLEES | PVKDGLLKPT | CGRKVSLPNK | ALELKDRETF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KAESPDKDGL | LKPTCGRKVS | LPNKALELKD | RETLKAESPD | NDGLLKPTCG | RKVSLPNKAL | ELKDRETFKA | AQMFPSESKQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KDDEENSWDF | ESFLETLLQN | DVCLPKATHQ | KEFDTLSGKL | EESPDKDGLL | KPTCGRKVSL | PNKALELKDR | ETLKAESPDK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DGLLKPTCVR | KVSLPNKALE | LKDRETLKAA | QMFPSESKQK | DDEENSWDFE | SFLEALLQND | GCLPKATHQK | EFDTLSGKLE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ESPDKDGLLK | PTCGMKISLP | NKALELKDRE | TFKAEDVSSV | ESTFSLFGKP | TTENSQSTKV | EEDFNLTTKE | GATKTVTGQQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ERDIGIIERA | PQDQTNKMPT | SELGRKEDTK | STSDSEIISV | SDTQNYECLP | EATYQKEIKT | TNGKIEESPE | KPSHFEPATE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| MQNSVPNKGL | EWKNKQTLRA | DSTTLSKILD | ALPSCERGRE | LKKDNCEQIT | AKMEQTKNKF | CVLQKELSEA | KEIKSQLENQ |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KAKWEQELCS | VRLTLNQEEE | KRRNVDILKE | KIRPEEQLRK | KLEVKQQLEQ | TLRIQDIELK | SVTSNLNQVS | HTHESENDLF |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| HENCMLKKEI | AMLKLEVATL | KHQHQVKENK | YFEDIKILQE | KNAELQMTLK | LKQKTVTKRA | SQYREQLKVL | TAENTMLTSK |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LKEKQDKEIL | ETEIESHHPR | LASALQDHDQ | SVTSRKNQEL | AFHSAGDAPL | QGIMNVDVSN | TIYNNEVLHQ | PLYEAQRKSK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| SPKINLNYAG | DDLRENALVS | EHAQRDRCET | QCQMKKAEHM | YQNEQDNVDK | HTEQQESLEQ | KLFQLESKNR | WLRQQLVYAH |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KKVNKSKVTI | NIQFPEMKMQ | RHLNEKNEEV | FNYGNHLKER | IDQYEKEKAE | REVSIKKYKY | FSNFLKESGL | G |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1677 | 1 | 619.9559 | -45.33 | 3 | 51.2 | 22.1 | 1 | 760-776 | K.LEESPDKDGLLKPTCGR.K | |

# Detailed Protein Report

## Protein 324: proteoglycan 4 isoform D precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|189181724 | **Score:** | 34.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 136.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.52 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.51 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MAWKTLPIYL LLLLSVFVIQ QVSSQELSCK GRCFESFERG RECDCDAQCK KYDKCCPDYE SFCAEVKDNK KNRTKKKPTP
        90        100        110        120        130        140        150        160
KPPVVDEAGS GLDNGDFKVT TPDTSTTQHN KVSTSPKITT AKPINPRPSL PPNSDTSKET SLTVNKETTV ETKETTTTNK
       170        180        190        200        210        220        230        240
QTSTDGKEKT TSAKETQSIE KTSAKDLAPT SKVLAKPTPK AETTTKGPAL TTPKEPTPTT PKEPASTTPK EPTPTTIKSA
       250        260        270        280        290        300        310        320
PTTPKEPAPT TTKSAPTTPK EPAPTTTKEP APTTPKEPAP TTTKEPAPTT TKSAPTTPKE PAPTTPKKPA PTTPKEPAPT
       330        340        350        360        370        380        390        400
TPKEPTPTTP KEPAPTTKEP APTTPKEPAP TAPKKPAPTT PKEPAPTTPK EPAPTTTKEP SPTTPKEPAP TTTKSAPTTT
       410        420        430        440        450        460        470        480
KEPAPTTTKS APTTPKEPSP TTTKEPAPTT PKEPAPTTPK KPAPTTPKEP APTTPKEPAP TTTKKPAPTT PKEPAPTTPK
       490        500        510        520        530        540        550        560
ETAPTTPKKL TPTTPEKLAP TTPEKPAPTT PEELAPTTPE EPTPTTPEEP APTTPKAAAP NTPKEPAPTT PKEPAPTTPK
       570        580        590        600        610        620        630        640
EPAPTTPKET APTTPKGTAP TTLKEPAPTT PKKPAPKELA PTTTKEPTST TCDKPAPTTP KGTAPTTPKE PAPTTPKEPA
       650        660        670        680        690        700        710        720
PTTPKGTAPT TLKEPAPTTP KKPAPKELAP TTTKGPTSTT SDKPAPTTPK ETAPTTPKEP APTTPKKPAP TTPETPPPTT
       730        740        750        760        770        780        790        800
SEVSTPTTTK EPTTIHKSPD ESTPELSAEP TPKALENSPK EPGVPTTKTP AATKPEMTTT AKDKTTERDL RTTPETTTAA
       810        820        830        840        850        860        870        880
PKMTKETATT TEKTTESKIT ATTTQVTSTT TQDTTPFKIT TLKTTTLAPK VTTTKKTITT TEIMNKPEET AKPKDRATNS
       890        900        910        920        930        940        950        960
KATTPKPQKP TKAPKKPTST KKPKTMPRVR KPKTTPTPRK MTSTMPELNP TSRIAEAMLQ TTTRPNQTPN SKLVEVNPKS
       970        980        990       1000       1010       1020       1030       1040
EDAGGAEGET PHMLLRPHVF MPEVTPDMDY LPRVPNQGII INPMLSDETN ICNGKPVDGL TTLRNGTLVA FRGHYFWMLS
      1050       1060       1070       1080       1090       1100       1110       1120
PFSPPSPARR ITEVWGIPSP IDTVFTRCNC EGKTFFFKDS QYWRFTNDIK DAGYPKPIFK GFGGLTGQIV AALSTAKYKN
      1130       1140       1150       1160       1170       1180       1190       1200
WPESVYFFKR GGSIQQYIYK QEPVQKCPGR RPALNYPVYG ETTQVRRRRF ERAIGPSQTH TIRIQYSPAR LAYQDKGVLH
      1210       1220       1230       1240       1250       1260       1270       1280
NEVKVSILWR GLPNVVTSAI SLPNIRKPDG YDYYAFSKDQ YYNIDVPSRT ARAITTRSGQ TLSKVWYNCP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2237 | 1 | 994.8741 | -142.64 | 2 | 57.8 | 23.9 | 2 | 785-802 | K.TTERDLRTTPETTTAAPK.M | | WUP:QUP 0.51<br>QU:MU 2.52 |
| 299 | 2 | 559.1629 | -227.93 | 2 | 33.4 | 10.6 | 0 | 792-802 | R.TTPETTTAAPK.M | | |

# Detailed Protein Report

**Protein 325:** **SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|325651836 | **Score:** | 34.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 121.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSAAEPPPP | PPPESAPSKP | AASIASGGSN | SSNKGGPEGV | AAQAVASAAS | AGPADAEMEE | IFDDASPGKQ | KEIQEPDPTY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EEKMQTDRAN | RFEYLLKQTE | LFAHFIQPAA | QKTPTSPLKM | KPGRPRIKKD | EKQNLLSVGD | YRHRRTEQEE | DEELLTESSK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ATNVCTRFED | SPSYVKWGKL | RDYQVRGLNW | LISLYENGIN | GILADEMGLG | KTLQTISLLG | YMKHYRNIPG | PHMVLVPKST |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LHNWMSEFKR | WVPTLRSVCL | IGDKEQRAAF | VRDVLLPGEW | DVCVTSYEML | IKEKSVFKKF | NWRYLVIDEA | HRIKNEKSKL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SEIVREFKTT | NRLLLTGTPL | QNNLHELWSL | LNFLLPDVFN | SADDFDSWFD | TNNCLGDQKL | VERLHMVLRP | FLLRRIKADV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EKSLPPKKEV | KIYVGLSKMQ | REWYTRILMK | DIDILNSAGK | MDKMRLLNIL | MQLRKCCNHP | YLFDGAEPGP | PYTTDMHLVT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NSGKMVVLDK | LLPKLKEQGS | RVLIFSQMTR | VLDILEDYCM | WRNYEYCRLD | GQTPHDERQD | SINAYNEPNS | TKFVFMLSTR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AGGLGINLAT | ADVVILYDSD | WNPQVDLQAM | DRAHRIGQTK | TVRVFRFITD | NTVEERIVER | AEMKLRLDSI | VIQQGRLVDQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NLNKIGKDEM | LQMIRHGATH | VFASKESEIT | DEDIDGILER | GAKKTAEMNE | KLSKMGESSL | RNFTMDTESS | VYNFEGEDYR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EKQKIAFTEW | IEPPKRERKA | NYAVDAYFRE | ALRVSEPKAP | KAPRPPKQPN | VQDFQFFPPR | LFELLEKEIL | FYRKTIGYKV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PRNPELPNAA | QAQKEEQLKI | DEAESLNDEE | LEEKEKLLTQ | GFTNWNKRDF | NQFIKANEKW | GRDDIENIAR | EVEGKTPEEV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| IEYSAVFWER | CNELQDIEKI | MAQIERGEAR | IQRRISIKKA | LDTKIGRYKA | PFHQLRISYG | TNKGKNYTEE | EDRFLICMLH |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KLGFDKENVY | DELRQCIRNS | PQFRFDWFLK | SRTAMELQRR | CNTLITLIER | ENMELEEKEK | AEKKKRGPKP | STQKRKMDGA |
| 1050 | 1060 | | | | | | |
| PDGRGRKKKL | KL | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 971 | 1 | 706.9594 | 14.52 | 2 | 42.2 | 20.7 | 2 | 485-496 | K.MVVLDKLLPKLK.E | Oxidation: 1 |

# Detailed Protein Report

| | | | |
|---|---|---|---|
| **Protein 326:** | **PREDICTED: chromodomain-helicase-DNA-binding protein 9 isoform X9 [Homo sapiens]** | | |
| **Accession:** | gi\|530424378 | **Score:** | 34.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 269.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***WUP:QUP*** | **Median:** | 4.90 | **CV:** | 0.00 % | **No. of Peptides:** | 1 | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSEKKQRKKV | ESESKQEKAN | RIISEAIAKA | KERGERNIPR | VMSPENFPTA | SVEGKEEKKG | RRMKSKPKDK | DSKKTKTCSK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LKEKTKIGKL | IITLGKKQKR | KNESSDEISD | AEQMPQHTLK | DQDSQKRRSN | RQIKRKKYAE | DIEGKQSEEE | VKGSMKIKKN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SAPLPGEQPL | QLFVENPSEE | DAAIVDKILS | SRTVKKEISP | GVMIDTEEFF | VKYKNYSYLH | CEWATEEQLL | KDKRIQQKIK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RFKLRQAQRA | HFFADMEEEP | FNPDYVEVDR | VLEVSFCEDK | DTGEPVIYYL | VKWCSLPYED | STWELKEDVD | LAKIEEFEQL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QASRPDTRRL | DRPPSNIWKK | IDQSRDYKNG | NQLREYQLEG | LNWLLFNWYN | RRNCILADEM | GLGKTIQSIT | FLYEILLTGI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RGPFLIIAPL | STIANWEREF | RTWTDINVVV | YHGSLISRQM | IQQYEMYFRD | SQGRIIRGAY | RFQAIITTFE | MILGGCGELN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AIEWRCVIID | EAHRLKNKNC | KLLEGLKLMN | LEHKVLLTGT | PLQNTVEELF | SLLHFLEPLR | FPSESTFMQE | FGDLKTEEQV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QKLQAILKPM | MLRRLKEDVE | KKLAPKEETI | IEVELTNIQK | KYYRAILEKN | FSFLSKGAGQ | TNVPNLVNTM | MELRKCCNHP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| YLIKGAEEKI | LGEFRDTYNP | AASDFHLQAM | IQSAGKLVLI | DKLLPKMKAG | GHKVLIFSQM | VRCLDILEDY | LIHKRYLYER |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| IDGRVRGNLR | QAAIDRFSKP | DSDRFVFLLC | TRAGGLGINL | TAADTCIIFD | SDWNPQNDLQ | AQARCHRIGQ | NKAVKVYRLV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TRNSYEREMF | DRASLKLGLD | KAVLQSMSGR | ESNVGGIQQL | SKKEIEDLLR | RGAYGAIMEE | EDEGSKFCEE | DIDQILLRRT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KTITIESEGR | GSTFAKASFV | ASGNRTDISL | DDPNFWQKWA | KKAEIDIEAI | SGRNSLVIDT | PRIRKQTRPF | SATKDELAEL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SEAESEGDEK | PKLRRPCDRS | NGYGRTECFR | VEKNLLVYGW | GRWREILSHG | RFKRQLNEHD | VEIICRALLA | YCLVHYRGDE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KIKGFIWDLI | TPTEDGQTRE | LQNHLGLSAP | VPRGRKGKKV | KTQTSSFDIQ | KAEWLRKYNP | EQLLQDEGYK | KHIKHHCNKV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LLRVRMLYYL | KQEVIGNECQ | KVFDGVDASD | IDVWVPEPDH | SEVPAEWWDF | DADKSLLIGV | FKHGYEKYNT | IRADPALCFL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ERVGKPDEKA | VAAEQRANDY | MDGDVEDPEY | KPAPAIFKDD | IEDDVSSPGD | LVIADGDGQL | MEGDKVYWPT | QSALTTRLRR |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LITAYQRTNK | NRQIQQIQPT | FSVPTSVMQP | IYEEATLNPK | MAAKIERQQR | WTRREEADFY | RVVSTFGVVF | DPDRGQFDWT |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KFRAMARLHK | KTDDSLEKYL | YAFMSMCRRV | CRLPSKEELV | DPNIFIQPIT | EERASRTLYR | IELLRKVREQ | ALRHPQLFER |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LKLCHPNPDL | PVWWECGPHD | RDLLIGAAKH | GVSRTDYHIL | RDPELSFMAA | QRNYSQSKMA | HSRTSTPLLQ | QYQVALSASP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| LTSLPRLLDA | KGIILEEMKV | KSENLKEEPQ | SSEEESMSSV | ETRTLIKSEP | VSPKNGVLPQ | ATGDQKSGGK | CETDRRMVAA |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| RTEPLTPNPA | SKKPRVHKRG | SESSSDSDSD | SERSSCSSRS | SSSSSSSSCS | HSRSGSSSSS | SSSCSSASSS | SSSSTSSSSS |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| SSSSSSEESD | SDEEEAQKRA | ESTTHMKAYD | EESVASLSTT | QDETQDSFQM | NNGTPESAYI | LQGGYMLAAS | YWPKDRVMIN |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| RLDSICQTVL | KGKWPSARRS | YDANTVASFY | TTKLLDSPGA | ATEYSDPSVP | TPPGAGVKEE | HDQSTQMSKV | KKHVREKEFT |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| VKIKDEGGLK | LTFQKQGLAQ | KRPFDGEDGA | LGQQQYLTRL | RELQSASETS | LVNFPKSIPV | SGTSIQPTLG | ANGVILDNQP |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| IVKKRRGRRK | NVEGVDIFFF | NRNKPPNHVS | LGLTSSQIST | GINPALSYTQ | PQGIPDTESP | VPVINLKDGT | RLAGDDAPKR |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| KDLEKWLKEH | PGYVEDLGAF | IPRMQLHEGR | PKQKRHRCRN | PNKLDVNSLT | GEERVQLINR | RNARKVGGAF | APPLKDLCRF |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| LKENSEYGVA | PEWGDVVKQS | GFLPESMYER | ILTGPVVREE | VSRRGRRPKS | GIAKATAAAA | AASATSVSGN | PLLANGLLPG |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1309 | 1 | 863.9074 | -143.00 | 2 | 46.0 | 10.4 | 2 | 563-576 | K.LQAILKPMMLRRLK.E | Oxidation: 8 | |
| 2019 | 1 | 719.3122 | -83.44 | 2 | 55.6 | 13.7 | 0 | 1342-1354 | R.VVSTFGVVFDPDR.G | | WUP:QUP 4.90 |

# Detailed Protein Report

## Protein 327: glutamine--tRNA ligase isoform b [Homo sapiens]

**Accession:** gi|441478305
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 34.3
**MW [kDa]:** 86.5
**pI:** 6.6
**Sequence Coverage [%]:** 5.6
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAALDSLSLF | TSLGLSEQKA | RETLKNSALS | AQLREAATQA | QQTLGSTIDK | ATGILLYGLA | SRLRDTRRLS | FLVSYIATAL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EYVRSHPLDP | IDTVDFEREC | GVGVIVTPEQ | IEEAVEAAIN | RHRPQLLVER | YHFNMGLLMG | EARAVLKWAD | GKMIKNEVDM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QVLHLLGPKL | EADLEKKFKV | AKARLEETDR | RTAKDVVENG | ETADQTLSLM | EQLRGEALKF | HKPGENYKTP | GYVVTPHTMN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LLKQHLEITG | GQVRTRFPPE | PNGILHIGHA | KAINFNFGYA | KANNGICFLR | FDDTNPEKEE | AKFFTAICDM | VAWLGYTPYK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VTYASDYFDQ | LYAWAVELIR | RGLAYVCHQR | GEELKGHNTL | PSPWRDRPME | ESLLLFEAMR | KGKFSEGEAT | LRMKLVMEDG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KMDPVAYRVK | YTPHHRTGDK | WCIYPTYDYT | HCLCDSIEHI | THSLCTKEFQ | ARRSSYFWLC | NALDVYCPVQ | WEYGRLNLHY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AVVSKRKILQ | LVATGAVRDW | DDPRLFTLTA | LRRRGFPPEA | INNFCARVGV | TVAQTTMEPH | LLEACVRDVL | NDTAPRAMAV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LESLRVIITN | FPAAKSLDIQ | VPNFPADETK | GFHQVPFAPI | VFIERTDFKE | EPEPGFKRLA | WGQPVGLRHT | GYVIELQHVV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KGPSGCVESL | EVTCRRADAG | EKPKAFIHWV | SQPLMCEVRL | YERLFQHKNP | EDPTEVPGGF | LSDLNLASLH | VVDAALVDCS |
| 730 | 740 | 750 | 760 | 770 | | | |
| VALAKPFDKF | QFERLGYFSV | DPDSHQGKLV | FNRTVTLKED | PGKV | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2780 | 1 | 841.6618 | -115.85 | 3 | 65.2 | 10.5 | 2 | 131-152 | R.YHFNMGLLMGEARAVLKWADGK.M | Oxidation: 9 |

# Detailed Protein Report

## Protein 328: sodium-driven chloride bicarbonate exchanger isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|295821221 | **Score:** | 34.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 125.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.10 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.37 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEIKDQGAQM | EPLLPTRNDE | EAVVDRGGTR | SILKTHFEKE | DLEGHRTLFI | GVHVPLGGRK | SHRRHRHRGH | KHRKRDRERD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SGLEDGRESP | SFDTPSQRVQ | FILGTEDDDE | EHIPHDLFTE | LDEICWREGE | DAEWRETARW | LKFEEDVEDG | GERWSKPYVA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TLSLHSLFEL | RSCILNGTVL | LDMHANTLEE | IADMVLDQQV | SSGQLNEDVR | HRVHEALMKQ | HHHQNQKKLT | NRIPIVRSFA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DIGKKQSEPN | SMDKNAGQVV | SPQSAPACVE | NKNDVSRENS | TVDFSKGLGG | QQKGHTSPCG | MKQRHEKGPP | HQQEREVDLH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FMKKIPPGAE | ASNILVGELE | FLDRTVVAFV | RLSPAVLLQG | LAEVPIPTRF | LFILLGPLGK | GQQYHEIGRS | IATLMTDEVF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HDVAYKAKDR | NDLVSGIDEF | LDQVTVLPPG | EWDPSIRIEP | PKNVPSQEKR | KIPAVPNGTA | AHGEAEPHGG | HSGPELQRTG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RIFGGLILDI | KRKAPYFWSD | FRDAFSLQCL | ASFLFLYCAC | MSPVITFGGL | LGEATEGRIS | AIESLFGASM | TGIAYSLFGG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QPLTILGSTG | PVLVFEKILF | KFCKEYGLSY | LSLRASIGLW | TATLCIILVA | TDASSLVCYI | TRFTEEAFAS | LICIIFIYEA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LEKLFELSEA | YPINMHNDLE | LLTQYSCNCV | EPHNPSNGTL | KEWRESNISA | SDIIWENLTV | SECKSLHGEY | VGRACGHDHP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YVPDVLFWSV | ILFFSTVTLS | ATLKQFKTSR | YFPTKVRSIV | SDFAVFLTIL | CMVLIDYAIG | IPSPKLQVPS | VFKPTRDDRG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| WFVTPLGPNP | WWTVIAAIIP | ALLCTILIFM | DQQITAVIIN | RKEHKLKKGC | GYHLDLLMVA | VMLGVCSIMG | LPWFVAATVL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SITHVNSLKL | ESECSAPGEQ | PKFLGIREQR | VTGLMIFILM | GSSVFMTSIL | KFIPMPVLYG | VFLYMGASSL | KGIQFFDRIK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LFWMPAKHQP | DFIYLRHVPL | RKVHLFTIIQ | MSCLGLLWII | KVSRAAIVFP | MMVLALVFVR | KLMDLLFTKR | ELSWLDDLMP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ESKKKKLEDA | EKEEEQSMLA | MEDEGTVQLP | LEGHYRDDPS | VINISDEMSK | TALWRNLLIT | ADNSKDKESS | FPSKSSPS |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 63 | 1 | 724.6832 | -193.81 | 2 | 29.7 | 11.3 | 1 | 128-139 | R.EGEDAEWRETAR.W | | QU:MU 2.10 |
| 1817 | 1 | 847.8355 | -100.68 | 2 | 52.5 | 10.3 | 1 | 278-293 | R.ENSTVDFSKGLGGQQK.G | | |
| 505 | 5 | 509.1120 | -289.14 | 2 | 36.3 | 12.7 | 0 | 705-713 | K.SLHGEYVGR.A | | WUP:QUP 2.37 |

# Detailed Protein Report

**Protein 329:** **monofunctional C1-tetrahydrofolate synthase, mitochondrial isoform 3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|337756507 | **Score:** | 34.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 99.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQSRRARPRR | EVIQNSKEVL | SLLQEKNPAF | KPVLAIIQAG | DDNLMQEINQ | NLAEEAGLNI | THICLPPDSS | EAEIIDEILK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| INEDTRVHGL | ALQISENLFS | NKVLNALKPE | KDVDGVTDIN | LGKLVRGDAH | ECFVSPVAKA | VIELLEKSVG | VNLDGKKILV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VGAHGSLEAA | LQCLFQRKGS | MTMSIQWKTR | QLQSKLHEAD | IVVLGSPKPE | EIPLTWIQPG | TTVLNCSHDF | LSGKVGCGSP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RIHFGGLIEE | DDVILLAAAL | RIQNMVSSGR | RWLREQQHRR | WRLHCLKLQP | LSPVPSDIEI | SRGQTPKAVD | VLAKEIGLLA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DEIEIYGKSK | AKVRLSVLER | LKDQADGKYV | LVAGITPTPL | GEGKSTVTIG | LVQALTAHLN | VNSFACLRQP | SQGPTFGVKG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GAAGGGYAQV | IPMEEFNLHL | TGDIHAITAA | NNLLAAAIDT | RILHENTQTD | KALYNRLVPL | VNGVREFSEI | QLARLKKLGI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NKTDPSTLTE | EEVSKFARLD | IDPSTITWQR | VLDTNDRFLR | KITIGQGNTE | KGHYRQAQFD | IAVASEIMAV | LALTDSLADM |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KARLGRMVVA | SDKSGQPVTA | DDLGVTGALT | VLMKDAIKPN | LMQTLEGTPV | FVHAGPFANI | AHGNSSVLAD | KIALKLVGEE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GFVVTEAGFG | ADIGMEKFFN | IKCRASGLVP | NVVVLVATVR | ALKMHGGGPS | VTAGVPLKKE | YTEENIQLVA | DGCCNLQKQI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QITQLFGVPV | VVALNVFKTD | TRAEIDLVCE | LAKRAGAFDA | VPCYHWSVGG | KGSVDLARAV | REAASKRSRF | QFLYDVQVPI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VDKIRTIAQA | VYGAKDIELS | PEAQAKIDRY | TQQGFGNLPI | CMAKTHLSLS | HQPDKKGVPR | DFILPISDVR | ASIGAGFIYP |
| 890 | 900 | 910 | 920 | | | | |
| LVGTMSTMPG | LPTRPCFYDI | DLDTETEQVK | GLF | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 228 | 1 | 801.7963 | -174.05 | 2 | 32.6 | 23.3 | 2 | 262-274 | R.IQNMVSSGRRWLR.E | |
| 1676 | 1 | 1045.0153 | -29.27 | 2 | 50.7 | 10.9 | 0 | 574-594 | K.SGQPVTADDLGVTGALTVLMK.D | Oxidation: 20 |

# Detailed Protein Report

**Protein 330:** **probable ATP-dependent RNA helicase DDX10 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|13514831 | **Score:** | 34.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 100.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| | | **Sequence Coverage [%]:** | 4.6 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGKTANSPGS | GARPDPVRSF | NRWKKKHSHR | QNKKKQLRKQ | LKKPEWQVER | ESISRLMQNY | EKINVNEITR | FSDFPLSKKT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LKGLQEAQYR | LVTEIQKQTI | GLALQGKDVL | GAAKTGSGKT | LAFLVPVLEA | LYRLQWTSTD | GLGVLIISPT | RELAYQTFEV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LRKVGKNHDF | SAGLIIGGKD | LKHEAERINN | INILVCTPGR | LLQHMDETVS | FHATDLQMLV | LDEADRILDM | GFADTMNAVI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ENLPKKRQTL | LFSATQTKSV | KDLARLSLKN | PEYVWVHEKA | KYSTPATLEQ | NYIVCELQQK | ISVLYSFLRS | HLKKKSIVFF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SSCKEVQYLY | RVFCRLRPGV | SILALHGRQQ | QMRRMEVYNE | FVRKRAAVLF | ATDIAARGLD | FPAVNWVLQF | DCPEDANTYI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HRAGRTARYK | EDGEALLILL | PSEKAMVQQL | LQKKVPVKEI | KINPEKLIDV | QKKLESILAQ | DQDLKERAQR | CFVSYVRSVY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LMKDKEVFDV | SKLPIPEYAL | SLGLAVAPRV | RFLQKMQKQP | TKELVRSQAD | KVIEPRAPSL | TNDEVEEFRA | YFNEKMSILQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KGGKRLEGTE | HRQDNDTGNE | EQEEEEDDEE | EMEEKLAKAK | GSQAPSLPNT | SEAQKIKEVP | TQFLDRDEEE | EDADFLKVKR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HNVFGLDLKD | EKTLQKKEPS | KSSIKKKMTK | VAEAKKVMKR | NFKVNKKITF | TDEGELVQQW | PQMQKSAIKD | AEEDDDTGGI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NLHKAKERLQ | EEDKFDKEEY | RKKIKAKHRE | KRLKEREARR | EANKRQAKAK | DEEEAFLDWS | DDDDDDDDGF | DPSTLPDPDK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| YRSSEDSDSE | DMENKISDTK | KKQGMKKRSN | SEVEDVGPTS | HNRKKARWDT | LEPLDTGLSL | AEDEELVLHL | LRSQS |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2045 | 3 | 599.9307 | -69.34 | 3 | 53.9 | 11.2 | 1 | 1-18 | -.MGKTANSPGSGARPDPVR.S | |
| 2761 | 2 | 713.3401 | -111.86 | 2 | 65.7 | 11.2 | 2 | 638-649 | K.VKRHNVFGLDLK.D | |

# Detailed Protein Report

## Protein 331: laminin subunit beta-2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|119703755 | **Score:** | 34.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 195.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530372442 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: laminin subunit beta-2 isoform X1 [Homo sapiens] |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MELTSRERGR | GQPLPWELRL | GLLLSVLAAT | LAQAPAPDVP | GCSRGSCYPA | TGDLLVGRAD | RLTASSTCGL | NGPQPYCIVS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HLQDEKKCFL | CDSRRPFSAR | DNPHSHRIQN | VVTSFAPQRR | AAWWQSENGI | PAVTIQLDLE | AEFHFTHLIM | TFKTFRPAAM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LVERSADFGR | TWHVYRYFSY | DCGADFPGVP | LAPPRHWDDV | VCESRYSEIE | PSTEGEVIYR | VLDPAIPIPD | PYSSRIQNLL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KITNLRVNLT | RLHTLGDNLL | DPRREIREKY | YYALYELVVR | GNCFCYGHAS | ECAPAPGAPA | HAEGMVHGAC | ICKHNTRGLN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CEQCQDFYRD | LPWRPAEDGH | SHACRKCECH | GHTHSCHFDM | AVYLASGNVS | GGVCDGCQHN | TAGRHCELCR | PFFYRDPTKD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LRDPAVCRSC | DCDPMGSQDG | GRCDSHDDPA | LGLVSGQCRC | KEHVVGTRCQ | QCRDGFFGLS | ISDRLGCRRC | QCNARGTVPG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| STPCDPNSGS | CYCKRLVTGR | GCDRCLPGHW | GLSHDLLGCR | PCDCDVGGAL | DPQCDEGTGQ | CHCRQHMVGR | RCEQVQPGYF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RPFLDHLIWE | AEDTRGQVLD | VVERLVTPGE | TPSWTGSGFV | RLQEGQTLEF | LVASVPKAMD | YDLLLRLEPQ | VPEQWAELEL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IVQRPGPVPA | HSLCGHLVPK | DDRIQGTLQP | HARYLIFPNP | VCLEPGISYK | LHLKLVRTGG | SAQPETPYSG | PGLLIDSLVL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LPRVLVLEMF | SGGDAAALER | QATFERYQCH | EEGLVPSKTS | PSEACAPLLI | SLSTLIYNGA | LPCQCNPQGS | LSSECNPHGG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QCLCKPGVVG | RRCDLCAPGY | YGFGPTGCQA | CQCSHEGALS | SLCEKTSGQC | LCRTGAFGLR | CDRCQRGQWG | FPSCRPCVCN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GHADECNTHT | GACLGCRDHT | GGEHCERCIA | GFHGDPRLPY | GGQCRPCPCP | EGPGSQRHFA | TSCHQDEYSQ | QIVCHCRAGY |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TGLRCEACAP | GHFGDPSRPG | GRCQLCECSG | NIDPMDPDAC | DPHTGQCLRC | LHHTEGPHCA | HCKPGFHGQA | ARQSCHRCTC |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| NLLGTNPQQC | PSPDQCHCDP | SSGQCPCLPN | VQGPSCDRCA | PNFWNLTSGH | GCQPCACHPS | RARGPTCNEF | TGQCHCRAGF |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GGRTCSECQE | LHWGDPGLQC | HACDCDSRGI | DTPQCHRFTG | HCSCRPGVSG | VRCDQCARGF | SGIFPACHPC | HACFGDWDRV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VQDLAARTQR | LEQRAQELQQ | TGVLGAFESS | FWHMQEKLGI | VQGIVGARNT | SAASTAQLVE | ATEELRREIG | EATEHLTQLE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| ADLTDVQDEN | FNANHALSGL | ERDRLALNLT | LRQLDQHLDL | LKHSNFLGAY | DSIRHAHSQS | AEAERRANTS | ALAVPSPVSN |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| SASARHRTEA | LMDAQKEDFN | SKHMANQRAL | GKLSAHTHTL | SLTDINELVC | GAPGDAPCAT | SPCGGAGCRD | EDGQPRCGGL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SCNGAAATAD | LALGRARHTQ | AELQRALAEG | GSILSRVAET | RRQASEAQQR | AQAALDKANA | SRGQVEQANQ | ELQELIQSVK |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| DFLNQEGADP | DSIEMVATRV | LELSIPASAE | QIQHLAGAIA | ERVRSLADVD | AILARTVGDV | RRAEQLLQDA | RRARSWAEDE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KQKAETVQAA | LEEAQRAQGI | AQGAIRGAVA | DTRDTEQTLY | QVQERMAGAE | RALSSAGERA | RQLDALLEAL | KLKRAGNSLA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| ASTAEETAGS | AQGRAQEAEQ | LLRGPLGDQY | QTVKALAERK | AQGVLAAQAR | AEQLRDEARD | LLQAAQDKLQ | RLQELEGTYE |
| 1770 | 1780 | 1790 | 1800 | | | | |
| ENERALESKA | AQLDGLEARM | RSVLQAINLQ | VQIYNTCQ | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2931 | 1 | 1051.5566 | 80.57 | 2 | 65.4 | 10.0 | 0 | 918-937 | R.LPYGGQCRPCPCPEGPGSQR.H | |

# Detailed Protein Report

## Protein 332: sacsin isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|491227401 | **Score:** | 34.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 504.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAPYQGPALY | VYNNAVFTPE | DWHGIQEIAR | SRKKDDPLKV | GRFGIGFNSV | YHITDVPCIF | SGDQIGMLDP | HQTLFGPHES |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GQCWNLKDDS | KEISELSDQF | APFVGIFGST | KETFINGNFP | GTFFRFPLRL | QPSQLSSNLY | NKQKVLELFE | SFRADADTVL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LFLKSVQDVS | LYVREADGTE | KLVFRVTSSE | SKALKHERPN | SIKILGTAIS | NYCKKTPSNN | ITCVTYHVNI | VLEEESTKDA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QKTSWLVCNS | VGGRGISSKL | DSLADELKFV | PIIGIAMPLS | SRDDEAKGAT | SDFSGKAFCF | LPLPPGEESS | TGLPVHISGF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FGLTDNRRSI | KWRELDQWRD | PAALWNEFLV | MNVVPKAYAT | LILDSIKRLE | MEKSSDFPLS | VDVIYKLWPE | ASKVKVHWQP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VLEPLFSELL | QNAVIYSISC | DWVRLEQVYF | SELDENLEYT | KTVLNYLQSS | GKQIAKVPGN | VDAAVQLTAA | SGTTPVRKVT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PAWVRQVLRK | CAHLGCAEEK | LHLLEFVLSD | QAYSELLGLE | LLPLQNGNFV | PFSSSVSDQD | VIYITSAEYP | RSLFPSLEGR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FILDNLKPHL | VAALKEAAQT | RGRPCTQLQL | LNPERFARLI | KEVMNTFWPG | RELIVQWYPF | DENRNHPSVS | WLKMVWKNLY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IHFSEDLTLF | DEMPLIPRTI | LEEGQTCVEL | IRLRIPSLVI | LDDESEAQLP | EFLADIVQKL | GGFVLKKLDA | SIQHPLIKKY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| IHSPLPSAVL | QIMEKMPLQK | LCNQITSLLP | THKDALRKFL | ASLTDSSEKE | KRIIQELAIF | KRINHSSDQG | ISSYTKLKGC |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KVLHHTAKLP | ADLRLSISVI | DSSDEATIRL | ANMLKIEQLK | TTSCLKLVLK | DIENAFYSHE | EVTQLMLWVL | ENLSSLKNEN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PNVLEWLTPL | KFIQISQEQM | VSAGELFDPD | IEVLKDLFCN | EEGTYFPPSV | FTSPDILHSL | RQIGLKNEAS | LKEKDVVQVA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KKIEALQVGA | CPDQDVLLKK | AKTLLLVLNK | NHTLLQSSEG | KMTLKKIKWV | PACKERPPNY | PGSLVWKGDL | CNLCAPPDMC |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| DVGHAILIGS | SLPLVESIHV | NLEKALGIFT | KPSLSAVLKH | FKIVVDWYSS | KTFSDEDYYQ | FQHILLEIYG | FMHDHLNEGK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DSFRALKFPW | VWTGKKFCPL | AQAVIKPIHD | LDLQPYLHNV | PKTMAKFHQL | FKVCGSIEEL | TSDHISMVIQ | KIYLKSDQDL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SEQESKQNLH | LMLNIIRWLY | SNQIPASPNT | PVPIHHSKNP | SKLIMKPIHE | CCYCDIKVDD | LNDLLEDSVE | PIILVHEDIP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| MKTAEWLKVP | CLSTRLINPE | NMGFEQSGQR | EPLTVRIKNI | LEEYPSVSDI | FKELLQNADD | ANATECSFLI | DMRRNMDIRE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| NLLDPGMAAC | HGPALWSFNN | SQFSDSDFVN | ITRLGESLKR | GEVDKVGKFG | LGFNSVYHIT | DIPIIMSREF | MIMFDPNINH |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ISKHIKDKSN | PGIKINWSKQ | QKRLRKFPNQ | FKPFIDVFGC | QLPLTVEAPY | SYNGTLFRLS | FRTQQEAKVS | EVSSTCYNTA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| DIYSLVDEFS | LCGHRLIIFT | QSVKSMYLKY | LKIEETNPSL | AQDTVIIKKK | SCSSKALNTP | VLSVLKEAAK | LMKTCSSSNK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KLPSDEPKSS | CILQITVEEF | HHVFRRIADL | QSPLFRGPDD | DPAALFEMAK | SGQSKKPSDE | LSQKTVECTT | WLLCTCMDTG |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| EALKFSLSES | GRRLGLVPCG | AVGVQLSEIQ | DQKWTVKPHI | GEVFCYLPLR | IKTGLPVHIN | GCFAVTSNRK | EIWKTDTKGR |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| WNTTFMRHVI | VKAYLQVLSV | LRDLATSGEL | MDYTYYAVWP | DPDLVHDDFS | VICQGFYEDI | AHGKGKELTK | VFSDGSTWVS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| MKNVRFLDDS | ILKRRDVGSA | AFKIFLKYLK | KTGSKNLCAV | ELPSSVKLGF | EEAGCKQILL | ENTFSEKQFF | SEVFFPNIQE |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| IEAELRDPLM | IFVLNEKVDE | FSGVLRVTPC | IPCSLEGHPL | VLPSRLIHPE | GRVAKLFDIK | DGRFPYGSTQ | DYLNPIILIK |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| LVQLGMAKDD | ILWDDMLERA | VSVAEINKSD | HVAACLRSSI | LLSLIDEKLK | IRDPRAKDFA | AKYQTIRFLP | FLTKPAGFSL |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| DWKGNSFKPE | TMFAATDLYT | AEHQDIVCLL | QPILNENSHS | FRGCGSVSLA | VKEFLGLLKK | PTVDLVINQL | KEVAKSVDDG |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1798 | 1 | 916.4469 | -78.82 | 2 | 50.8 | 10.5 | 2 | 1570-1586 | K.KSCSSKALNTPVLSVLK.E | Carbamidomethyl: 3 |
| 362 | 1 | 529.2876 | -26.74 | 3 | 34.5 | 12.9 | 2 | 4347-4361 | R.GKSDKDVKPTALAQK.I | |

# Detailed Protein Report

## Protein 333: leucine-, glutamate- and lysine-rich protein 1 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|262263420 | **Score:** | 34.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 81.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.5 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530374591 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: leucine-, glutamate- and lysine-rich protein 1 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDHHIPMHAL | PEEIQKMLPE | EKVCKYCGVS | YLILHEFKAM | EEKVKAMEKE | MKFYQGSVDR | EKRLQEKLHS | LSQELEQYKI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DNKSKTERIY | DVGMQLKSQQ | NEFQKVKKQL | SHLQDELKIK | YRQSYIFSQR | LSEYKYFWNK | TLSLLTFTKR | ELTSIKNEVY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DNYQNWTSLK | GAVFLQIKSI | SETALTEIDI | LNKSLTVSQR | NKVCLEKEMK | NLKLLSDAAI | LRSQQIRTSR | QQEVNLQTRC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YDLQKEVLDL | QCLVEALGLK | LQKAVTEMDN | YKEMLMNKSN | EADDCQRELK | KLKFESIISE | SQHTMLLKEK | EDSLMTCQQI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YKALQEELTV | KEKQEEDIKR | RINLAENELE | ITKTLLNQTR | EEVLTLKNER | ELMLISHQKS | IEQLQETLRQ | KLLSDDNWKE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KIEAELAKER | AQHLVEFEEQ | ALLFKEETKL | QLDIEKEKHQ | DVIQKYKKEQ | EELQMKISDL | ITGATRDLRQ | EVTTLKEKLH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KSHIRYTEES | NSKEKEIENL | KNLVAEFESR | LKKEIDSNDS | VSENLRKEME | QKSDELKRVM | LAQTQLIEQF | NQSQEENTFL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QETVRRECEE | RFELTEALSQ | AREQLLELSK | LRGSLPFSPC | SLSKGSLTSP | AAAVSNHGER | SLARLNSEKG | IQIPNLRGVS |
| 650 | 660 | 670 | 680 | 690 | 700 | | |
| KPTTFPTSDK | PKRVRSGVPI | LPQPHPPRGG | ASSANETRQR | LAAILRRRRS | QQ | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1884 | 1 | 734.7526 | -169.10 | 2 | 53.9 | 10.2 | 1 | 86-97 | K.TERIYDVGMQLK.S | Oxidation: 9 |
| 538 | 1 | 501.6964 | -160.45 | 2 | 36.7 | 11.2 | 1 | 494-501 | K.EKEIENLK.N | |

# Detailed Protein Report

## Protein 334: dynein heavy chain domain-containing protein 1 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|222144249 | **Score:** | 34.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 533.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 1.73 | **CV:** 0.00 % | **No. of Peptides:** 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVPEERRVGL | SSDETSSDSL | KSWHSICVLD | SKEQPLACQQ | KQRQFVKPVT | ESEQPTVLEL | LLAELRTLFS | AVLQDSSPAA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| WRYLHAVLGL | LPPYRELLVG | HLDLLPFLEQ | LYCWAPWVQT | HLHLDLLGAI | VQAFPPDSSL | LDSASHADCC | PQKRRLHHRP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PCPACPFVQA | QWSRQQVKEE | LATWLRPLTL | PELQRCLGIV | GAQVALEEAV | WLDGLSLLPL | ALAADIPVRY | ESSDTDNAEV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EPVGRKETRS | QLDYEVPREK | AFQKSSTGFS | PETSFLDSQV | MTALKMERYL | KKIHFLYLNV | APSRYFRPYS | LMVVPPDKVN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PEHYIFSPFG | ILHVHPVEGS | ETMTLGTWHH | HCVLWQQLQF | IPFFKYCLLR | KSFTCWKKNV | RLQGLHRLQK | FLENHLLLAV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PHFGAGLLHI | SRLLQELHSV | SWLPQELDRC | YELLDLQTAL | AEEKHKALRL | LHRCLNLCTS | ILRLVHEDTY | HMQQCLQERV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QNCDRIRTGQ | GSIYLQRVQH | KQLEQKLKQA | EAWWLQLGKF | ARLVDYMICQ | SLISVLEEQI | TSFVANILQA | PRQKPFLSSQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LVFDDHGQLS | HVPCVENMIQ | TLTGGLQSVK | TSALQVVQSA | DLKTSSDSLY | SEEEDEEEDS | KDEFLMPKFQ | GQPSDAVSIF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CGPNVGLVWP | WKSHPIAGIL | EVRGCRLRGQ | YFPHNYKQLE | EDLDNNPKIQ | QALNIQQVLL | EGVLCKVQEF | CREHHWITGI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YEFLQSWGPQ | KLEDMRGGPI | KNYVTLVSRL | NVWQARVSSM | PIELLTKGGL | LLLSCHDVQA | EMESKLNSIR | KDILAHVQNE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| CWNLSQQLMT | ELTDFMHIFR | TINSDIHAIA | QCTQKLNEAN | EQYVELEERM | EYVRALHELI | RNHFSLFSAE | NEALDISVRR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QFGESPIPPC | PPPPQPHLLH | CPLLAPQLLD | MWEAFQFEKS | QASEFLLSKR | HAIMPKLQQL | MAAALAELEG | LLAKALSGPF |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| MDPTQDQRST | EHQLVSLERQ | FQNTVSDLSE | LHHAYAIFTE | DETPVPLPIC | GTRPIVQQQR | IWHLYRVISE | NISEWKCMAF |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AKFSPAMAQE | KTEGWLTEAA | RMSTTLELHS | PVLQHCMRIL | GEFRSYLPLL | TKLGSLHPQS | LNCQCLLRAL | GLGSLQTIEL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LTLGQLLTYP | LLEFADRINQ | VWQNENERIH | AQETIRRLQR | YWEARQLRLL | NFILHVPYEP | PASERSKRQV | LRSPQWEVVD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KDSGTFILSD | YSNLQDSIQE | SLQVLSKILA | IEKSGDLNKI | ALEWVAIMHG | LGALLEVWLT | FQQKWIFLNK | VLHEMKIQFP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| NADLNSRFKV | MDDQYRTLMR | ISVADPMVLS | LVVPSAERSP | YFQGQQLQQL | LQAGSVELEG | IIMSLESVLY | GVCAHFPRLF |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| FLSDSELVAL | LAARLESCEA | QLWVRRCFPH | VHAVSFRSCP | TGEKNTDDWE | SSPNTQTQVE | ALAVLGAGGE | EVKLQGPLPL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| HPDLPKWLAS | LEKCLRLALV | HMLQGCVAAR | LARGPSLGEA | LKQLPKQNKL | YLQLYVQHWI | DLVQAFPWQC | VLVAEEVVWR |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| AEMEEALLEW | GTLAMVSMHM | RKLEVLVNFM | RAQRASQGGQ | SLPSVRQTSL | LSALLVMAVT | HRDIAQLLEQ | HQVSDLTDFH |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| WVRQLKYHLG | SPHIIPKSPL | QSLKTIASSE | PSLSPAACWI | DVLGRSFLYN | YEYLGPRLGP | LPSLLPERPA | LVLLLALEEV |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| ACGTVLGPNG | VGKRAIVNSL | AQALGRQLVM | LPCSPQIEAQ | CLSNYLNGAL | QGGAWLLLEK | VHQLPPGLLS | ALGQRLGELH |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| HLYAPLYQEA | SRNTSTIDPT | QPQLLGSSFF | EKHHVSVRLG | YGCLLVLRAL | SSAVPANLHL | LLRPVALALP | DLRQVAELTL |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| LGAGMRDAFQ | MATRLSKFFS | LERELVSGPL | PCRLPLLKQI | LEDTIRTLNV | TKEEPKCQKP | RSLAAIEEAA | LLRSPLFSIL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| NGLHLHNLRG | LLCALFPSAS | QVLAEPMTYK | LMKPLVVEEL | QQVGLDPSPD | ILGSLEQLSQ | ALSRASGILL | LGPAGSGKTT |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| CWHSLFKIQN | RLAAMEDTST | QGCQPVEITH | LYPSGLSPQE | FLGWLEGSCW | HHGIFPKVLR | AAGQCNNMGQ | KRQTEESIGI |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| QHWIICDGAS | NGAWLDSITC | LLSELPQLSL | PSGQQIARPP | GTFLLMEVAD | TTGISPTVVG | CCALVWCGGE | QTWQCILSAL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2480 | 3 | 625.3103 | -20.67 | 2 | 61.5 | 13.4 | 0 | 454-463 | R.CLNLCTSILR.L | Carbamidomethyl: 1, 5 | QU:MU 1.73 |

# Detailed Protein Report

## Protein 335: R-spondin-1 isoform 3 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|339276103 | **Score:** | 34.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 26.5 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRLGLCVVAL | VLSWTHLTIS | SRGIKGKRQR | RISAEGSQAC | AKGCELCSEV | NGCLKCSPKL | FILLERNDIR | QVGVCLPSCP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PGYFDARNPD | MNKCIKCKIE | HCEACFSHNF | CTKCKEGLYL | HKGRCYPACP | EGSSAANGTM | ECSSPGQKRR | KGGQGRRENA |
| 170 | 180 | 190 | 200 | 210 | | | |
| NRNLARKESK | EAGAGSRRRK | GQQQQQQQGT | VGPLTSAGPA | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2673 | 1 | 913.9847 | 93.98 | 2 | 63.5 | 12.9 | 1 | 43-59 | K.GCELCSEVNGCLKCSPK.L | Carbamidomethyl: 2 |
| 1684 | 1 | 1273.9976 | -19.18 | 2 | 50.8 | 10.8 | 1 | 125-149 | R.CYPACPEGSSAANGTMECSSPGQKR.R | Oxidation: 16 |

# Detailed Protein Report

## Protein 336: myotubularin-related protein 8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21361759 | **Score:** | 34.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 78.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDHITVPKVE | NVKLVDRYVS | KKPANGILYL | TATHLIYVEA | SGAARKETWI | ALHHIATVEK | LPITSLGCPL | TLRCKNFRVA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HFVLDSDLVC | HEVYISLLKL | SQPALPEDLY | AFSYNPKSSK | EMRESGWKLI | DPISDFGRMG | IPNRNWTITD | ANRNYEICST |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YPPEIVVPKS | VTLGTVVGSS | KFRSKERVPV | LSYLYKENNA | AICRCSQPLS | GFYTRCVDDE | LLLEAISQTN | PGSQFMYVVD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TRPKLNAMAN | RAAGKGYENE | DNYANIRFRF | MGIENIHVMR | SSLQKLLEVC | ELKTPTMSEF | LSGLESSGWL | RHIKAIMDAG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IFITKAVKVE | KASVLVHCSD | GWDRTAQVCS | VASILLDPFY | RTFKGLMILI | EKEWISMGHK | FSQRCGHLDG | DSKEVSPIFT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QFLDCIWQLM | EQFPCAFEFN | ENFLLEIHDH | VFSCQFGNFL | GNCQKDREDL | RVYEKTHSVW | PFLVQRKPDF | RNPLYKGFTM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YGVLNPSTVP | YNIQFWCGMY | NRFDKGLQPK | QSMLESLLEI | KKQRAMLETD | VHELEKKLKV | RDEPPEEICT | CSQLGNILSQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HLGSPLTNPL | GFMGINGDLN | TLMENGTLSR | EGGLRAQMDQ | VKSQGADLHH | NCCEIVGSLR | AINISGDVGI | SEAMGISGDM |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | |
| CTFEATGFSK | DLGICGAMDI | SEATGISGNL | GISEARGFSG | DMGILGDTGI | SKASTKEADY | SKHQ | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1315 | 8 | 956.5835 | 100.93 | 1 | 46.6 | 16.9 | 0 | 1-8 | -.MDHITVPK.V | Oxidation: 1 |

# Detailed Protein Report

## Protein 337: PREDICTED: NEDD8 ultimate buster 1 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530387034 | **Score:** | 33.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 67.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKTNGGRCRI | RALCWSRREW | RGAGMAQKKY | LQAKLTQFLR | EDRIQLWKPP | YTDENKKVGL | ALKDLAKQYS | DRLECCENEV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EKVIEEIRCK | AIERGTGNDN | YRTTGIATIE | VFLPPRLKKD | RKNLLETRLH | ITGRELRSKI | AETFGLQENY | IKIVINKKQL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QLGKTLEEQG | VAHNVKAMVL | ELKQSEEDAR | KNFQLEEEEQ | NEAKLKEKQI | QRTKRGLEIL | AKRAAETVVD | PEMTPYLDIA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NQTGRSIRIP | PSERKALMLA | MGYHEKGRAF | LKRKEYGIAL | PCLLDADKYF | CECCRELLDT | VDNYAVLQLD | IVWCYFRLEQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LECLDDAEKK | LNLAQKCFKN | CYGENHQRLV | HIKGNCGKEK | VLFLRLYLLQ | GIRNYHSGND | VEAYEYLNKA | RQLFKELYID |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PSKVDNLLQL | GFTAQEARLG | LRACDGNVDH | AATHITNRRE | ILLSNPQMWW | LNDSNPETDN | RQESPSQENI | DRLVYMGFDA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LVAEAALRVF | RGNVQLAAQT | LAHNGGSLPP | ELPLSPEDSL | SPPATSPSDS | AGTSSASTDE | DMETEAVNEI | LEDIPEHEED |
| 570 | 580 | 590 | 600 | | | | |
| YLDSTLEDEE | IIIAEYLSYV | ENRKSATKKN | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2092 | 1 | 625.2489 | -174.33 | 2 | 54.5 | 12.9 | 2 | 330-339 | K.KLNLAQKCFK.N | Carbamidomethyl: 8 |

# Detailed Protein Report

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## Protein 338: EH domain-binding protein 1 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|217330572 | **Score:** | 33.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 132.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.96 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.29 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|217330574 | refseq_human (refseq_human_20140103.fasta) | EH domain-binding protein 1 isoform 3 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MASVWKRLQR VGKHASKFQF VASYQELMVE CTKKWQPDKL VVVWTRRSRR KSSKAHSWQP GIKNPYRGVV VWPVPENIEI
        90        100        110        120        130        140        150        160
TVTLFKDPHA EEFEDKEWTF VIENESPSGR RKALATSSIN MKQYASPMPT QTDVKLKFKP LSKKVVSAAL QFSLSCIFLR
       170        180        190        200        210        220        230        240
EGKATDEDMQ SLASLMSMKQ ADIGNLDDFE EDNEDDDENR VNQEEKAAKI TELINKLNFL DEAEKDLATV NSNPFDDPDA
       250        260        270        280        290        300        310        320
AELNPFGDPD SEEPITETAS PRKTEDSFYN NSYNPFKEVQ TPQYLNPFDE PEAFVTIKDS PPQSTKRKNI RPVDMSKYLY
       330        340        350        360        370        380        390        400
ADSSKTEEEE LDESNPFYEP KSTPPPNNLV NPVQELETER RVKRKAPAPP VLSPKTGVLN ENTVSAGKDL STSPKPSPIP
       410        420        430        440        450        460        470        480
SPVLGRKPNA SQSLLVWCKE VTKNYRGVKI TNFTTSWRNG LSFCAILHHF RPDLIDYKSL NPQDIKENNK KAYDGFASIG
       490        500        510        520        530        540        550        560
ISRLLEPSDM VLLAIPDKLT VMTYLYQIRA HFSGQELNVV QIEENSSKST YKVGNYETDT NSSVDQEKFY AELSDLKREP
       570        580        590        600        610        620        630        640
ELQQPISGAV DFLSQDDSVF VNDSGVGESE SEHQTPDDHL SPSTASPYCR RTKSDTEPQK SQQSSGRTSG SDDPGICSNT
       650        660        670        680        690        700        710        720
DSTQAQVLLG KKRLLKAETL ELSDLYVSDK KKDMSPPFIC EETDEQKLQT LDIGSNLEKE KLENSRSLEC RSDPESPIKK
       730        740        750        760        770        780        790        800
TSLSPTSKLG YSYSRDLDLA KKKHASLRQT ESDPDADRTT LNHADHSSKI VQHRLLSRQE ELKERARVLL EQARRDAALK
       810        820        830        840        850        860        870        880
AGNKHNTNTA TPFCNRQLSD QQDEERRRQL RERARQLIAE ARSGVKMSEL PSYGEMAAEK LKERSKASGE QNSKLVDLKL
       890        900        910        920        930        940        950        960
KKLLEVQPQV ANSPSSAAQK AVTESSEQDM KSGTEDLRTE RLQKTTERFR NPVVFSKDST VRKTQLQSFS QYIENRPEMK
       970        980        990       1000       1010       1020       1030       1040
RQRSIQEDTK KGNEEKAAIT ETQRKPSEDE VLNKGFKDTS QYVVGELAAL ENEQKQIDTR AALVEKRLRY LMDTGRNTEE
      1050       1060       1070       1080       1090       1100       1110       1120
EEAMMQEWFM LVNKKNALIR RMNQLSLLEK EHDLERRYEL LNRELRAMLA IEDWQKTEAQ KRREQLLLDE LVALVNKRDA
      1130       1140       1150       1160       1170
LVRDLDAQEK QAEEEDEHLE RTLEQNKGKM AKKEEKCVLQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 804 | 1 | 660.3468 | -45.46 | 2 | 38.5 | 12.3 | 2 | 111-122 | R.RKALATSSINMK.Q | | |
| 192 | 2 | 688.2999 | -17.82 | 2 | 32.1 | 10.3 | 0 | 805-816 | K.HNTNTATPFCNR.Q | | WUP:QUP 1.29<br>QU:MU 0.96 |

# Detailed Protein Report

## Protein 339: PREDICTED: uncharacterized protein C1orf159 isoform X8 [Homo sapiens]

**Accession:** gi|578799328

**Database:** refseq_human(refseq_human_20140103.fasta)

**Database Date:** 2015-11-30

**Score:** 33.9

**MW [kDa]:** 30.9

**pI:** 11.7

**Sequence Coverage [%]:** 8.9

**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSVVPILEGQ | PHSISLAPHA | PPCGRLCASA | PGMALRHLAL | LAGLLVGVAS | KSMENTAQLP | ECCVDVVGVN | ASCPGASLCG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PGCYRRWNAD | GSASCVRCGN | GTLPAYNGSE | CRSFAGPGAP | FPMNRSSGTP | GRPHPGAPRV | AASLFLGTFF | ISSGLILSVA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GFFYLKRSSK | LPRACYRRNK | APALQPGEAA | AMIPPPQSSG | PTLTSPVSDP | FQYGSRATSG | GSGPWTGPRI | PLPSRGRPVS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | |
| AMSDLEAETT | PRTWRQGPGG | RPLGGNQHKV | LASPGARDSP | GHSLGSESLR | LPATDAKGSR | AA | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2555 | 1 | 701.8644 | -5.90 | 2 | 61.9 | 10.1 | 0 | 256-269 | R.QGPGGRPLGGNQHK.V | |

# Detailed Protein Report

## Protein 340: metabotropic glutamate receptor 4 isoform 5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|378548216 | **Score:** | 33.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 83.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| | | **Sequence Coverage [%]:** | 6.3 |
| | | **No. of unique Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MSCKIPQISY ASTAPDLSDN SRYDFFSRVV PSDTYQAQAM VDIVRALKWN YVSTVASEGS YGESGVEAFI QKSREDGGVC
        90        100        110        120        130        140        150        160
IAQSVKIPRE PKAGEFDKII RRLLETSNAR AVIIFANEDD IRRVLEAARR ANQTGHFFWM GSDSWGSKIA PVLHLEEVAE
       170        180        190        200        210        220        230        240
GAVTILPKRM SVRGFDRYFS SRTLDNNRRN IWFAEFWEDN FHCKLSRHAL KKGSHVKKCT NRERIGQDSA YEQEGKVQFV
       250        260        270        280        290        300        310        320
IDAVYAMGHA LHAMHRDLCP GRVGLCPRMD PVDGTQLLKY IRNVNFSGIA GNPVTFNENG DAPGRYDIYQ YQLRNDSAEY
       330        340        350        360        370        380        390        400
KVIGSWTDHL HLRIERMHWP GSGQQLPRSI CSLPCQPGER KKTVKGMPCC WHCEPCTGYQ YQVDRYTCKT CPYDMRPTEN
       410        420        430        440        450        460        470        480
RTGCRPIPII KLEWGSPWAV LPLFLAVVGI AATLFVVITF VRYNDTPIVK ASGRELSYVL LAGIFLCYAT TFLMIAEPDL
       490        500        510        520        530        540        550        560
GTCSLRRIFL GLGMSISYAA LLTKTNRIYR IFEQGKRSVS APRFISPASQ LAITFSLISL QLLGICVWFV VDPSHSVVDF
       570        580        590        600        610        620        630        640
QDQRTLDPRF ARGVLKCDIS DLSLICLLGY SMLLMVTCTV YAIKTRGVPE TFNEAKPIGF TMYTTCIVWL AFIPIFFGTS
       650        660        670        680        690        700        710        720
QSADKLYIQT TTLTVSVSLS ASVSLGMLYM PKVYIILFHP EQNVPKRKRS LKAVVTAATM SNKFTQKGNF RPNGEAKSEL
       730        740        750
CENLEAPALA TKQTYVTYTN HAI
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2591 | 1 | 701.8584 | -42.25 | 2 | 62.4 | 10.3 | 2 | 90-101 | R.EPKAGEFDKIIR.R | |
| 1390 | 1 | 977.5200 | -44.32 | 2 | 47.5 | 12.4 | 1 | 487-504 | R.RIFLGLGMSISYAALLTK.T | |

# Detailed Protein Report

## Protein 341: PREDICTED: nuclear pore complex protein Nup214 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530427224 | **Score:** | 33.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 209.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 2 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRGQLRAAGA | EGRKFAVERP | GFRGQGRGRQ | RWLLRHTEGG | AMGDEMDAMI | PEREMKDFQF | RALKKVRIFD | SPEELPKERS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SLLAVSNKYG | LVFAGGASGL | QIFPTKNLLI | QNKPGDDPNK | IVDKVQGLLV | PMKFPIHHLA | LSCDNLTLSA | CMMSSEYGSI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IAFFDVRTFS | NEAKQQKRPF | AYHKLLKDAG | GMVIDMKWNP | TVPSMVAVCL | ADGSIAVLQV | TETVKVCATL | PSTVAVTSVC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| WSPKGKQLAV | GKQNGTVVQY | LPTLQEKKVI | PCPPFYESDH | PVRVLDVLWI | GTYVFAIVYA | AADGTLETSP | DVVMALLPKK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EEKHPEIFVN | FMEPCYGSCT | ERQHHYYLSY | IEEWDLVLAA | SAASTEVSIL | ARQSDQINWE | SWLLEDSSRA | ELPVTDKSDD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SLPMGVVVDY | TNQVEITISD | EKTLPPAPVL | MLLSTDGVLC | PFYMINQNPG | VKSLIKTPER | LSLEGERQPK | SPASLAPTPA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ASPVAPSAAS | FSFGSSGFKP | TLESTPVPSV | SAPNIAMKPS | FPPSTSAVKV | NLSEKFTAAA | TSTPVSSSQS | APPMSPFSSA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SKPAASGPLS | HPTPLSAPPS | SVPLKSSVLP | SPSAGRSAQG | SSSPVPSMVQ | KSPRITPPAA | KPGSPQAKSL | QPAVAEKQGH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QWKDSDPVMA | GIGEEIAHFQ | KELEELKART | SKACFQVGTS | EEMKMLRTES | DDLHTFLLEI | KETTESLHGD | ISSLKTTLLE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GFAGVEEARE | QNERNRDSGY | LHLLYKRPLD | PKSEAQLQEI | RRLHQYVKFA | VQDVNDVLDL | EWDQHLEQKK | KQRHLLVPER |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ETLFNTLANN | REIINQQRKR | LNHLVDSLQQ | LRLYKQTSLW | SLSSAVPSQS | SIHSFDSDLE | SLCNALLKTT | IESHTKSLPK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VPAKLSPMKQ | AQLRNFLAKR | KTPPVRSTAP | ASLSRSAFLS | QRYYEDLDEV | SSTSSVSQSL | ESEDARTSCK | DDEAVVQAPR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| HAPVVRTPSI | QPSLLPHAAP | FAKSHLVHGS | SPGVMGTSVA | TSASKIIPQG | ADSTMLATKT | VKHGAPSPSH | PISAPQAAAA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AALRRQMASQ | APAVNTLTES | TLKNVPQVVN | VQELKNNPAT | PSTAMGSSVP | YSTAKTPHPV | LTPVAANQAK | QGSLINSLKP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SGPTPASGQL | SSGDKASGTA | KIETAVTSTP | SASGQFSKPF | SFSPSGTGFN | FGIITPTPSS | NFTAAQGATP | STKESSQPDA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| FSSGGGSKPS | YEAIPESSPP | SGITSASNTT | PGEPAASSSR | PVAPSGTALS | TTSSKLETPP | SKLGELLFPS | SLAGETLGSF |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SGLRVGQADD | STKPTNKASS | TSLTSTQPTK | TSGVPSGFNF | TAPPVLGKHT | EPPVTSSATT | TSVAPPAATS | TSSTAVFGSL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PVTSAGSSGV | ISFGGTSLSA | GKTSFSFGSQ | QTNSTVPPSA | PPPTTAATPL | PTSFPTLSFG | SLLSSATTPS | LPMSAGRSTE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EATSSALPEK | PGDSEVSASA | ASLLEEQQSA | QLPQAPPQTS | DSVKKEPVLA | QPAVSNSGTA | ASSTSLVALS | AEATPATTGV |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PDARTEAVPP | ASSFSVPGQT | AVTAAAISSA | GPVAVETSST | PIASSTTSIV | APGPSAEAAA | FGTVTSGSSV | FAQPPAASSS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| SAFNQLTNNT | ATAPSATPVF | GQVAASTAPS | LFGQQTGSTA | STAAATPQVS | SSGFSSPAFG | TTAPGVFGQT | TFGQASVFGQ |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| SASSAASVFS | FSQPGFSSVP | AFGQPASSTP | TSTSGSVFGA | ASSTSSSSSF | SFGQSSPNTG | GGLFGQSNAP | AFGQSPGFGQ |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| GGSVFGGTSA | ATTTAATSGF | SFCQASGFGS | SNTGSVFGQA | ASTGGIVFGQ | QSSSSSGSVF | GSGNTGRGGG | FFSGLGGKPS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| QDAANKNPFS | SASGGFGSTA | TSNTSNLFGN | SGAKTFGGFA | SSSFGEQKPT | GTFSSGGGSV | ASQGFGFSSP | NKTGGFGAAP |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| VFGSPPTFGG | SPGFGGVPAF | GSAPAFTSPL | GSTGGKVFGE | GTAAASAGGF | GFGSSSNTTS | FGTLASQNAP | TFGSLSQQTS |
| 2010 | 2020 | 2030 | 2040 | | | | |
| GFGTQSSGFS | GFGSGTGGFS | FGSNNSSVQG | FGGWRS | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2741 | 1 | 715.3112 | -107.27 | 2 | 62.7 | 17.4 | 1 | 66-77 | K.VRIFDSPEELPK.E | |
| 1945 | 4 | 1023.3932 | -98.93 | 2 | 54.7 | 16.5 | 2 | 670-687 | R.TSKACFQVGTSEEMKMLR.T | |

# Detailed Protein Report

**Protein 342:** **PREDICTED: leucine-rich repeat serine/threonine-protein kinase 2 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530399725 | **Score:** | 33.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 285.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.46 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.75 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASGSCQGCE | EDEETLKKLI | VRLNNVQEGK | QIETLVQILE | DLLVFTYSER | ASKLFQGKNI | HVPLLIVLDS | YMRVASVQQV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GWSLLCKLIE | VCPGTMQSLM | GPQDVGNDWE | VLGVHQLILK | MLTVHNASVN | LSVIGLKTLD | LLLTSGKITL | LILDEESDIF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MLIFDAMHSF | PANDEVQKLG | CKALHVLFER | VSEEQLTEFV | ENKDYMILLS | ALTNFKDEEE | IVLHVLHCLH | SLAIPCNNVE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VLMSGNVRCY | NIVVEAMKAF | PMSERIQEVS | CCLLHRLTLG | NFFNILVLNE | VHEFVVKAVQ | QYPENAALQI | SALSCLALLT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ETIFLNQDLE | EKNENQENDD | EGEEDKLFWL | EACYKALTWH | RKNKHVQEAA | CWALNNLLMY | QNSLHEKIGD | EDGHFPAHRE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VMLSMLMHSS | SKEVFQASAN | ALSTLLEQNV | NFRKILLSKG | IHLNVLELMQ | KHIHSPEVAE | SGCKMLNHLF | EGSNTSLDIM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AAVVPKILTV | MKRHETSLPV | QLEALRAILH | FIVPGMPEES | REDTEFHHKL | NMVKKQCFKN | DIHKLVLAAL | NRFIGNPGIQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KCGLKVISSI | VHFPDALEML | SLEGAMDSVL | HTLQMYPDDQ | EIQCLGLSLI | GYLITKKNVF | IGTGHLLAKI | LVSSLYRFKD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VAEIQTKGFQ | TILAILKLSA | SFSKLLVHHS | FDLVIFHQMS | SNIMEQKDQQ | FLNLCCKCFA | KVAMDDYLKN | VMLERACDQN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NSIMVECLLL | LGADANQAKE | GSSLICQVCE | KESSPKLVEL | LLNSGSREQD | VRKALTISIG | KGDSQIISLL | LRRLALDVAN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NSICLGGFCI | GKVEPSWLGP | LFPDKTSNLR | KQTNIASTLA | RMVIRYQMKS | AVEEGTASGS | DGNFSEDVLS | KFDEWTFIPD |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SSMDSVFAQS | DDLDSEGSEG | SFLVKKKSNS | ISVGEFYRDA | VLQRCSPNLQ | RHSNSLGPIF | DHEDLLKRKR | KILSSDDSLR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SSKLQSHMRH | SDSISSLASE | REYITSLDLS | ANELRDIDAL | SQKCCISVHL | EHLEKLELHQ | NALTSFPQQL | CETLKSLTHL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| DLHSNKFTSF | PSYLLKMSCI | ANLDVSRNDI | GPSVVLDPTV | KCPTLKQFNL | SYNQLSFVPE | NLTDVVEKLE | QLILEGNKIS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GICSPLRLKE | LKILNLSKNH | ISSLSENFLE | ACPKVESFSA | RMNFLAAMPF | LPPSMTILKL | SQNKFSCIPE | AILNLPHLRS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LDMSSNDIQY | LPGPAHWKSL | NLRELLFSHN | QISILDLSEK | AYLWSRVEKL | HLSHNKLKEI | PPEIGCLENL | TSLDVSYNLE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LRSFPNEMGK | LSKIWDLPLD | ELHLNFDFKH | IGCKAKDIIR | FLQQRLKKAV | PYNRMKLMIV | GNTGSGKTTL | LQQLMKTKKS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| DLGMQSATVG | IDVKDWPIQI | RDKRKRDLVL | NVWDFAGREE | FYSTHPHFMT | QRALYLAVYD | LSKGQAEVDA | MKPWLFNIKA |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| RASSSPVILV | GTHLDVSDEK | QRKACMSKIT | KELLNKRGFP | AIRDYHFVNA | TEESDALAKL | RKTIINESLN | FKIRDQLVVG |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| QLIPDCYVEL | EKIILSERKN | VPIEFPVIDR | KRLLQLVREN | QLQLDENELP | HAVHFLNESG | VLLHFQDPAL | QLSDLYFVEP |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KWLCKIMAQI | LTVKVEGCPK | HPKGIISRRD | VEKFLSKKRK | FPKNYMSQYF | KLLEKFQIAL | PIGEEYLLVP | SSLSDHRPVI |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| ELPHCENSEI | IIRLYEMPYF | PMGFWSRLIN | RLLEISPYML | SGRERALRPN | RMYWRQGIYL | NWSPEAYCLV | GSEVLDNHPE |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SFLKITVPSC | RKGCILLGQV | VDHIDSLMEE | WFPGLLEIDI | CGEGETLLKK | WALYSFNDGE | EHQKILLDDL | MKKAEEGDLL |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| VNPDQPRLTI | PISQIAPDLI | LADLPRNIML | NNDELEFEQA | PEFLLGDGSF | GSVYRAAYEG | EEVAVKIFNK | HTSLRLLRQE |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LVVLCHLHHP | SLISLLAAGI | RPRMLVMELA | SKGSLDRLLQ | QDKASLTRTL | QHRIALHVAD | GLRYLHSAMI | IYRDLKPHNV |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| LLFTLYPNAA | IIAKIADYGI | AQYCCRMGIK | TSEGTPGFRA | PEVARGNVIY | NQQADVYSFG | LLLYDILTTG | GRIVEGLKFP |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| NEFDELEIQG | KLPDPVKEYG | CAPWPMVEKL | IKQCLKENPQ | ERPTSAQVFD | ILNSAELVCL | TRRILLPKNV | IVECMVATHH |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 394 | 1 | 591.8037 | -59.20 | 2 | 34.9 | 10.0 | 1 | 1964-1973 | K.ASLTRTLQHR.I | | QU:MU 0.46<br>WUP:QUP 1.75 |
| 1730 | 1 | 796.0646 | -20.88 | 3 | 51.4 | 11.0 | 1 | 2457-2477 | R.VMMTAQLGSLKNVMLVLGYNR.K | Oxidation: 2, 3, 14 | |

# Detailed Protein Report

**Protein 343:** **PREDICTED: zinc finger protein 708 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578833563 | **Score:** | 33.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***QU:MU*** **Median:** 2.98 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MKRHEMAAKP PAMCSHFAKD LRPEQYIKNS FQQVILRRYG KCGYQKGCKS VDEHKLHKGG HKGLNRCVTT TQSKIVQCDK

        90        100        110        120        130        140        150        160
YVKVFHKYSN AKRHKIRHTG KNPFKCKECG KSFCMLSQLT QHEIIHTGEK PYKCEECGKA FKKSSNLTNH KIIHTGEKPY

       170        180        190        200        210        220        230        240
KCEECGKAFN QSSTLTRHKI IHTGEKLYKC EECGKAFNRS SNLTKHKIVH TGEKPYKCEE CGKAFKQSSN LTNHKKIHTG

       250        260        270        280        290        300        310        320
EKPYKCGECG KAFTLSSHLT THKRIHTGEK PYKCEECGKA FSVFSTLTKH KIIHTEEKPY KCEECGKAFN RSSHLTNHKV

       330        340        350        360        370        380        390        400
IHTGEKPYKC EECGKAFTKS STLTYHKVIH TGKKPYKCEE CGKAFSIFSI LTKHKVIHTE DKPYKCEECG KTFNYSSNFT

       410        420        430        440        450        460        470        480
NHKKIHTGEK PYKCEECGKS FILSSHLTTH KIIHTGEKPY KCKECGKAFN QSSTLMKHKI IHTGEKPYKC EECGKAFNQS

       490        500
PNLTKHKRIH TKEKPYKCK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 252 | 1 | 605.6643 | -205.83 | 2 | 32.9 | 12.7 | 2 | 102-111 | K.NPFKCKECGK.S | Carbamidomethyl: 8 | QU:MU | 2.98 |
| 1258 | 2 | 586.7739 | 28.23 | 2 | 45.9 | 20.9 | 1 | 330-339 | K.CEECGKAFTK.S | Carbamidomethyl: 4 | | |

# Detailed Protein Report

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**Protein 344:** **PREDICTED: ras-specific guanine nucleotide-releasing factor 2 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530379425 | **Score:** | 33.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 133.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQKSVRYNEG | HALYLAFLAR | KEGTKRGFLS | KKTAEASRWH | EKWFALYQNV | LFYFEGEQSC | RPAGMYLLEG | CSCERTPAPP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RAGAGQGGVR | DALDKQYYFT | VLFGHEGQKP | LELRCEEEQD | GKEWMEAIHQ | ASYADILIER | EVLMQKYIHL | VQIVETEKIA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ANQLRHQLED | QDTEIERLKS | EIIALNKTKE | RMRPYQSNQE | DEDPDIKKIK | KVQSFMRGWL | CRRKWKTIVQ | DYICSPHAES |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MRKRNQIVFT | MVEAESEYVH | QLYILVNGFL | RPLRMAASSK | KPPISHDDVS | SIFLNSETIM | FLHEIFHQGL | KARIANWPTL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ILADLFDILL | PMLNIYQEFV | RNHQYSLQVL | ANCKQNRDFD | KLLKQYEANP | ACEGRMLETF | LTYPMFQIPR | YIITLHELLA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HTPHEHVERK | SLEFAKSKLE | ELSRVMHDEV | SDTENIRKNL | AIERMIVEGC | DILLDTSQTF | IRQGSLIQVP | SVERGKLSKV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RLGSLSLKKE | GERQCFLFTK | HFLICTRSSG | GKLHLLKTGG | VLSLIDCTLI | EEPDASDDDS | KGSGQVFGHL | DFKIVVEPPD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AAAFTVVLLA | PSRQEKAAWM | SDISQCVDNI | RCNGLMTIVF | EENSKVTVPH | MIKSDARLHK | DDTDICFSKT | LNSCKVPQIR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| YASVERLLER | LTDLRFLSID | FLNTFLHTYR | IFTTAAVVLG | KLSDIYKRPF | TSIPVRSLEL | FFATSQNNRG | EHLVDGKSPR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LCRKFSSPPP | LAVSRTSSPV | RARKLSLTSP | LNSKIGALDL | TTSSSPTTTT | QSPAASPPPH | TGQIPLDLSR | GLSSPEQSPG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TVEENVDNPR | VDLCNKLKRS | IQKGFNNTER | TCDKEFIIRR | TATNRVLNVL | RHWVSKHAQD | FELNNELKMN | VLNLLEEVLR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DPDLLPQERK | AAANILRALS | QDDQDDIHLK | LEDIIQMTDC | MKAECFESLS | AMELAEQITL | LDHVIFRSIP | YEEFLGQGWM |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KLDKNERTPY | IMKTSQHFND | MSNLVASQIM | NYADVSSRAN | AIEKWVAVAD | ICRCLHNYNG | VLEITSALNR | SAIYRLKKTW |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AKVSKQTKAL | MDKLQKTVSS | EGRFKNLRET | LKNCNPPAVP | YLGMYLTDLA | FIEEGTPNFT | EEGLVNFSKM | RMISHIIREI |
| 1130 | 1140 | 1150 | 1160 | 1170 | | | |
| RQFQQTSYRI | DHQPKVAQYL | LDKDLIIDED | TLYELSLKIE | PRLPA | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1027 | 1 | 984.1548 | 34.58 | 3 | 42.4 | 33.5 | 1 | 898-922 | R.ALSQDDQDDIHLKLEDIIQMTDCMK.A | Oxidation: 20, 24 |

# Detailed Protein Report

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**Protein 345:** **PREDICTED: nascent polypeptide-associated complex subunit alpha isoform X6 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578823772 | **Score:** | 33.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 201.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 2 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPGEATETVP | ATEQELPQPQ | AETAVLPMSS | ALSVTAALGQ | PGPTLPPPCS | PAPQQCPLSA | ANQASPFPSP | STIASTPLEV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PFPQSSSGTA | LPLGTAPEAP | TFLPNLIGPP | ISPAALALAS | PMIAPTLKGT | PSSSAPLALV | ALAPHSVQKS | SAFPPNLLTS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PPSVAVAESG | SVITLSAPIA | PSEPKTNLNK | VPSEVVPNPK | GTPSPPCIVS | TVPYHCVTPM | ASIQSGVASL | PQTTPTTTLA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IASPQVKDTT | ISSVLISPQN | PGSLSLKGPV | SPPAALSLST | QSLPVVTSSQ | KTAGPNTPPD | FPISLGSHLA | PLHQSSFGSV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QLLGQTGPSA | LSDPTVKTIS | VDHSSTGASY | PSQRSVIPPL | PSRNEVVPAT | VAAFPVVAPS | VDKGPSTISS | ITCSPSGSLN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VATSFSLSPT | TSLILKSSPN | ATYHYPLVAQ | MPVSSVGTTP | LVVTNPCTIA | AAPTTTFEVA | TCVSPPMSSG | PISNIEPTSP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AALVMAPVAP | KEPSTQVATT | LRIPVSPPLP | DPEDLKNLPS | SVLVKFPTQK | DLQTVPASLE | GAPFSPAQAG | LTTKKDPTVL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PLVQAAPKNS | PSFQSTSSSP | EIPLSPEATL | AKKSLGEPLP | IGKPASSMTS | PLGVNSSASV | IKTDSYAGPD | SAGPLLKSSL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ITPTVAAFPL | ESADPAGVAP | TTAKGTSTYT | TTASPFLEGT | VSLAPKNHPV | KEGTLTTLPL | VPTASENCPV | APSPQNTCAP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LATLVLAPEI | PKSVPSPSLP | PAGTPPGTKK | VDGISHTSAL | APVASSPKEC | PTEDSGASAT | ASSKGTLTYL | ADSPSPLGVS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VSPQTKRPPT | KKGSAGPDTP | IGNLSSPVSP | VEASFLPENS | LSFQGSKDSP | ATTHSPTPPS | PKGAPTPSAV | TPLSPKGVTL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PPKETPTPSV | VNLPFPKEGP | ATPAPKQAPA | LSMTSSSPKK | ARATPAPKGI | PASPSPKGAP | TPPAATPPSP | KGGPATPSPK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| WAPTPPAATP | PSPKGGPATP | SPKGAPTPPA | ATPPSPKGSP | AATPLPKGAP | TTPAATLPSP | KGGPATPSLK | GAPTPPAATP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PSPKGGPATP | SPKGAPMPPA | ATPPSPKGGL | ATPPHKGAPT | TPAATPPSPK | GGLATPPPKG | APTTPAATPP | SPKGGLATPP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PKGAPTTPAA | TPPSPKGGLA | TPSPKGAPTT | PAATPPSPKG | GLATPSPKGA | PTTPAATPPS | PKGGLATPSP | KGAPTTPAAT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PPSPKGGPAT | PPPKGAPTPP | AATPPSLKGG | LATPPHKGAP | NPAVVTPPSP | KGGPATSPPK | GAPTPPAATP | PSPKGSPGTP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PPKGAPTPPA | VTPPSPKGTP | TLPATTPSSK | GGPTTPSSKE | GPTPPAATPS | HKGGPAMTPP | SPKRGPAIPS | PKGDPTSPAV |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| IPLSPKKAPA | TPVTREGAAT | PSKGDLTPPA | VTPVSLKKAP | ATSAPKGGPA | TPSSKGDPTL | PAVTPPSPKE | PPAPKQVATS |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SSPKKAPATP | APMGAPTLPA | VIPSSPKEVP | ATPSSRRDPI | APTATLLSKK | TPATLAPKEA | LIPPAMTVPS | PKKTPAIPTP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| KEAPATPSSK | EASSPPAVTP | STYKGAPSPK | ELLIPPAVTS | PSPKEAPTPP | AVTPPSPEKG | PATPAPKGTP | TSPPVTPSSL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KDSPTSPASV | TCKMGATVPQ | ASKGLPAKKG | PTALKEVLVA | PAPESTPIIT | APTRKGPQTK | KSSATSPPIC | PDPSAKNGSK |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| GPLSTVAPAP | LLPVQKDSSK | TAKGKDASHS | PKGPLAPPES | KASTPLTAAA | FEKVLPKPES | ASVSAAPSPP | VSLPLAPSPV |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| PTLPPKQQFL | PSSPGLVLES | PSKPLAPADE | DELLPLIPPE | PISGGVPFQS | VLVNMPTPKS | AGIPVPTPSA | KQPVTKNNKG |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| SGTESDSDES | VPELEEQDST | QATTQQAQLA | AAAEIDEEPV | SKAKQSRSEK | KARKAMSKLG | LRQVTGVTRV | TIRKSKNILF |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| VITKPDVYKS | PASDTYIVFG | EAKIEDLSQQ | AQLAAAEKFK | VQGEAVSNIQ | ENTQTPTVQE | ESEEEEVDET | GVEVKDIELV |
| 2010 | 2020 | 2030 | 2040 | | | | |
| MSQANVSRAK | AVRALKNNSN | DIVNAIMVSV | QAFVP | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 732 | 1 | 472.2592 | 28.32 | 2 | 39.1 | 11.0 | 0 | 1468-1476 | K.EVPATPSSR.R | |
| 52 | 1 | 717.7555 | -144.48 | 2 | 30.5 | 11.1 | 0 | 1531-1544 | K.EASSPPAVTPSTYK.G | |

# Detailed Protein Report

## Protein 346: semaphorin-3A precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5174673 | **Score:** | 33.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 88.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.2 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.64 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.31 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578813881 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: semaphorin-3A isoform X4 [Homo sapiens] |
| gi\|578813879 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: semaphorin-3A isoform X3 [Homo sapiens] |
| gi\|530385417 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: semaphorin-3A isoform X2 [Homo sapiens] |
| gi\|530385415 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: semaphorin-3A isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGWLTRIVCL | FWGVLLTARA | NYQNGKNNVP | RLKLSYKEML | ESNNVITFNG | LANSSSYHTF | LLDEERSRLY | VGAKDHIFSF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DLVNIKDFQK | IVWPVSYTRR | DECKWAGKDI | LKECANFIKV | LKAYNQTHLY | ACGTGAFHPI | CTYIEIGHHP | EDNIFKLENS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HFENGRGKSP | YDPKLLTASL | LIDGELYSGT | AADFMGRDFA | IFRTLGHHHP | IRTEQHDSRW | LNDPKFISAH | LISESDNPED |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DKVYFFFREN | AIDGEHSGKA | THARIGQICK | NDFGGHRSLV | NKWTTFLKAR | LICSVPGPNG | IDTHFDELQD | VFLMNFKDPK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NPVVYGVFTT | SSNIFKGSAV | CMYSMSDVRR | VFLGPYAHRD | GPNYQWVPYQ | GRVPYPRPGT | CPSKTFGGFD | STKDLPDDVI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TFARSHPAMY | NPVFPMNNRP | IVIKTDVNYQ | FTQIVVDRVD | AEDGQYDVMF | IGTDVGTVLK | VVSIPKETWY | DLEEVLLEEM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TVFREPTAIS | AMELSTKQQQ | LYIGSTAGVA | QLPLHRCDIY | GKACAECCLA | RDPYCAWDGS | ACSRYFPTAK | RRTRRQDIRN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GDPLTHCSDL | HHDNHHGHSP | EERIIYGVEN | SSTFLECSPK | SQRALVYWQF | QRRNEERKEE | IRVDDHIIRT | DQGLLLRSLQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QKDSGNYLCH | AVEHGFIQTL | LKVTLEVIDT | EHLEELLHKD | DDGDGSKTKE | MSNSMTPSQK | VWYRDFMQLI | NHPNLNTMDE |
| 730 | 740 | 750 | 760 | 770 | 780 | | |
| FCEQVWKRDR | KQRRQRPGHT | PGNSNKWKHL | QENKKGRNRR | THEFERAPRS | V | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1358 | 2 | 436.6061 | -206.99 | 2 | 47.1 | 18.6 | 0 | 213-219 | R.TEQHDSR.W | | QU:MU 0.64<br>WUP:QUP 1.31 |
| 2058 | 1 | 722.8469 | -17.26 | 2 | 56.1 | 14.8 | 1 | 265-277 | R.IGQICKNDFGGHR.S | | |

# Detailed Protein Report

## Protein 347: transmembrane protein 169 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|19923913 | **Score:** | 33.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 33.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 13.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578805184 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: transmembrane protein 169 isoform X1 [Homo sapiens] |
| gi\|214831834 | refseq_human(refseq_human_20140103.fasta) | transmembrane protein 169 [Homo sapiens] |
| gi\|214831799 | refseq_human(refseq_human_20140103.fasta) | transmembrane protein 169 [Homo sapiens] |
| gi\|214831780 | refseq_human(refseq_human_20140103.fasta) | transmembrane protein 169 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MEEPTAVEGQ VQLPSPHQGS LRKAVAAALA LDGESTMGHR KKKRKESRPE SIIIYRSDNE KTDEEPGESE GGDQPKEEEG
        90        100        110        120        130        140        150        160
DDFLDYPVDD DMWNLPLDSR YVTLTGTITR GKKKGQMVDI HVTLTEKELQ ELTKPKESSR ETTPEGRMAC QMGADRGPHV
       170        180        190        200        210        220        230        240
VLWTLICLPV VFILSFVVSF YYGTITWYNI FLVYNEERTF WHKISYCPCL VLFYPVLIMA MASSLGLYAA VVQLSWSWEA
       250        260        270        280        290        300
WWQAARDMEK GFCGWLCSKL GLEDCSPYSI VELLESDNIS STLSNKDPIQ EVETSTV
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 77 | 1 | 845.3458 | -96.16 | 3 | 30.7 | 10.3 | 1 | 1-23 | -.MEEPTAVEGQVQLPSPHQGSLRK.A | Oxidation: 1 |

# Detailed Protein Report

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## Protein 348: heat shock 70 kDa protein 1A/1B [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|167466173 | **Score:** | 33.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 70.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 0.62 | **CV:** 0.00 % | **No. of Peptides:** 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|194248072 | refseq_human(refseq_human_20140103.fasta) | heat shock 70 kDa protein 1A/1B [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAKAAAIGID | LGTTYSCVGV | FQHGKVEIIA | NDQGNRTTPS | YVAFTDTERL | IGDAAKNQVA | LNPQNTVFDA | KRLIGRKFGD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PVVQSDMKHW | PFQVINDGDK | PKVQVSYKGE | TKAFYPEEIS | SMVLTKMKEI | AEAYLGYPVT | NAVITVPAYF | NDSQRQATKD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AGVIAGLNVL | RIINEPTAAA | IAYGLDRTGK | GERNVLIFDL | GGGTFDVSIL | TIDDGIFEVK | ATAGDTHLGG | EDFDNRLVNH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FVEEFKRKHK | KDISQNKRAV | RRLRTACERA | KRTLSSSTQA | SLEIDSLFEG | IDFYTSITRA | RFEELCSDLF | RSTLEPVEKA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LRDAKLDKAQ | IHDLVLVGGS | TRIPKVQKLL | QDFFNGRDLN | KSINPDEAVA | YGAAVQAAIL | MGDKSENVQD | LLLLDVAPLS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LGLETAGGVM | TALIKRNSTI | PTKQTQIFTT | YSDNQPGVLI | QVYEGERAMT | KDNNLLGRFE | LSGIPPAPRG | VPQIEVTFDI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DANGILNVTA | TDKSTGKANK | ITITNDKGRL | SKEEIERMVQ | EAEKYKAEDE | VQRERVSAKN | ALESYAFNMK | SAVEDEGLKG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KISEADKKKV | LDKCQEVISW | LDANTLAEKD | EFEHKRKELE | QVCNPIISGL | YQGAGGPGPG | GFGAQGPKGG | SGSGPTIEEV |
| 650 | | | | | | | |
| D | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 602 | 1 | 744.3677 | 18.07 | 2 | 37.5 | 10.9 | 0 | 37-49 | R.TTPSYVAFTDTER.L | | QU:MU 0.62 |
| 1835 | 2 | 599.2683 | -138.16 | 2 | 53.3 | 22.4 | 0 | 160-171 | K.DAGVIAGLNVLR.I | | |

# Detailed Protein Report

## Protein 349: PREDICTED: coiled-coil domain-containing protein 60 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530401235 | **Score:** | 33.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 47.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 7.4 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTKVPATKKL | QSSPNSGAVR | PFYASENLRQ | VPDKPMKSIK | YMDKEIINLK | KDLIRSRFLI | QSVKIGRGYF | AILREETAKK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KKQQQLQKLK | EEERNKFQPA | EKISEIHYGD | TLLSTYDDEK | LKTLGARVTR | RPFTPIHSCI | ISPSLTEAHV | EPLFRQLCAL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HWLLEALTID | HTHHTMKPVI | TCWNPKDPGG | SKSTIKKINK | DKSMGQKWEH | FITAPKTKKF | KIPTMRVTNR | KPSRRGSTLS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LSRASGGSSP | QSSMISVNPG | SDEPPSVNTQ | VTSSKDIEDN | ESSSTKPDEE | PLYMNLQKLL | EMVREDARRT | VTIENGMQRK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| APSILSVLKQ | NKSNSAYKEM | QTTLKSSERS | SSTSAESHIQ | PVQKKSKNRT | NCDINIHYKS | GVCNTMRAKF | YSVAQEAGFC |
| 410 | 420 | 430 | | | | | |
| LQDKMEILMN | LLLDSRDHPS | R | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2869 | 1 | 724.8749 | -14.66 | 2 | 64.6 | 19.1 | 2 | 309-320 | R.RTVTIENGMQRK.A | Oxidation: 9 |
| 2374 | 1 | 1022.9281 | -68.61 | 2 | 59.6 | 14.2 | 1 | 346-364 | K.SSERSSSTSAESHIQPVQK.K | |

# Detailed Protein Report

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**Protein 350:** **PREDICTED: cylicin-1 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530421958 | **Score:** | 33.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 74.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSLPRLKVNI | RTYDNSIPIS | ESSRKSWNQK | HFALTFPKPL | QRGTNDKSRP | LKSQITVTRH | DKRKLEEGQK | PAHKWIRHSF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RKILQWPPIY | TAAREQTPFR | HLYTSKTHLK | KAEYKKSKDE | KGGTPLKKDS | KKKGGSYATN | PESKQIVEEK | TKRQNEADKT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PLKSSHENEQ | SKKSKSSSET | NPESQNSKTV | SKNCSQKDKK | DSKNSKKTNT | EFLHTKNNPK | KDLKRSKTSN | DPISEICSEN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SLNVDFLMLV | GQSDDESINF | DAWLRNYSQN | NSKNYSLKYT | KYTKKDTKKN | AKKSSDAESE | DSKDAKKDSK | KVKKNVKKDD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KKKDVKKDTE | STDAESGDSK | DERKDTKKDK | KKLKKDDKKK | DTKKYPESTD | TESGDAKDAR | NDSRNLKKAS | KNDDKKKDAK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KITFSTDSES | ELESKESQKD | EKKDKKDSKT | DNKKSVKNDE | ESTDADSEPK | GDSKKGKKDE | KKGKKDSKKD | DKKKDAKKNA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ESTEMESDLE | LKKDKKHSKE | KKGSKKDIKK | DARKDTESTD | AEFDESSKTG | FKTSTKIKGS | DTESEESLYK | PGAKKKIDES |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DGTSANSKME | GLESKRGFRM | SSKKTTFNEK | GEKASTGRVP | PSREKPPLPA | CEPSLPSPKV | RRLCWCKMPP | PPPKPRYAPL |
| 650 | 660 | | | | | | |
| PEAPWIHKLL | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 547 | 1 | 472.6490 | -226.33 | 2 | 35.3 | 16.3 | 1 | 119-127 | K.DEKGGTPLK.K | |

# Detailed Protein Report

## Protein 351: PREDICTED: lysine-specific demethylase 2A isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578821239 | **Score:** | 33.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 120.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVDVMDVNTQ | KGIEMTMAQW | TRYYETPEEE | REKLYNVISL | EFSHTRLENM | VQRPSTVDFI | DWVDNMWPRH | LKESQTESTN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AILEMQYPKV | QKYCLMSVRG | CYTDFHVDFG | GTSVWYHIHQ | GGKVFWLIPP | TAHNLELYEN | WLLSGKQGDI | FLGDRVSDCQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RIELKQGYTF | VIPSGWIHAV | YTPTDTLVFG | GNFLHSFNIP | MQLKIYNIED | RTRVPNKFRY | PFYYEMCWYV | LERYVYCITN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RSHLTKEFQK | ESLSMDLELN | GLESGNGDEE | AVDREPRRLS | SRRSVLTSPV | ANGVNLDYDG | LGKTCRSLPS | LKKTLAGDSS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SDCSRGSHNG | QVWDPQCAPR | KDRQVHLTHF | ELEGLRCLVD | KLESLPLHKK | CVPTGIEDED | ALIADVKILL | EELANSDPKL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ALTGVPIVQW | PKRDKLKFPT | RPKVRVPTIP | ITKPHTMKPA | PRLTPVRPAA | ASPIVSGARR | RRVRCRKCKA | CVQGECGVCH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YCRDMKKFGG | PGRMKQSCVL | RQCLAPRLPH | SVTCSLCGEV | DQNEETQDFE | KKLMECCICN | EIVHPGCLQM | DGEGLLNEEL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PNCWECPKCY | QEDSSEKAQK | RKMEESDEEA | VQAKVLRPLR | SCDEPLTPPP | HSPTSMLQLI | HDPVSPRGMV | TRSSPGAGPS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DHHSASRDER | FKRRQLLRLQ | ATERTMVREK | ENNPSGKKEL | SEVEKAKIRG | SYLTVTLQRP | TKELHGTSIV | PKLQAITASS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ANLRHSPRVL | VQHCPARTPQ | RGDEEGLGGE | EEEEEEEEEE | DDSAEEGGAA | RLNGRGSWAQ | DGDESWMQRE | VWMSVFRYLS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RRELCECMRV | CKTWYKWCCD | KRLWTKIDLS | RCKAIVPQAL | SGIIKRQPVS | LDLSWTNISK | KQLTWLVNRL | PGLKDLLLAG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| CSWSAVSALS | TSSCPLLRTL | DLRWAVGIKD | PQIRDLLTPP | ADKPGQDNRS | KLRNMTDFRL | AGLDITDATL | RLIIRHMPLL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SRLDLSHCSH | LTDQSSNLLT | AVGSSTRYSL | TELNMAGCNK | LTDQTLIYLR | RIANVTLIDL | RGCKQITRKA | CEHFISDLSI |
| 1050 | 1060 | | | | | | |
| NSLYCLSDEK | LIQKIS | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 846 | 1 | 663.6790 | -184.30 | 2 | 40.6 | 10.3 | 1 | 313-325 | K.KTLAGDSSSDCSR.G | |
| 762 | 1 | 599.6213 | -221.03 | 2 | 39.5 | 10.5 | 0 | 314-325 | K.TLAGDSSSDCSR.G | |

# Detailed Protein Report

**Protein 352:** **constitutive coactivator of peroxisome proliferator-activated receptor gamma isoform a [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|556503397 | **Score:** | 33.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 105.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 5.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.86 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.76 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDRQMILSRS | SVMGVRGLQG | FVGSTCPHIC | TVVNFKELAE | HHRSKYPGCT | PTIVVDAMCC | LRYWYTPESW | ICGGQWREYF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SALRDFVKTF | TAAGIKLIFF | FDGMVEQDKR | DEWVKRRLKN | NREISRIFHY | IKSHKEQPGR | NMFFIPSGLA | VFTRFALKTL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GQETLCSLQE | ADYEVASYGL | QHNCLGILGE | DTDYLIYDTC | PYFSISELCL | ESLDTVMLCR | EKLCESLGLC | VADLPLLACL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LGNDIIPEGM | FESFRYKCLS | SYTSVKENFD | KKGNIILAVS | DHISKVLYLY | QGEKKLEEIL | PLGPNKALFY | KGMASYLLPG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QKSPWFFQKP | KGVITLDKQV | ISTSSDAESR | EEVPMCSDAE | SRQEVPMCTG | PESRREVPVY | TDSEPRQEVP | MCSDPEPRQE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VPTCTGPESR | REVPMCSDPE | PRQEVPMCTG | PEARQEVPMY | TDSEPRQEVP | MYTDSEPRQE | VPMYTGSEPR | QEVPMYTGPE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SRQEVPMYTG | PESRQEVLIR | TDPESRQEIM | CTGHESKQEV | PICTDPISKQ | EDSMCTHAEI | NQKLPVATDF | EFKLEALMCT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NPEIKQEDPT | NVGPEVKQQV | TMVSDTEILK | VARTHHVQAE | SYLVYNIMSS | GEIECSNTLE | DELDQALPSQ | AFIYRPIRQR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VYSLLLEDCQ | DVTSTCLAVK | EWFVYPGNPL | RHPDLVRPLQ | MTIPGGTPSL | KILWLNQEPE | IQVRRLDTLL | ACFNLSSSRE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ELQAVESPFQ | ALCCLLIYLF | VQVDTLCLED | LHAFIAQALC | LQGKSTSQLV | NLQPDYINPR | AVQLGSLLVR | GLTTLVLVNS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ACGFPWKTSD | FMPWNVFDGK | LFHQKYLQSE | KGYAVEVLLE | QNRSRLTKFH | NLKAVVCKAC | MKENRRITGR | AHWGSHHAGR |
| 890 | 900 | 910 | 920 | 930 | | | |
| WGRQGSSYHR | TGSGYSRSSQ | GQPWRDQGPG | SRQYEHDQWR | RY | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1242 | 1 | 666.6715 | -165.15 | 2 | 45.6 | 11.1 | 0 | 412-422 | R.EVPMCSDPEPR.Q | Carbamidomethyl: 5;<br>Oxidation: 4 | WUP:QUP 0.76<br>QU:MU 1.86 |

# Detailed Protein Report

**Protein 353:** **PREDICTED: acetyl-CoA acetyltransferase, cytosolic isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530383698 | **Score:** | 33.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 44.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| | | **Sequence Coverage [%]:** | 9.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGSHPVLRIW | GNRRATAASL | GRSGGRLSSP | RLLRVVAPTL | TFAQTSRCSF | NGALAAVPVQ | DLGSTVIKEV | LKRATVAPED |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VSEVIFGHVL | AAGCGQNPVR | QASVGAGIPY | SVPAWSCQMI | CGSGLKAVCL | AVQSIGIGDS | SIVVAGGMEN | MSKAPHLAYL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RTGVKIGEMP | LTDSILCDGL | TDAFHNCHMG | ITAENVAKKW | QVSREDQDKV | AVLSQNRTEN | AQKAGHFDKE | IVPVLVSTRK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GLIEVKTDEF | PRHGSNIEAM | SKLKPYFLTD | GTGTVTPANA | SGINDGAAAV | VLMKKSEADK | RGLTPLARIV | SWSQVGVEPS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IMGIGPIPAI | KQAVTKAGWS | LEDVDIFEIN | EAFAAVSAAI | VKELGLNPEK | VNIEGGAIAL | GHPLGASGCR | ILVTLLHTLE |
| 410 | 420 | 430 | | | | | |
| RMGRSRGVAA | LCIGGGMGIA | MCVQRE | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2173 | 1 | 1045.4885 | -59.90 | 2 | 57.0 | 15.6 | 0 | 48-68 | R.CSFNGALAAVPVQDLGSTVIK.E | |

# Detailed Protein Report

## Protein 354: PREDICTED: latent-transforming growth factor beta-binding protein 1 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530367595 | **Score:** | 33.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 134.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAGAWLRWGL | LLWAGLLASS | AHGRLRRITY | VVHPGPGLAA | GALPLSGPPR | SRTFNVALNA | RYSRSSAAAG | APSRASPGVP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SERTRRTSKP | GGAALQGLRP | PPPPPPEPAR | PAVPGGQLHP | NPGGHPAAAP | FTKQGRQVVR | SKVPQETQSG | GGSRLQVHQK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QQLQGVNVCG | GRCCHGWSKA | PGSQRCTKPS | CVPPCQNGGM | CLRPQLCVCK | PGTKGKACET | IAAQDTSSPV | FGGQSPGAAS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SWGPPEQAAK | HTSSKKADTL | PRVSPVAQMT | LTLKPKPSVG | LPQQIHSQVT | PLSSQSVVIH | HGQTQEYVLK | PKYFPAQKGI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SGEQSTEGSF | PLRYVQDQVA | APFQLSNHTG | RIKVVFTPSI | CKVTCTKGSC | QNSCEKGNTT | TLISENGHAA | DTLTATNFRV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VICHLPCMNG | GQCSSRDKCQ | CPPNFTGKLC | QIPVHGASVP | KLYQHSQQPG | KALGTHVIHS | THTLPLTVTS | QQGVKVKFPP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NIVNIHVKHP | PEASVQIHQV | SRIDGPTGQK | TKEAQPGQSQ | VSYQGLPVQK | TQTIHSTYSH | QQVIPHVYPV | AAKTQLGRCF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QETIGSQCGK | ALPGLSKQED | CCGTVGTSWG | FNKCQKCPKK | PSYHGYNQMM | ECLPGYKRVN | NTFCQDINEC | QLQGVCPNGE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CLNTMGSYRC | TCKIGFGPDP | TFSSCVPDPP | VISEEKGPCY | RLVSSGRQCM | HPLSVHLTKQ | LCCCSVGKAW | GPHCEKCPLP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GTAAFKEICP | GGMGYTVSGV | HRRRPIHHHV | GKGPVFVKPK | NTQPVAKSTH | PPPLPAKEEP | VEALTFSREH | GPGVAEPEVA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TAPPEKEIPS | LDQEKTKLEP | GQPQLSPGIS | TIHLHPQFPV | VIEKTSPPVP | VEVAPEASTS | SASQVIAPTQ | VTEINECTVN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PDICGAGHCI | NLPVRYTCIC | YEGYRFSEQQ | RKCVDIDECT | QVQHLCSQGR | CENTEGSFLC | ICPAGFMASE | EGTNCIDVDE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| CLRPDVCGEG | HCVNTVGAFR | CEYCDSGYRM | TQRGRCEDID | ECLNPSTCPD | EQCVNSPGSY | QCVPCTEGFR | GWNGQCLDVD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ECLEPNVCAN | GDCSNLEGSY | MCSCHKGYTR | TPDHKHCRDI | DECQQGNLCV | NGQCKNTEGS | FRCTCGQGYQ | LSAAKDQCED |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| IDECQHRHLC | AHGQCRNTEG | SFQCVCDQGY | RASGLGDHCE | DINECLEDKS | VCQRGDCINT | AGSYDCTCPD | GFQLDDNKTC |
| 1210 | 1220 | 1230 | 1240 | 1250 | | | |
| QDINECEHPG | LCGPQGECLN | TEGSFHCVCQ | QGFSISADGR | TCEDVNE | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2143 | 1 | 1052.3999 | -77.45 | 2 | 57.2 | 10.8 | 1 | 400-418 | R.VVICHLPCMNGGQCSSRDK.C | Carbamidomethyl: 8 |

# Detailed Protein Report

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## Protein 355: zinc finger protein 90 [Homo sapiens]

**Accession:** gi|209862791
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 33.0
**MW [kDa]:** 69.0
**pI:** 10.3
**Sequence Coverage [%]:** 4.3
**No. of unique Peptides:** 1

## Quantitation

***WUP:QUP*** **Median:** 2.83 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MGPLEFRDVA IEFSLEEWHC LDTAQQNLYR DVMLENYRHL VFLGIVVTKP DLITCLEQGK KPFTVKRHEM IAKSPVMCFH

        90        100        110        120        130        140        150        160
FAQDLCPEQS LKDSFQKVIV TRYEKREYGN LELKKGCESV DEGKVHKRGY NGLNQCLTAT QSKVFQCDTY VKVSHIFSNS

       170        180        190        200        210        220        230        240
NRHKIRDTGK KPFKCIECGK AFNQSSTLAT HKKIHTGEIT CKCEECGKAF NRSSHLTSHK RIHTGEKRYK CEDCGKELKY

       250        260        270        280        290        300        310        320
SSTLTAHKRI HTGEKRYKCE DCGKELKYSS TLTAHKRIHT GEKPYKCDKC GRAFISSSIL YVHKISHTEE KPYKCEECGK

       330        340        350        360        370        380        390        400
AFKLSSILST HKRIHTGEKP YKCEECGKAF RRSLVLRTHK RIHTGEKPYK CDKCGKAFIS SSLLYKHKIS HSEKKPYKCE

       410        420        430        440        450        460        470        480
ECGKAFKRSS TLTIHKISHT EEKPYKCQEC DKVFKRSSAL STHKIIHSGE KPYKCEECGK AFKRSSNLTT HKISHTEEKL

       490        500        510        520        530        540        550        560
YKCQECDKAF KYSSALSTHK IIHSGENPYK CEECGKAFKR SSVLSKHKII HTGAKPYKCE ECGKAFKRSS QLTSHKISHT

       570        580        590        600        610
GEKPYKCEEC GKAFNLSSDL NTHKRIHIGQ KAYIVKNMAN L
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1099 | 1 | 917.4452 | -8.48 | 2 | 43.8 | 11.6 | 1 | 529-544 | K.IIHTGAKPYKCEECGK.A | Carbamidomethyl: 11 | WUP:QUP 2.83 |

# Detailed Protein Report

**Protein 356:** **E3 ubiquitin-protein ligase MARCH7 isoform c [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|544346219 | **Score:** | 33.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 73.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MIGNYDHLMS LVTSTSASAS ASPFQSAWYS ESEITQGARS RSQNQQRDHD SKRPKLSCTN CTTSAGRNVG NGLNTLSDSS
        90        100        110        120        130        140        150        160
WRHSQVPRSS SMVLGSFGTD LMRERRDLER RTDSSISNLM DYSHRSGDFT TSSYVQDRVP SYSQGARPKE NSMSTLQLNT
       170        180        190        200        210        220        230        240
SSTNHQLPSE HQTILSSRDS RNSLRSNFSS RESESSRSNT QPGFSYSSSR DEAPIISNSE RVVSSQRPFQ ESSDNEGRRT
       250        260        270        280        290        300        310        320
TRRLLSRIAS SMSSTFFSRR SSQDSLNTRS LNSENSYVSP RILTASQSRS NVPSASEVPD NRASEASQGF RFLRRRWGLS
       330        340        350        360        370        380        390        400
SLSHNHSSES DSENFNQESE GRNTGPWLSS SLRNRCTPLF SRRRREGRDE SSRIPTSDTS SRSHIFRRES NEVVHLEAQN
       410        420        430        440        450        460        470        480
DPLGAAANRP QASAASSSAT TGGSTSDSAQ GGRNTGISGI LPGSLFRFAV PPALGSNLTD NVMITVDIIP SGWNSADGKS
       490        500        510        520        530        540        550        560
DKTKSAPSRD PERLQKIKES LLLEDSEEEE GDLCRICQMA AASSSNLLIE PCKCTGSLQY VHQDCMKKWL QAKINSGSSL
       570        580        590        600        610        620        630        640
EAVTTCELCK EKLELNLEDF DIHELHRAHA NEQAEYEFIS SGLYLVVLLH LCEQSFSDMM GNTNEPSTRV RFINLARTLQ
       650        660        670
AHMEDLETSE DDSEEDGDHN RTFDIA
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1613 | 1 | 682.3429 | 11.62 | 3 | 50.4 | 22.6 | 2 | 89-106 | R.SSSMVLGSFGTDLMRERR.D | Oxidation: 4 |

# Detailed Protein Report

## Protein 357: E3 ubiquitin-protein ligase RNF213 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|366039979 | **Score:** | 32.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 591.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 0.6 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MECPSCQHVS | KEETPKFCSQ | CGERLPPAAP | IADSENNNST | MASASEGEME | CGQELKEEGG | PCLFPGSDSW | QENPEEPCSK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ASWTVQESKK | KKRKKKKKGN | KSASSELASL | PLSPASPCHL | TLLSNPWPQD | TALPHSQAQQ | SGPTGQPSQP | PGTATTPLEG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DGLSAPTEVG | DSPLQAQALG | EAGVATGSEA | QSSPQFQDHT | EGEDQDASIP | SGGRGLSQEG | TGPPTSAGEG | HSRTEDAAQE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LLLPESKGGS | SEPGTELQTT | EQQAGASASM | AVDAVAEPAN | AVKGAGKEMK | EKTQRMKQPP | ATTPPFKTHC | QEAETKTKDE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MAAAEEKVGK | NEQGEPEDLK | KPEGKNRSAA | AVKNEKEQKN | QEADVQEVKA | STLSPGGGVT | VFFHAIISLH | FPFNPDLHKV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FIRGGEEFGE | SKWDSNICEL | HYTRDLGHDR | VLVEGIVCIS | KKHLDKYIPY | KYVIYNGESF | EYEFIYKHQQ | KKGEYVNRCL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FIKSSLLGSG | DWHQYYDIVY | MKPHGRLQKV | MNHITDGPRK | DLVKGKQIAA | ALMLDSTFSI | LQTWDTINLN | SFFTQFEQFC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FVLQQPMIYE | GQAQLWTDLQ | YREKEVKRYL | WQHLKKHVVP | LPDGKSTDFL | PVDCPVRSKL | KTGLIVLFVV | EKIELLLEGS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LDWLCHLLTS | DASSPDEFHR | DLSHILGIPQ | SWRLYLVNLC | QRCMDTRTYT | WLGALPVLHC | CMELAPRHKD | AWRQPEDTWA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ALEGLSFSPF | REQMLDTSSL | LQFMREKQHL | LSIDEPLFRS | WFSLLPLSHL | VMYMENFIEH | LGRFPAHILD | CLSGIYYRLP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GLEQVLNTQD | VQDVQNVQNI | LEMLLRLLDT | YRDKIPEEAL | SPSYLTVCLK | LHEAICSSTK | LLKFYELPAL | SAEIVCRMIR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LLSLVDSAGQ | RDETGNNSVQ | TVFQGTLAAT | KRWLREVFTK | NMLTSSGASF | TYVKEIEVWR | RLVEIQFPAE | HGWKESLLGD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| MEWRLTKEEP | LSQITAYCNS | CWDTKGLEDS | VAKTFEKCII | EAVSSACQSQ | TSILQGFSYS | DLRKFGIVLS | AVITKSWPRT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ADNFNDILKH | LLTLADVKHV | FRLCGTDEKI | LANVTEDAKR | LIAVADSVLT | KVVGDLLSGT | ILVGQLELII | KHKNQFLDIW |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QLREKSLSPQ | DEQCAVEEAL | DWRREELLLL | KKEKRCVDSL | LKMCGNVKHL | IQVDFGVLAV | RHSQDLSSKR | LNDTVTVRLS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TSSNSQRATH | YHLSSQVQEM | AGKIDLLRDS | HIFQLFWREA | AEPLSEPKED | QEAAELLSEP | EEESERHILE | LEEVYDYLYQ |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PSYRKFIKLH | QDLKSGEVTL | AEIDVIFKDF | VNKYTDLDSE | LKIMCTVDHQ | DQRDWIKDRV | EQIKEYHHLH | QAVHAAKVIL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| QVKESLGLNG | DFSVLNTLLN | FTDNFDDFRR | ETLDQINQEL | IQAKKLLQDI | SEARCKGLQA | LSLRKEFICW | VREALGGINE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LKVFVDLASI | SAGENDIDVD | RVACFHDAVQ | GYASLLFKLD | PSVDFSAFMK | HLKKLWKALD | KDQYLPRKLC | DSARNLEWLK |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| TVNESHGSVE | RSSLTLATAI | NQRGIYVIQA | PKGGQKISPD | TVLHLILPES | PGSHEESREY | SLEEVKELLN | KLMLMSGKKD |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| RNNTEVERFS | EVFCSVQRLS | QAFIDLHSAG | NMLFRTWIAM | AYCSPKQGVS | LQMDFGLDLV | TELKEGGDVT | ELLAALCRQM |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| EHFLDSWKRF | VTQKRMEHFY | LNFYTAEQLV | YLSTELRKQP | PSDAALTMLS | FIKSNCTLRD | VLRASVGCGS | EAARYRMRRV |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| MEELPLMLLS | EFSLVDKLRI | IMEQSMRCLP | AFLPDCLDLE | TLGHCLAHLA | GMGGSPVERC | LPRGLQVGQP | NLVVCGHSEV |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| LPAALAVYMQ | TPSQPLPTYD | EVLLCTPATT | FEEVALLLRR | CLTLGSLGHK | VYSLLFADQL | SYEVARQAEE | LFHNLCTQQH |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| REDYQLVMVC | DGDWEHCYLP | SAFSQHKVFV | TPQAPLEAIQ | AYLAGHYRVP | KQTLSAAAVF | NDRLCVGIVA | SERAGVGKSL |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| YVKRLHDKMK | MQLNVKNVPL | KTIRLIDPQV | DESRVLGALL | PFLDAQYQKV | PVLFHLDVTS | SVQTGIWVFL | FKLLILQYLM |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| DINGKMWLRN | PCHLYIVEIL | ERRTSVPSRS | SSALRTRVPQ | FSFLDIFPKV | TCRPPKEVID | MELSALRSDT | EPGMDLWEFC |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1737 | 1 | 863.0655 | 110.54 | 2 | 51.5 | 19.4 | 1 | 746-759 | R.EKQHLLSIDEPLFR.S | |

# Detailed Protein Report

**Protein 358:** **spectrin beta chain, non-erythrocytic 4 isoform sigma1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|115430237 | **Score:** | 32.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 288.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 4.03 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 3.65 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAQVPGEVDN | MEGLPAPNNN | PAARWESPDR | GWEREQPAAS | TAAASLFECS | RIKALADERE | AVQKKTFTKW | VNSHLARVGC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HIGDLYVDLR | DGFVLTRLLE | VLSGEQLPRP | TRGRMRIHSL | ENVDKALQFL | KEQRVHLENV | GSHDIVDGNH | RLTLGLVWTI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ILRFQIQVIK | IETEDNRETR | SAKDALLLWC | QMKTAGYPEV | NIQNFTTSWR | DGLAFNALIH | RHRPDLVDFS | KLTKSNANYN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LQRAFRTAEQ | HLGLARLLDP | EDVNMEAPDE | KSIITYVVSF | YHYFSKMKAL | AVEGKRIGKV | LDQVLEVGKI | IERYEELAAE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LLAWIHRTVG | LISNQKFANS | LSGVQQQLQA | FTAYCTLEKP | VKFQEKGNLE | VLLFSIQSKL | RACNRRLFVP | REGCGIWDID |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KAWGELEKAE | HEREAALRAE | LIRQEKLELL | AQRFDHKVAM | RESWLNENQR | LVSQDNFGYE | LPAVEAAMKK | HEAIEADIAA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YEERVQGVAE | LAQALAAEGY | YDIRRVAAQR | DSVLRQWALL | TGLVGARRTR | LEQNLALQKV | FQEMVYMVDW | MEEMQAQLLS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RECGQHLVEA | DDLLQKHGLL | EGDIAAQSER | VEALNAAALR | FSQLQGYQPC | DPQVICNRVN | HVHGCLAELQ | EQAARRRAEL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EASRSLWALL | QELEEAESWA | RDKERLLEAA | GGGGAAGAAG | AAGTAGGAHD | LSSTARLLAQ | HKILQGELGG | RRALLQQALR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CGEELVAAGG | AVGPGADTVH | LVGLAERAAS | ARRRWQRLEE | AAARRERRLQ | EARALHQFGA | DLDGLLDWLR | DAYRLAAAGD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FGHDEASSRR | LARQHRALTG | EVEAHRGPVS | GLRRQLATLG | GASGAGPLVV | ALQVRVVEAE | QLFAEVTEVA | ALRRQWLRDA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LAVYRMFGEV | HACELWIGEK | EQWLLSMRVP | DSLDDVEVVQ | HRFESLDQEM | NSLMGRVLDV | NHTVQELVEG | GHPSSDEVRS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| CQDHLNSRWN | RIVELVEQRK | EEMSAVLLVE | NHVLEVAEVR | AQVREKRRAV | ESAPRAGGAL | QWRLSGLEAA | LQALEPRQAA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LLEEAALLAE | RFPAQAARLH | QGAEELGAEW | GALASAAQAC | GEAVAAAGRL | QRFLHDLDAF | LDWLVRAQEA | AGGSEGPLPN |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SLEEADALLA | RHAALKEEVD | QREEDYARIV | AASEALLAAD | GAELGPGLAL | DEWLPHLELG | WHKLLGLWEA | RREALVQAHI |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| YQLFLRDLRQ | ALVVLRNQEM | ALSGAELPGT | VESVEEALKQ | HRDFLTTMEL | SQQKMQVAVQ | AAEGLLRQGN | IYGEQAQEAV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TRLLEKNQEN | QLRAQQWMQK | LHDQLELQHF | LRDCHELDGW | IHEKMLMARD | GTREDNHKLH | KRWLRHQAFM | AELAQNKEWL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| EKIEREGQQL | MQEKPELAAS | VRKKLGEIRQ | CWAELESTTQ | AKARQLFEAS | KADQLVQSFA | ELDKKLLHME | SQLQDVDPGG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DLATVNSQLK | KLQSMESQVE | EWYREVGELQ | AQTAALPLEP | ASKELVGERQ | NAVGERLVRL | LEPLQERRRL | LLASKELHQV |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| AHDLDDELAW | VQERLPLAMQ | TERGNGLQAV | QQHIKKNQGL | RREIQAHGPR | LEEVLERAGA | LASLRSPEAE | AVRRGLEQLQ |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| SAWAGLREAA | ERRQQVLDAA | FQVEQYYFDV | AEVEAWLGEQ | ELLMMSEDKG | KDEQSTLQLL | KKHLQLEQGV | ENYEESIAQL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| SRQCRALLEM | GHPDSEQISR | RQSQVDRLYV | ALKELGEERR | VALEQQYWLY | QLSRQVSELE | HWIAEKEVVA | GSPELGQDFE |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| HVSVLQEKFS | EFASETGMAG | RERLAAVNQM | VDELIECGHT | AAATMAEWKD | GLNEAWAELL | ELMGTRAQLL | AASRELHKFF |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| SDARELQGQI | EEKRRRLPRL | TTPPEPRPSA | SSMQRTLRAF | EHDLQLLVSQ | VRQLQEGAAQ | LRTVYAGEHA | EAIASREQEV |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LQGWKELLSA | CEDARLHVSS | TADALRFHSQ | VRDLLSWMDG | IASQIGAADK | PRDVSSVEVL | MNYHQGLKTE | LEARVPELTT |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| CQELGRSLLL | NKSAMADEIQ | AQLDKLGTRK | EEVSEKWDRH | WEWLQQMLEV | HQFAQEAVVA | DAWLTAQEPL | LQSRELGSSV |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| DEVEQLIRRH | EAFRKAAAAW | EERFSSLRRL | TTIEKIKAEQ | SKQPPTPLLG | RKFFGDPTEL | AAKAAPLLRP | GGYERGLEPL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1131 | 7 | 530.7679 | 3.99 | 2 | 44.3 | 18.5 | 2 | 2553-2562 | R.EGGDRRASGR.R |  | WUP:QUP 3.65<br>QU:MU 4.03 |

# Detailed Protein Report

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**Protein 359:** **PREDICTED: calcium-binding mitochondrial carrier protein SCaMC-3 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578833593 | **Score:** | 32.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 6.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.17 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.48 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRGSPGDAER | RQRWGRLFEE | LDSNKDGRVD | VHELRQGLAR | LGGGNPDPGA | QQGISSEGDA | DPDGGLDLEE | FSRYLQEREQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RLLLMFHSLD | RNQDGHIDVS | EIQQSFRALG | ISISLEQAEK | ILHSMDRDGT | MTIDWQEWRD | HFLLHSLENV | EDVLYFWKHS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TVLDIGECLT | VPDEFSKQEK | LTGMWWKQLV | AGAVAGAVSR | TGTAPLDRLK | VFMQVHASKT | NRLNILGGLR | SMVLEGGIRS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LWRGNGINVL | KIAPESAIKF | MAYEQIKRAI | LGQQETLHVQ | ERFVAGSLAG | ATAQTIIYPM | ETLKNWWLQQ | YSHDSADPGI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LVLLACGTIS | STCGQIASYP | LALVRTRMQA | QASIEGGPQL | SMLGLLRHIL | SQEGMRGLYR | GIAPNFMKVI | PAVSISYVVY |
| 410 | 420 | | | | | | |
| ENMKQALGVT | SR | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1190 | 4 | 644.3159 | -77.32 | 2 | 45.0 | 18.2 | 1 | 209-219 | R.LKVFMQVHASK.T | | QU:MU 1.17<br>WUP:QUP 1.48 |

# Detailed Protein Report

## Protein 360: PREDICTED: uncharacterized protein KIAA1210 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578838720 | **Score:** | 32.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 167.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| | | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAESLSEISD | SLDVLEAGDE | GKKKCKFKAL | KSFFVKKKEK | EAEDTQEEEM | LELSLSSSNI | NISSLQPVRE | NQPTKARAKS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SMGSKALSHD | SIFMLGPEPE | RSASKMFPSM | DPQRGRPQQR | SHISRTLPKP | RSKVPGVVSG | AMSGAVLQNV | PTSAVWVAGP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KITENPPSRR | RRLSIIPPVI | QPEIISKNLV | EISLDDESPK | NPQKKALPHK | SLTATQSFSE | LSSGPDCSQS | LTAFATLAST |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SSTQLPIGFS | TPATTQGCLD | SSAARHKMTL | NPRKQKKNLQ | VIVEPKEEEP | NLPLVSEEEK | SITKPKEINE | KKLGMDSADS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SSQKQNNKTE | MYDKKTTDQA | PNTDASRSQG | YPMSAAYGRR | WRRKGASVSG | LSGCEFKGRS | LKQSSEGYGL | GDRAGSSPTN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KTARNVPFSH | LSLEKDNMEQ | PTTSQPETTT | PQGLLSDKDD | MGRRNAGIDF | GSRKASAAQP | IPENMDNSMV | SDPQPYHEDA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ASGAEKTEAR | ASLSLMVESL | STTQEEAILS | VAAEAQVFMN | PSHIQLEDQE | AFSFDLQKAQ | SKMESAQDVQ | TICKEKPSGN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VHQTFTASVL | GMTSTTAKGD | VYAKTLPPRS | LFQSSRKPDA | EEVSSDSENI | PEEGDGSEEL | AHGHSSQSLG | KFEDEQEVFS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ESKSFVEDLS | SSEEELDLRC | LSQALEEPED | AEVFTESSSY | VEKYNTSDDC | SSSEEDLPLR | HPAQALGKPK | NQQEVSSASN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NTPEEQNDFM | QQLPSRCPSQ | PIMNPTVQQQ | VPTSSVGTSI | KQSDSVEPIP | PRHPFQPWVN | PKVEQEVSSS | PKSMAVEESI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SMKPLPPKLL | CQPLMNPKVQ | QNMFSGSEDI | AVERVISVEP | LLPRYSPQSL | TDPQIRQISE | STAVEEGTYV | EPLPPRCLSQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PSERPKFLDS | MSTSAEWSSP | VAPTPSKYTS | PPWVTPKFEE | LYQLSAHPES | TTVEEDISKE | QLLPRHLSQL | TVGNKVQQLS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SNFERAAIEA | DISGSPLPPQ | YATQFLKRSK | VQEMTSRLEK | MAVEGTSNKS | PIPRRPTQSF | VKFMAQQIFS | ESSALKRGSD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VAPLPPNLPS | KSLSKPEVKH | QVFSDSGSAN | PKGGISSKML | PMKHPLQSLG | RPEDPQKVFS | YSERAPGKCS | SFKEQLSPRQ |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LSQALRKPEY | EQKVSPVSAS | SPKEWRNSKK | QLPPKHSSQA | SDRSKFQPQM | SSKGPVNVPV | KQSSGEKHLP | SSSPFQQQVH |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SSSVNAAARR | SVFESNSDNW | FLGRDEAFAI | KTKKFSQGSK | NPIKSIPAPA | TKPGKFTIAP | VRQTSTSGGI | YSKKEDLESG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DGNNNQHANL | SNQDDVEKLF | GVRLKRAPPS | QKYKSEKQDN | FTQLASVPSG | PISSSVGRGH | KIRSTSQGLL | DAAGNLTKIS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| YVADKQQSRP | KSESMAKKQP | ACKTPGKPAG | QQSDYAVSEP | VWITMAKQKQ | KSFKAHISVK | ELKTKSNAGA | DAETKEPKYE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GAGSANENQP | KKMFTSSVHK | QEKTAQMKPP | KPTKSVGFEA | QKILQVPAME | KETKRSSTLP | AKFQNPVEPI | EPVWFSLARK |
| 1530 | 1540 | | | | | | |
| KAKAWSHMAE | ITQ | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1818 | 1 | 582.2582 | -176.44 | 1 | 53.1 | 16.6 | 0 | 1151-1155 | K.QLPPK.H | |

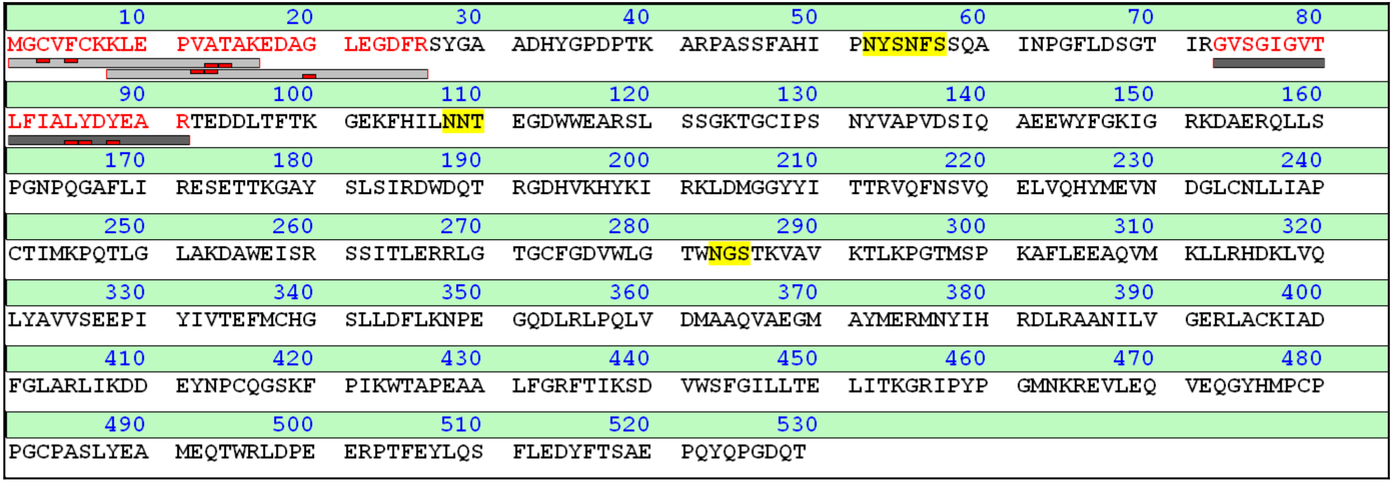
# Detailed Protein Report

## Protein 361: tyrosine-protein kinase Fgr [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4885235 | **Score:** | 32.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 8.5 |
| | | **No. of unique Peptides:** | 3 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578798632 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: tyrosine-protein kinase Fgr isoform X1 [Homo sapiens] |
| gi\|112382244 | refseq_human (refseq_human_20140103.fasta) | tyrosine-protein kinase Fgr [Homo sapiens] |
| gi\|112382241 | refseq_human (refseq_human_20140103.fasta) | tyrosine-protein kinase Fgr [Homo sapiens] |



```
        10         20         30         40         50         60         70         80
MGCVFCKKLE PVATAKEDAG LEGDFRSYGA ADHYGPDPTK ARPASSFAHI PNYSNFSSQA INPGFLDSGT IRGVSGIGVT
        90        100        110        120        130        140        150        160
LFIALYDYEA RTEDDLTFTK GEKFHILNNT EGDWWEARSL SSGKTGCIPS NYVAPVDSIQ AEEWYFGKIG RKDAERQLLS
       170        180        190        200        210        220        230        240
PGNPQGAFLI RESETTKGAY SLSIRDWDQT RGDHVKHYKI RKLDMGGYYI TTRVQFNSVQ ELVQHYMEVN DGLCNLLIAP
       250        260        270        280        290        300        310        320
CTIMKPQTLG LAKDAWEISR SSITLERRLG TGCFGDVWLG TWNGSTKVAV KTLKPGTMSP KAFLEEAQVM KLLRHDKLVQ
       330        340        350        360        370        380        390        400
LYAVVSEEPI YIVTEFMCHG SLLDFLKNPE GQDLRLPQLV DMAAQVAEGM AYMERMNYIH RDLRAANILV GERLACKIAD
       410        420        430        440        450        460        470        480
FGLARLIKDD EYNPCQGSKF PIKWTAPEAA LFGRFTIKSD VWSFGILLTE LITKGRIPYP GMNKREVLEQ VEQGYHMPCP
       490        500        510        520        530
PGCPASLYEA MEQTWRLDPE ERPTFEYLQS FLEDYFTSAE PQYQPGDQT
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2000 | 1 | 899.3791 | -86.20 | 2 | 53.4 | 11.8 | 2 | 1-16 | -.MGCVFCKKLEPVATAK.E | Carbamidomethyl: 6;<br>Oxidation: 1 |
| 2074 | 1 | 682.6660 | -32.64 | 3 | 56.3 | 10.3 | 2 | 8-26 | K.KLEPVATAKEDAGLEGDFR.S | |
| 1458 | 1 | 1022.6515 | 107.92 | 2 | 46.6 | 10.7 | 0 | 73-91 | R.GVSGIGVTLFIALYDYEAR.T | |

# Detailed Protein Report

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**Protein 362:** **PREDICTED: NAD-dependent protein deacylase sirtuin-5, mitochondrial isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530381706 | **Score:** | 32.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 14.1 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.99 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.07 | **CV:** | 115.25 % | **No. of Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRPLQIVPSR | LISQLYCGLK | PPASTRNQIC | LKMARPSSSM | ADFRKFFAKA | KHIVIISGAG | VSAESGVPTF | RGAGGYWRKW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QAQDLATPLA | FAHNPSRVWE | FYHYRREVMG | SKEPNAGHRA | IAECETRLGK | QGRRVVVITQ | NIDELHRKAG | TKNLLEIHGS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LFKTRCTSCG | VVAENYKSPI | CPALSGKGAP | EPGTQDASIP | VEKLPRWALP | LWCTQQPCLP | PRWLPGACQW | LNLTRRPPQL |
| 250 | 260 | 270 | 280 | 290 | | | |
| RTDSGFISRD | PVERLFLKPL | PVMKMKLFLK | CPGEERNYSI | SKN | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 324 | 1 | 686.3446 | 49.16 | 2 | 32.7 | 11.4 | 0 | 33-44 | K.MARPSSSMADFR.K | Oxidation: 8 | WUP:QUP 0.43<br>QU:MU 1.99 |
| 553 | 1 | 731.0325 | 126.18 | 2 | 36.5 | 10.4 | 1 | 255-266 | R.LFLKPLPVMKMK.L | Oxidation: 9 | WUP:QUP 2.69 |

# Detailed Protein Report

## Protein 363: adenomatous polyposis coli protein isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|306922386 | **Score:** | 32.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 308.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | |
|---|---|---|---|
| ***WUP:QUP*** | **Median:** 0.63 | **CV:** 0.00 % | **No. of Peptides:** 1 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MYASLGSGPV APLPASVPPS VLGSWSTGGS RSCVRQETKS PGGARTSGHW ASVWQEVLKQ LQGSIEDEAM ASSGQIDLLE
        90        100        110        120        130        140        150        160
RLKELNLDSS NFPGVKLRSK MSLRSYGSRE GSVSSRSGEC SPVPMGSFPR RGFVNGSRES TGYLEELEKE RSLLLADLDK
       170        180        190        200        210        220        230        240
EEKEKDWYYA QLQNLTKRID SLPLTENFSL QTDMTRRQLE YEARQIRVAM EEQLGTCQDM EKRAQRSSQN KHETGSHDAE
       250        260        270        280        290        300        310        320
RQNEGQGVGE INMATSGNGQ GSTTRMDHET ASVLSSSSTH SAPRRLTSHL GTKVEMVYSL LSMLGTHDKD DMSRTLLAMS
       330        340        350        360        370        380        390        400
SSQDSCISMR QSGCLPLLIQ LLHGNDKDSV LLGNSRGSKE ARARASAALH NIIHSQPDDK RGRREIRVLH LLEQIRAYCE
       410        420        430        440        450        460        470        480
TCWEWQEAHE PGMDQDKNPM PAPVEHQICP AVCVLMKLSF DEEHRHAMNE LGGLQAIAEL LQVDCEMYGL TNDHYSITLR
       490        500        510        520        530        540        550        560
RYAGMALTNL TFGDVANKAT LCSMKGCMRA LVAQLKSESE DLQQVIASVL RNLSWRADVN SKKTLREVGS VKALMECALE
       570        580        590        600        610        620        630        640
VKKESTLKSV LSALWNLSAH CTENKADICA VDGALAFLVG TLTYRSQTNT LAIIESGGGI LRNVSSLIAT NEDHRQILRE
       650        660        670        680        690        700        710        720
NNCLQTLLQH LKSHSLTIVS NACGTLWNLS ARNPKDQEAL WDMGAVSMLK NLIHSKHKMI AMGSAAALRN LMANRPAKYK
       730        740        750        760        770        780        790        800
DANIMSPGSS LPSLHVRKQK ALEAELDAQH LSETFDNIDN LSPKASHRSK QRHKQSLYGD YVFDTNRHDD NRSDNFNTGN
       810        820        830        840        850        860        870        880
MTVLSPYLNT TVLPSSSSSR GSLDSSRSEK DRSLERERGI GLGNYHPATE NPGTSSKRGL QISTTAAQIA KVMEEVSAIH
       890        900        910        920        930        940        950        960
TSQEDRSSGS TTELHCVTDE RNALRRSSAA HTHSNTYNFT KSENSNRTCS MPYAKLEYKR SSNDSLNSVS SSDGYGKRGQ
       970        980        990       1000       1010       1020       1030       1040
MKPSIESYSE DDESKFCSYG QYPADLAHKI HSANHMDDND GELDTPINYS LKYSDEQLNS GRQSPSQNER WARPKHIIED
      1050       1060       1070       1080       1090       1100       1110       1120
EIKQSEQRQS RNQSTTYPVY TESTDDKHLK FQPHFGQQEC VSPYRSRGAN GSETNRVGSN HGINQNVSQS LCQEDDYEDD
      1130       1140       1150       1160       1170       1180       1190       1200
KPTNYSERYS EEEQHEEEER PTNYSIKYNE EKRHVDQPID YSLKYATDIP SSQKQSFSFS KSSSGQSSKT EHMSSSSENT
      1210       1220       1230       1240       1250       1260       1270       1280
STPSSNAKRQ NQLHPSSAQS RSGQPQKAAT CKVSSINQET IQTYCVEDTP ICFSRCSSLS SLSSAEDEIG CNQTTQEADS
      1290       1300       1310       1320       1330       1340       1350       1360
ANTLQIAEIK EKIGTRSAED PVSEVPAVSQ HPRTKSSRLQ GSSLSSESAR HKAVEFSSGA KSPSKSGAQT PKSPPEHYVQ
      1370       1380       1390       1400       1410       1420       1430       1440
ETPLMFSRCT SVSSLDSFES RSIASSVQSE PCSGMVSGII SPSDLPDSPG QTMPPSRSKT PPPPPQTAQT KREVPKNKAP
      1450       1460       1470       1480       1490       1500       1510       1520
TAEKRESGPK QAAVNAAVQR VQVLPDADTL LHFATESTPD GFSCSSSLSA LSLDEPFIQK DVELRIMPPV QENDNGNETE
      1530       1540       1550       1560       1570       1580       1590       1600
SEQPKESNEN QEKEAEKTID SEKDLLDDSD DDDIEILEEC IISAMPTKSS RKAKKPAQTA SKLPPPVARK PSQLPVYKLL
      1610       1620       1630       1640       1650       1660       1670       1680
PSQNRLQPQK HVSFTPGDDM PRVYCVEGTP INFSTATSLS DLTIESPPNE LAAGEGVRGG AQSGEFEKRD TIPTEGRSTD
      1690       1700       1710       1720       1730       1740       1750       1760
EAQGGKTSSV TIPELDDNKA EEGDILAECI NSAMPKGKSH KPFRVKKIMD QVQQASASSS APNKNQLDGK KKKPTSPVKP
      1770       1780       1790       1800       1810       1820       1830       1840
IPQNTEYRTR VRKNADSKNN LNAERVFSDN KDSKKQNLKN NSKVFNDKLP NNEDRVRGSF AFDSPHHYTP IEGTPYCFSR
      1850       1860       1870       1880       1890       1900       1910       1920
NDSLSSLDFD DDDVDLSREK AELRKAKENK ESEAKVTSHT ELTSNQQSAN KTQAIAKQPI NRGQPKPILQ KQSTFPQSSK
      1930       1940       1950       1960       1970       1980       1990       2000
DIPDRGAATD EKLQNFAIEN TPVCFSHNSS LSSLSDIDQE NNNKENEPIK ETEPPDSQGE PSKPQASGYA PKSFHVEDTP
      2010       2020       2030       2040       2050       2060       2070       2080
VCFSRNSSLS SLSIDSEDDL LQECISSAMP KKKKPSRLKG DNEKHSPRNM GGILGEDLTL DLKDIQRPDS EHGLSPDSEN
      2090       2100       2110       2120       2130       2140       2150       2160
FDWKAIQEGA NSIVSSLHQA AAAACLSRQA SSDSDSILSL KSGISLGSPF HLTPDQEEKP FTSNKGPRIL KPGEKSTLET
      2170       2180       2190       2200       2210       2220       2230       2240
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2988 | 1 | 619.0064 | -1.40 | 3 | 66.1 | 10.6 | 0 | 1753-1768 | K.KPTSPVKPIPQNTEYR.T | | WUP:QUP 0.63 |
| 1774 | 1 | 620.2541 | -173.92 | 2 | 52.0 | 10.5 | 1 | 1892-1902 | K.TQAIAKQPINR.G | | |

# Detailed Protein Report

## Protein 364: PREDICTED: MAGUK p55 subfamily member 6 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530384825 | **Score:** | 32.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 48.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 10.0 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNNSSINNQL | LPVDAIRILG | IHKRAGEPLG | VTFRVENNDL | VIARILHGGM | IDRQGLLHVG | DIIKEVNGHE | VGNNPKELQE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LLKNISGSVT | LKILPSYRDT | ITPQQVFVKC | HFDYNPYNDN | LIPCKEAGLK | FSKGEILQIV | NREDPNWWQA | SHVKEGGSAG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LIPSQFLEEK | RKAFVRRDWD | NSGPFCGTIS | SKKKKKMMYL | TTRNAEFDRH | EIQIYEEVAK | MPPFQRKTLV | LIGAQGVGRR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SLKNRFIVLN | PTRFGTTVPF | TSRKPREDEK | DGQAYKFVSR | SEMEADIKAG | KYLEHGEYEG | NLYGTKIDSI | LEVVQTGRTC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ILDVNPQALK | VLRTSEFMPY | VVFIAAPELE | TLRAMHKAVV | DAGITTKLLT | DSDLKKTVDE | SARIQRAYNH | YFDLIIINDN |
| 410 | 420 | 430 | | | | | |
| LDKAFEKLQT | AIEKLRMEPQ | WVPISWVY | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2335 | 1 | 938.2188 | 84.20 | 3 | 57.5 | 10.4 | 1 | 334-357 | R.TSEFMPYVVFIAAPELETLRAMHK.A | Oxidation: 5, 22 |
| 2850 | 1 | 994.4934 | -74.35 | 2 | 64.3 | 22.2 | 2 | 358-376 | K.AVVDAGITTKLLTDSDLKK.T | |

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# Detailed Protein Report

## Protein 365: PREDICTED: gamma-2-syntrophin isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578802555 | **Score:** | 32.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 53.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| | | **Sequence Coverage [%]:** | 8.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLSVWAEATR | AGITVTLRRQ | PVGGLGLSIK | GGSEHNVPVV | ISKIFEDQAA | DQTGMLFVGD | AVLQVNGIHV | ENATHEEVVH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LLRNAGDEVT | ITVEYLREAP | AFLKLPLGSP | GPSSDHSSGA | SSPLFDSGLH | LNGNSSTTAP | SSPSSPIAKD | PRYEKRWLDT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LSVPLSMARI | SRYKAGTEKL | RWNAFEVLAL | DGVSSGILRF | YTAQDGTDWL | RAVSANIREL | TLQNMKMANK | CCSPSDQVVH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MGWVNEKLQG | ADSSQTFRPK | FLALKGPSFY | VFSTPPVSTF | DWVRAERTYH | LCEVLFKVHK | FWLTEDCWLQ | ANLYLGLQDF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DFEDQRPYCF | SIVAGHGKSH | VFNVELGSEL | AMWEKSFQRA | TFMEVQRTGS | RTYMCSWQGE | MLCFTVDFAL | GFTCFESKTK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NVLWRFKFSQ | LKGSSDDGKT | RVKLLFQNLD | TKQIETKELE | FQDLRAVLHC | IHSFIAAKVA | SVDPGFMDSQ | SLARKYMYSS |
| 490 | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2101 | 1 | 788.3311 | -169.19 | 2 | 56.1 | 10.1 | 2 | 420-432 | K.TRVKLLFQNLDTK.Q | |

# Detailed Protein Report

## Protein 366: PREDICTED: CAS1 domain-containing protein 1 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578814529 | **Score:** | 32.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 72.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.55 | **CV:** | 0.00 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 0.30 | **CV:** | 0.00 % | **No. of Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MGRCVLFSRN CSSIAPTWAQ VAASKLGDSP KARVRARRVP LVLSPHTPMA LPQPPPPAGA RDPVTPEHWA SGPPSQAQPL
        90        100        110        120        130        140        150        160
LRQEAKEEEE GEETGVQGAW GTGTAEQRRR GWGEAAESAA AEEGQAEVGG AAAAGSGSPA GGAGGGLGSW RPLLAWLQRR
       170        180        190        200        210        220        230        240
QPQCCPCAAP LSRSAAHCCH GGTKMAALAY NLGKREINHY FSVRSAKVLA LVAVLLLAAC HLASRRYRGN DSCEYLLSSG
       250        260        270        280        290        300        310        320
RFLGEKVWQP HSCMMHKYKI SEAKNCLVDK HIAFIGDSRI RQLFYSFVKI INPQFKEEGN KHENIPFEDK TASVKVDFLW
       330        340        350        360        370        380        390        400
HPEVNGSMKQ CIKVWTEDSI AKPHVIVAGA ATWSIKIHNG SSEALSQYKM NITSIAPLLE KLAKTSDVYW VLQDPVYEDL
       410        420        430        440        450        460        470        480
LSENRKMITN EKIDAYNEAA VSILNSSTRN SKSNVKMFSV SKLIAQETIM ESLDGLHLPE SSRETTAMIL MNVYCNKILK
       490        500        510        520        530        540        550        560
PVDGSCCQPR PPVTLIQKLA ACFFTLSIIG YLIFYIIHRN AHRKNKPCTD LESGEEKKNI INTPVSSLEI LLQSFCKLGL
       570        580        590        600        610        620        630        640
IMAYFYMCDR ANLFMKENKF YTHSSFFIPI IYILVLGVFY NENTKETKVL NREQTDEWKG WMQLVILIYH ISGASTIVGA
       650        660
IGTQEGEMTF I
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 149 | 2 | 793.8480 | -29.08 | 2 | 31.6 | 11.2 | 1 | 160-173 | R.RQPQCCPCAAPLSR.S | Carbamidomethyl: 6 | WUP:QUP<br>QU:MU | 0.30<br>1.55 |
| 175 | 4 | 793.8315 | -49.90 | 2 | 32.2 | 21.3 | 1 | 160-173 | R.RQPQCCPCAAPLSR.S | Carbamidomethyl: 8 | WUP:QUP<br>QU:MU | 0.30<br>1.55 |

# Detailed Protein Report

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## Protein 367: PREDICTED: PAX3- and PAX7-binding protein 1 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578836733 | **Score:** | 32.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 86.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| | | **Sequence Coverage [%]:** | 5.7 |
| | | **No. of unique Peptides:** | 3 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFRKARRVNV | RKRNDSEEEE | RERDEEQEPP | PLLPPPGTGE | EAGPGGGDRA | PGGESLLGPG | PSPPSALTPG | LGAEAGGGFP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GGAEPGNGLK | PRKRPRENKE | VPRASLLSFQ | DEEEENEEVF | KVKKSSYSKK | IVKLLKKEYK | EDLEKSKIKT | ELNSSAESEQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PLDKTGHVKD | TNQEDGVIIS | EHGEDEMDME | SEKEEEKPKT | GGAFSNALSS | LNVLRPGEIP | DAAFIHAARK | KRQMARELGD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FTPHDNEPGK | GRLVREDEND | ASDDEDDDEK | RRIVFSVKEK | SQRQKIAEEI | GIEGSDDDAL | VTGEQDEELS | RWEQEQIRKG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| INIPQVQASQ | PAEVNMYYQN | TYQTMPYGSS | YGIPYSYTAY | GSSDAKSQKT | DNTVPFKTPS | NEMTPVTIDL | VKKQLKDRLD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SMKELHKTNR | QQHEKHLQSR | VDSTRAIERL | EGSSGGIGER | YKFLQEMRGY | VQDLLECFSE | KVPLINELES | AIHQLYKQRA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SRLVQRRQDD | IKDESSEFSS | HSNKALMAPN | LDSFGRDRAL | YQEHAKRRIA | EREARRTRRR | QAREQTGKMA | DHLEGLSSDD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EETSTDITNF | NLEKDRISKE | SGKVFEDVLE | SFYSIDCIKS | QFEAWRSKYY | TSYKDAYIGL | CLPKLFNPLI | RLQLLTWTPL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EAKCRDFENM | LWFESLLFYG | CEEREQEKDD | VDVALLPTIV | EKVILPKLTV | IAENMWDPFS | TTQTSRMVGI | TLKLINGYPS |
| 730 | 740 | 750 | 760 | | | | |
| VVNAENKNTQ | VYLKALLLRM | RRTLDDDVFM | PLYPKNC | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 584 | 1 | 824.2497 | -169.01 | 2 | 36.9 | 10.9 | 0 | 150-164 | K.TELNSSAESEQPLDK.T | |
| 156 | 1 | 822.7809 | -180.37 | 2 | 31.7 | 11.6 | 0 | 378-392 | K.TPSNEMTPVTIDLVK.K | |
| 2673 | 1 | 676.8390 | -7.24 | 2 | 61.8 | 10.0 | 1 | 430-442 | R.LEGSSGGIGERYK.F | |

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# Detailed Protein Report

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## Protein 368: kinesin-like protein KIF6 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|573459724 | **Score:** | 32.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 86.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 3.8 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MVKQTIQIFA RVKPPVRKHQ QGIYSIDEDE KLIPSLEIIL PRDLADGFVN NKRESYKFKF QRIFDQDANQ ETVFENIAKP
        90        100        110        120        130        140        150        160
VAGSVLAGYN GTIFAYGQTG SGKTFTITGG AERYSDRGII PRTLSYIFEQ LQKDSSKIYT THISYLEIYN ECGYDLLDPR
       170        180        190        200        210        220        230        240
HEASSLEDLP KVTILEDPDQ NIHLKNLTLH QATTEEEALN LLFLGDTNRM IAETPMNQAS TRSHCIFTIH LSSKEPGSAT
       250        260        270        280        290        300        310        320
VRHAKLHLVD LAGSERVAKT GVGGHLLTEA KYINLSLHYL EQVIIALSEK HRSHIPYRNS MMTSVLRDSL GGNCMTTMIA
       330        340        350        360        370        380        390        400
TLSLEKRNLD ESISTCRFAQ RVALIKNEAV LNEEINPRLV IKRLQKEIQE LKDELAMVTG EQRTEALTEA ELLQLEKLIT
       410        420        430        440        450        460        470        480
SFLEDQDSDS RLEVGADMRK VHHCFHHLKK LLNDKKILEN NTVSSESKDQ DCQEPLKEEE YRKLRDILKQ RDNEISILSE
       490        500        510        520        530        540        550        560
VMKKLPLSWF ERGMREEMSL GCQEAFEIFK RDHADSVTID DNKQILKQRF SEAKALGESI NEARSKIGHL KEEITQRHIQ
       570        580        590        600        610        620        630        640
QVALGISENM AVPLMPDQQE EKLRSQLEEE KRRYKTMFTR LKALKVEIEH LQLLMDKAKV KLQKEFEVWW AEEATNLQVN
       650        660        670        680        690        700        710        720
SPAVNSLDHT KPFLQTSDSQ HEWSQLLSNK SSGGWEVQDQ GTGRFDVCDV NARKILPSPC PSPHSQKQSS TSTPLEDSIP
       730        740        750        760
KRPVSSIPLT GDSQTDSDII AFIKARQSIL QKQCLGSN
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2648 | 1 | 994.9726 | -29.06 | 2 | 63.2 | 15.8 | 1 | 367-383 | K.EIQELKDELAMVTGEQR.T | |

# Detailed Protein Report

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## Protein 369: nucleus accumbens-associated protein 1 [Homo sapiens]

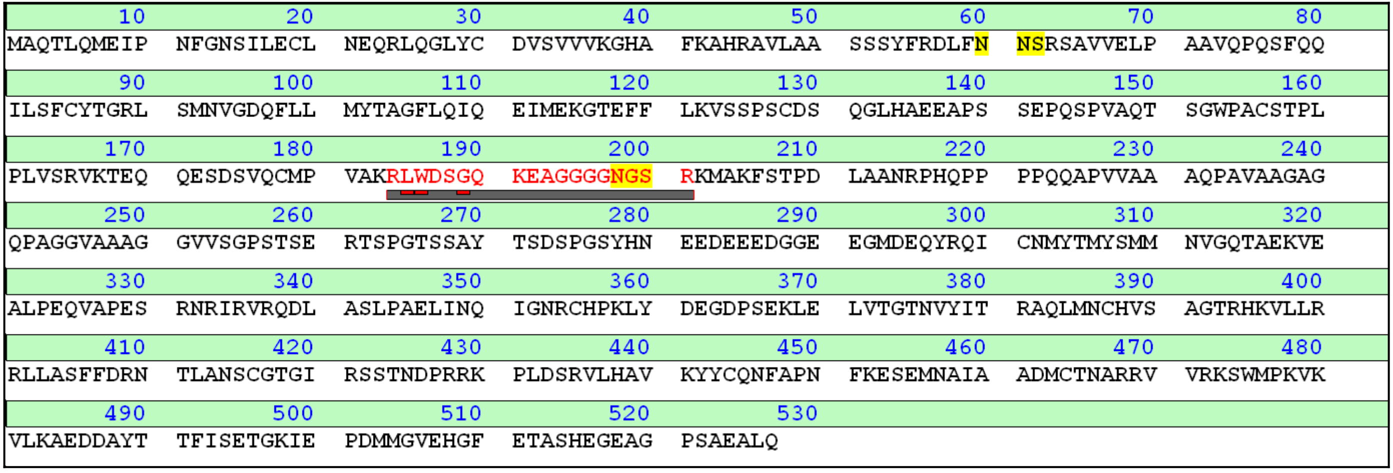
| | | | |
|---|---|---|---|
| **Accession:** | gi\|16418383 | **Score:** | 32.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 4.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***WUP:QUP*** | **Median:** | 1.25 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578832952 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: nucleus accumbens-associated protein 1 isoform X2 [Homo sapiens] |
| gi\|530414464 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: nucleus accumbens-associated protein 1 isoform X1 [Homo sapiens] |



| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAQTLQMEIP | NFGNSILECL | NEQRLQGLYC | DVSVVVKGHA | FKAHRAVLAA | SSSYFRDLFN | NSRSAVVELP | AAVQPQSFQQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ILSFCYTGRL | SMNVGDQFLL | MYTAGFLQIQ | EIMEKGTEFF | LKVSSPSCDS | QGLHAEEAPS | SEPQSPVAQT | SGWPACSTPL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PLVSRVKTEQ | QESDSVQCMP | VAKRLWDSGQ | KEAGGGGNGS | RKMAKFSTPD | LAANRPHQPP | PPQQAPVVAA | AQPAVAAGAG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QPAGGVAAAG | GVVSGPSTSE | RTSPGTSSAY | TSDSPGSYHN | EEDEEEDGGE | EGMDEQYRQI | CNMYTMYSMM | NVGQTAEKVE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ALPEQVAPES | RNRIRVRQDL | ASLPAELINQ | IGNRCHPKLY | DEGDPSEKLE | LVTGTNVYIT | RAQLMNCHVS | AGTRHKVLLR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RLLASFFDRN | TLANSCGTGI | RSSTNDPRRK | PLDSRVLHAV | KYYCQNFAPN | FKESEMNAIA | ADMCTNARRV | VRKSWMPKVK |
| 490 | 500 | 510 | 520 | 530 | | | |
| VLKAEDDAYT | TFISETGKIE | PDMMGVEHGF | ETASHEGEAG | PSAEALQ | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1731 | 6 | 916.4065 | -40.21 | 2 | 51.4 | 20.9 | 2 | 184-201 | K.RLWDSGQKEAGGGGNGSR.K | | WUP:QUP 1.25 |

# Detailed Protein Report

## Protein 370: ubiquinone biosynthesis protein COQ7 homolog isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|25453484 | **Score:** | 32.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 14.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSCAGAAAAP | RLWRLRPGAR | RSLSAYGRRT | SVRFRSSGMT | LDNISRAAVD | RIIRVDHAGE | YGANRIYAGQ | MAVLGRTSVG |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| PVIQKMWDQE | KDHLKKFNEL | MVTFRVRPTV | LMPLWNVLGF | ALGAGTALLG | KEGAMACTVA | VEESIAHHYN | NQIRTLMEED |
| **170** | **180** | **190** | **200** | **210** | **220** | | |
| PEKYEELLQL | IKKFRDEELE | HHDIGLDHDA | ELAPAYAVLK | SIIQAGCRVA | IYLSERL | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1373 | 1 | 1045.9338 | -113.36 | 2 | 45.5 | 20.1 | 2 | 36-54 | R.SSGMTLDNISRAAVDRIIR.V | Oxidation: 4 |

# Detailed Protein Report

## Protein 371: potassium channel subfamily K member 10 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|20143944 | **Score:** | 32.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 60.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***QU:MU*** **Median:** 0.42 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKFPIETPRK | QVNWDPKVAV | PAAAPVCQPK | SATNGQPPAP | APTPTPRLSI | SSRATVVARM | EGTSQGGLQT | VMKWKTVVAI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FVVVVVYLVT | GGLVFRALEQ | PFESSQKNTI | ALEKAEFLRD | HVCVSPQELE | TLIQHALDAD | NAGVSPIGNS | SNNSSHWDLG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SAFFFAGTVI | TTIGYGNIAP | STEGGKIFCI | LYAIFGIPLF | GFLLAGIGDQ | LGTIFGKSIA | RVEKVFRKKQ | VSQTKIRVIS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TILFILAGCI | VFVTIPAVIF | KYIEGWTALE | SIYFVVVTLT | TVGFGDFVAG | GNAGINYREW | YKPLVWFWIL | VGLAYFAAVL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SMIGDWLRVL | SKKTKEEVGE | IKAHAAEWKA | NVTAEFRETR | RRLSVEIHDK | LQRAATIRSM | ERRRLGLDQR | AHSLDMLSPE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KRSVFAALDT | GRFKASSQES | INNRPNNLRL | KGPEQLNKHG | QGASEDNIIN | KFGSTSRLTK | RKNKDLKKTL | PEDVQKIYKT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | |
| FRNYSLDEEK | KEEETEKMCN | SDNSSTAMLT | DCIQQHAELE | NGMIPTDTKD | REPENNSLLE | DRN | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1557 | 2 | 494.2527 | -64.89 | 2 | 49.7 | 17.6 | 1 | 3-10 | K.FPIETPRK.Q | | QU:MU 0.42 |
| 2750 | 1 | 741.8557 | 7.67 | 2 | 64.8 | 14.8 | 0 | 60-73 | R.MEGTSQGGLQTVMK.W | Oxidation: 13 | |

# Detailed Protein Report

## Protein 372: PREDICTED: nardilysin isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530362704 | **Score:** | 32.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 105.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVFMGSLKYP | DENGFDAFLK | KHGGSDNAST | DCERTVFQFD | VQRKYFKEAL | DRWAQFFIHP | LMIRDAIDRE | VEAVDSEYQL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ARPSDANRKE | MLFGSLARPG | HPMGKFFWGN | AETLKHEPRK | NNIDTHARLR | EFWMRYYSSH | YMTLVVQSKE | TLDTLEKWVT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EIFSQIPNNG | LPRPNFGHLT | DPFDTPAFNK | LYRVVPIRKI | HALTITWALP | PQQQHYRVKP | LHYISWLVGH | EGKGSILSFL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RKKCWALALF | GGNGETGFEQ | NSTYSVFSIS | ITLTDEGYEH | FYEVAYTVFQ | YLKMLQKLGP | EKRIFEEIRK | IEDNEFHYQE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QTDPVEYVEN | MCENMQLYPL | QDILTGDQLL | FEYKPEVIGE | ALNQLVPQKA | NLVLLSGANE | GKCDLKEKWF | GTQYSIEDIE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NSWAELWNSN | FELNPDLHLP | AENKYIATDF | TLKAFDCPET | EYPVKIVNTP | QGCLWYKKDN | KFKIPKAYIR | FHLISPLIQK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SAANVVLFDI | FVNILTHNLA | EPAYEADVAQ | LEYKLVAGEH | GLIIRVKGFN | HKLPLLFQLI | IDYLAEFNST | PAVFTMITEQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LKKTYFNILI | KPETLAKDVR | LLILEYARWS | MIDKYQALMD | GLSLESLLSF | VKEFKSQLFV | EGLVQGNVTS | TESMDFLKYV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VDKLNFKPLE | QEMPVQFQVV | ELPSGHHLCK | VKALNKGDAN | SEVTVYYQSG | TRSLREYTLM | ELLVMHMEEP | CFDFLRTKQT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LGYHVYPTCR | NTSGILGFSV | TVGTQATKYN | SEVVDKKIEE | FLSSFEEKIE | NLTEEAFNTQ | VTALIKLKEC | EDTHLGEEVD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RNWNEVVTQQ | YLFDRLAHEI | EALKSFSKSD | LVNWFKAHRG | PGSKMLSVHV | VGYGKYELEE | DGTPSSEDSN | SSCEVMQLTY |
| 890 | 900 | 910 | 920 | | | | |
| LPTSPLLADC | IIPITDIRAF | TTTLNLLPYH | KIVK | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2877 | 2 | 703.3682 | 134.70 | 2 | 66.7 | 17.6 | 0 | 22-34 | K.HGGSDNASTDCER.T | Carbamidomethyl: 11 |
| 923 | 1 | 512.2392 | -109.51 | 2 | 41.6 | 14.7 | 0 | 816-824 | R.LAHEIEALK.S | |

# Detailed Protein Report

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**Protein 373:** **protein scribble homolog isoform b [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|355390315 | **Score:** | 32.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 174.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLKCIPLWRC | NRHVESVDKR | HCSLQAVPEE | IYRYSRSLEE | LLLDANQLRE | LPKPFFRLLN | LRKLGLSDNE | IQRLPPEVAN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FMQLVELDVS | RNDIPEIPES | IKFCKALEIA | DFSGNPLSRL | PDGFTQLRSL | AHLALNDVSL | QALPGDVGNL | ANLVTLELRE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NLLKSLPASL | SFLVKLEQLD | LGGNDLEVLP | DTLGALPNLR | ELWLDRNQLS | ALPPELGNLR | RLVCLDVSEN | RLEELPAELG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GLVLLTDLLL | SQNLLRRLPD | GIGQLKQLSI | LKVDQNRLCE | VTEAIGDCEN | LSELILTENL | LMALPRSLGK | LTKLTNLNVD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RNHLEALPPE | IGGCVALSVL | SLRDNRLAVL | PPELAHTTEL | HVLDVAGNRL | QSLPFALTHL | NLKALWLAEN | QAQPMLRFQT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EDDARTGEKV | LTCYLLPQQP | PPSLEDAGQQ | GSLSETWSDA | PPSRVSVIQF | LEAPIGDEDA | EEAAAEKRGL | QRRATPHPSE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LKVMKRSIEG | RRSEACPCQP | DSGSPLPAEE | EKRLSAESGL | SEDSRPSAST | VSEAEPEGPS | AEAQGGSQQE | ATTAGGEEDA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EEDYQEPTVH | FAEDALLPGD | DREIEEGQPE | APWTLPGGRQ | RLIRKDTPHY | KKHFKISKLP | QPEAVVALLQ | GMQPDGEGPV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| APGGWHNGPH | APWAPRAQKE | EEEEEEGSPQ | EEEEEEEEEN | RAEEEEASTE | EEDKEGAVVS | APSVKGVSFD | QANNLLIEPA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RIEEEELTLT | ILRQTGGLGI | SIAGGKGSTP | YKGDDEGIFI | SRVSEEGPAA | RAGVRVGDKL | LEVNGVALQG | AEHHEAVEAL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RGAGTAVQMR | VWRERMVEPE | NAVTITPLRP | EDDYSPRERR | GGGLRLPLLP | PESPGPLRQR | HVACLARSER | GLGFSIAGGK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GSTPYRAGDA | GIFVSRIAEG | GAAHRAGTLQ | VGDRVLSING | VDVTEARHDH | AVSLLTAASP | TIALLLEREA | GGPLPPSPLP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| HSSPPTAAVA | TTSITTATPG | VPGLPSLAPS | LLAAALEGPY | PVEEIRLPRA | GGPLGLSIVG | GSDHSSHPFG | VQEPGVFISK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VLPRGLAARS | GLRVGDRILA | VNGQDVRDAT | HQEAVSALLR | PCLELSLLVR | RDPAPPGLRE | LCIQKAPGER | LGISIRGGAR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GHAGNPRDPT | DEGIFISKVS | PTGAAGRDGR | LRVGLRLLEV | NQQSLLGLTH | GEAVQLLRSV | GDTLTVLVCD | GFEASTDAAL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EVSPGVIANP | FAAGIGHRNS | LESISSIDRE | LSPEGPGKEK | ELPGQTLHWG | PEATEAAGRG | LQPLKLDYRA | LAAVPSAGSV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| QRVPSGAAGG | KMAESPCSPS | GQQPPSPPSP | DELPANVKQA | YRAFAAVPTS | HPPEDAPAQP | PTPGPAASPE | QLSFRERQKY |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| FELEVRVPQA | EGPPKRVSLV | GADDLRKMQE | EEARKLQQKR | AQMLREAAEA | GAEARLALDG | ETLGEEEQED | EQPPWASPSP |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| TSRQSPASPP | PLGGGAPVRT | AKAERRHQER | LRVQSPEPPA | PERALSPAEL | RALEAEKRAL | WRAARMKSLE | QDALRAQMVL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| SRSQEGRGTR | GPLERLAEAP | SPAPTPSPTP | VEDLGPQTST | SPGRLSPDFA | EELRSLEPSP | SPGPQEEDGE | VALVLLGRPS |
| 1610 | 1620 | 1630 | 1640 | | | | |
| PGAVGPEDVA | LCSSRRPVRP | GRRGLGPVPS | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 129 | 2 | 696.1281 | 130.45 | 3 | 31.3 | 16.1 | 2 | 861-880 | R.HVACLARSERGLGFSIAGGK.G | Carbamidomethyl: 4 |

# Detailed Protein Report

## Protein 374: tumor suppressor candidate gene 1 protein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|51944974 | **Score:** | 32.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 23.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 8.5 |
| | | **No. of unique Peptides:** | 3 |

## Quantitation

***WUP:QUP*** **Median:** 1.49 **CV:** 0.00 % **No. of Peptides:** 2

```
        10         20         30         40         50         60         70         80
MGPMWRMRGG ATRRGSCCGG DGAADGRGPG RSGRARGGGS PSGGGGGVGW RGRADGARQQ LEERFADLAA SHLEAIRARD
```

```
        90        100        110        120        130        140        150        160
EWDRQNARLR QENARLRLEN RRLKRENRSL FRQALRLPGE GGNGTPAEAR RVPEEASTNR RARDSGREDE PGSPRALRAR

       170        180        190        200        210        220
LEKLEAMYRR ALLQLHLEQR GPRPSGDKEE QPLQEPDSGL RSRDSEPSGP WL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1612 | 1 | 853.3687 | 3.55 | 2 | 49.9 | 10.3 | 2 | 14-31 | R.RGSCCGGDGAADGRGPGR.S | Carbamidomethyl: 5 | WUP:QUP 1.49 |
| 1610 | 1 | 853.3997 | 39.87 | 2 | 48.5 | 10.6 | 2 | 14-31 | R.RGSCCGGDGAADGRGPGR.S | Carbamidomethyl: 4 | WUP:QUP 1.49 |
| 474 | 1 | 775.3888 | 94.96 | 2 | 35.9 | 11.4 | 1 | 15-31 | R.GSCCGGDGAADGRGPGR.S | Carbamidomethyl: 3 | |

# Detailed Protein Report

## Protein 375: PREDICTED: protein Shroom4 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578838225 | **Score:** | 32.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 147.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 4.76 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.17 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MESLEQPGQA | TYESHLLPID | QNMYPNQRDS | AYSSFSASSN | ASDCALSLRP | EEPASTDCIM | QGPGPTKAPS | GRPNVAETSG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GSRRTNGGHL | TPSSQMSSRP | QEGYQSGPAK | AVRGPPQPPV | RRDSLQASRA | QLLNGEQRRA | SEPVVPLPQK | EKLSLEPVLP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ARNPNRFCCL | SGHDQVTSEG | HQNCEFSQPP | ESSQQGSEHL | LMQASTKAVG | SPKACDRASS | VDSNPLNEAS | AELAKASFGR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PPHLIGPTGH | RHSAPEQLLA | SHLQHVHLDT | RGSKGMELPP | VQDGHQWTLS | PLHSSHKGKK | SPCPPTGGTH | DQSSKERKTR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QVDDRSLVLG | HQSQSSPPHG | EADGHPSEKG | FLDPNRTSRA | ASELANQQPS | ASGSLVQQAT | DCSSTTKAAS | GTEAGEEGDS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EPKECSRMGG | RRSGGTRGRS | IQNRRKSERF | ATNLRNEIQR | RKAQLQKSKG | PLSQLCDTKE | PVEETQEPPE | SPPLTASNTS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LLSSCKKPPS | PRDKLFNKSM | MLRARSSECL | SQAPESHESR | TGLEGRISPG | QRPGQSSLGL | NTWWKAPDPS | SSDPEKAHAH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| CGVRGGHWRW | SPEHNSQPLV | AAAMEGPSNP | GDNKELKAST | AQAGEDAILL | PFADRRKFFE | ESSKSLSTSH | LPGLTTHSNK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TFTQRPKPID | QNFQPMSSSC | RELRRHPMDQ | SYHSADQPYH | ATDQSYHSMS | PLQSETPTYS | ECFASKGLEN | SMCCKPLHCG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DFDYHRTCSY | SCSVQGALVH | DPCIYCSGEI | CPALLKRNMM | PNCYNCRCHH | HQCIRCSVCY | HNPQHSALED | SSLAPGNTWK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PRKLTVQEFP | GDKWNPITGN | RKTSQSGREM | AHSKTSFSWA | TPFHPCLENP | ALDLSSYRAI | SSLDLLGDFK | HALKKSEETS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VYEEGSSLAS | MPHPLRSRAF | SESHISLAPQ | STRAWGQHRR | ELFSKGDETQ | SDLLGARKKA | FPPPRPPPPN | WEKYRLFRAA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QQQKQQQQQQ | KQQEEEEEEE | EEEEEEEEEE | EEEAEEEEEE | LPPQYFSSET | SGSCALNPEE | VLEQPQPLSF | GHLEGSRQGS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QSVPAEQESF | ALHSSDFLPP | IRGHLGSQPE | QAQPPCYYGI | GGLWRTSGQE | ATESAKQEFQ | HFSPPSGAPG | IPTSYSAYYN |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ISVAKAELLN | KLKDQPEMAE | IGLGEEEVDH | ELAQKKIQLI | ESISRKLSVL | REAQRGLLED | INANSALGEE | VEANLKAVCK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SNEFEKYHLF | VGDLDKVVNL | LLSLSGRLAR | VENALNSIDS | EANQEKLVLI | EKKQQLTGQL | ADAKELKEHV | DRREKLVFGM |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | | |
| VSRYLPQDQL | QDYQHFVKMK | SALIIEQREL | EEKIKLGEEQ | LKCLRESLLL | GPSNF | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 43 | 1 | 750.8112 | -65.69 | 2 | 30.4 | 14.4 | 1 | 557-569 | K.AHAHCGVRGGHWR.W | Carbamidomethyl: 5 | WUP:QUP<br>QU:MU | 0.17<br>4.76 |

# Detailed Protein Report

## Protein 376: PREDICTED: exosome complex exonuclease RRP44 isoform X1 [Homo sapiens]

**Accession:** gi|530402172
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 32.2
**MW [kDa]:** 90.5
**pI:** 6.5
**Sequence Coverage [%]:** 3.1
**No. of unique Peptides:** 2

```
        10         20         30         40         50         60         70         80
MSADNQLQVI FITNDRRNKE KAIEEGIPAF TCEEYVKSLT ANPELIDRLA CLSEEGNEIE SGKIIFSEHL PLSKLQQGIK
        90        100        110        120        130        140        150        160
SGTYLQGTFR ASRENYLEAT VWIHGDNEEN KEIILQGLKH LNRAVHEDIV AVELLPKSQW VAPSSVVLHD EGQNEEDVEK
       170        180        190        200        210        220        230        240
EEETERMLKT AVSEKMLKPT GRVVGIIKRN WRPYCGMLSK SDIKESRRHL FTPADKRIPR IRIETRQAST LEGRRIIVAI
       250        260        270        280        290        300        310        320
DGWPRNSRYP NGHFVRNLGD VGEKETETEV LLLEHDVPHQ PFSQAVLSFL PKMPWSITEK DMKNREDLRH LCICSVDPPG
       330        340        350        360        370        380        390        400
CTDIDDALHC RELENGNLEV GVHIADVSHF IRPGNALDQE SARRGTTVYL CEKRIDMVPE LLSSNLCSLK CDVDRLAFSC
       410        420        430        440        450        460        470        480
IWEMNHNAEI LKTKFTKSVI NSKASLTYAE AQLRIDSANM NDDITTSLRG LNKLAKILKK RRIEKGALTL SSPEVRFHMD
       490        500        510        520        530        540        550        560
SETHDPIDLQ TKELRETNSM VEEFMLLANI SVAKKIHEEF SEHALLRKHP APPPSNYEIL VKAARSRNLE IKTDTAKSLA
       570        580        590        600        610        620        630        640
ESLDQAESPT FPYLNTLLRI LATRCMMQAV YFCSGMDNDF HHYGLASPIY THFTSPIRRY ADVIVHRLLA VAIGADCTYP
       650        660        670        680        690        700        710        720
ELTDKHKLAD ICKNLNFRHK MAQYAQRASV AFHTQLFFKS KGIVSEEAYI LFVRKNAIVV LIPKYGLEGT VFFEEKDKPN
       730        740        750        760        770        780        790        800
PQLIYDDEIP SLKIEDTVFH VFDKVKVKIM LDSSNLQHQK IRMSLVEPQI PGISIPTDTS NMDLNGPKKK KMKLGK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1167 | 1 | 977.5217 | 29.45 | 2 | 44.2 | 19.3 | 2 | 189-204 | K.RNWRPYCGMLSKSDIK.E | |
| 2612 | 1 | 588.6601 | -226.00 | 2 | 60.9 | 13.0 | 2 | 301-309 | K.DMKNREDLR.H | |

# Detailed Protein Report

## Protein 377: PREDICTED: ankyrin-3 isoform X15 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578819314 | **Score:** | 32.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 386.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.57 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.19 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MALPQSEDAM | TGDTDKYLGP | QDLKELGDDS | LPAEGYMGFS | LGARSASSDR | SYTLNRSSYA | RDSMMIEELL | VPSKEQHLTF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TREFDSDSLR | HYSWAADTLD | NVNLVSSPIH | SGFLVSFMVD | ARGGSMRGSR | HHGMRIIIPP | RKCTAPTRIT | CRLVKRHKLA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NPPPMVEGEG | LASRLVEMGP | AGAQFLGPVI | VEIPHFGSMR | GKERELIVLR | SENGETWKEH | QFDSKNEDLT | ELLNGMDEEL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DSPEELGKKR | ICRIITKDFP | QYFAVVSRIK | QESNQIGPEG | GILSSTTVPL | VQASFPEGAL | TKRIRVGLQA | QPVPDEIVKK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ILGNKATFSP | IVTVEPRRRK | FHKPITMTIP | VPPPSGEGVS | NGYKGDTTPN | LRLLCSITGG | TSPAQWEDIT | GTTPLTFIKD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CVSFTTNVSA | RFWLADCHQV | LETVGLATQL | YRELICVPYM | AKFVVFAKMN | DPVESSLRCF | CMTDDKVDKT | LEQQENFEEV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ARSKDIEVLE | GKPIYVDCYG | NLAPLTKGGQ | QLVFNFYSFK | ENRLPFSIKI | RDTSQEPCGR | LSFLKEPKTT | KGLPQTAVCN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LNITLPAHKK | ETESDQDDEI | EKTDRRQSFA | SLALRKRYSY | LTEPGMKTVE | RSTGATRSLP | TTYSYKPFFS | TRPYQSWTTA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PITVPGPAKS | GFTSLSSSSS | NTPSASPLKS | IWSVSTPSPI | KSTLGASTTS | SVKSISDVAS | PIRSFRTMSS | PIKTVVSQSP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YNIQVSSGTL | ARAPAVTEAT | PLKGLASNST | FSSRTSPVTT | AGSLLERSSI | TMTPPASPKS | NINMYSSSLP | FKSIITSAAP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LISSPLKSVV | SPVKSAVDVI | SSAKITMASS | LSSPVKQMPG | HAEVALVNGS | ISPLKYPSSS | TLINGCKATA | TLQEKISSAT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| NSVSSVVSAA | TDTVEKVFST | TTAMPFSPLR | SYVSAAPSAF | QSLRTPSASA | LYTSLGSSIS | ATTSSVTSSI | ITVPVYSVVN |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VLPEPALKKL | PDSNSFTKSA | AALLSPIKTL | TTETHPQPHF | SRTSSPVKSS | LFLAPSALKL | STPSSLSSSQ | EILKDVAEMK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EDLMRMTAIL | QTDVPEEKPF | QPELPKEGRI | DDEEPFKIVE | KVKEDLVKVS | EILKKDVCVD | NKGSPKSPKS | DKGHSPEDDW |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| IEFSSEEIRE | ARQQAAASQS | PSLPERVQVK | AKAASEKDYN | LTKVIDYLTN | DIGSSSLTNL | KYKFEDAKKD | GEERQKRVLK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PAIALQEHKL | KMPPASMRTS | TSEKELCKMA | DSFFGTDTIL | ESPDDFSQHD | QDKSPLSDSG | FETRSEKTPS | APQSAESTGP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KPLFHEVPIP | PVITETRTEV | VHVIRSYDPS | AGDVPQTQPE | EPVSPKPSPT | FMELEPKPTT | SSIKEKVKAF | QMKASSEEDD |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| HNRVLSKGMR | VKEETHITTT | TRMVYHSPPG | GEGASERIEE | TMSVHDIMKA | FQSGRDPSKE | LAGLFEHKSA | VSPDVHKSAA |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ETSAQHAEKD | NQMKPKLERI | IEVHIEKGNQ | AEPTEVIIRE | TKKHPEKEMY | VYQKDLSRGD | INLKDFLPEK | HDAFPCSEEQ |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| GQQEEEELTA | EESLPSYLES | SRVNTPVSQE | EDSRPSSAQL | ISDDSYKTLK | LLSQHSIEYH | DDELSELRGE | SYRFAEKMLL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| SEKLDVSHSD | TEESVTDHAG | PPSSELQGSD | KRSREKIATA | PKKEILSKIY | KDVSENGVGK | VSKDEHFDKV | TVLHYSGNVS |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| SPKHAMWMRF | TEDRLDRGRE | KLIYEDRVDR | TVKEAEEKLT | EVSQFFRDKT | EKLNDELQSP | EKKARPKNGK | EYSSQSPTSS |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SPEKVLLTEL | LASNDEWVKA | RQHGPDGQGF | PKAEEKAPSL | PSSPEKMVLS | QQTEDSKSTV | EAKGSISQSK | APDGPQSGFQ |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| LKQSKLSSIR | LKFEQGTHAK | SKDMSQEDRK | SDGQSRIPVK | KIQESKLPVY | QVFAREKQQK | AIDLPDESVS | VQKDFMVLKT |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| KDEHAQSNEI | VVNDSGSDNV | KKQRTEMSSK | AMPDSFSEQQ | AKDLACHITS | DLATRGPWDK | KVFRTWESSG | ATNNKSQKEK |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| LSHVLVHDVR | ENHIGHPESK | SVDQKNEFMS | VTERERKLLT | NGSLSEIKEM | TVKSPSKKVL | YREYVVKEGD | HPGGLLDQPS |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| RRSESSAVSH | IPVRVADERR | MLSSNIPDGF | CEQSAFPKHE | LSQKLSQSSM | SKETVETQHF | NSIEDEKVTY | SEISKVSKHQ |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 534 | 1 | 676.8481 | -14.81 | 2 | 35.1 | 20.1 | 1 | 3029-3041 | K.TKALTTSSCVDVK.S | | WUP:QUP 1.19<br>QU:MU 1.57 |

# Detailed Protein Report

## Protein 378: PREDICTED: alpha-actinin-4 isoform X1 [Homo sapiens]

**Accession:** gi|530417302
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 32.1
**MW [kDa]:** 104.3
**pI:** 5.2
**Sequence Coverage [%]:** 2.4
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVDYHAANQS | YQYGPSSAGN | GAGGGGSMGD | YMAQEDDWDR | DLLLDPAWEK | QQRKTFTAWC | NSHLRKAGTQ | IENIDEDFRD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GLKLMLLLEV | ISGERLPKPE | RGKMRVHKIN | NVNKALDFIA | SKGVKLVSIG | AEEIVDGNAK | MTLGMIWTII | LRFAIQDISV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EETSAKEGLL | LWCQRKTAPY | KNVNVQNFHI | SWKDGLAFNA | LIHRHRPELI | EYDKLRKDDP | VTNLNNAFEV | AEKYLDIPKM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LDAEDIVNTA | RPDEKAIMTY | VSSFYHAFSG | AQKAETAANR | ICKVLAVNQE | NEHLMEDYEK | LASDLLEWIR | RTIPWLEDRV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PQKTIQEMQQ | KLEDFRDYRR | VHKPPKVQEK | CQLEINFNTL | QTKLRLSNRP | AFMPSEGKMV | SDINNGWQHL | EQAEKGYEEW |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LLNEIRRLER | LDHLAEKFRQ | KASIHEAWTD | GKEAMLKHRD | YETATLSDIK | ALIRKHEAFE | SDLAAHQDRV | EQIAAIAQEL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NELDYYDSHN | VNTRCQKICD | QWDALGSLTH | SRREALEKTE | KQLEAIDQLH | LEYAKRAAPF | NNWMESAMED | LQDMFIVHTI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EEIEGLISAH | DQFKSTLPDA | DREREAILAI | HKEAQRIAES | NHIKLSGSNP | YTTVTPQIIN | SKWEKVQQLV | PKRDHALLEE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QSKQQSNEHL | RRQFASQANV | VGPWIQTKME | EIGRISIEMN | GTLEDQLSHL | KQYERSIVDY | KPNLDLLEQQ | HQLIQEALIF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DNKHTNYTME | HIRVGWEQLL | TTIARTINEV | ENQILTRDAK | GISQEQMQEF | RASFNHFDKK | QTGSMDSDDF | RALLISTGYS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LGEAEFNRIM | SLVDPNHSGL | VTFQAFIDFM | SRETTDTDTA | DQVIASFKVL | AGDKNFITAE | ELRRELPPDQ | AEYCIARMAP |
| 890 | 900 | 910 | | | | | |
| YQGPDAVPGA | LDYKSFSTAL | YGESDL | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2706 | 1 | 693.8970 | 9.14 | 2 | 64.9 | 20.3 | 0 | 734-745 | R.VGWEQLLTTIAR.T | |

# Detailed Protein Report

## Protein 379: PREDICTED: centrosomal protein of 95 kDa isoform X10 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578831608 | **Score:** | 32.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 71.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578831610 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: centrosomal protein of 95 kDa isoform X11 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKICCTLLVF | CPRVGHPLLK | TVSCNGSETL | SVSGIPNARK | LGEPIRAAIP | LHPPYHPSEP | RAPCPIGKEY | LHSSHCSPAV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NSTGEHTEFS | GDLDDGLFLI | SKLPKGSKWE | VYPAQVQGPR | TRKPPKGKRN | ENRATASSCN | SPFPQRPRKR | LTEQELHDVS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EKLSQRLSEL | DWMLKSALGD | RIKEKTDHKE | ENTGNEEVED | GTEETLSQHS | DGIVEYGPKK | SRPGLSMRRK | PPYRSHSLSP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SPVNKHKQFH | LERKRQRKPR | ETDVRQFQAQ | AFTEAFEREL | RRHKVQENIG | PLRIHEKEEE | TEKIYRGEAV | RKGTPECSQP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WKIYSRKTTT | QSLRGGLPKP | NKAVPMKVSE | HSLLPLMLEQ | FPFLYVSGPT | LSKMWKQQIA | QVEQLKKEAC | RENRSKKKLQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DEIEEALRRH | DLLTTLVKKE | YEHNKRLQDF | KDCIRRQRLT | QSKIKENRQQ | IVRARKYYDD | YRVQLCAKMM | RMRTREEMIF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KKLFEEGLNI | QKQRLRDLRN | YAKEKRDEQR | RRHQDELDSM | ENYYKDQFSL | LAEAISQEHQ | ELKAREKSQA | QVIIKIEAKS |
| 570 | 580 | 590 | 600 | 610 | 620 | | |
| CTAWQCFFQQ | GTSYIGGWSN | RLYHIAPVCS | GLYSLGLCKY | TDILHNNKII | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1748 | 1 | 568.7494 | -72.31 | 2 | 52.2 | 14.3 | 1 | 463-471 | R.VQLCAKMMR.M | Carbamidomethyl: 4 |

# Detailed Protein Report

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## Protein 380: macrophage mannose receptor 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4505245 | **Score:** | 32.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 165.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRLPLLLVFA | SVIPGAVLLL | DTRQFLIYNE | DHKRCVDAVS | PSAVQTAACN | QDAESQKFRW | VSESQIMSVA | FKLCLGVPSK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TDWVAITLYA | CDSKSEFQKW | ECKNDTLLGI | KGEDLFFNYG | NRQEKNIMLY | KGSGLWSRWK | IYGTTDNLCS | RGYEAMYTLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GNANGATCAF | PFKFENKWYA | DCTSAGRSDG | WLWCGTTTDY | DTDKLFGYCP | LKFEGSESLW | NKDPLTSVSY | QINSKSALTW |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HQARKSCQQQ | NAELLSITEI | HEQTYLTGLT | SSLTSGLWIG | LNSLSFNSGW | QWSDRSPFRY | LNWLPGSPSA | EPGKSCVSLN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PGKNAKWENL | ECVQKLGYIC | KKGNTTLNSF | VIPSESDVPT | HCPSQWWPYA | GHCYKIHRDE | KKIQRDALTT | CRKEGGDLTS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IHTIEELDFI | ISQLGYEPND | ELWIGLNDIK | IQMYFEWSDG | TPVTFTKWLR | GEPSHENNRQ | EDCVVMKGKD | GYWADRGCEW |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PLGYICKMKS | RSQGPEIVEV | EKGCRKGWKK | HHFYCYMIGH | TLSTFAEANQ | TCNNENAYLT | TIEDRYEQAF | LTSFVGLRPE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KYFWTGLSDI | QTKGTFQWTI | EEEVRFTHWN | SDMPGRKPGC | VAMRTGIAGG | LWDVLKCDEK | AKFVCKHWAE | GVTHPPKPTT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TPEPKCPEDW | GASSRTSLCF | KLYAKGKHEK | KTWFESRDFC | RALGGDLASI | NNKEEQQTIW | RLITASGSYH | KLFWLGLTYG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SPSEGFTWSD | GSPVSYENWA | YGEPNNYQNV | EYCGELKGDP | TMSWNDINCE | HLNNWICQIQ | KGQTPKPEPT | PAPQDNPPVT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EDGWVIYKDY | QYYFSKEKET | MDNARAFCKR | NFGDLVSIQS | ESEKKFLWKY | VNRNDAQSAY | FIGLLISLDK | KFAWMDGSKV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DYVSWATGEP | NFANEDENCV | TMYSNSGFWN | DINCGYPNAF | ICQRHNSSIN | ATTVMPTMPS | VPSGCKEGWN | FYSNKCFKIF |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GFMEEERKNW | QEARKACIGF | GGNLVSIQNE | KEQAFLTYHM | KDSTFSAWTG | LNDVNSEHTF | LWTDGRGVHY | TNWGKGYPGG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RRSSLSYEDA | DCVVIIGGAS | NEAGKWMDDT | CDSKRGYICQ | TRSDPSLTNP | PATIQTDGFV | KYGKSSYSLM | RQKFQWHEAE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TYCKLHNSLI | ASILDPYSNA | FAWLQMETSN | ERVWIALNSN | LTDNQYTWTD | KWRVRYTNWA | ADEPKLKSAC | VYLDLDGYWK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TAHCNESFYF | LCKRSDEIPA | TEPPQLPGRC | PESDHTAWIP | FHGHCYYIES | SYTRNWGQAS | LECLRMGSSL | VSIESAAESS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| FLSYRVEPLK | SKTNFWIGLF | RNVEGTWLWI | NNSPVSFVNW | NTGDPSGERN | DCVALHASSG | FWSNIHCSSY | KGYICKRPKI |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| IDAKPTHELL | TTKADTRKMD | PSKPSSNVAG | VVIIVILLIL | TGAGLAAYFF | YKKRRVHLPQ | EGAFENTLYF | NSQSSPGTSD |
| 1450 | 1460 | | | | | | |
| MKDLVGNIEQ | NEHSVI | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2976 | 1 | 928.0036 | 17.04 | 2 | 66.0 | 14.3 | 2 | 126-140 | K.NIMLYKGSGLWSRWK.I | Oxidation: 3 |

BRUKER

# Detailed Protein Report

## Protein 381: desmoglein-2 preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|116534898 | **Score:** | 32.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 122.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| | | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MARSPGRAYA | LLLLLICFNV | GSGLHLQVLS | TRNENKLLPK | HPHLVRQKRA | WITAPVALRE | GEDLSKKNPI | AKIHSDLAEE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RGLKITYKYT | GKGITEPPFG | IFVFNKDTGE | LNVTSILDRE | ETPFFLLTGY | ALDARGNNVE | KPLELRIKVL | DINDNEPVFT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QDVFVGSVEE | LSAAHTLVMK | INATDADEPN | TLNSKISYRI | VSLEPAYPPV | FYLNKDTGEI | YTTSVTLDRE | EHSSYTLTVE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ARDGNGEVTD | KPVKQAQVQI | RILDVNDNIP | VVENKVLEGM | VEENQVNVEV | TRIKVFDADE | IGSDNWLANF | TFASGNEGGY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FHIETDAQTN | EGIVTLIKEV | DYEEMKNLDF | SVIVANKAAF | HKSIRSKYKP | TPIPIKVKVK | NVKEGIHFKS | SVISIYVSES |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MDRSSKGQII | GNFQAFDEDT | GLPAHARYVK | LEDRDNWISV | DSVTSEIKLA | KLPDFESRYV | QNGTYTVKIV | AISEDYPRKT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ITGTVLINVE | DINDNCPTLI | EPVQTICHDA | EYVNVTAEDL | DGHPNSGPFS | FSVIDKPPGM | AEKWKIARQE | STSVLLQQSE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KKLGRSEIQF | LISDNQGFSC | PEKQVLTLTV | CECLHGSGCR | EAQHDSYVGL | GPAAIALMIL | AFLLLLLVPL | LLLMCHCGKG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AKGFTPIPGT | IEMLHPWNNE | GAPPEDKVVP | SFLPVDQGGS | LVGRNGVGGM | AKEATMKGSS | SASIVKGQHE | MSEMDGRWEE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HRSLLSGRAT | QFTGATGAIM | TTETTKTARA | TGASRDMAGA | QAAAVALNEE | FLRNYFTDKA | ASYTEEDENH | TAKDCLLVYS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QEETESLNAS | IGCCSFIEGE | LDDRFLDDLG | LKFKTLAEVC | LGQKIDINKE | IEQRQKPATE | TSMNTASHSL | CEQTMVNSEN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TYSSGSSFPV | PKSLQEANAE | KVTQEIVTER | SVSSRQAQKV | ATPLPDPMAS | RNVIATETSY | VTGSTMPPTT | VILGPSQPQS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LIVTERVYAP | ASTLVDQPYA | NEGTVVVTER | VIQPHGGGSN | PLEGTQHLQD | VPYVMVRERE | SFLAPSSGVQ | PTLAMPNIAV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GQNVTVTERV | LAPASTLQSS | YQIPTENSMT | ARNTTVSGAG | VPGPLPDFGL | EESGHSNSTI | TTSSTRVTKH | STVQHSYS |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1168 | 1 | 955.7541 | 206.12 | 1 | 44.8 | 19.8 | 1 | 33-40 | R.NENKLLPK.H | |

# Detailed Protein Report

## Protein 382: PREDICTED: zinc finger protein 665 isoform X5 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|578834915 | **Score:** | 32.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 76.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.6 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVCPCSGLLL | AVGGMPPRCQ | GRTLEEEEEE | GKGVRDGSSS | DISCKCVNTD | LPPKGKNNMG | EAFYTVKLER | LESCDTVGLS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FQEVQKNTYD | FECQWKDDEG | NYKTVLMLQK | ENLPGRRAQR | DRRAAGNRHI | ENQLGVSFQS | HLPELQQFQH | EGKIYEYNQV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EKSPNNRGKH | YKCDECGKVF | SQNSRLTSHK | RIHTGEKPYQ | CNKCGKAFTV | RSNLTIHQVI | HTGEKPYKCN | ECGKVFSQPS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NLAGHQRIHT | GEKPYKCNEC | GKAFRAHSKL | TTHQVIHTGE | KPYKCKECGK | CFTQNSHLAS | HRRIHTGEKP | YKCNECGKAF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SVRSSLTTHQ | TIHTGEKPYK | CNECGKVFRH | NSYLAKHRRI | HTGEKPYKCN | ECGKAFSMHS | NLTKHQIIHT | GEKPFKCNEC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VKVFTQYSHL | ANHRRIHTGE | KPYRCDECGK | AFSVRSSLTT | HQAIHTGEKP | YKCNDCGKVF | TQNSHLASHR | GIHSGEKPYK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CDECGKAFSQ | TSQLARHWRV | HTGEKPYKCN | ECGKAFSVHS | SLTIHQTIHT | GQKPYKCNDC | GKVFRHNSYL | AIHQRIHTGE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KPYKCNECGK | AFSVHSNLAT | HQVIHTGEKP | YKCNECGKVF | TQNSHLANHR | RIHTGEKPYR | CNECGKAFSV | RSTLTTHMAV |
| 650 | 660 | 670 | 680 |  |  |  |  |
| HTGDKPYKCN | QCGKVFTQNS | NLAKHRRIHS | G |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1354 | 1 | 684.3815 | 97.70 | 2 | 46.5 | 12.8 | 1 | 33-45 | K.GVRDGSSSDISCK.C | Carbamidomethyl: 12 |

# Detailed Protein Report

**Protein 383:** **unconventional myosin-Ie [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|55956916 | **Score:** | 32.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 127.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGSKGVYQYH | WQSHNVKHSG | VDDMVLLSKI | TENSIVENLK | KRYMDDYIFT | YIGSVLISVN | PFKQMPYFGE | KEIEMYQGAA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QYENPPHIYA | LADNMYRNMI | IDRENQCVII | SGESGAGKTV | AAKYIMSYIS | RVSGGGTKVQ | HVKDIILQSN | PLLEAFGNAK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TVRNNNSSRF | GKYFEIQFSP | GGEPDGGKIS | NFLLEKSRVV | MRNPGERSFH | IFYQLIEGAS | AEQKHSLGIT | SMDYYYYLSL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SGSYKVDDID | DRREFQETLH | AMNVIGIFAE | EQTLVLQIVA | GILHLGNISF | KEVGNYAAVE | SEEFLAFPAY | LLGINQDRLK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EKLTSRQMDS | KWGGKSESIH | VTLNVEQACY | TRDALAKALH | ARVFDFLVDS | INKAMEKDHE | EYNIGVLDIY | GFEIFQKNGF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EQFCINFVNE | KLQQIFIELT | LKAEQEEYVQ | EGIRWTPIEY | FNNKIVCDLI | ENKVNPPGIM | SILDDVCATM | HAVGEGADQT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LLQKLQMQIG | SHEHFNSWNQ | GFIIHHYAGK | VSYDMDGFCE | RNRDVLFMDL | IELMQSSELP | FIKSLFPENL | QADKKGRPTT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AGSKIKKQAN | DLVSTLMKCT | PHYIRCIKPN | ETKKPRDWEE | SRVKHQVEYL | GLKENIRVRR | AGYAYRRIFQ | KFLQRYAILT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KATWPSWQGE | EKQGVLHLLQ | SVNMDSDQFQ | LGRSKVFIKA | PESLFLLEEM | RERKYDGYAR | VIQKSWRKFV | ARKKYVQMRE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EASDLLLNKK | ERRRNSINRN | FIGDYIGMEE | HPELQQFVGK | REKIDFADTV | TKYDRRFKGV | KRDLLLTPKC | LYLIGREKVK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QGPDKGLVKE | VLKRKIEIER | ILSVSLSTMQ | DDIFILHEQE | YDSLLESVFK | TEFLSLLAKR | YEEKTQKQLP | LKFSNTLELK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LKKENWGPWS | AGGSRQVQFH | QGFGDLAVLK | PSNKVLQVSI | GPGLPKNSRP | TRRNTTQNTG | YSSGTQNANY | PVRAAPPPPG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| YHQNGVIRNQ | YVPYPHAPGS | QRSNQKSLYT | SMARPPLPRQ | QSTSSDRVSQ | TPESLDFLKV | PDQGAAGVRR | QTTSRPPPAG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | |
| GRPKPQPKPK | PQVPQCKALY | AYDAQDTDEL | SFNANDIIDI | IKEDPSGWWT | GRLRGKQGLF | PNNYVTKI | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1182 | 1 | 478.1928 | -225.01 | 2 | 43.0 | 13.4 | 1 | 782-789 | K.RDLLLTPK.C | |

# Detailed Protein Report

## Protein 384: cleavage and polyadenylation specificity factor subunit 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|34101288 | **Score:** | 32.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 88.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530403998 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: cleavage and polyadenylation specificity factor subunit 2 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTSIIKLTTL | SGVQEESALC | YLLQVDEFRF | LLDCGWDEHF | SMDIIDSLRK | HVHQIDAVLL | SHPDPLHLGA | LPYAVGKLGL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NCAIYATIPV | YKMGQMFMYD | LYQSRHNTED | FTLFTLDDVD | AAFDKIQQLK | FSQIVNLKGK | GHGLSITPLP | AGHMIGGTIW |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KIVKDGEEEI | VYAVDFNHKR | EIHLNGCSLE | MLSRPSLLIT | DSFNATYVQP | RRKQRDEQLL | TNVLETLRGD | GNVLIAVDTA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GRVLELAQLL | DQIWRTKDAG | LGVYSLALLN | NVSYNVVEFS | KSQVEWMSDK | LMRCFEDKRN | NPFQFRHLSL | CHGLSDLARV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PSPKVVLASQ | PDLECGFSRD | LFIQWCQDPK | NSIILTYRTT | PGTLARFLID | NPSEKITEIE | LRKRVKLEGK | ELEEYLEKEK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LKKEAAKKLE | QSKEADIDSS | DESDIEEDID | QPSAHKTKHD | LMMKGEGSRK | GSFFKQAKKS | YPMFPAPEER | IKWDEYGEII |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KPEDFLVPEL | QATEEEKSKL | ESGLTNGDEP | MDQDLSDVPT | KCISTTESIE | IKARVTYIDY | EGRSDGDSIK | KIINQMKPRQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LIIVHGPPEA | SQDLAECCRA | FGGKDIKVYM | PKLHETVDAT | SETHIYQVRL | KDSLVSSLQF | CKAKDAELAW | IDGVLDMRVS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KVDTGVILEE | GELKDDGEDS | EMQVEAPSDS | SVIAQQKAMK | SLFGDDEKET | GEESEIIPTL | EPLPPHEVPG | HQSVFMNEPR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | |
| LSDFKQVLLR | EGIQAEFVGG | VLVCNNQVAV | RRTETGRIGL | EGCLCQDFYR | IRDLLYEQYA | IV | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 303 | 1 | 1292.7280 | 120.56 | 1 | 33.5 | 21.9 | 1 | 439-449 | K.HDLMMKGEGSR.K | Oxidation: 4, 5 |
| 1834 | 1 | 734.4148 | 23.62 | 2 | 51.3 | 10.2 | 1 | 610-622 | R.LKDSLVSSLQFCK.A | |

# Detailed Protein Report

## Protein 385: protein phosphatase 1 regulatory subunit 26 [Homo sapiens]

**Accession:** gi|45387958
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 32.0
**MW [kDa]:** 127.3
**pI:** 9.8
**Sequence Coverage [%]:** 2.4
**No. of unique Peptides:** 2

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.43 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.34 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578818032 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein phosphatase 1 regulatory subunit 26 isoform X5 [Homo sapiens] |
| gi\|578818030 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein phosphatase 1 regulatory subunit 26 isoform X4 [Homo sapiens] |
| gi\|578818028 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein phosphatase 1 regulatory subunit 26 isoform X3 [Homo sapiens] |
| gi\|530426639 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein phosphatase 1 regulatory subunit 26 isoform X2 [Homo sapiens] |
| gi\|530426637 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein phosphatase 1 regulatory subunit 26 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFLMNASPVV | ALQSKWEAFG | PPGSCRFPRC | FSEADEGVES | ASVSARVQML | ISTLQRDGAA | RGTSDERAAQ | RGHRAEGCHD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ARPAAKPTVH | KEPPALAVCG | LVADFDPMGE | EETTDFGPLV | LDSDSDDSVD | RDIEEAIQEY | LKAKSGAAQP | GAGGAQPGAA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QPSRAAGGGS | RCKPEPAHGS | APTALCPPKL | VPGSGGGPGS | QVGSSKDQGS | ASPVSVSSDD | SFEQSIRAEI | EQFLNEKRQH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ETQKCDGSVE | KKPDTNENSA | KSLLKSHQEP | PTKVVHRQGL | LGVQKEFAFR | KPPRLAKMNV | QPRSLRSKVT | TTQENEGSTK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PATPCRPSEA | AQNKGGIKRS | ASAARRGKRV | MSAAQASEAS | DSSSDDGIEE | AIQLYQLQKT | RKEADGDLPQ | RVQLREERAP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DPPAHSTSSA | TKSALPETHR | KTPSKKKLVA | TKTMDPGPGG | LDTDHAPKLL | KETKAPPPAS | PASRSEFVER | SSCRADTSAE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LMCAEAILDI | SKTILPAPVE | GSDGSLSASP | LFYSPNVPSR | SDGDSSSVDS | DDSIEQEIRT | FLALKAQSGS | LLARGESCPQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AAQGPLLPPG | LNSQTGGHKT | PLSKTPDPLL | GCKRKRRGGG | HVRPSTPKKM | QEVVKDGSQD | ADHSQGRAEP | GHERRDLPIQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GKASEALGGE | GTARGPGDTR | MSQGQGKTDE | ARRLDEKESS | EDKSSSLDSD | EDLDTAIKDL | LRSKRKLKKR | CREPRAACRK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KVRFSTAQTH | FLEQLGGLRR | DWKDRGPPVL | KSCLSKSKRD | SGEGPGKKPP | SVFGSTAERM | RQEGAASQDA | ALAFRVRRPA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SASASEGNPF | PRESQGPAPS | PGSLSDDSSS | VDSNDSIELE | IRKFLAEKAK | ESVSSSEVQA | EGPTALGTGG | PARPEVLCRK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EPAPPPGVCT | RSQRARGVPH | LAEGLRGTES | AGAQGTAGLF | SQGGKGLPAA | PARGDPVPPR | STSGGVSAKG | LSVSRRNVYV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| HKDQSPRGAE | PAAKSAFGQL | PSCATAGTEA | GGARGTFHMG | CGSPSFLTPS | PGAERDAGAQ | ADRTPPWSDF | AHQSRLPSPW |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VLRSEGRDAV | WRGGVGSERD | KGSEGPARGL | PSLPLAGFSP | LLSTQLFHFG | KGVSWGGRQA | GLFSPHLGLP | LQGPSFSAFR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EAQAGPSPVF | GSPHLLAKKD | GGPWPTRKAQ | AGLSLHDRRS | SGSEESILDL | RYRRRVNRDD | QEQDALGSDA | SDFSDTSTED |
| 1210 | | | | | | | |
| SGGSSVVKV | | | | | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1424 | 1 | 627.5982 | -62.69 | 3 | 46.2 | 13.9 | 0 | 475-492 | R.ADTSAELMCAEAILDISK.T | | |
| 1803 | 1 | 590.7798 | -21.71 | 2 | 52.9 | 18.1 | 0 | 881-891 | K.EPAPPPGVCTR.S | Carbamidomethyl: 9 | QU:MU 0.43<br>WUP:QUP 2.34 |

# Detailed Protein Report

## Protein 386: pregnancy zone protein precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|162809334 | **Score:** | 31.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 163.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRKDRLLHLC | LVLLLILLSA | SDSNSTEPQY | MVLVPSLLHT | EAPKKGCVLL | SHLNETVTVS | ASLESGRENR | SLFTDLVAEK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DLFHCVSFTL | PRISASSEVA | FLSIQIKGPT | QDFRKRNTVL | VLNTQSLVFV | QTDKPMYKPG | QTVRFRVVSV | DENFRPRNEL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IPLIYLENPR | RNRIAQWQSL | KLEAGINQLS | FPLSSEPIQG | SYRVVVQTES | GGRIQHPFTV | EEFVLPKFEV | KVQVPKIISI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MDEKVNITVC | GEYTYGKPVP | GLATVSLCRK | LSRVLNCDKQ | EVCEEFSQQL | NSNGCITQQV | HTKMLQITNT | GFEMKLRVEA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RIREEGTDLE | VTANRISEIT | NIVSKLKFVK | VDSHFRQGIP | FFAQVLLVDG | KGVPIPNKLF | FISVNDANYY | SNATTNEQGL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AQFSINTTSI | SVNKLFVRVF | TVHPNLCFHY | SWVAEDHQGA | QHTANRVFSL | SGSYIHLEPV | AGTLPCGHTE | TITAHYTLNR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QAMGELSELS | FHYLIMAKGV | IVRSGTHTLP | VESGDMKGSF | ALSFPVESDV | APIARMFIFA | ILPDGEVVGD | SEKFEIENCL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ANKVDLSFSP | AQSPPASHAH | LQVAAAPQSL | CALRAVDQSV | LLMKPEAELS | VSSVYNLLTV | KDLTNFPDNV | DQQEEEQGHC |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PRPFFIHNGA | IYVPLSSNEA | DIYSFLKGMG | LKVFTNSKIR | KPKSCSVIPS | VSAGAVGQGY | YGAGLGVVER | PYVPQLGTYN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VIPLNNEQSS | GPVPETVRSY | FPETWIWELV | AVNSSGVAEV | GVTVPDTITE | WKAGAFCLSE | DAGLGISSTA | SLRAFQPFFV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ELTMPYSVIR | GEVFTLKATV | LNYLPKCIRV | SVQLKASPAF | LASQNTKGEE | SYCICGNERQ | TLSWTVTPKT | LGNVNFSVSA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EAMQSLELCG | NEVVEVPEIK | RKDTVIKTLL | VEAEGIEQEK | TFSSMTCASG | ANVSEQLSLK | LPSNVVKESA | RASFSVLGDI |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LGSAMQNIQN | LLQMPYGCGE | QNMVLFAPNI | YVLNYLNETQ | QLTQEIKAKA | VGYLITGYQR | QLNYKHQDGS | YSTFGERYGR |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| NQGNTWLTAF | VLKTFAQARS | YIFIDEAHIT | QSLTWLSQMQ | KDNGCFRSSG | SLLNNAIKGG | VEDEATLSAY | VTIALLEIPL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PVTNPIVRNA | LFCLESAWNV | AKEGTHGSHV | YTKALLAYAF | SLLGKQNQNR | EILNSLDKEA | VKEDNLVHWE | RPQRPKAPVG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| HLYQTQAPSA | EVEMTSYVLL | AYLTAQPAPT | SGDLTSATNI | VKWIMKQQNA | QGGFSSTQDT | VVALHALSRY | GAATFTRTEK |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TAQVTVQDSQ | TFSTNFQVDN | NNLLLLQQIS | LPELPGEYVI | TVTGERCVYL | QTSMKYNILP | EKEDSPFALK | VQTVPQTCDG |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| HKAHTSFQIS | LTISYTGNRP | ASNMVIVDVK | MVSGFIPLKP | TVKMLERSSS | VSRTEVSNNH | VLIYVEQVTN | QTLSFSFMVL |
| 1450 | 1460 | 1470 | 1480 | 1490 | | | |
| QDIPVGDLKP | AIVKVYDYYE | TDESVVAEYI | APCSTDTEHG | NV | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 705 | 1 | 802.0356 | 159.48 | 2 | 38.8 | 16.0 | 1 | 322-335 | R.IREEGTDLEVTANR.I | |

# Detailed Protein Report

## Protein 387: cystatin-B [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|4503117 | **Score:** | 31.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 11.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.9 |
|  |  | **Sequence Coverage [%]:** | 12.2 |
|  |  | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 4.54 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MMCGAPSATQ PATAETQHIA DQVRSQLEEK ENKKFPVFKA VSFKSQVVAG TNYFIKVHVG DEDFVHLRVF QSLPHENKPL
        90        100
TLSNYQTNKA KHDELTYF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 695 | 1 | 663.8458 | -15.71 | 2 | 37.1 | 31.9 | 0 | 45-56 | K.SQVVAGTNYFIK.V |  | WUP:QUP 4.54 |

# Detailed Protein Report

## Protein 388: peroxisome biogenesis factor 1 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|544186104 | **Score:** | 31.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 119.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMKELQTKQL | QSNTVGITES | NENESEIPVD | SSSVASLWTM | IGSIFSFQSE | KKQETSWGLT | EINAFKNMQS | KVVPLDNIFR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VCKSQPPSIY | NASATSVFHK | HCAIHVFPWD | QEYFDVEPSF | TVTYGKLVKL | LSPKQQQSKT | KQNVLSPEKE | KQMSEPLDQK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KIRSDHNEED | EKACVLQVVW | NGLEELNNAI | KYTKNVEVLH | LGKVWIPDDL | RKRLNIEMHA | VVRITPVEVT | PKIPRSLKLQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PRENLPKDIS | EEDIKTVFYS | WLQQSTTTML | PLVISEEEFI | KLETKDGLKE | FSLSIVHSWE | KEKDKNIFLL | SPNLLQKTTI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QVLLDPMVKE | ENSEEIDFIL | PFLKLSSLGG | VNSLGVSSLE | HITHSLLGRP | LSRQLMSLVA | GLRNGALLLT | GGKGSGKSTL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AKAICKEAFD | KLDAHVERVD | CKALRGKRLE | NIQKTLEVAF | SEAVWMQPSV | VLLDDLDLIA | GLPAVPEHEH | SPDAVQSQRL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AHALNDMIKE | FISMGSLVAL | IATSQSQQSL | HPLLVSAQGV | HIFQCVQHIQ | PPNQEQRCEI | LCNVIKNKLD | CDINKFTDLD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LQHVAKETGG | FVARDFTVLV | DRAIHSRLSR | QSISTREKLV | LTTLDFQKAL | RGFLPASLRS | VNLHKPRDLG | WDKIGGLHEV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RQILMDTIQL | PAKYPELFAN | LPIRQRTGIL | LYGPPGTGKT | LLAGVIARES | RMNFISVKGP | ELLSKYIGAS | EQAVRDIFIR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AQAAKPCILF | FDEFESIAPR | RGHDNTGVTD | RVVNQLLTQL | DGVEGLQGVY | VLAATSRPDL | IDPALLRPGR | LDKCVYCPPP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DQVSRLEILN | VLSDSLPLAD | DVDLQHVASV | TDSFTGADLK | ALLYNAQLEA | LHGMLLSSGL | QDGSSSSDSD | LSLSSMVFLN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| HSSGSDDSAG | DGECGLDQSL | VSLEMSEILP | DESKFNMYRL | YFGSSYESEL | GNGTSSDLSS | QCLSAPSSMT | QDLPGVPGKD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QLFSQPPVLR | TASQEGCQEL | TQEQRDQLRA | DISIIKGRYR | SQSGEDESMN | QPGPIKTRLA | ISQSHLMTAL | GHTRPSISED |
| 1050 | 1060 | 1070 | 1080 | | | | |
| DWKNFAELYE | SFQNPKRRKN | QSGTMFRPGQ | KVTLA | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1073 | 4 | 1207.9210 | 130.55 | 1 | 43.0 | 31.9 | 2 | 233-242 | K.IPRSLKLQPR.E | |

# Detailed Protein Report

## Protein 389: PREDICTED: serine/threonine-protein kinase 31 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578813577 | **Score:** | 31.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 95.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.8 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 2 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.59 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.20 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MWVQGHSSRA SATESVSFSG IVQMDEDTHY DKVEDVVGSH IEDAVTFWAQ SINRNKDIMK IGCSLSEVCP QASSVLGNLD
        90        100        110        120        130        140        150        160
PNKIYGGLFS EDQCWYRCKV LKIISVEKCL VRYIDYGNTE ILNRSDIVEI PLELQFSSVA KKYKLWGLHI PSDQEVTQFD
       170        180        190        200        210        220        230        240
QQEKAAAVDL TNHLEYTLKT YIDTRMKNLA AKMEILKEMR HVDISVRFGK DLSDAIQVLD EGCFTTPASL NGLEIIWAEY
       250        260        270        280        290        300        310        320
SLAQENIKTC EYVSEGNILI AQRNEMQQKL YMSVEDFILE VDESSLNKRL KTLQDLSVSL EAVYGQAKEG ANSDEILKKF
       330        340        350        360        370        380        390        400
YDWKCDKREE FTSVRSETDA SLHRLVAWFQ RTLKVFDLSV EGSLISEDAM DNIDEILEKT ESSVCKELEI ALVDQGDADK
       410        420        430        440        450        460        470        480
EIISNTYSQV LQKIHSEERL IATVQAKYKD SIEFKKQLIE YLNKSPSVDH LLSIKKTLKS LKALLRWKLV EKSNLEESDD
       490        500        510        520        530        540        550        560
PDGSQIEKIK EEITQLRNNV FQEIYHEREE YEMLTSLAQK WFPELPLLHP EIGLLKYMNS GGLLTMSLER DLLDAEPMKE
       570        580        590        600        610        620        630        640
LSSKRPLVRS EVNGQIILLK GYSVDVDTEA KVIERAATYH RAWREAEGDS GLLPLIFLFL CKSDPMAYLM VPYYPRANLN
       650        660        670        680        690        700        710        720
AVQANMPLNS EETLKVMKGV AQGLHTLHKA DIIHGSLHQN NVFALNREQG IVGDFDFTKS VSQRASVNMM VGDLSLMSPE
       730        740        750        760        770        780        790        800
LKMGKPASPG SDLYAYGCLL LWLSVQNQEF EINKDGIPKV DQFHLDDKVK SLLCSLICYR SSMTAEQVLN AECFLMPKEQ
       810        820        830        840        850
SVPNPEKDTE YTLYKKEEEI KTENLDKCME KTRNGEANFD C
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 181 | 8 | 592.2959 | 31.07 | 2 | 31.1 | 21.2 | 0 | 581-591 | K.GYSVDVDTEAK.V | | QU:MU 1.59<br>WUP:QUP 0.20 |
| 1907 | 1 | 734.2871 | -85.93 | 2 | 52.2 | 10.5 | 2 | 822-833 | K.TENLDKCMEKTR.N | | |

# Detailed Protein Report

## Protein 390: formin-1 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|472235321 | **Score:** | 31.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 71.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 5.7 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***QU:MU*** **Median:** 2.49 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MEGTHCTLQL HKPITELCYI SFCLPKGEVR GFSYKGTVTL DRSNKGFHNC YQVREESDII SLSQEPDEHP GDIFFKQTPT
        90        100        110        120        130        140        150        160
KDILTELYKL TTERERLLTN LLSSDHILGI TMGNQEGKLQ ELSVSLAPED DCFQSAGDWQ GELPVGPLNK RSTHGNKKPR
       170        180        190        200        210        220        230        240
RSSGRRESFG ALPQKRTKRK GRGGRESAPL MGKDKICSSH SLPLSRTRPN LWVLEEKGNL LPNGALACSL QRRESCPPDI
       250        260        270        280        290        300        310        320
PKTPDTDLGF GSFETAFKDT GLGREVLPPD CSSTEAGGDG IRRPPSGLEH QQTGLSESHQ DPEKHPEAEK DEMEKPAKRT
       330        340        350        360        370        380        390        400
CKQKPVSKVV AKVQDLSSQV QRVVKTHSKG KETIAIRPAA HAEFVPKADL LTLPGAEAGA HGSRRQGKER QGDRSSQSPA
       410        420        430        440        450        460        470        480
GETASISSVS ASAEGAVNKV PLKVIESEKL DEAPEGKRLG FPVHTSVPHT RPETRNKRRA GLPLGGHKSL FLDLPHKVGP
       490        500        510        520        530        540        550        560
DSSQPRGDKK KPSPPAPAAL GKVFNNSASQ SSTHKQTSPV PSPLSPRLPS PQQHHRILRL PALPGEREAA LNDSPCRKSR
       570        580        590        600        610        620        630        640
VFSGCVSADT LEPPSSAKVT ETKGASPAFL RAGQPRLVPG ETLEKSLGPG KTTAEPQHQS PPAFHWDLQQ HFQEPVIRTV
       650        660        670
SISCASNLIK EEAGKGKESR SG
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 787 | 1 | 509.7081 | -159.31 | 2 | 38.3 | 16.9 | 1 | 320-328 | R.TCKQKPVSK.V | | QU:MU 2.49 |
| 1018 | 1 | 920.4993 | 28.10 | 3 | 42.8 | 14.8 | 1 | 395-423 | R.<br>SSQSPAGETASISSVSASAEGAVN<br>V | | |

# Detailed Protein Report

**Protein 391:** **bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase isoform 3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|298566325 | **Score:** | 31.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 78.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPIGDCSVAA | KPRKQLLCSL | FQTTLGYRAR | ASGWKPMVIC | RGSHAFKDLI | NTYRMIEQDD | FDINTRLHTI | VRGEDEAAMV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ESVGLALVKL | PDVLNRLKPD | IMIVHGDRFD | ALALATSAAL | MNIRILHIEG | GEVSGTIDDS | IRHAITKLAH | YHVCCTRSAE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QHLISMCEDH | DRILLAGCPS | YDKLLSAKNK | DYMSIIRMWL | GDDVKSKDYI | VALQHPVTTD | IKHSIKMFEL | TLDALISFNK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RTLVLFPNID | AGSKEMVRVM | RKKGIEHHPN | FRAVKHVPFD | QFIQLVAHAG | CMIGNSSCGV | REVGAFGTPV | INLGTRQIGR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ETGENVLHVR | DADTQDKILQ | ALHLQFGKQY | PCSKIYGDGN | AVPRILKFLK | SIDLQEPLQK | KFCFPPVKEN | ISQDIDHILE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TLSALAVDLG | GTNLRVAIVS | MKGEIVKKYT | QFNPKTYEER | INLILQMCVE | AAAEAVKLNC | RILGVGISTG | GRVNPREGIV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LHSTKLIQEW | NSVDLRTPLS | DTLHLPVWVD | NDGNCAALAE | RKFGQGKGLE | NFVTLITGTG | IGGGIIHQHE | LIHGSSFCAA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ELGHLVVSLD | GPDCSCGSHG | CIEAYASGMA | LQREAKKLHD | EDLLLVEGMS | VPKDEAVGAL | HLIQAAKLGN | AKAQSILRTA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GTALGLGVVN | ILHTMNPSLV | ILSGVLASHY | IHIVKDVIRQ | QALSSVQDVD | VVVSDLVDPA | LLGAASMVLD | YTTRRIY |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1574 | 1 | 1051.4917 | -54.07 | 2 | 49.4 | 15.4 | 2 | 29-47 | R.ARASGWKPMVICRGSHAFK.D | |
| 2066 | 1 | 1044.9156 | -88.64 | 2 | 56.2 | 16.2 | 2 | 191-207 | K.DYMSIIRMWLGDDVKSK.D | Oxidation: 3, 8 |

# Detailed Protein Report

## **Protein 392:** PDZ domain-containing protein MAGIX isoform d [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|532164745 | **Score:** | 31.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 26.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.6 |
| | | **Sequence Coverage [%]:** | 11.9 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***QU:MU*** **Median:** 1.32 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEPRTGDAAD | PRGSRGGRGP | SPLAGPSARQ | LLARLDARPL | AARAAVDVAA | LVRRAGATLR | LRRKEAVSVL | DSADIEVTDS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RLPHATIVDH | RPQVGDLVLH | INGESTQGLT | HAQAVERIRA | GGPQLHLVIR | RPLETHPGKP | RGVGEPRKGV | DRSPDPGGPE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VTGSRSSSTS | LVQHPPSRTT | LKKTRGSPEP | SPEAAADGPT | VSPPERRAED | PNDQIPGSPG | PWLVPSEERL | SRALGVRGAA |
| 250 | 260 | | | | | | |
| QLAQEMAAGR | RRH | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1080 | 1 | 841.9573 | 58.27 | 2 | 43.1 | 19.2 | 1 | 149-165 | K.GVDRSPDPGGPEVTGSR.S | | QU:MU 1.32 |
| 1707 | 2 | 1273.8380 | 161.91 | 1 | 51.6 | 12.4 | 0 | 238-250 | R.GAAQLAQEMAAGR.R | | |

# Detailed Protein Report

| | | | |
|---|---|---|---|
| **Protein 393:** | serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B beta isoform isoform e [Homo sapiens] | | |
| **Accession:** | gi\|430727947 | **Score:** | 31.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 62.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| | | **Sequence Coverage [%]:** | 6.6 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MHQPPPASCS | SSSSSSSSSC | ECARVGVRVS | ALAPAAAPCP | APRQLPYPRL | PEPPSRGTST | LIPARLGPWC | SPTGSPAPLS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CETGCGEGSW | ILVCRLLVPT | QVSLLSMEED | IDTRKINNSF | LRDHSYATEA | DIISTVEFNH | TGELLATGDK | GGRVVIFQRE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QESKNQVHRR | GEYNVYSTFQ | SHEPEFDYLK | SLEIEEKINK | IRWLPQQNAA | YFLLSTNDKT | VKLWKVSERD | KRPEGYNLKD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EEGRLRDPAT | ITTLRVPVLR | PMDLMVEATP | RRVFANAHTY | HINSISVNSD | YETYMSADDL | RINLWNFEIT | NQSFNIVDIK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PANMEELTEV | ITAAEFHPHH | CNTFVYSSSK | GTIRLCDMRA | SALCDRHTKF | FEEPEDPSNR | SFFSEIISSI | SDVKFSHSGR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YIMTRDYLTV | KVWDLNMENR | PIETYQVHDY | LRSKLCSLYE | NDCIFDKFEC | VWNGSDSVIM | TGSYNNFFRM | FDRNTKRDVT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | |
| LEASRENSKP | RAILKPRKVC | VGGKRRKDEI | SVDSLDFSKK | ILHTAWHPSE | NIIAVAATNN | LYIFQDKVN | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1632 | 1 | 1073.5401 | -40.07 | 2 | 48.7 | 20.8 | 1 | 29-49 | R.VSALAPAAAPCPAPRQLPYPR.L | |

# Detailed Protein Report

## Protein 394: protein Hook homolog 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|7705415 | **Score:** | 31.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 84.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530362743 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein Hook homolog 1 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEETQPPPQP | KLPLCDSLMI | WLQTFNTASP | CQDVKQLTSG | VAMAQVLHQI | DAAWFNESWL | SRIKEDVGDN | WRIKASNVKK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VLQGIMSYYH | EFLGQQISEA | LIPDLNQITE | CSDPVELGRL | LQLILGCAIN | CEKKQEHIQN | IMTLEESVQH | VVMTAIQELM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SKEILSSPPN | DAVGELEQQL | KRALEELQEA | LAEKEELRQR | CEELDMQVTT | LQDEKNSLVS | ENEMMNEKLD | QLDGSFDDPN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TVVAKKYFHA | QLQLEQLQEE | NFRLEAAKDD | YRVHCEELEK | QLIEFQHRND | ELTSLAEETR | ALKDEIDVLR | ATSDKANKLE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| STVEIYRQKL | QDLNDLRKQV | KTLQETNMMY | MHNTVSLEEE | LKKANAARTQ | LETYKRQVQD | LHVKLSSESK | RADTLAFEMK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RLEEKHEALL | KEKERLIEQR | DTLKETNEEL | RCSQVQQDHL | NQTDASATKS | YENLAAEIMP | VEYREVFIRL | QHENKMLRLQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QEGSENERIE | ELQEQLEQKH | RKMNELETEQ | RLSKERIREL | QQQIEDLQKS | LQEQGSKSEG | ESSSKLKQKL | EAHMEKLTEV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HEELQKKQEL | IEDLQPDINQ | NVQKINELEA | ALQKKDEDMK | AMEERYKMYL | EKARNVIKTL | DPKLNPASAE | IMLLRKQLAE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KERRIEILES | ECKVAKFRDY | EEKLIVSAWY | NKSLAFQKLG | MESRLVSGGG | ACSDTGACTP | ARSFLAQQRH | ITNTRRNLSV |
| 730 | | | | | | | |
| KVPATTSD | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1597 | 1 | 685.8641 | -18.30 | 2 | 48.3 | 10.6 | 2 | 546-556 | K.LKQKLEAHMEK.L | Oxidation: 9 |

# Detailed Protein Report

## Protein 395: PREDICTED: ribosomal protein S6 kinase-like 1 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530404733 | **Score:** | 31.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 10.3 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.47 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.80 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSLVACECLP SPGLEPEPCS RARSQAHVYL EQIRNRVALG VPDMTKRDYL VDAATQIRLA LERDVSEDYE AAFNHYQNGV
        90        100        110        120        130        140        150        160
DVLLRGIHVD PNKERREAVK LKITKYLRRA EEIFNCHLQR PLSSGASPSA GFSSLRLRPI RTLSSAVEQL RGCRVVGVIE
       170        180        190        200        210        220        230        240
KVQLVQDPAT GGTFVVKSLP RCHMVSRERL TIIPHGVPYM TKLLRYFVSE DSIFLHLEHV QGGTLWSHLL SQAHSRHSGL
       250        260        270        280        290        300        310        320
SSGSTQERMK AQLNPHLNLL TPARLPSGHA PGQDRIALEP PRTSPNLLLA GEAPSTRPQR EAEGEPTART STSGSSDLPK
       330        340        350        360        370        380        390        400
APGGHLHLQA RRAGQNSDAG PPRGLTWVPE GAGPVLGGCG RGMDQSCLSA DGAGRGCGRA TWSVREEQVK QWAAEMLVAL
       410        420        430        440        450        460        470        480
EALHEQGVLC RDLHPGNLLL DQAGHIRLTY FGQWSEVEPQ CCGEAVDNLY SAPEVGGISE LTEACDWWSF GSLLYELLTG
       490        500        510        520        530
MALSQSHPSG IQAHTQLQLP EWLSRPAASL LTEVRCSPAR GSSCLA
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2112 | 1 | 1072.4083 | -80.50 | 2 | 56.8 | 10.0 | 0 | 2-21 | M.SLVACECLPSPGLEPEPCSR.A | Carbamidomethyl: 18 | |
| 2285 | 1 | 884.8843 | -103.89 | 2 | 59.0 | 10.7 | 0 | 412-427 | R.DLHPGNLLLDQAGHIR.L | | WUP:QUP 1.80<br>QU:MU 0.47 |

# Detailed Protein Report

**Protein 396:** **PREDICTED: sodium bicarbonate transporter-like protein 11 isoform X2 [Homo sapiens]**

**Accession:** gi|530426013
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 31.4
**MW [kDa]:** 96.0
**pI:** 8.9
**Sequence Coverage [%]:** 2.8
**No. of unique Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSQNGYFEDS | SYYKCDTDDT | FEAREEILGD | EAFDTANSSI | VSGESIRFFV | NVNLEMQATN | TENEATSGGC | VLLHTSRKYL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KLKNFKEEIR | AHRDLDGFLA | QASIVLNETA | TSLDNVLRTM | LRRFARDPDN | NEPNCNLDLL | MAMLFTDAGA | PMRGKVHLLS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DTIQGVTATV | TGVRYQQSWL | CIICTMKALQ | KRHVCISRLV | RPQNWGENSC | EVRFVILVLA | PPKMKSTKTA | MEVARTFATM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FSDIAFRQKL | LETRTEEEFK | EALVHQRQLL | TMVSHGPVAP | RTKERSTVSL | PAHRHPEPPK | CKDFVPFGKG | IREDIARRFP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LYPLDFTDGI | IGKNKAVGKY | ITTTLFLYFA | CLLPTIAFGS | LNDENTDGAI | DVQKTIAGQS | IGGLLYALFS | GQPLVILLTT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| APLALYIQVI | RVICDDYDLD | FNSFYAWTGL | WNSFFLALYA | FFNLSLVMSL | FKRSTEEIIA | LFISITFVLD | AVKGTVKIFW |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KYYYGHYLDD | YHTKRTSSLV | SLSGLGASLN | ASLHTALNAS | FLASPTELPS | ATHSGQATAV | LSLLIMLGTL | WLGYTLYQFK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KSPYLHPCVR | EILSDCALPI | AVLAFSLISS | HGFREIEMSK | FRYNPSESPF | AMAQIQSLSL | RAVSGAMGLG | FLLSMLFFIE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QNLVAALVNA | PENRLVKGTA | YHWDLLLLAI | INTGLSLFGL | PWIHAAYPHS | PLHVRALALV | EERVENGHIY | DTIVNVKETR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LTSLGASVLV | GLSLLLLPVP | LQWIPKPVLY | GLFLYIALTS | LDGNQLVQRV | ALLLKEQTAY | PPTHYIRRVP | QRKIHYFTGL |
| 810 | 820 | 830 | 840 | 850 | 860 | | |
| QVLQLLLLCA | FGMSSLPYMK | MIFPLIMIAM | IPIRYILLPR | IIEAKYLDVM | DAEHRP | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 823 | 1 | 711.9737 | 188.22 | 2 | 38.7 | 20.7 | 0 | 236-247 | R.TFATMFSDIAFR.Q | Oxidation: 5 |

# Detailed Protein Report

**Protein 397:** **PREDICTED: myelin transcription factor 1-like protein isoform X7 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578802502 | **Score:** | 31.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 130.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEVDTEEKRH | RTRSKGVRVP | VEPAIQELFS | CPTPGCDGSG | HVSGKYARHR | SVYGCPLAKK | RKTQDKQPQE | PAPKRKPFAV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KADSSSVDEC | DDSDGTEDMD | EKEEDEGEEY | SEDNDEPGDE | DEEDEEGDRE | EEEEIEEEDE | DDDEDGEDVE | DEEEEEEEEE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EEEEEEEENED | HQMNCHNTRI | MQDTEKDDNN | NDEYDNYDEL | VAKSLLNLGK | IAEDAAYRAR | TESEMNSNTS | NSLEDDSDKN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ENLGRKSELS | LDLDSDVVRE | TVDSLKLLAQ | GHGVVLSENM | NDRNYADSMS | QQDSRNMNYV | MLGKPMNNGL | MEKMVEESDE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EVCLSSLECL | RNQCFDLARK | LSETNPQERN | PQQNMNIRQH | VRPEEDFPGR | TPDRNYSDML | NLMRLEEQLS | PRSRVFASCA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KEDGCHERDD | DTTSVNSDRS | EEVFDMTKGN | LTLLEKAIAL | ETERAKAMRE | KMAMEAGRRD | NMRSYEDQSP | RQLPGEDRKP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KSSDSHVKKP | YYVLAMHESV | LKCPTPGCTG | RGHVNSNRNS | HRSLSGCPIA | AAEKLAKAQE | KHQSCDVSKS | SQASDRVLRP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MCFVKQLEIP | QYGYRNNVPT | TTPRSNLAKE | LEKYSKTSFE | YNSYDNHTYG | KRAIAPKVQT | RDISPKGYDD | AKRYCKDPSP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SSSSTSSYAP | SSSSNLSCGG | GSSASSTCSK | SSFDYTHDME | AAHMAATAIL | NLSTRCREMP | QNLSTKPQDL | CATRNPDMEV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DENGTLDLSM | NKQRPRDSCC | PILTPLEPMS | PQQQAVMNNR | CFQLGEGDCW | DLPVDYTKMK | PRRIDEDESK | DITPEDLDPF |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QEALEERRYP | GEVTIPSPKP | KYPQCKESKK | DLITCPTPGC | DGSGHVTGNY | ASHRSLSGCP | LADKSIRSML | ATSSQELKCP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TPGCDGSGHI | TGNYASHRSL | SGCPRAKKSG | IRIAQSKEDK | EDQEPIRCPV | PGCDGQGHIT | GKYASHRSAS | GCPLAAKRQK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DGYLNGSQFS | WKSVKTEGMS | CPTPGCDGSG | HVSGSFLTHR | SLSGCPRATS | AMKKAKLSGE | QMLTIKQRAS | NGIENDEEIK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QLDEEIKELN | ESNSQMEADM | IKLRTQVTIT | TMESNLKTIE | EENKVIEQQN | ESLLHELANL | SQSLIHSLAN | IQLPHMDPIN |
| 1130 | 1140 | 1150 | 1160 | 1170 | | | |
| EQNFDAYVTT | LTEMYTNQDR | YQSPENKALL | ENIKQAVRGI | QV | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1852 | 2 | 612.7877 | 57.61 | 2 | 53.5 | 15.8 | 0 | 409-419 | R.DDDTTSVNSDR.S | |
| 2754 | 2 | 639.3511 | 58.06 | 2 | 62.9 | 15.6 | 1 | 512-522 | R.GHVNSNRNSHR.S | |

# Detailed Protein Report

**Protein 398:** **arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|7661880 | **Score:** | 31.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 81.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTVKLDFEEC | LKDSPRFRAS | IELVEAEVSE | LETRLEKLLK | LGTGLLESGR | HYLAASRAFV | VGICDLARLG | PPEPMMAECL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EKFTVSLNHK | LDSHAELLDA | TQHTLQQQIQ | TLVKEGLRGF | REARRDFWRG | AESLEAALTH | NAEVPRRRAQ | EAEEAGAALR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TARAGYRGRA | LDYALQINVI | EDKRKFDIME | FVLRLVEAQA | THFQQGHEEL | SRLSQYRKEL | GAQLHQLVLN | SAREKRDMEQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RHVLLKQKEL | GGEEPEPSLR | EGPGGLVMEG | HLFKRASNAF | KTWSRRWFTI | QSNQLVYQKK | YKDPVTVVVD | DLRLCTVKLC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PDSERRFCFE | VVSTSKSCLL | QADSERLLQL | WVSAVQSSIA | SAFSQARLDD | SPRGPGQGSG | HLAIGSAATL | GSGGMARGRE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PGGVGHVVAQ | VQSVDGNAQC | CDCREPAPEW | ASINLGVTLC | IQCSGIHRSL | GVHFSKVRSL | TLDSWEPELV | KLMCELGNVI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| INQIYEARVE | AMAVKKPGPS | CSRQEKEAWI | HAKYVEKKFL | TKLPEIRGRR | GGRGRPRGQP | PVPPKPSIRP | RPGSLRSKPE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PPSEDLGSLH | PGALLFRASG | HPPSLPTMAD | ALAHGADVNW | VNGGQDNATP | LIQATAANSL | LACEFLLQNG | ANVNQADSAG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RGPLHHATIL | GHTGLACLFL | KRGADLGARD | SEGRDPLTIA | METANADIVT | LLRLAKMREA | EAAQGQAGDE | TYLDIFRDFS |
| 730 | 740 | 750 | | | | | |
| LMASDDPEKL | SRRSHDLHTL | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1185 | 1 | 984.5174 | 36.04 | 2 | 44.4 | 11.5 | 2 | 1-16 | -.MTVKLDFEECLKDSPR.F | Carbamidomethyl: 10 |
| 2485 | 1 | 821.9375 | 18.65 | 2 | 61.6 | 19.9 | 1 | 261-275 | R.EGPGGLVMEGHLFKR.A | Oxidation: 8 |

# Detailed Protein Report

## Protein 399: calponin-3 isoform 2 [Homo sapiens]

**Accession:** gi|554506520
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 31.3
**MW [kDa]:** 31.4
**pI:** 6.1
**Sequence Coverage [%]:** 8.1
**No. of unique Peptides:** 1

```
         10         20         30         40         50         60         70         80
MTHFNKGPSY GLSAEVKNKI ASKYDHQAEE DLRNWIEEVT GMSIGPNFQL GLKDGIILCE LINKLQPGSV KKVNESSLNW
         90        100        110        120        130        140        150        160
PQAKTKGFHT TIDIGVKYAE KQTRRFDEGK LKAGQSVIGL QMGTNKCASQ AGMTAYGTRR HLYDPKMQTD KPFDQTTISL
        170        180        190        200        210        220        230        240
QMGTNKGASQ AGMLAPGTRR DIYDQKLTLQ PVDNSTISLQ MGTNKVASQK GMSVYGLGRQ VYDPKYCAAP TEPVIHNGSQ
        250        260        270        280        290
GTGTNGSEIS DSDYQAEYPD EYHGEYQDDY PRDYQYSDQG IDY
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1867 | 1 | 702.3265 | -60.80 | 2 | 53.7 | 14.0 | 0 | 113-126 | K.AGQSVIGLQMGTNK.C | |

# Detailed Protein Report

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## Protein 400: ATP-binding cassette sub-family F member 2 isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|27881506 | **Score:** | 31.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 71.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPSDLAKKKA | AKKKEAAKAR | QRPRKGHEEN | GDVVTEPQVA | EKNEANGRET | TEVDLLTKEL | EDFEMKKAAA | RAVTGVLASH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PNSTDVHIIN | LSLTFHGQEL | LSDTKLELNS | GRRYGLIGLN | GIGKSMLLSA | IGKREVPIPE | HIDIYHLTRE | MPPSDKTPLH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CVMEVDTERA | MLEKEAERLA | HEDAECEKLM | ELYERLEELD | ADKAEMRASR | ILHGLGFTPA | MQRKKLKDFS | GGWRMRVALA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RALFIRPFML | LLDEPTNHLD | LDACVWLEEE | LKTFKRILVL | VSHSQDFLNG | VCTNIIHMHN | KKLKYYTGNY | DQYVKTRLEL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EENQMKRFHW | EQDQIAHMKN | YIARFGHGSA | KLARQAQSKE | KTLQKMMASG | LTERVVSDKT | LSFYFPPCGK | IPPPVIMVQN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VSFKYTKDGP | CIYNNLEFGI | DLDTRVALVG | PNGAGKSTLL | KLLTGELLPT | DGMIRKHSHV | KIGRYHQHLQ | EQLDLDLSPL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EYMMKCYPEI | KEKEEMRKII | GRYGLTGKQQ | VSPIRNLSDG | QKCRVCLAWL | AWQNPHMLFL | DEPTNHLDIE | TIDALADAIN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| EFEGGMMLVS | HDFRLIQQVA | QEIWVCEKQT | ITKWPGDILA | YKEHLKSKLV | DEEPQLTKRT | HNV | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2422 | 1 | 1044.2014 | 104.18 | 2 | 60.8 | 16.5 | 1 | 437-455 | K.STLLKLLTGELLPTDGMIR.K | Oxidation: 17 |

# Detailed Protein Report

## Protein 401: coilin [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4758024 | **Score:** | 31.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 62.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 5.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAASETVRLR | LQFDYPPPAT | PHCTAFWLLV | DLNRCRVVTD | LISLIRQRFG | FSSGAFLGLY | LEGGLLPPAE | SARLVRDNDC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LRVKLEERGV | AENSVVISNG | DINLSLRKAK | KRAFQLEEGE | ETEPDCKYSK | KHWKSRENNN | NNEKVLDLEP | KAVTDQTVSK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KNKRKNKATC | GTVGDDNEEA | KRKSPKKKEK | CEYKKKAKNP | KSPKVQAVKD | WANQRCSSPK | GSARNSLVKA | KRKGSVSVCS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KESPSSSSES | ESCDESISDG | PSKVTLEARN | SSEKLPTELS | KEEPSTKNTT | ADKLAIKLGF | SLTPSKGKTS | GTTSSSSDSS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AESDDQCLMS | SSTPECAAGF | LKTVGLFAGR | GRPGPGLSSQ | TAGAAGWRRS | GSNGGGQAPG | ASPSVSLPAS | LGRGWGREEN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LFSWKGAKGR | GMRGRGRGRG | HPVSCVVNRS | TDNQRQQQLN | DVVKNSSTII | QNPVETPKKD | YSLLPLLAAA | PQVGEKIAFK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LLELTSSYSP | DVSDYKEGRI | LSHNPETQQV | DIEILSSLPA | LREPGKFDLV | YHNENGAEVV | EYAVTQESKI | TVFWKELIDP |
| 570 | 580 | | | | | | |
| RLIIESPSNT | SSTEPA | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1773 | 1 | 835.3568 | -43.51 | 2 | 52.0 | 11.4 | 2 | 132-144 | K.HWKSRENNNNNEK.V | |

# Detailed Protein Report

**Protein 402:** **PREDICTED: oleosin-B4-like [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|410170263 | **Score:** | 31.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.9 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSPVLEPSP | GPRSPYLHGP | YLLLGEVLGH | SALGAQHAQP | ANGDADELLE | LPALLQHPTG | CDPCASLRDS | RVTPATALLL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LSHRGRAQRR | SIQAAAAQEQ | STGRGCLGKE | PPSQESWTRS | DPRRCLSQDA | VRSGSRVCRS | RPQTRGGGGK | QPRRQKAAVA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GAKSRGGEGK | KPQRRGQKAA | TAGAKSRGGG | VRSLGGKKMR | RGQKGAAGAK | RCGGGKQPRR | RGQKASKSGG | VRCQTPQKAA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AQGVKSRKKL | RQRGQKAAAA | GQEAAAGKTC | GGGGEKHRGG | GDKKPLRKNS | RWRGQKAAAA | GGKKPQKAAA | AGGERRKKLR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RQKAAVARAK | SPKKPRWRGQ | NSGNGVEGQR | SLAFLEFDVE | GKVQRKTKIP | GGVVKQFVPA | DQGPLWQKAA | NLHKMSLPHQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | |
| LALKMEWNGI | IIEWNRMELS | SNGINRDHHR | MEPNGVIIEW | NRKASSCNGI | EWHHQRMDSK | GIIIE | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1321 | 1 | 1045.0547 | 21.73 | 2 | 44.8 | 13.5 | 2 | 90-109 | R.RSIQAAAAQEQSTGRGCLGK.E | Carbamidomethyl: 17 |
| 928 | 1 | 573.2590 | -111.53 | 2 | 41.2 | 17.7 | 2 | 176-187 | R.GQKAATAGAKSR.G | |

# Detailed Protein Report

## Protein 403: ATP-dependent RNA helicase DDX42 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|45446743 | **Score:** | 31.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 102.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578830314 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: ATP-dependent RNA helicase DDX42 isoform X1 [Homo sapiens] |
| gi\|45446747 | refseq_human (refseq_human_20140103.fasta) | ATP-dependent RNA helicase DDX42 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNWNKGGPGT | KRGFGFGGFA | ISAGKKEEPK | LPQQSHSAFG | ATSSSSGFGK | SAPPQLPSFY | KIGSKRANFD | EENAYFEDEE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EDSSNVDLPY | IPAENSPTRQ | QFHSKPVDSD | SDDDPLEAFM | AEVEDQAARD | MKRLEEKDKE | RKNVKGIRDD | IEEEDDQEAY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FRYMAENPTA | GVVQEEEEDN | LEYDSDGNPI | APTKKIIDPL | PPIDHSEIDY | PPFEKNFYNE | HEEITNLTPQ | QLIDLRHKLN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LRVSGAAPPR | PGSSFAHFGF | DEQLMHQIRK | SEYTQPTPIQ | CQGVPVALSG | RDMIGIAKTG | SGKTAAFIWP | MLIHIMDQKE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LEPGDGPIAV | IVCPTRELCQ | QIHAECKRFG | KAYNLRSVAV | YGGGSMWEQA | KALQEGAEIV | VCTPGRLIDH | VKKKATNLQR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VSYLVFDEAD | RMFDMGFEYQ | VRSIASHVRP | DRQTLLFSAT | FRKKIEKLAR | DILIDPIRVV | QGDIGEANED | VTQIVEILHS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GPSKWNWLTR | RLVEFTSSGS | VLLFVTKKAN | AEELANNLKQ | EGHNLGLLHG | DMDQSERNKV | ISDFKKKDIP | VLVATDVAAR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GLDIPSIKTV | INYDVARDID | THTHRIGRTG | RAGEKGVAYT | LLTPKDSNFA | GDLVRNLEGA | NQHVSKELLD | LAMQNAWFRK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SRFKGGKGKK | LNIGGGGLGY | RERPGLGSEN | MDRGNNNVMS | NYEAYKPSTG | AMGDRLTAMK | AAFQSQYKSH | FVAASLSNQK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AGSSAAGASG | WTSAGSLNSV | PTNSAQQGHN | SPDSPVTSAA | KGIPGFGNTG | NISGAPVTYP | SAGAQGVNNT | ASGNNSREGT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GGSNGKRERY | TENRGSSRHS | HGETGNRHSD | SPRHGDGGRH | GDGYRHPESS | SRHTDGHRHG | ENRHGGSAGR | HGENRGANDG |
| 890 | 900 | 910 | 920 | 930 | 940 | | |
| RNGESRKEAF | NRESKMEPKM | EPKVDSSKMD | KVDSKTDKTA | DGFAVPEPPK | RKKSRWDS | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2100 | 1 | 753.3769 | 8.39 | 2 | 56.6 | 15.7 | 2 | 896-908 | K.MEPKMEPKVDSSK.M | |

# Detailed Protein Report

## Protein 404: 28S ribosomal protein S31, mitochondrial [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|186928854 | **Score:** | 31.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 2 |

### Quantitation

***WUP:QUP*** **Median:** 0.38 **CV:** 33.11 % **No. of Peptides:** 2

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFPRVSTFLP | LRPLSRHPLS | SGSPETSAAA | IMLLTVRHGT | VRYRSSALLA | RTKNNIQRYF | GTNSVICSKK | DKQSVRTEET |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SKETSESQDS | EKENTKKDLL | GIIKGMKVEL | STVNVRTTKP | PKRRPLKSLE | ATLGRLRRAT | EYAPKKRIEP | LSPELVAAAS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AVADSLPFDK | QTTKSELLSQ | LQQHEEESRA | QRDAKRPKIS | FSNIISDMKV | ARSATARVRS | RPELRIQFDE | GYDNYPGQEK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TDDLKKRKNI | FTGKRLNIFD | MMAVTKEAPE | TDTSPSLWDV | EFAKQLATVN | EQPLQNGFEE | LIQWTKEGKL | WEFPINNEAG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FDDDGSEFHE | HIFLEKHLES | FPKQGPIRHF | MELVTCGLSK | NPYLSVKQKV | EHIEWFRNYF | NEKKDILKES | NIQFN |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2703 | 1 | 724.8604 | -42.02 | 2 | 64.9 | 19.1 | 2 | 384-395 | K.KDILKESNIQFN.- | | WUP:QUP | 0.28 |
| 1539 | 1 | 660.8309 | -18.83 | 2 | 48.9 | 12.0 | 1 | 385-395 | K.DILKESNIQFN.- | | WUP:QUP | 0.53 |

# Detailed Protein Report

## Protein 405: ubiquitin-conjugating enzyme E2 J2 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|37577130 | **Score:** | 31.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 22.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| | | **Sequence Coverage [%]:** | 5.8 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|37577132 | refseq_human (refseq_human_20140103.fasta) | ubiquitin-conjugating enzyme E2 J2 isoform 3 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MTPYEGGYYH GKLIFPREFP FKPPSIYMIT PNGRFKCNTR LCLSITDFHP DTWNPAWSVS TILTGLLSFM VEKGPTLGSI
        90        100        110        120        130        140        150        160
ETSDFTKRQL AVQSLAFNLK DKVFCELFPE VVEEIKQKQK AQDELSSRPQ TLPLPDVVPD GETHLVQNGI QLLNGHAPGA
       170        180        190        200        210
VPNLAGLQQA NRHHGLLGGA LANLFVIVGF AAFAYTVKYV LRSIAQE
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 188 | 1 | 636.3948 | 167.51 | 2 | 32.1 | 12.9 | 0 | 2-12 | M.TPYEGGYYHGK.L | |

# Detailed Protein Report

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## Protein 406: zinc finger protein 568 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|325651958 | **Score:** | 31.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 67.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.65 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|325651960 | refseq_human (refseq_human_20140103.fasta) | zinc finger protein 568 isoform 3 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MKPAQRNLYR DVMLENYSNL VTVGCQVTKP DVIFKLEQEE EPWVMEEEMF GRHCPEVWEV DEQIKKQQET LVRKVTSISK
        90        100        110        120        130        140        150        160
KILIKEKVIE CKKVAKIFPL SSDIVTSRQS FYDCDSLDKG LEHNLDLLRY EKGCVREKQS NEFGKPFYHC ASYVVTPFKC
       170        180        190        200        210        220        230        240
NQCGQDFSHK FDLIRHERIH AGEKPYECKE CGKAFSRKEN LITHQKIHTG EKPYKCNECG KAFIQMSNLI RHHRIHTGEK
       250        260        270        280        290        300        310        320
PYACKDCWKA FSQKSNLIEH ERIHTGEKPY ECKECGKSFS QKQNLIEHEK IHTGEKPYAC NECGRAFSRM SSVTLHMRSH
       330        340        350        360        370        380        390        400
TGEKPYKCNK CGKAFSQCSV FIIHMRSHTG EKPYVCSECG KAFSQSSSLT VHMRNHTAEK PYECKECGKA FSRKENLITH
       410        420        430        440        450        460        470        480
QKIHTGEKPY ECSECGKAFI QMSNLIRHQR IHTGEKPYAC TVCGKAFSQK SNLTEHEKIH TGEKPYHCNQ CGKAFSQRQN
       490        500        510        520        530        540        550        560
LLEHEKIHTG EKPFKCNECG KAFSRISSLT LHVRSHTGEK PYECNKCGKA FSQCSLLIIH MRSHTGEKPF ECNECGKAFS
       570        580        590
QRASLSIHKR GHTGERHQVY
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 858 | 1 | 501.2115 | -157.63 | 2 | 39.1 | 12.8 | 1 | 66-73 | K.KQQETLVR.K | | QU:MU 0.65 |

# Detailed Protein Report

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## Protein 407: cartilage intermediate layer protein 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|145699139 | **Score:** | 30.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 126.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASLLPLLCL | CVVAAHLAGA | RDATPTEEPM | ATALGLERRS | VYTGQPSPAL | EDWEEASEWT | SWFNVDHPGG | DGDFESLAAI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RFYYGPARVC | PRPLALEART | TDWALPSAVG | ERVHLNPTRG | FWCLNREQPR | GRRCSNYHVR | FRCPLEASWG | AWGPWGPCSG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SCGPGRRLRR | RHCPSPAGDA | CPGRPLEAQK | CVRPRCPGCS | LDTCECPDHI | LLGSVVTPSG | QPLLGARVSL | RDQPGTVATS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DAHGTFRVPG | VCADSRANIR | AQMDGFSAGE | AQAQANGSIS | VVTIILDKLE | KPYLVKHPES | RVREAGQNVT | FCCKASGTPM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PKKYSWFHNG | TLLDRRAHGY | GAHLELRGLR | PDQAGIYHCK | AWNEAGAVRS | GTARLTVLAP | GQPACDPRPR | EYLIKLPEDC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GQPGSGPAYL | DVGLCPDTRC | PSLAGSSPRC | GDASSRCCSV | RRLERREIHC | PGYVLPVKVV | AECGCQKCLP | PRGLVRGRVV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AADSGEPLRF | ARILLGQEPI | GFTAYQGDFT | IEVPPSTQRL | VVTFVDPSGE | FMDAVRVLPF | DPRGAGVYHE | VKAMRKKAPV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ILHTSQSNTI | PLGELEDEAP | LGELVLPSGA | FRRADGKPYS | GPVEARVTFV | DPRDLTSAAS | APSDLRFVDS | DGELAPLRTY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GMFSVDLRAP | GSAEQLQVGP | VAVRVAASQI | HMPGHVEALK | LWSLNPETGL | WEEESGFRRE | GSSGPRVRRE | ERVFLVGNVE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| IRERRLFNLD | VPERRRCFVK | VRAYANDKFT | PSEQVEGVVV | TLVNLEPAPG | FSANPRAWGR | FDSAVTGPNG | ACLPAFCDAD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RPDAYTALVT | ATLGGEELEP | APSLPRPLPA | TVGVTQPYLD | RLGYRRTDHD | DPAFKRNGFR | INLAKPRPGD | PAEANGPVYP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| WRSLRECQGA | PVTASHFRFA | RVEADKYEYN | VVPFREGTPA | SWTGDLLAWW | PNPQEFRACF | LKVKIQGPQE | YMVRSHNAGG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SHPRTRGQLY | GLRDARSVRD | PERPGTSAAC | VEFKCSGMLF | DQRQVDRTLV | TIMPQGSCRR | VAVNGLLRDY | LTRHPPPVPA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EDPAAFSMLA | PLDPLGHNYG | VYTVTDQSPR | LAKEIAIGRC | FDGSSDGFSR | EMKADAGTAV | TFQCREPPAG | RPSLFQRLLE |
| 1130 | 1140 | 1150 | 1160 | | | | |
| SPATALGDIR | REMSEAAQAQ | ARASGPLRTR | RGRVRQ | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1629 | 1 | 534.3438 | 61.87 | 2 | 50.6 | 13.1 | 1 | 468-476 | K.CLPPRGLVR.G | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 408: regulator of G-protein signaling 9 isoform 2 [Homo sapiens]

**Accession:** gi|126366080
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 30.9
**MW [kDa]:** 76.6
**pI:** 10.0
**Sequence Coverage [%]:** 3.6
**No. of unique Peptides:** 2

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.13 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.17 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTIRHQGQQY | RPRMAFLQKI | EALVKDMQNP | ETGVRMQNQR | VLVTSVPHAM | TGSDVLQWIV | QRLWISSLEA | QNLGNFIVRY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GYIYPLQDPK | NLILKPDGSL | YRFQTPYFWP | TQQWPAEDTD | YAIYLAKRNI | KKKGILEEYE | KENYNFLNQK | MNYKWDFVIM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QAKEQYRAGK | ERNKADRYAL | DCQEKAYWLV | HRCPPGMDNV | LDYGLDRVTN | PNEVKKQTVV | AVKKEIMYYQ | QALMRSTVKS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SVSLGGIVKY | SEQFSSNDAI | MSGCLPSNPW | ITDDTQFWDL | NAKLVEIPTK | MRVERWAFNF | SELIRDPKGR | QSFQYFLKKE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FSGENLGFWE | ACEDLKYGDQ | SKVKEKAEEI | YKLFLAPGAR | RWINIDGKTM | DITVKGLKHP | HRYVLDAAQT | HIYMLMKKDS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YARYLKSPIY | KDMLAKAIEP | QETTKKSSTL | PFMRRHLRSS | PSPVILRQLE | EEAKAREAAN | TVDITQPGQH | MAPSPHLTVY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TGTCMPPSPS | SPFSSSCRSP | RKPFASPSRF | IRRPSTTICP | SPIRVALESS | SGLEQKGECS | GSMAPRGPSV | TESSEASLDT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SWPRSRPRAP | PKARMALSFS | RFLRRGCLAS | PVFARLSPKC | PAVSHGRVQP | LGDVGQQLPR | LKSKRVANFF | QIKMDVPTGS |
| 650 | 660 | 670 | 680 | | | | |
| GTCLMDSEDA | GTGESGDRAT | EKEVICPWES | L | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2782 | 1 | 681.4961 | 134.76 | 2 | 63.3 | 19.3 | 1 | 436-447 | R.HLRSSPSPVILR.Q | | |
| 461 | 1 | 626.3269 | -12.81 | 2 | 35.8 | 11.6 | 1 | 596-607 | R.LSPKCPAVSHGR.V | | WUP:QUP 0.17<br>QU:MU 1.13 |

# Detailed Protein Report

## Protein 409: steroid hormone receptor ERR2 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|238550159 | **Score:** | 30.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.9 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSDDRHLGS | SCGSFIKTEP | SSPSSGIDAL | SHHSPSGSSD | ASGGFGLALG | THANGLDSPP | MFAGAGLGGT | PCRKSYEDCA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SGIMEDSAIK | CEYMLNAIPK | RLCLVCGDIA | SGYHYGVASC | EACKAFFKRT | IQGNIEYSCP | ATNECEITKR | RRKSCQACRF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MKCLKVGMLK | EGVRLDRVRG | GRQKYKRRLD | SESSPYLSLQ | ISPPAKKPLT | KIVSYLLVAE | PDKLYAMPPP | GMPEGDIKAL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TTLCDLADRE | LVVIIGWAKH | IPGFSSLSLG | DQMSLLQSAW | MEILILGIVY | RSLPYDDKLV | YAEDYIMDEE | HSRLAGLLEL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YRAILQLVRR | YKKLKVEKEE | FVTLKALALA | NSDSMYIEDL | EAVQKLQDLL | HEALQDYELS | QRHEEPWRTG | KLLLTLPLLR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QTAAKAVQHF | YSVKLQGKVP | MHKLFLEMLE | AKVGQEQLRG | SPKDERMSSH | DGKCPFQSAA | FTSRDQSNSP | GIPNPRPSSP |
| 490 | 500 | 510 |  |  |  |  |  |
| TPLNERGRQI | SPSTRTPGGQ | GKHLWLTM |  |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1383 | 2 | 1179.1487 | 0.19 | 2 | 47.4 | 17.9 | 1 | 239-259 | K.ALTTLCDLADRELVVIIGWAK.H | Carbamidomethyl: 6 |

# Detailed Protein Report

## Protein 410: PREDICTED: rho GTPase-activating protein 23 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578831178 | **Score:** | 30.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 153.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578840369 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: rho GTPase-activating protein 23 isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNGVAFCLVG | IPPRPEPRPP | QLPLGPRDGC | SPRRPFPWQG | PRTLLLYKSP | QDGFGFTLRH | FIVYPPESAV | HCSLKEEENG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GRGGGPSPRY | RLEPMDTIFV | KNVKEDGPAH | RAGLRTGDRL | VKVNGESVIG | KTYSQVIALI | QNSDDTLELS | IMPKDEDILQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LAYSQDAYLK | GNEPYSGEAR | SIPEPPPICY | PRKTYAPPAR | ASTRATMVPE | PTSALPSDPR | SPAAWSDPGL | RVPPAARAHL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DNSSLGMSQP | RPSPGAFPHL | SSEPRTPRAF | PEPGSRVPPS | RLECQQALSH | WLSNQVPRRA | GERRCPAMAP | RARSASQDRL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EEVAAPRPWP | CSTSQDALSQ | LGQEGWHRAR | SDDYLSRATR | SAEALGPGAL | VSPRFERCGW | ASQRSSARTP | ACPTRDLPGP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QAPPPSGLQG | LDDLGYIGYR | SYSPSFQRRT | GLLHALSFRD | SPFGGLPTFN | LAQSPASFPP | EASEPPRVVR | PEPSTRALEP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PAEDRGDEVV | LRQKPPTGRK | VQLTPARQMN | LGFGDESPEP | EASGRGERLG | RKVAPLATTE | DSLASIPFID | EPTSPSIDLQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AKHVPASAVV | SSAMNSAPVL | GTSPSSPTFT | FTLGRHYSQD | CSSIKAGRRS | SYLLAITTER | SKSCDDGLNT | FRDEGRVLRR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LPNRIPSLRM | LRSFFTDGSL | DSWGTSEDAD | APSKRHSTSD | LSDATFSDIR | REGWLYYKQI | LTKKGKAEDR | DDMLGWIRAI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RENSRAEGED | PGCANQALIS | KKLNDYRKVS | HSSGPKADSS | PKGSRGLGGL | KSEFLKQSAA | RGLRTQDLPA | GSKDDSAAAP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KTPWGINIIK | KNKKAAPRAF | GVRLEECQPA | TENQRVPLIV | AACCRIVEAR | GLESTGIYRV | PGNNAVVSSL | QEQLNRGPGD |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| INLQDERWQD | LNVISSLLKS | FFRKLPEPLF | TDDKYNDFIE | ANRIEDARER | MRTLRKLIRD | LPGHYYETLK | FLVGHLKTIA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DHSEKNKMEP | RNLALVFGPT | LVRTSEDNMT | DMVTHMPDRY | KIVETLIQHS | DWFFSDEEDK | GERTPVGDKE | PQAVPNIEYL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LPNIGRTVPP | GDPGSDSTTC | SSAKSKGSWA | PKKEPYAREM | LAISFISAVN | RKRKKRREAR | GLGSSTDDDS | EQEAHKPGAG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ATAPGTQERP | QGPLPGAVAP | EAPGRLSPPA | APEERPAADT | RSIVSGYSTL | STMDRSVCSG | ASGRRAGAGD | EADDERSELS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| HVETDTEGAA | GAGPGGRLTR | RPSFSSHHLM | PCDTLARRRL | ARGRPDGEGA | GRGGPRAPEP | PGSASSSSQE | SLRPPAAALA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SRPSRMEALR | LRLRGTADDM | LAVRLRRPLS | PETRRRRSSW | RRHTVVVQSP | LTDLNFNEWK | ELGGGGPPEP | AGARAHSDNK |
| 1370 | 1380 | 1390 | 1400 | 1410 | | | |
| DSGLSSLEST | KARAPSSAAS | QPPAPGDTGS | LQSQPPRRSA | ASRLHQCL | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2089 | 2 | 734.3401 | -78.89 | 2 | 54.5 | 12.7 | 2 | 1239-1252 | R.RLARGRPDGEGAGR.G | |

# Detailed Protein Report

**Protein 411:** **PREDICTED: maestro heat-like repeat-containing protein family member 1 isoform X10 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578816157 | **Score:** | 30.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 163.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTESSMKKLA | STLLDAITDK | DPLVQEQVCS | ALCSLGEARP | VETLRACEEY | LRQHDKLAHP | YRAAVLRAME | RVLSSRASEL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DKDTASTIIL | LASSEMTKTK | DLVWDWQQAA | SGVLVAVGRQ | FISKVMEELL | RRLHPGTLPH | CAVLHTLASL | SVANAFGVVP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FLPSVLSSLL | PVLGVAKQDT | VRVAFCSALQ | RFSEGALEYL | ANLDRAPDPT | VRKDAFATDI | FSAYDVLFHQ | WLQSREAKLR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LAVVEALGPM | SHLLPSERLE | EQLPKLLPGI | LALYKKHAET | FYLSKSLGQI | LEAAVSVGSR | TLETQLDALL | AALHSQICVP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VESSSPLVMS | NQKEVLRCFT | VLACSSPDRL | LAFLLPRLDT | SNERTRVGTL | QVVRHVINSA | AAQMEDKKPF | ILSSMRLPLL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DTNSKVKRAV | VQVISAMAHH | GYLEQPGGEA | MIEYIVQQCA | LPPEQEPEKP | GPGSKDPKAD | SVRAISVRTL | YLVSTTVDRM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SHVLWPYLLQ | FLTPVRFTGA | LTPLCRSLVH | LAQKRQEAGA | DAFLIQYDAH | ASLPSPYAVT | GRLLVVSSSP | YLGDGRGAAA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LRLLSVLHPN | IHPLLGQHWE | TTVPLLLGYL | DEHTEETLPQ | EEWEEKLLMF | LRDTLAIISD | NAWICQLSLE | LCRQLPCYDE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| APQEKNFLYK | CIGTTLGAAS | SKEVVRKHLQ | ELLETARYQE | EAEREGLACC | FGICAISHLE | DTLAQLEDFV | RSEVFRKSIG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ILNIFKDRSE | NEVEKVKSAL | ILCYGHVAAR | APRELVLAKV | ESDILRNICQ | HFSTKVLGIK | VETKDPALKL | CLVQSVCMVS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RAICSSTQAG | SFHFTRKAEL | VAQMMEFIRA | EPPDSLRTPI | RKKAMLTCTY | LVSVEPALDE | QARADVIHGC | LHSIMALLPE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PKEEDGGCQK | SLYLETLHAL | EDLLTSLLQR | NMTPQGLQIM | IEHLSPWIKS | PRGHERARAL | GLSALLLRYF | LEHLRVSALV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PFHNLGLLIG | LFSPRCADLW | PATRQEAVDC | VYSLLYLQLG | YEGFSRDYRD | DVAERLLSLK | DGLVHPDPAI | LFHTCHSVGQ |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| IIAKRLPPDQ | LISLLLTMFE | ALGDPEKNCS | RAATVMINCL | LQERGGVLQE | KVPEIVSVLR | SKLQEAQGEH | VLPAAQHSVY |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LLATQHCAAV | VSSLLGSPLP | LDSHTCMLWR | ALAVEPRLAA | QVLGLLLEKM | SRDVPFKESR | AFLLGRTPDR | VATLLPLSAT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| CALFEVMSTP | AAGPAVLELY | PQLFVVLLLR | VSCTVGVQLP | RNLQAQERRG | ASPALATRNL | EPCSSAVDTL | RSMLLRSGSE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DVVQRMDLEG | GWELLRTSAG | HEEGATRLAR | AMAEHAGPRL | PLVLKTLACT | HSSAYENQRV | TTTAFLAELL | NSNVANDLML |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LDSLLESLAA | RQKDTCASVR | RLVLRGLANL | ASGCPDKVRT | HGPQLLTAMI | GGLDDGDNPH | SPVALEAMLG | LARLVHLVES |
| 1450 | 1460 | 1470 | 1480 | 1490 | | | |
| WDLRSGLLHV | AIRIRPFFDS | VTVESADLQG | CCFAGPGSPH | P | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2554 | 1 | 821.4177 | -87.55 | 2 | 61.9 | 12.2 | 1 | 1158-1172 | R.LAAQVLGLLLEKMSR.D | |

# Detailed Protein Report

**Protein 412:** **NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial isoform 5 [Homo sapiens]**

**Accession:** gi|316983160
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 30.8
**MW [kDa]:** 80.9
**pI:** 6.2
**Sequence Coverage [%]:** 2.7
**No. of unique Peptides:** 1

## Quantitation

***WUP:QUP*** **Median:** 2.24 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MRIRGSSGTL | SRINMLRIPV | RKALVGLSKS | PKGCVRTTAT | AASNLIEVFV | DGQSVMVEPG | TTVLQACEKV | GMQIPRFCYH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ERLSVAGNCR | MCLVEIEKAP | KVVAACAMPV | MKGWNILTNS | EKSKKAREGV | MEFLLANHPL | DCPICDQGGE | CDLQDQSMMF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GNDRSRFLEG | KRAVEDKNIG | PLVKTIMTRC | IQCTRCIRFA | SEIAGVDDLG | TTGRGNDMQV | GTYIEKMFMS | ELSGNIIDIC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PVGALTSKPY | AFTARPWETR | KTESIDVMDA | VGSNIVVSTR | TGEVMRILPR | MHEDINEEWI | SDKTRFAYDG | LKRQRLTEPM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VRNEKGLLTY | TSWEDALSRV | AGMLQSFQGK | DVAAIAGGLV | DAEALVALKD | LLNRVDSDTL | CTEEVFPTAG | AGTDLRSNYL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LNTTIAGVEE | ADVVLLVGTN | PRFEAPLFNA | RIRKSWLHND | LKVALIGSPV | DLTYTYDHLG | DSPKILQDIA | SGSHPFSQVL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KEAKKPMVVL | GSSALQRNDG | AAILAAVSSI | AQKIRMTSGV | TGDWKVMNIL | HRIASQVAAL | DLGYKPGVEA | IRKNPPKVLF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LLGADGGCIT | RQDLPKDCFI | IYQGHHGDVG | APIADVILPG | AAYTEKSATY | VNTEGRAQQT | KVAVTPPGLA | REDWKIIRAL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SEIAGMTLPY | DTLDQVRNRL | EEVSPNLVRY | DDIEGANYFQ | QANELSKLVN | QQLLADPLVP | PQLTIKDFYM | TDSISRASQT |
| 730 | 740 | 750 | | | | | |
| MAKCVKAVTE | GAQAVEEPSI | C | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2481 | 1 | 449.6389 | -246.99 | 2 | 61.0 | 14.1 | 0 | 526-532 | K.VMNILHR.I | Oxidation: 2 | WUP:QUP 2.24 |

# Detailed Protein Report

## Protein 413: scaffold attachment factor B1 isoform 4 [Homo sapiens]

**Accession:** gi|321267473
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 30.8
**MW [kDa]:** 95.1
**pI:** 6.0
**Sequence Coverage [%]:** 2.6
**No. of unique Peptides:** 1

### Quantitation

***QU:MU*** **Median:** 4.03 **CV:** 0.00 % **No. of Peptides:** 1
***WUP:QUP*** **Median:** 3.65 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAETLSGLGD | SGAAGAAALS | SASSETGTRR | LSDLRVIDLR | AELRKRNVDS | SGNKSVLMER | LKKAIEDEGG | NPDEIEITSE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GNKKTSKRSS | KGRKPEEEGV | EDNGLEENSG | DGQIEDKETI | NNLDTSSSDF | TILQEIEEPS | LEPENEKILD | ILGETCKSEP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VKEESSELEQ | PFAQDTSSVG | PDRKLAEEED | LFDSAHPEEG | DLDLASESTA | HAQSSKADSL | LAVVKREPAE | QPGDGERTDC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EPVGLEPAVE | QSSAASELAE | ASSEELAEAP | TEAPSPEARD | SKEDGRKFDF | DACNEVPPAP | KESSTSEGAD | QKMSSPEDDS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DTKRLSKEEK | GRSSCGRNFW | VSGLSSTTRA | TDLKNLFSKY | GKVVGAKVVT | NARSPGARCY | GFVTMSTAEE | ATKCINHLHK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TELHGKMISV | EKAKNEPVGK | KTSDKRDSDG | KKEKSSNSDR | STNLKRDDKC | DRKDDAKKGD | DGSGEKSKDQ | DDQKPGPSER |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SRATKSGSRG | TERTVVMDKS | KGVPVISVKT | SGSKERASKS | QDRKSASREK | RSVVSFDKVK | EPRKSRDSES | HSRVRERSER |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EQRMQAQWER | EERERLEIAR | ERLAFQRQRL | ERERMERERL | ERERMHVEHE | RRREQERIHR | EREELRRQQE | LRYEQERRPA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VRRPYDLDRR | DDAYWPEAKR | AALDERYHSD | FNRQDRFHDF | DHRDRGRYPD | HSVDRREGSR | SMMGEREGQH | YPERHGGPER |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HGRDSRDGWG | GYGSDKRMSE | GRGLPPPPRG | RRDWGDHGRR | EDDRSWQGTA | DGGMMDRDHK | RWQGGERSMS | GHSGPGHMMN |
| 810 | 820 | 830 | 840 | 850 | | | |
| RGGMSGRGSF | APGGASRGHP | IPHGGMQGGF | GGQSRGSRPS | DARFTRRY | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 980 | 2 | 530.6065 | -255.21 | 2 | 40.6 | 14.1 | 1 | 545-553 | K.SRDSESHSR.V | | WUP:QUP 3.65<br>QU:MU 4.03 |

# Detailed Protein Report

## Protein 414: putative sodium-coupled neutral amino acid transporter 10 isoform a [Homo sapiens]

**Accession:** gi|83921602
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 30.8
**MW [kDa]:** 119.7
**pI:** 5.4
**Sequence Coverage [%]:** 3.5
**No. of unique Peptides:** 2

## Quantitation

***QU:MU*** **Median:** 0.94 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTAAAASNWG | LITNIVNSIV | GVSVLTMPFC | FKQCGIVLGA | LLLVFCSWMT | HQSCMFLVKS | ASLSKRRTYA | GLAFHAYGKA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GKMLVETSMI | GLMLGTCIAF | YVVIGDLGSN | FFARLFGFQV | GGTFRMFLLF | AVSLCIVLPL | SLQRNMMASI | QSFSAMALLF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YTVFMFVIVL | SSLKHGLFSG | QWLRRVSYVR | WEGVFRCIPI | FGMSFACQSQ | VLPTYDSLDE | PSVKTMSSIF | ASSLNVVTTF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YVMVGFFGYV | SFTEATAGNV | LMHFPSNLVT | EMLRVGFMMS | VAVGFPMMIL | PCRQALSTLL | CEQQQKDGTF | AAGGYMPPLR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FKALTLSVVF | GTMVGGILIP | NVETILGLTG | ATMGSLICFI | CPALIYKKIH | KNALSSQVVL | WVGLGVLVVS | TVTTLSVSEE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VPEDLAEEAP | GGRLGEAEGL | MKVEAARLSA | QDPVVAVAED | GREKPKLPKE | REELEQAQIK | GPVDVPGRED | GKEAPEEAQL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DRPGQGIAVP | VGEAHRHEPP | VPHDKVVVDE | GQDREVPEEN | KPPSRHAGGK | APGVQGQMAP | PLPDSEREKQ | EPEQGEVGKR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PGQAQALEEA | GDLPEDPQKV | PEADGQPAVQ | PAKEDLGPGD | RGLHPRPQAV | LSEQQNGLAV | GGGEKAKGGP | PPGNAAGDTG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QPAEDSDHGG | KPPLPAEKPA | PGPGLPPEPR | EQRDVERAGG | NQAASQLEEA | GRAEMLDHAV | LLQVIKEQQV | QQKRLLDQQE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KLLAVIEEQH | KEIHQQRQED | EEDKPRQVEV | HQEPGAAVPR | GQEAPEGKAR | ETVENLPPLP | LDPVLRAPGG | RPAPSQDLNQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RSLEHSEGPV | GRDPAGPPDG | GPDTEPRAAQ | AKLRDGQKDA | APRAAGTVKE | LPKGPEQVPV | PDPAREAGGP | EERLAEEFPG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QSQDVTGGSQ | DRKKPGKEVA | ATGTSILKEA | NWLVAGPGAE | TGDPRMKPKQ | VSRDLGLAAD | LPGGAEGAAA | QPQAVLRQPE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LRVISDGEQG | GQQGHRLDHG | GHLEMRKARG | GDHVPVSHEQ | PRGGEDAAVQ | EPRQRPEPEL | GLKRAVPGGQ | RPDNAKPNRD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LKLQAGSDLR | RRRRDLGPHA | EGQLAPRDGV | IIGLNPLPDV | QVNDLRGALD | AQLRQAAGGA | LQVVHSRQLR | QAPGPPEES |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2229 | 1 | 701.2999 | -60.69 | 3 | 57.7 | 11.7 | 0 | 275-293 | R.VGFMMSVAVGFPMMILPCR.Q | Oxidation: 13 | QU:MU 0.94 |
| 203 | 1 | 1043.9225 | -84.97 | 2 | 32.5 | 19.1 | 1 | 854-873 | K.GPEQVPVPDPAREAGGPEER.L | | |

# Detailed Protein Report

**Protein 415:** **PREDICTED: nuclear envelope pore membrane protein POM 121C isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578813833 | **Score:** | 30.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 128.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTWRARDDAT | RGAVHAGIFK | SPPRRGAAMS | PAAAAAGAGE | RRRPIASVRD | GRGRGCGGPA | GAALLGLSLV | GLLLYLVPAA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AALAWLAVGT | TAAWWGLSRE | PRGSRPLSSF | VQKARHRRTL | FASPPAKSTA | NGNLLEPRTL | LEGPDPAELL | LMGSYLGKPG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PPQPAPAPEG | QDLRNRPGRR | PPARPAPRST | PPSQPTHRVH | HFYPSLPTPL | LRPSGRPSPR | DRGTLPDRFV | ITPRRRYPIH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QTQYSCPGVL | PTVCWNGYHK | KAVLSPRNSR | MVCSPVTVRI | APPDRRFSRS | AIPEQIISST | LSSPSSNAPD | PCAKETVLSA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LKEKKKKRTV | EEEDQIFLDG | QENKRRRHDS | SGSGHSAFEP | LVASGVPASF | VPKPGSLKRG | LNSQSSDDHL | NKRSRSSSMS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SLTGAYTSGI | PSSSRNAITS | SYSSTRGISQ | LWKRNGPSSS | PFSSPASSRS | QTPERPAKKI | REEELCHHSS | SSTPLAADKE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SQGEKAADTT | PRKKQNSNSQ | STPGSSGQRK | RKVQLLPSRR | GEQLTLPPPP | QLGYSITAED | LDLEKKASLQ | WFNQALEDKS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DAASNSVTET | PPTTQPSFTF | TLPAAATASP | PTSLLAPSTN | PLLESLKKMQ | TPPSLPPCPE | SAGAATTEAL | SPPKTPSLLP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PLGLSQSGPP | GLLPSPSFDS | KPPTTLLGLI | PAPSMVPATD | TKAPPTLQAE | TATKPQATSA | PSPAPKQSFL | FGTQNTSPSS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PAAPAASSAS | PMFKPIFTAP | PKSEKEGLTP | PGPSVSATAP | SSSSLPTTTS | TTAPTFQPVF | SSMGPPASVP | LPAPFFKQTT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TPATAPTTTA | PLFTGLASAT | SAVAPITSAS | PSTDSASKPA | FGFGINSVSS | SSVSTTTSTA | TAASQPFLFG | APQASAASFT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PAMGSIFQFG | KPPALPTTTT | VTTFSQSLPT | AVPTATSSSA | ADFSGFGSTL | ATSAPATSSQ | PTLTFSNTST | PTFNIPFGSS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| AKSPLPSYPG | ANPQPAFGAA | EGQPPGAAKP | ALTPSFGSSF | TFGNSAAPAP | ATAPTPAPAS | TIKIVPAHVP | TPIQPTFGGA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| THSAFGLKAT | ASAFGAPASS | QPAFGGSTAV | FSFGAATSSG | FGATTQTASS | GSSSSVFGST | TPSPFTFGGS | AAPAGSGSFG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| INVATPGSSA | TTGAFSFGAG | QSGSTATSTP | FTGGLGQNAL | GTTGQSTPFA | FNVGSTTESK | PVFGGTATPT | FGQNTPAPGV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | | |
| GTSGSSLSFG | ASSAPAQGFV | GVGPFGSAAP | SFSIGAGSKT | PGARQRLQAR | RQHTRKK | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2272 | 1 | 703.3240 | -44.91 | 2 | 56.7 | 10.4 | 1 | 268-279 | R.NSRMVCSPVTVR.I | Carbamidomethyl: 6 |
| 39 | 1 | 1103.4999 | -21.74 | 2 | 30.2 | 20.4 | 1 | 394-415 | R.SRSSSMSSLTGAYTSGIPSSSR.N | |

BRUKER

# Detailed Protein Report

**Protein 416:** **amyloid beta A4 precursor protein-binding family B member 1 isoform b [Homo sapiens]**

**Accession:** gi|22035554
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 30.7
**MW [kDa]:** 76.9
**pI:** 4.8
**Sequence Coverage [%]:** 5.6
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSVPSSLSQS | AINANSHGGP | ALSLPLPLHA | AHNQLLNAKL | QATAVGPKDL | RSAMGEGGGP | EPGPANAKWL | KEGQNQLRRA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ATAHRDQNRN | VTLTLAEEAS | QEPEMAPLGP | KGLIHLYSEL | ELSAHNAANR | GLRGPGLIIS | TQEQGPDEGE | EKAAGEAEEE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EEDDDDEEEE | EDLSSPPGLP | EPLESVEAPP | RPQALTDGPR | EHSKSASLLF | GMRNSAASDE | DSSWATLSQG | SPSYGSPEDT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DSFWNPNAFE | TDSDLPAGWM | RVQDTSGTYY | WHIPTGTTQW | EPPGRASPSQ | GSSPQEESQL | TWTGFAHGEG | FEDGEFWKDE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PSDEAPMELG | LKEPEEGTLT | FPAQSLSPEP | LPQEEEKLPP | RNTNPGIKCF | AVRSLGWVEM | TEEELAPGRS | SVAVNNCIRQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LSYHKNNLHD | PMSGGWGEGK | DLLLQLEDET | LKLVEPQSQA | LLHAQPIISI | RVWGVGRDSG | RDFAYVARDK | LTQMLKCHVF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RCEAPAKNIA | TSLHEICSKI | MAERRNARCL | VNGLSLDHSK | LVDVPFQVEF | PAPKNELVQK | FQVYYLGNVP | VAKPVGVDVI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NGALESVLSS | SSREQWTPSH | VSVAPATLTI | LHQQTEAVLG | ECRVRFLSFL | AVGRDVHTFA | FIMAAGPASF | CCHMFWCEPN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | |
| AASLSEAVQA | ACMLRYQKCL | DARSQASTSC | LPAPPAESVA | RRVGWTVRRG | VQSLWGSLKP | KRLGAHTP | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2594 | 1 | 946.7123 | -95.55 | 3 | 60.7 | 13.7 | 1 | 86-111 | R.DQNRNVTLTLAEEASQEPEMAPLGPK.G | |

# Detailed Protein Report

## Protein 417: ras/Rap GTPase-activating protein SynGAP [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|194248068 | **Score:** | 30.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 148.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSRSRASIHR | GSIPAMSYAP | FRDVRGPSMH | RTQYVHSPYD | RPGWNPRFCI | ISGNQLLMLD | EDEIHPLLIR | DRRSESSRNK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LLRRTVSVPV | EGRPHGEHEY | HLGRSRRKSV | PGGKQYSMEG | APAAPFRPSQ | GFLSRRLKSS | IKRTKSQPKL | DRTSSFRQIL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PRFRSADHDR | ARLMQSFKES | HSHESLLSPS | SAAEALELNL | DEDSIIKPVH | SSILGQEFCF | EVTTSSGTKC | FACRSAAERD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KWIENLQRAV | KPNKDNSRRV | DNVLKLWIIE | ARELPPKKRY | YCELCLDDML | YARTTSKPRS | ASGDTVFWGE | HFEFNNLPAV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RALRLHLYRD | SDKKRKKDKA | GYVGLVTVPV | ATLAGRHFTE | QWYPVTLPTG | SGGSGGMGSG | GGGGSGGGSG | GKGKGGCPAV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RLKARYQTMS | ILPMELYKEF | AEYVTNHYRM | LCAVLEPALN | VKGKEEVASA | LVHILQSTGK | AKDFLSDMAM | SEVDRFMERE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HLIFRENTLA | TKAIEEYMRL | IGQKYLKDAI | GEFIRALYES | EENCEVDPIK | CTASSLAEHQ | ANLRMCCELA | LCKVVNSHCV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FPRELKEVFA | SWRLRCAERG | REDIADRLIS | ASLFLRFLCP | AIMSPSLFGL | MQEYPDEQTS | RTLTLIAKVI | QNLANFSKFT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SKEDFLGFMN | EFLELEWGSM | QQFLYEISNL | DTLTNSSSFE | GYIDLGRELS | TLHALLWEVL | PQLSKEALLK | LGPLPRLLND |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ISTALRNPNI | QRQPSRQSER | PRPQPVVLRG | PSAEMQGYMM | RDLNSSIDLQ | SFMARGLNSS | MDMARLPSPT | KEKPPPPPPG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GGKDLFYVSR | PPLARSSPAY | CTSSSDITEP | EQKMLSVNKS | VSMLDLQGDG | PGGRLNSSSV | SNLAAVGDLL | HSSQASLTAA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LGLRPAPAGR | LSQGSGSSIT | AAGMRLSQMG | VTTDGVPAQQ | LRIPLSFQNP | LFHMAADGPG | PPGGHGGGGG | HGPPSSHHHH |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| HHHHHHRGGE | PPGDTFAPFH | GYSKSEDLSS | GVPKPPAASI | LHSHSYSDEF | GPSGTDFTRR | QLSLQDNLQH | MLSPPQITIG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PQRPAPSGPG | GGSGGGSGGG | GGGQPPPLQR | GKSQQLTVSA | AQKPRPSSGN | LLQSPEPSYG | PARPRQQSLS | KEGSIGGSGG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SGGGGGGGLK | PSITKQHSQT | PSTLNPTMPA | SERTVAWVSN | MPHLSADIES | AHIEREEYKL | KEYSKSMDES | RLDRVKEYEE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EIHSLKERLH | MSNRKLEEYE | RRLLSQEEQT | SKILMQYQAR | LEQSEKRLRQ | QQAEKDSQIK | SIIGRLMLVE | EELRRDHPAM |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | |
| AEPLPEPKKR | LLDAQERQLP | PLGPTNPRVT | LAPPWNGLAP | PAPPPPPRLQ | ITENGEFRNT | ADH | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1986 | 1 | 687.3345 | 70.59 | 2 | 55.2 | 10.1 | 0 | 750-761 | R.GPSAEMQGYMMR.D | Oxidation: 10 |

# Detailed Protein Report

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## Protein 418: PREDICTED: uncharacterized protein C4orf50 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530358255 | **Score:** | 30.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 97.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 3.4 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPLLQGEASV | SKEGPESLSR | RERVEGYVWG | LRGGLSSENE | EVAPPATFSR | AHETKEPWPT | DSQLLAGKVR | ATGRTARGKE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ENQVWLGNAL | LLQGGSLEDK | GLEEEDEMPH | QEASGLGCRG | APEEPDSQEH | ESKEMLFFAG | ETGLPLFPRF | ALSVEGAEPT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DHGHPQAVSK | GHDRCALTID | ELAQDVEACF | QQLSTLQPGS | RGWQCSASAC | RGENWSFAQK | WHSGWERAHS | QQVWGNWGIC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SNEEAKSKES | GEGDKPGKTT | ALGTSEVPGN | PGTLPHWDEA | SPNPPQGPAE | PWGALERVRS | RFHQLISGLK | KQRSQILHDN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TKLHGDQERF | HERVCALERE | REREVTKISR | LERDNHRLVG | DISQLKKELD | QYLQAISDLE | DCNGKSYCKI | LELEEENETL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KGNLGQLQKA | TSESVRKSKD | TMEQVTLENW | KLQTLISELG | VSYKELIKDI | VLGIEDMIRA | LSGENEHLLR | RVHVLEREVT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LQRSTDQGRL | VRGREHLQGK | AKMHALDKEV | QVTPLTGQLL | SRACGPPLEE | EMSLAAGQTG | PSTGTGNSRR | GADSPPPSLV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| WRNTGVANAL | QGNVSGAEVK | EAHLEKEEKR | PRCSVAQGQA | LSSLSNGPML | RDSEAEVTEE | DPRLRAQQLH | HRVLTLQCQL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RDQGAAHQAS | LDEATRLQEE | LQAKLEELQK | KQHEAKLAVT | PLKAKIASLV | RKCRERNRLI | THLLQELHRH | GLGNLLLSEL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AQNMLNDVAL | AEYTATFLAP | GVPETSHHLD | VKSEMTAALR | AQTYLLNPEM | DSVLQSSLSS | ESWPVPEPEW | PAQTAQLDSL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KLPLSLVSTL | DPGTCLAAVT | VEPGLPAQRL | QEKGGMPCPA | LQVDNVPAPS | ELLSPARILA | FHQELRQSIC | SNSQVHKSPL |
| 890 | | | | | | | |
| ELEM | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1506 | 1 | 1058.4824 | 21.34 | 2 | 48.5 | 10.4 | 1 | 202-220 | R.GWQCSASACRGENWSFAQK.W | |

# Detailed Protein Report

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## Protein 419: hypoxia up-regulated protein 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5453832 | **Score:** | 30.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 111.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|195976805 | refseq_human (refseq_human_20140103.fasta) | hypoxia up-regulated protein 1 precursor [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MADKVRRQRP | RRRVCWALVA | VLLADLLALS | DTLAVMSVDL | GSESMKVAIV | KPGVPMEIVL | NKESRRKTPV | IVTLKENERF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FGDSAASMAI | KNPKATLRYF | QHLLGKQADN | PHVALYQARF | PEHELTFDPQ | RQTVHFQISS | QLQFSPEEVL | GMVLNYSRSL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AEDFAEQPIK | DAVITVPVFF | NQAERRAVLQ | AARMAGLKVL | QLINDNTATA | LSYGVFRRKD | INTTAQNIMF | YDMGSGSTVC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TIVTYQMVKT | KEAGMQPQLQ | IRGVGFDRTL | GGLEMELRLR | ERLAGLFNEQ | RKGQRAKDVR | ENPRAMAKLL | REANRLKTVL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SANADHMAQI | EGLMDDVDFK | AKVTRVEFEE | LCADLFERVP | GPVQQALQSA | EMSLDEIEQV | ILVGGATRVP | RVQEVLLKAV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GKEELGKNIN | ADEAAAMGAV | YQAAALSKAF | KVKPFVVRDA | VVYPILVEFT | REVEEEPGIH | SLKHNKRVLF | SRMGPYPQRK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VITFNRYSHD | FNFHINYGDL | GFLGPEDLRV | FGSQNLTTVK | LKGVGDSFKK | YPDYESKGIK | AHFNLDESGV | LSLDRVESVF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ETLVEDSAEE | ESTLTKLGNT | ISSLFGGGTT | PDAKENGTDT | VQEEEESPAE | GSKDEPGEQV | ELKEEAEAPV | EDGSQPPPPE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PKGDATPEGE | KATEKENGDK | SEAQKPSEKA | EAGPEGVAPA | PEGEKKQKPA | RKRRMVEEIG | VELVVLDLPD | LPEDKLAQSV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QKLQDLTLRD | LEKQEREKAA | NSLEAFIFET | QDKLYQPEYQ | EVSTEEQREE | ISGKLSAAST | WLEDEGVGAT | TVMLKEKLAE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LRKLCQGLFF | RVEERKKWPE | RLSALDNLLN | HSSMFLKGAR | LIPEMDQIFT | EVEMTTLEKV | INETWAWKNA | TLAEQAKLPA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TEKPVLLSKD | IEAKMMALDR | EVQYLLNKAK | FTKPRPRPKD | KNGTRAEPPL | NASASDQGEK | VIPPAGQTED | AEPISEPEKV |
| 970 | 980 | 990 | 1000 | | | | |
| ETGSEPGDTE | PLELGGPGAE | PEQKEQSTGQ | KRPLKNDEL | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 419 | 1 | 643.8239 | -17.73 | 2 | 35.2 | 10.7 | 2 | 298-308 | K.DVRENPRAMAK.L | |

# Detailed Protein Report

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**Protein 420:** **PREDICTED: myotubularin-related protein 12 isoform X2 [Homo sapiens]**

**Accession:** gi|530378835
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl, Oxidation

**Score:** 30.5
**MW [kDa]:** 81.7
**pI:** 6.4
**Sequence Coverage [%]:** 3.0
**No. of unique Peptides:** 2

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLGKGVVGGG | GGTKAPKPSF | VSYVRPEEIH | TNEKEVTEKE | VTLHLLPGEQ | LLCEASTVLK | YVQEDSCQHG | VYGRLVCTDF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KIAFLGDDES | ALDNDETQFK | NKVIGENDIT | LHCVDQIYGV | FDEKKKTLFG | QLKKYPEKLI | IHCKDLRVFQ | FCLRYTKEEE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VKRIVSGIIH | HTQAPKLLKR | LFLFSYATAA | QNNTVTDPKN | HTVMFDTLKD | WCWELERTKG | NMKYKAVSVN | EGYKVCERLP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AYFVVPTPLP | EENVQRFQGH | GIPIWCWSCH | NGSALLKMSA | LPKEQDDGIL | QIQKSFLDGI | YKTIHRPPYE | IVKTEDLSSN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FLSLQEIQTA | YSKFKQLFLI | DNSTEFWDTD | IKWFSLLESS | SWLDIIRRCL | KKAIEITECM | EAQNMNVLLL | EENASDLCCL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ISSLVQLMMD | PHCRTRIGFQ | SLIQKEWVMG | GHCFLDRCNH | LRQNDKEEGR | EGQDTQSKPL | NLLTVWDWSV | QFEPKAQTLL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KNPLYVEKPK | LDKGQRKGMR | FKLCLQAQNF | SPTESTKERA | VMHQRQLSLP | LTQSKSSPKR | GFFREETDHL | IKNLLGKRIS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KLINSSDELQ | DNFREFYDSW | HSKSTDYHGL | LLPHIEGPEI | KVWAQRYLRW | IPEAQILGGG | QVATLSKLLE | MMEEVQSLQE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KIDERHHSQQ | APQAEAPCLL | RNSARLSSLF | PFALLQRHSS | KPVLPTSGWK | ALGDEDDLAK | REDEFVDLGD | V |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1197 | 1 | 662.2827 | -107.94 | 1 | 45.1 | 19.7 | 0 | 278-283 | K.MSALPK.E | Oxidation: 1 |
| 1995 | 1 | 862.3137 | -122.84 | 2 | 54.8 | 10.8 | 0 | 503-517 | K.LCLQAQNFSPTESTK.E | Carbamidomethyl: 2 |

# Detailed Protein Report

**Protein 421:** **PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 2 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530394565 | **Score:** | 30.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 6.3 |
| | | **No. of unique Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MLLKHRKEFW WFPHMWSHMQ PHLFHNRSVL ADQMRLNKQF ALEHGIPTDL GYAVAPHHSG VYPIHTQLYE AWKSVWGIQV
        90        100        110        120        130        140        150        160
TSTEEYPHLR PARYRRGFIH NGIMVLPRQT CGLFTHTIFY NEYPGGSREL DRSIRGGELF LTVLLNPISI FMTHLSNYGN
       170        180        190        200        210        220        230        240
DRLGLYTFES LVRFLQCWTR LRLQTLPPVP LAQKYFELFP QERSPLWQNP CDDKRHKDIW SKEKTCDRLP KFLIVGPQKT
       250        260        270        280        290        300        310        320
GTTAIHFFLS LHPAVTSSFP SPSTFEEIQF FNSPNYHKGI DWYMDFFPVP SNASTDFLFE KSATYFDSEV VPRRGAALLP
       330        340        350        360        370        380        390        400
RAKIITVLTN PADRAYSWYQ HQRAHGDPVA LNYTFYQVIS ASSQTPLALR SLQNRCLVPG YYSTHLQRWL TYYPSGQLLI
       410        420        430        440        450        460        470        480
VDGQELRTNP AASMESIQKF LGITPFLNYT RTLRFDDDKG FWCQGLEGGK TRCLGRSKGR RYPDMDTESR LFLTDFFRNH
       490        500        510
NLELSKLLSR LGQPVPSWLR EELQHSSLG
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 618 | 1 | 677.3937 | 25.26 | 2 | 37.3 | 10.3 | 0 | 97-108 | R.GFIHNGIMVLPR.Q | |
| 1699 | 1 | 1045.7064 | 77.05 | 2 | 51.0 | 20.0 | 2 | 315-334 | R.GAALLPRAKIITVLTNPADR.A | |

# Detailed Protein Report

## Protein 422: PREDICTED: serine/threonine-protein kinase ULK2 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578830126 | **Score:** | 30.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 110.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***WUP:QUP*** **Median:** 0.50 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MEVVGDFEYS KRDLVGHGAF AVVFRGRHRQ KTDWEVAIKS INKKNLSKSQ ILLGKEIKIL KELQHENIVA LYDVQELPNS
        90        100        110        120        130        140        150        160
VFLVMEYCNG GDLADYLQAK GTLSEDTIRV FLHQIAAAMR ILHSKGIIHR DLKPQNILLS YANRRKSSVS GIRIKIADFG
       170        180        190        200        210        220        230        240
FARYLHSNMM AATLCGSPMY MAPEVIMSQH YDAKADLWSI GTVIYQCLVG KPPFQANSPQ DLRMFYEKNR SLMPSIPRET
       250        260        270        280        290        300        310        320
SPYLANLLLG LLQRNQKDRM DFEAFFSHPF LEQGPVKKSC PVPVPMYSGS VSGSSCGSSP SCRFASPPSL PDMQHIQEEN
       330        340        350        360        370        380        390        400
LSSPPLGPPN YLQVSKDSAS TSSKNSSCDT DDFVLVPHNI SSDHSCDMPV GTAGRRASNE FLVCGGQCQP TVSPHSETAP
       410        420        430        440        450        460        470        480
IPVPTQIRNY QRIEQNLTST ASSGTNVHGS PRSAVVRRSN TSPMGFLRPG SCSPVPADTA QTVGRRLSTG SSRPYSPSPL
       490        500        510        520        530        540        550        560
VGTIPEQFSQ CCCGHPQGHD SRSRNSSGSP VPQAQSPQSL LSGARLQSAP TLTDIYQNKQ KLRKQHSDPV CPSHTGAGYS
       570        580        590        600        610        620        630        640
YSPQPSRPGS LGTSPTKHLG SSPRSSDWFF KTPLPTIIGS PTKTTAPFKI PKTQASSNLL ALVTRHGPAE EQSKDGNEPR
       650        660        670        680        690        700        710        720
ECAHCLLVQG SERQRAEQQS KAVFGRSVST GKLSDQQGKT PICRHQGSTD SLNTERPMDI GSPPHSAAAP TCTHMFLRTR
       730        740        750        760        770        780        790        800
TTSVGPSNSG GSLCAMSGRV CVGSPPGPGF GSSPPGAEAA PSLRYVPYGA SPPSLEGLIT FEAPELPEET LMEREHTDTL
       810        820        830        840        850        860        870        880
RHLNVMLMFT ECVLDLTAMR GGNPELCTSA VSLYQIQESV VVDQISQLSK DWGRVEQLVL YMKAAQLLAA SLHLAKAQIK
       890        900        910        920        930        940        950        960
SGKLSPSTAV KQVVKNLNER YKFCITMCKK LTEKLNRFFS DKQRFIDEIN SVTAEKLIYN CAVEMVQSAA LDEMFQQTED
       970        980        990       1000       1010
IVYRYHKAAL LLEGLSRILQ DPADIENVHK YKCSIERRLS ALCHSTATV
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1434 | 1 | 458.6103 | -303.83 | 2 | 48.1 | 18.1 | 0 | 231-238 | R.SLMPSIPR.E | Oxidation: 3 | WUP:QUP 0.50 |
| 2561 | 2 | 913.4770 | 71.20 | 2 | 62.0 | 12.3 | 0 | 721-739 | R.TTSVGPSNSGGSLCAMSGR.V | Carbamidomethyl: 14 | |

BRUKER

# Detailed Protein Report

**Protein 423:** **PREDICTED: leukocyte immunoglobulin-like receptor subfamily B member 5 isoform X5 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578833860 | **Score:** | 30.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 6.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTLTLSVLIC | LGLSVGPRTC | VQAGTLPKPT | LWAEPASVIA | RGKPVTLWCQ | GPLETEEYRL | DKEGLPWARK | RQNPLEPGAK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AKFHIPSTVY | DSAGRYRCYY | ETPAGWSEPS | DPLELVATGF | YAEPTLLALP | SPVVASGGNV | TLQCDTLDGL | LTFVLVEEEQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KLPRTLYSQK | LPKGPSQALF | PVGPVTPSCR | WRFRCYYYYR | KNPQVWSNPS | DLLEILVPGV | SRKPSLLIPQ | GSVVARGGSL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TLQCRSDVGY | DIFVLYKEGE | HDLVQGSGQQ | PQAGLSQANF | TLGPVSRSHG | GQYRCYGAHN | LSPRWSAPSD | PLDILIAGLI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PDIPALSVQP | GPKVASGENV | TLLCQSWHQI | DTFFLTKEGA | AHPPLCLKSK | YQSYRHQAEF | SMSPVTSAQG | GTYRCYSAIR |
| 410 | 420 | 430 | 440 | 450 | 460 | | |
| SYPYLLSSPS | YPQELVVSGP | SGDPSLSPTG | STPTPGPEDQ | PLTPTGLDPQ | SGE | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2477 | 1 | 973.4893 | -56.45 | 2 | 61.5 | 15.4 | 0 | 1-18 | -.MTLTLSVLICLGLSVGPR.T | Carbamidomethyl: 10;<br>Oxidation: 1 |

# Detailed Protein Report

## Protein 424: PREDICTED: tetratricopeptide repeat protein 13 isoform X7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578802328 | **Score:** | 30.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| | | **Sequence Coverage [%]:** | 4.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMLYHHGSLQ | EALKNFKRCL | QLEPYNEVCQ | YMKGLSHVAM | GQFYEGIKAQ | TKVMLNDPLP | GQKASPEYLK | VKYLREYSRY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LHAHLDTPLT | EYNIDVDLPG | SFKDHWAKNL | PFLIEDYEEQ | PGLQPHIKDV | LHQNFESYKP | EVQELICVAD | RLGSLMQYET |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PGFLPNKRIH | RAMGLAALEV | MQAVQRTWTN | SKVRMNGKTR | LMQWRDMFDI | AVKWRRIADP | DQPVLWLDQM | PARSLSRGFN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NHINLIRGQV | INMRYLEYFE | KILHFIKDRI | LVYHGANNPK | GLLEVREALE | KVHKVEDLLP | IMKQFNTKTK | DGFTVNTKVP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SLKDQGKEYD | GFTITITGDK | VGNILFSVET | QTTEERTQLY | HAEIDALYKD | LTAKGKVLIL | SSEFGEADAV | CNLILSLVYY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FYNLMPLSRG | SSVIAYSVIV | GALMASGKEV | AGKIPKGKLV | DFEAMTAPGS | EAFSKVAKSW | MNLKSISPSY | KTLPSVSETF |
| 490 | 500 | 510 | | | | | |
| PTLRSMIEVL | NTDSSPRCLK | KL | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1682 | 4 | 820.8728 | -97.18 | 2 | 49.4 | 15.9 | 1 | 234-247 | R.SLSRGFNNHINLIR.G | |

# Detailed Protein Report

## Protein 425: storkhead-box protein 1 isoform d [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|194328693 | **Score:** | 30.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 98.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578819078 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: storkhead-box protein 1 isoform X2 [Homo sapiens] |
| gi\|578819076 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: storkhead-box protein 1 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNPITQSQFV | PLGEVLCCAI | SDMNTAQIVV | TQESLLERLM | KHYPGIAIPS | EDILYTTLGT | LIKERKIYHT | GEGYFIVTPQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TYFITNTTTQ | ENKRMLPSDE | SRLMPASMTY | LVSMESCAES | AQENAAPISH | CQSCQCFRDM | HTQDVQEAPV | AAEVTRKSHR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GLGESVSWVQ | NGAVSVSAEH | HICESTKPLP | YTRDKEKGKK | FGFSLLWRSL | SRKEKPKTEH | SSFSAQFPPE | EWPVRDEDDL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DNIPRDVEHE | IIKRINPILT | VDNLIKHTVL | MQKYEEQKKY | NSQGTSTDML | TIGHKYPSKE | GVKKRQGLSA | KPQGQGHSRR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DRHKARNQGS | EFQPGSIRLE | KHPKLPATQP | IPRIKSPNEM | VGQKPLGEIT | TVLGSHLIYK | KRISNPFQGL | SHRGSTISKG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HKIQKTSDLK | PSQTGPKEKP | FQKPRSLDSS | RIFDGKAKEP | YAEQPNDKME | AESIYINDPT | VKPINDDFRG | HLFSHPQQSM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LQNDGKCCPF | MESMLRYEVY | GGENEVIPEV | LRKSHSHFDK | LGETKQTPHS | LPSRGASFSD | RTPSACRLVD | NTIHQFQNLG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LLDYPVGVNP | LRQAARQDKD | SEELLRKGFV | QDAETTSLEN | EQLSNDDQAL | YQNEVEDDDG | ACSSLYLEED | DISENDDLRQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| MLPGHSQYSF | TGGSQGNHLG | KQKVIERSLT | EYNSTMERVE | SQVLKRNECY | KPTGLHATPG | ESQEPNLSAE | SCGLNSGAQF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GFNYEEEPSV | AKCVQASAPA | DERIFDYYSA | RKASFEAEVI | QDTIGDTGKK | PASWSQSPQN | QEMRKHFPQK | FQLFNTSHMP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VLAQDVQYEH | SHLEGTENHS | MAGDSGIDSP | RTQSLGSNNS | VILDGLKRRQ | NFLQNVEGTK | SSQPLTSNSL | LPLTPVINV |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1771 | 1 | 823.3088 | -161.08 | 2 | 52.5 | 16.3 | 0 | 832-847 | R.TQSLGSNNSVILDGLK.R | |

# Detailed Protein Report

## Protein 426: homeobox protein Hox-A6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|13489077 | **Score:** | 30.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 26.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 11.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSYFVNPTF | PGSLPSGQDS | FLGQLPLYQA | GYDALRPFPA | SYGASSLPDK | TYTSPCFYQQ | SNSVLACNRA | SYEYGASCFY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SDKDLSGASP | SGSGKQRGPG | DYLHFSPEQQ | YKPDSSSGQG | KALHDEGADR | KYTSPVYPWM | QRMNSCAGAV | YGSHGRRGRQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TYTRYQTLEL | EKEFHFNRYL | TRRRRIEIAN | ALCLTERQIK | IWFQNRRMKW | KKENKLINST | QPSGEDSEAK | AGE |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2519 | 1 | 701.8340 | -53.57 | 2 | 61.5 | 17.0 | 0 | 186-197 | R.IEIANALCLTER.Q | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 427: PREDICTED: ubl carboxyl-terminal hydrolase 18 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578836791 | **Score:** | 30.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 8.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.31 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.38 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MNVDFTRILK | RITVPRGADE | QRRSVPFQML | LLLEKMQDSR | QKAVRPLELA | YCLQKCNVPL | FVQHDAAQLY | LKLWNLIKDQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ITDVHLVERL | QALYTIRVKD | SLICVDCAME | SSRNSSMLTL | PLSLFDVDSK | PLKTLEDALH | CFFQPRELSS | KSKCFCENCG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KKTRGKQVLK | LTHLPQTLTI | HLMRFSIRNS | QTRKICHSLY | FPQSLDFSQI | LPMKRESCDA | EEQSGGQYEL | FAVIAHVGMA |
| 250 | 260 | 270 | 280 | 290 | 300 | | |
| DSGHYCVYIR | NAVDGKWFCF | NDSNICLVSW | EDIQCTYGNP | NYHWQETAYL | LVYMKMEC | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 374 | 1 | 795.4149 | -53.97 | 2 | 34.7 | 14.0 | 1 | 23-35 | R.RSVPFQMLLLLEK.M | Oxidation: 7 | WUP:QUP 0.38<br>QU:MU 2.31 |

# Detailed Protein Report

## Protein 428: endothelial cell-specific molecule 1 isoform b precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|208022668 | **Score:** | 30.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 14.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| | | **Sequence Coverage [%]:** | 16.4 |
| | | **No. of unique Peptides:** | 1 |

```
         10         20         30         40         50         60         70         80
MKSVLLLTTL LVPAHLVAAW SNNYAVDCPQ HCDSSECKSS PRCKRTVLDD CGCCRVCAAG RGETCYRTVS GMDGMKCGPG
         90        100        110        120        130        140
LRCQPSNGED PFGEEFGICK EHDMASGDGN IVREEVVKEN AAGSPVMRKW LNPR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1903 | 1 | 643.3133 | 32.48 | 2 | 54.2 | 15.5 | 1 | 56-67 | R.VCAAGRGETCYR.T | |

# Detailed Protein Report

## Protein 429: kinesin light chain 4 isoform d [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|573459761 | **Score:** | 30.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| | | **Sequence Coverage [%]:** | 5.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSGLVLGQRD | EPAGHRLSQE | EILGSTRLVS | QGLEALRSEH | QAVLQSLSQT | IECLQQGGHE | EGLVHEKARQ | LRRSMENIEL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GLSEAQEEKE | GDATKDSLDD | LFPNEEEEDP | SNGLSRGQGA | TAAQQGGYEI | PARLRTLHNL | VIQYAAQGRY | EVAVPLCKQA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LEDLERTSGR | GHPDVATMLN | ILALVYRDQN | KYKEAAHLLN | DALSIRESTL | GPDHPAVAAT | LNNLAVLYGK | RGKYKEAEPL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CQRALEIREK | VLGTNHPDVA | KQLNNLALLC | QNQGKYEAVE | RYYQRALAIY | EGQLGPDNPN | VARTKNNLAS | CYLKQGKYAE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AETLYKEILT | RAHVQEFGSV | DDDHKPIWMH | AEEREEMSKS | RHHEGGTPYA | EYGGWYKACK | VSSPTVNTTL | RNLGALYRRQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GKLEAAETLE | ECALRSRRQG | TDPISQTKVA | ELLGESDGRR | TSQEGPGDSV | KFEGGEDASV | AVEWSGDGSG | TLQRSGSLGK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | |
| IRDVLRRSSE | LLVRKLQGTE | PRPSSSNMKR | AASLNYLNQP | SAAPLQVSRG | LSASTMDLSS | SS | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2084 | 1 | 900.3300 | -81.09 | 3 | 54.4 | 16.9 | 2 | 355-377 | R.EEMSKSRHHEGGTPYAEYGGWYK.A | |

# Detailed Protein Report

**Protein 430:** **PREDICTED: sprouty-related, EVH1 domain-containing protein 2 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530367354 | **Score:** | 30.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 25.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 14.0 |
| | | **No. of unique Peptides:** | 2 |

```
        10          20          30          40          50          60          70          80
MPRPYRQVSF  PDDDEEIVRI  NPREKIWMTG  YEDYRHAPVR  GKYPDPSEDA  DSSYVRFAKG  EVPKHDYNYP  YVDSSDFGLG
        90         100         110         120         130         140         150         160
EDPKGRGGSV  IKTQPSRGKS  RRRKEDGERS  RCVYCRDMFN  HEENRRGHCQ  DAPDSVRTCI  RRVSCMWCAD  SMLYHCMSDP
       170         180         190         200         210         220         230
EGDYTDPCSC  DTSDEKFCLR  WMALIALSFL  APCMCCYLPL  RACYHCGVMC  RCCGGKHKAA  A
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2553 | 3 | 973.5096 | 122.27 | 2 | 62.6 | 16.7 | 1 | 112-125 | R.CVYCRDMFNHEENR.R | Carbamidomethyl: 1, 4;<br>Oxidation: 7 |
| 1552 | 3 | 993.4662 | 70.96 | 2 | 49.6 | 13.4 | 2 | 202-218 | R.ACYHCGVMCRCCGGKHK.A | Carbamidomethyl: 2, 5;<br>Oxidation: 8 |

# Detailed Protein Report

## Protein 431: cytochrome b-245 heavy chain [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|6996021 | **Score:** | 30.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 65.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 4.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.65 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 5.33 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGNWAVNEGL | SIFVILVWLG | LNVFLFVWYY | RVYDIPPKFF | YTRKLLGSAL | ALARAPAACL | NFNCMLILLP | VCRNLLSFLR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GSSACCSTRV | RRQLDRNLTF | HKMVAWMIAL | HSAIHTIAHL | FNVEWCVNAR | VNNSDPYSVA | LSELGDRQNE | SYLNFARKRI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KNPEGGLYLA | VTLLAGITGV | VITLCLILII | TSSTKTIRRS | YFEVFWYTHH | LFVIFFIGLA | IHGAERIVRG | QTAESLAVHN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ITVCEQKISE | WGKIKECPIP | QFAGNPPMTW | KWIVGPMFLY | LCERLVRFWR | SQQKVVITKV | VTHPFKTIEL | QMKKKGFKME |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VGQYIFVKCP | KVSKLEWHPF | TLTSAPEEDF | FSIHIRIVGD | WTEGLFNACG | CDKQEFQDAW | KLPKIAVDGP | FGTASEDVFS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YEVVMLVGAG | IGVTPFASIL | KSVWYKYCNN | ATNLKLKKIY | FYWLCRDTHA | FEWFADLLQL | LESQMQERNN | AGFLSYNIYL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TGWDESQANH | FAVHHDEEKD | VITGLKQKTL | YGRPNWDNEF | KTIASQHPNT | RIGVFLCGPE | ALAETLSKQS | ISNSESGPRG |
| 570 | 580 | | | | | | |
| VHFIFNKENF | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 906 | 1 | 676.2230 | -177.87 | 2 | 41.4 | 13.2 | 1 | 560-570 | R.GVHFIFNKENF.- | | QU:MU 0.65<br>WUP:QUP 5.33 |

# Detailed Protein Report

## Protein 432: zinc finger protein 831 [Homo sapiens]

**Accession:** gi|123701326
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 30.1
**MW [kDa]:** 177.8
**pI:** 9.7
**Sequence Coverage [%]:** 1.7
**No. of unique Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578835748 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 831 isoform X5 [Homo sapiens] |
| gi\|530417822 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 831 isoform X3 [Homo sapiens] |
| gi\|530417820 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 831 isoform X2 [Homo sapiens] |
| gi\|530417818 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 831 isoform X1 [Homo sapiens] |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEVPEPTCPA | PPARDQPAPT | PGPPGAPGGQ | ASPHLTLGPV | LLPPEQGLAP | PTVFLKALPI | PLYHTVPPGG | LQPRAPLVTG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SLDGGNVPFI | LSPVLQPEGP | GPTQVGKPAA | PTLTVNIVGT | LPVLSPGLGP | TLGSPGKVRN | AGKYLCPHCG | RDCLKPSVLE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KHIRSHTGER | PFPCATCGIA | FKTQSNLYKH | RRTQTHLNNS | RLSSESEGAG | GGLLEEGDKA | GEPPRPEGRG | ESRCQGMHEG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ASERPLSPGA | HVPLLAKNLD | VRTEAAPCPG | SAFADREAPW | DSAPMASPGL | PAASTQPWRK | LPEQKSPTAG | KPCALQRQQA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TAAEKPWDAK | APEGRLRKCE | STDSGYLSRS | DSAEQPHAPC | SPLHSLSEHS | AESEGEGGPG | PGPGVAGAEP | GAREAGLELE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KKRLEERIAQ | LISHNQAVVD | DAQLDNVRPR | KTGLSKQGSI | DLPTPYTYKD | SFHFDIRALE | PGRRRAPGPV | RSTWTPPDKS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RPLFFHSVPT | QLSTTVECVP | VTRSNSLPFV | EGSRTWLEPR | EPRDPWSRTQ | KPLSPRPGPA | RLGCRSGLSS | TDVPSGHPRA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LVRQAAVEDL | PGTPIGDALV | PAEDTDAKRT | AAREAMAGKG | RAGGRKCGQR | RLKMFSQEKW | QVYGDETFKR | IYQKMKASPH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GGKKAREVGM | GSGAELGFPL | QKEAAGSSGT | VPTQDRRTPV | HEDISAGATP | EPWGNPPALE | ASLVTEPTKH | GETVARRGDS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DRPRVEEAVS | SPALGGRDSP | CSGSRSPLVS | PNGRLELGWQ | MPPAPGPLKG | GDVEAPRPVW | PDPKLEGGAR | GVGDVQETCL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| WAQTVLRWPS | RGSGEDKLPS | ERKKLKVEDL | HSWKQPEPVS | AETPGGPTQP | ASLSSQKQDA | DPGEVPGGSK | ESARQVGEPL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ESSGASLAAA | SVALKRVGPR | DKATPLHPAA | PAPAEHPSLA | TPPQAPRVLS | ALADNAFSPK | YLLRLPQAET | PLPLPIPWGP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RHSQDSLCSS | GWPEERASFV | GSGLGTPLSP | SPASGPSPGE | ADSILEDPSC | SRPQDGRKGA | QLGGDKGDRM | ATSRPAAREL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PISAPGAPRE | ATSSPPTPTC | EAHLVQDMEG | DSHRIHRLCM | GSTLARARLS | GDVLNPWVPN | WELGEPPGNA | PEDPSSGPLV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GPDPCSPLQP | GSFLTALTRP | QGVPPGWPEL | ALSSHSGTSR | SHSTRSPHST | QNPFPSLKAE | PRLTWCCLSR | SVPLPAEQKA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KAASVYLAVH | FPGSSLRDEG | PNGPPGSNGG | WTWTSPGEGG | PAQMSKFSYP | TVPGVMPQHQ | VSEPEWKKGL | PWRAKMSRGN |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SKQRKLKINP | KRYKGNFLQS | CVQLRASRLR | TPTWVRRRSR | HPPALEGLKP | CRTPGQTSSE | IAGLNLQEEP | SCATSESPPC |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| CGKEEKKEGD | CRQTLGTLSL | GTSSRIVREM | DKRTVKDISP | SAGEHGDCTT | HSTAATSGLS | LQSDTCLAVV | NDVPLPPGKG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LDLGLLETQL | LASQDSVSTD | PKPYIFSDAQ | RPSSFGSKGT | FPHHDIATSV | AAVCISLPVR | TDHIAQEIHS | AESRDHSQTA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| GRTLTSSSPD | SKVTEEGRAQ | TLLPGRPSSG | QRISDSVPLE | STEKTHLEIP | ASGPSSASSH | HKEGRHKTFF | PSRGQYGCGE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| MTVPCPSLGS | DGRKRQVSGL | ITRKDSVVPS | KPEQPIEIPE | APSKSLKKRS | LEGMRKQTRV | EFSDTSSDDE | DRLVIEI |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2187 | 8 | 1023.8998 | -84.84 | 2 | 57.2 | 18.3 | 1 | 258-276 | K.NLDVRTEAAPCPGSAFADR.E | Carbamidomethyl: 11 |

# Detailed Protein Report

## Protein 433: transient receptor potential cation channel subfamily V member 5 [Homo sapiens]

**Accession:** gi|17505200
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 30.0
**MW [kDa]:** 82.5
**pI:** 6.0
**Sequence Coverage [%]:** 3.0
**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MGGFLPKAEG PGSQLQKLLP SFLVREQDWD QHLDKLHMLQ QKRILESPLL RASKENDLSV LRQLLLDCTC DVRQRGALGE

        90        100        110        120        130        140        150        160
TALHIAALYD NLEAALVLME AAPELVFEPT TCEAFAGQTA LHIAVVNQNV NLVRALLTRR ASVSARATGT AFRRSPRNLI

       170        180        190        200        210        220        230        240
YFGEHPLSFA ACVNSEEIVR LLIEHGADIR AQDSLGNTVL HILILQPNKT FACQMYNLLL SYDGHGDHLQ PLDLVPNHQG

       250        260        270        280        290        300        310        320
LTPFKLAGVE GNTVMFQHLM QKRRHIQWTY GPLTSILYDL TEIDSWGEEL SFLELVVSSD KREARQILEQ TPVKELVSFK

       330        340        350        360        370        380        390        400
WNKYGRPYFC ILAALYLLYM ICFTTCCVYR PLKFRGGNRT HSRDITILQQ KLLQEAYETR EDIIRLVGEL VSIVGAVIIL

       410        420        430        440        450        460        470        480
LLEIPDIFRV GASRYFGKTI LGGPFHVIII TYASLVLVTM VMRLTNTNGE VVPMSFALVL GWCSVMYFTR GFQMLGPFTI

       490        500        510        520        530        540        550        560
MIQKMIFGDL MRFCWLMAVV ILGFASAFYI IFQTEDPTSL GQFYDYPMAL FTTFELFLTV IDAPANYDVD LPFMFSIVNF

       570        580        590        600        610        620        630        640
AFAIIATLLM LNLFIAMMGD THWRVAQERD ELWRAQVVAT TVMLERKLPR CLWPRSGICG CEFGLGDRWF LRVENHNDQN

       650        660        670        680        690        700        710        720
PLRVLRYVEV FKNSDKEDDQ EHPSEKQPSG AESGTLARAS LALPTSSLSR TASQSSSHRG WEILRQNTLG HLNLGLNLSE

       730
GDGEEVYHF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 87 | 1 | 829.3594 | 10.76 | 2 | 30.8 | 10.5 | 1 | 653-666 | K.NSDKEDDQEHPSEK.Q | |

# Detailed Protein Report

**Protein 434:** **PREDICTED: microtubule-associated protein 4 isoform X15 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530372482 | **Score:** | 30.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 241.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MADLSLADAL | TEPSPDIEGE | IKRDFIATLE | AEAFDDVVGE | TVGKTDYIPL | LDVDEKTGNS | ESKKKPCSET | SQIEDTPSSK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PTLLANGGHG | VEGSDTTGSP | TEFLEEKMAY | QEYPNSQNWP | EDTNFCFQPE | QVVDPIQTDP | FKMYHDDDLA | DLVFPSSATA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DTSIFAGQND | PLKDSYVPLE | LAKEIEMASE | ERPPAQALEI | MMGLKTTDMA | PSKETEMALA | KDMALATKTE | VALAKDMESP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TKLDVTLAKD | MQPSMESDMA | LVKDMELPTE | KEVALVKDVR | WPTETDVSSA | KNVVLPTETE | VAPAKDVTLL | KETERASPIK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MDLAPSKDMG | PPKENKKETE | RASPIKMDLA | PSKDMGPPKE | NKIVPAKDLV | LLSEIEVAQA | NDIISSTEIS | SAEKVALSSE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TEVALARDMT | LPPETNVILT | KDKALPLEAE | VAPVKDMAQL | PETEIAPAKD | VAPSTVKEVG | LLKDMSPLSE | TEMALGKDVT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PPPETEVVLI | KNVCLPPEME | VALTEDQVPA | LKTEAPLAKD | GVLTLANNVT | PAKDVPPLSE | TEATPVPIKD | MEIAQTQKGI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SEDSHLESLQ | DVGQSAAPTF | MISPETVTGT | GKKCSLPAEE | DSVLEKLGER | KPCNSQPSEL | SSETSANFMY | CGTPPTQAKQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VCRPSDRRST | RPKPARVPPE | LLGGSPPWKT | LDHRLGHCSL | SESGWVSGSS | SCGGPGNQRK | SIHVDSLEPQ | RDLGREAWDI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ESTPIMMKKK | KKKPKQKRYS | QPRAGGPSDD | DNADKPKGHP | FAADTQKSGV | LPSQPTTMGT | EYGLVSGENL | KRECLVNSSA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ARLVAENFVS | ESLRIPLYPS | EEAPKTAISS | QSKLRVEEES | KSNKSVLQNQ | DKKLLKQHEY | KPQPAPHLKT | PVDKSQSVGP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LNLKGPLAEV | SAYNVETPLD | IRLKEGCSPF | LDQEVMGVVS | KPTAAKEIPN | LVPTLIASNP | LECNLKEGNN | ESKMTKLQNV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KLKEFPEGAE | EDKELKKEAF | PNERQEISIF | TSEQLQGQVL | VQVPGVENEP | FKRMAGDGKS | RKGRGSSGKM | RTDSGKVKAK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SELPFLLDSQ | KDGRAVLIPS | EPVSKTEGMT | TQDKSEELGL | NSSKQPGTKA | DLTEAVVMGE | PKEMTQPKVA | GTMQALIPLE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SGSGMTQTSG | VSTETGDVVK | DMGVNNQSKE | GRCPWKDHEA | APWISEKPKK | RGNEGKSKKF | KNNYSTQPAR | MERKEEILNP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PFEGKDGDTG | SIPHKSKEIG | FTFPKMHDSS | FSHTPDTPTV | EAVDRKGGNF | QVNFVELGTL | GENKISTVKA | STVTEPPAKV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TDVSCQEQIQ | GAGFVPSVVS | EENKTDAANR | YTAVADKPSK | RSNDGKSKKV | KNSSPEKHIL | ENKIDATKIH | VPMETTGDQG |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| IEGMAYMDEN | RNITFTCPRT | PSELINKSSP | LEVLESAACE | KLPTPTPQVV | KEGDSFPDTL | AKNGQEIAPA | QISKSLMVDN |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| YTKDGVPGQE | RPKGPSAVVP | STSTGGVALP | ITTAIETVNI | HGDHSLKNKA | ELADSMKNEA | GIDEGHVIGE | SESVHSGASK |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| HSVEKVTELA | KGHLLPGVPV | EDQSLPGEAR | ALEGYADRGN | FPAHPVNEEK | ETKEGSVAVQ | IPDLLEDKAQ | KLSFCEDQNA |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QDRNSKGSDS | LNKKVDLTLL | SPKSENDKLK | EISLACKITE | LESVSLPTPE | IQSDFLHSKV | EAPPSEVADT | LVIMTASKGV |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| RLPEPKDKIL | ETPQKMTEKS | ESKTPGEGKK | EDKSRMAEPM | KGYMRPTKSR | GLTPLLPKST | IQEQERHKQL | KSAVCLSSST |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| VYQQLGMSVY | GIARPEEGRP | VVSGTGNDIT | TPPNKELPPS | PEKKTKPLAT | TQPAKTSTSK | AKTQPTSLPK | QPAPTTIGGL |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| NKKPMSLASG | LVPAAPPKRP | AVASARPSIL | PSKDVKPKPI | ADAKAPEKRA | SPSKPASAPA | SRSGSKSTQT | VAKTTTAAAV |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| ASTGPSSRSP | STLLPKKPTA | IKTEGKPAEV | KKMTAKSVPA | DLSRPKSTST | SSMKKTTTLS | GTAPAAGVVP | SRVKATPMPS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| RPSTTPFIDK | KPTSAKPSST | TPRLSRLATN | TSAPDLKNVR | SKVGSTENIK | HQPGGGRAKV | EKKTEAAATT | RKPESNAVTK |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| TAGPIASAQK | QPAGKVQIVS | KKVSYSHIQS | KCGSKDNIKH | VPGGGNVQIQ | NKKVDISKVS | SKCGSKANIK | HKPGGGDVKI |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1574 | 1 | 949.4919 | -30.30 | 2 | 49.9 | 14.9 | 1 | 2072-2090 | R.KPESNAVTKTAGPIASAQK.Q | |

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# Detailed Protein Report

## Protein 435: E3 ubiquitin-protein ligase Hakai isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|546230945 | **Score:** | 29.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 6.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDHTDNELQG | TNSSGSLGGL | DVRRRIPIKL | ISKQANKAKP | APRTQRTINR | MPAKAPPGDE | GFDYNEEERY | DCKGGELFAN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QRRFPGHLFW | DFQINILGEK | DDTPVHFCDK | CGLPIKIYGR | MIPCKHVFCY | DCAILHEKKG | DKMCPGCSDP | VQRIEQCTRG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SLFMCSIVQG | CKRTYLSQRD | LQAHINHRHM | RAGKPVTRAS | LENVHPPIAP | PPTEIPERFI | MPPDKHHMSH | IPPKQHIMMP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PPPLQHVPHE | HYNQPHEDIR | APPAELSMAP | PPPRSVSQET | FRISTRKHSN | LITVPIQDDS | NSGAREPPPP | APAPAHHHPE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YQGQPVVSHP | HHIMPPQQHY | APPPPPPPPI | SHPMPHPPQA | AGTPHLVYSQ | APPPPMTSAP | PPITPPPGHI | IAQMPPYMNH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PPPGPPPPQH | GGPPVTAPPP | HHYNPNSLPQ | FTEDQGTLSP | PFTQPGGMSP | GIWPAPRGPP | PPPRLQGPPS | QTPLPGPHHP |
| 490 | 500 | | | | | | |
| DQTRYRPYYQ | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2201 | 1 | 753.7596 | 78.65 | 3 | 57.9 | 16.7 | 2 | 154-173 | R.IEQCTRGSLFMCSIVQGCKR.T | |

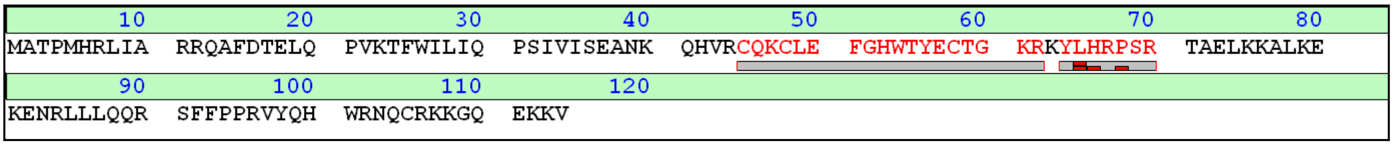
# Detailed Protein Report

**Protein 436:** **PREDICTED: zinc finger CCHC domain-containing protein 10 isoform X4 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530380033 | **Score:** | 29.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 13.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.3 |
| | | **Sequence Coverage [%]:** | 21.9 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.79 | **CV:** | 15.24 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 1.67 | **CV:** | 23.19 % | **No. of Peptides:** | 2 |



```
        10         20         30         40         50         60         70         80
MATPMHRLIA RRQAFDTELQ PVKTFWILIQ PSIVISEANK QHVRCQKCLE FGHWTYECTG KRKYLHRPSR TAELKKALKE
        90        100        110        120
KENRLLLQQR SFFPPRVYQH WRNQCRKKGQ EKKV
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1467 | 1 | 1095.0485 | 53.51 | 2 | 48.5 | 15.5 | 2 | 45-62 | R.CQKCLEFGHWTYECTGKR.K | | QU:MU 0.92<br>WUP:QUP 2.10 |
| 380 | 1 | 464.6667 | -199.17 | 2 | 34.4 | 14.4 | 0 | 64-70 | K.YLHRPSR.T | | QU:MU 0.68<br>WUP:QUP 1.33 |

# Detailed Protein Report

## Protein 437: zinc finger C4H2 domain-containing protein isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|295842335 | **Score:** | 29.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 23.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.9 |
| | | **Sequence Coverage [%]:** | 13.9 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|345091006 | refseq_human (refseq_human_20140103.fasta) | zinc finger C4H2 domain-containing protein isoform 2 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MEKIKARLKA EFEALESEER HLKEYKQEMD LLLQEKMAHV EELRLIHADI NVMENTIKQS ENDLNKLLES TRRLHDEYKP

        90        100        110        120        130        140        150        160
LKEHVDALRM TLGLQRLPDL CEEEEKLSLD YFEKQKAEWQ TEPQEPPIPE SLAAAAAAAQ QLQVARKQDT RQTATFRQQP

       170        180        190        200        210
PPMKACLSCH QQIHRNAPIC PLCKAKSRSR NPKKPKRKQD E
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2312 | 1 | 1051.3738 | -133.19 | 2 | 58.8 | 13.3 | 1 | 158-175 | R.QQPPPMKACLSCHQQIHR.N | |

# Detailed Protein Report

## Protein 438: PREDICTED: coiled-coil domain-containing protein 108 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578804012 | **Score:** | 29.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 87.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.4 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.17 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.74 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MDSLCVSSAY ISLISSERPV HNWRGKSVQK KQAESKSQIK LHTQSAPFGL CPKDMMLTQA PSSVVRSRNS RNHTVNSGGS
        90        100        110        120        130        140        150        160
CLSASTVAIP AINDSSAAMS ACSTISAQPA SSMDTQMHSP KKQERVNKRV IWGIEVAEEL HWKGWELGKE TTRNLVLKNR
       170        180        190        200        210        220        230        240
SLKLQKMKYR PPKTKFFFTV IPQPIFLSPG ITLTLPIVFR PLEAKEYMDQ LWFEKAEGMF CVGLRATLPC HRLICRPPSL
       250        260        270        280        290        300        310        320
QLPMCAVGDT TEAFFCLDNV GDLPTFFTWE FSSPFQMLPA TGLLEPGQAS QIKVTFQPLT AVIYEVQATC WYGAGSRQRS
       330        340        350        360        370        380        390        400
SIQLQAVAKC AQLLVSIKHK CPEDQDAEGF QKLLYFGSVA VGCTSERQIR LHNPSAVNAP FRIEISPDEL AEDQAFSCPT
       410        420        430        440        450        460        470        480
AHGIVLPGEK KCVSVFFHPK TLDTRTVDYC SIMPSGCASK TLLKVVGFCR GPAVSLQHYC VNFSWVNLGE RSEQPLWIEN
       490        500        510        520        530        540        550        560
QSDCTAHFQF AIDCLESVFT IRPAFGTLVG KARMTLHCAF QPTHPIICFR RVACLIHHQD PLFLDLMGTC HSDSTKPAIL
       570        580        590        600        610        620        630        640
KPQHLTWYRT HLARGLTLYP PDILDAMLKE KKLAQDQNGA LMIPIQDLED MPAPQYPYIP PMTEFFFDGT SDITIFPPPI
       650        660        670        680        690        700        710        720
SVEPVEVDFG ACPGPEAPNP VPLCLMNHTK GKIMVVWTRR SDCPFWVTPE SCDVPPLKSM AMRLHFQPPH PNCLYTVELE
       730        740        750        760        770        780        790
AFAIYKVCAR NEREECGVSA RSLSGLVGWQ EVTEGSFRLH PLRARLSLGW TVTPMSLSPP KLLA
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 745 | 1 | 712.1831 | -154.73 | 2 | 39.3 | 12.8 | 0 | 341-352 | K.CPEDQDAEGFQK.L | Carbamidomethyl: 1 | WUP:QUP 1.74<br>QU:MU 0.17 |

# Detailed Protein Report

## Protein 439: glycerol-3-phosphate dehydrogenase, mitochondrial precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|285002231 | **Score:** | 29.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 80.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530370176 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: glycerol-3-phosphate dehydrogenase, mitochondrial isoform X1 [Homo sapiens] |
| gi\|285002233 | refseq_human (refseq_human_20140103.fasta) | glycerol-3-phosphate dehydrogenase, mitochondrial precursor [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAFQKAVKGT | ILVGGGALAT | VLGLSQFAHY | RRKQMNLAYV | KAADCISEPV | NREPPSREAQ | LLTLQNTSEF | DILVIGGGAT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GSGCALDAVT | RGLKTALVER | DDFSSGTSSR | STKLIHGGVR | YLQKAIMKLD | IEQYRMVKEA | LHERANLLEI | APHLSAPLPI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MLPVYKWWQL | PYYWVGIKLY | DLVAGSNCLK | SSYVLSKSRA | LEHFPMLQKD | KLVGAIVYYD | GQHNDARMNL | AIALTAARYG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AATANYMEVV | SLLKKTDPQT | GKVRVSGARC | KDVLTGQEFD | VRAKCVINAT | GPFTDSVRKM | DDKDAAAICQ | PSAGVHIVMP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GYYSPESMGL | LDPATSDGRV | IFFLPWQKMT | IAGTTDTPTD | VTHHPIPSEE | DINFILNEVR | NYLSCDVEVR | RGDVLAAWSG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IRPLVTDPKS | ADTQSISRNH | VVDISESGLI | TIAGGKWTTY | RSMAEDTINA | AVKTHNLKAG | PSRTVGLFLQ | GGKDWSPTLY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IRLVQDYGLE | SEVAQHLAAT | YGDKAFEVAK | MASVTGKRWP | IVGVRLVSEF | PYIEAEVKYG | IKEYACTAVD | MISRRTRLAF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LNVQAAEEAL | PRIVELMGRE | LNWDDYKKQE | QLETARKFLY | YEMGYKSRSE | QLTDRSEISL | LPSDIDRYKK | RFHKFDADQK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GFITIVDVQR | VLESINVQMD | ENTLHEILNE | VDLNKNGQVE | LNEFLQLMSA | IQKGRVSGSR | LAILMKTAEE | NLDRRVPIPV |
| 730 | | | | | | | |
| DRSCGGL | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 810 | 2 | 491.6440 | -225.52 | 2 | 38.5 | 17.3 | 0 | 34-41 | K.QMNLAYVK.A | Oxidation: 2 |

# Detailed Protein Report

**Protein 440:** **uncharacterized protein C9orf172 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|148762978 | **Score:** | 29.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 106.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MTRTDPPDLL VSTVYQDIKV ATPGPASKCS PCERSVARPA EPAPFNKRHC RSFDFLEALD GPAMETLPEP PPPESAVPRA
        90        100        110        120        130        140        150        160
RTREAEPRRR ARSKSAPRAP PGLTPAPASP PVLPRRGREA QRAARAEASP RREPAYPALR ALANELHPIK LQPQRGGPGR
       170        180        190        200        210        220        230        240
VAPLCAAAGR CAPPEPPAGP APHVRCRLDI KPDDAVLQHA TRGSRSCGPT EAAHWARPAP QFHGLTVPGP RHMALSRTPT
       250        260        270        280        290        300        310        320
PSDSYCADPR AFYCDGPLPG PRDYAERRSL PFTTPPGPTQ FFYTEEPQGF RGSFAASPGP TFDAYYPRPY PSEELSGPSP
       330        340        350        360        370        380        390        400
RRMGGYYAGE VRTFPIQEPP SRSYYGEAPR AYGLPYGPRY VPEEPRAHST ARPFYTEDFG RYRERDVLAR TYPHPRSSPA
       410        420        430        440        450        460        470        480
WADWGPRPYR TLQVVPPSDP DPLLASWHGG TGTSPPRLAT DSRHYSRSWD NILAPGPRRE DPLGRGRSYE NLLGREVREP
       490        500        510        520        530        540        550        560
RGVSPEGRRP PVVVNLSTSP RRYAALSLSE TSLTEKGRAG EGLGRNWYVT PEITITDNDL RATERPSARA WELPGGRTRP
       570        580        590        600        610        620        630        640
PPHAAPDGPT SGRQRSLEQL DELITDLVID SRPTAGQASE PAADCLGPQL RRLLDSRPAG SGAPALAPPR SPPASAGSAE
       650        660        670        680        690        700        710        720
EPAAPGEAAD ASPEPSADED DLMTCSNARC RRTETMFNAC LYFKSCHSCY TYYCSRLCRR EDWDAHKARC VYGRVGSVCR
       730        740        750        760        770        780        790        800
HVLQFCRDSG PVHRAFSRIA RVGFLSRGRG VLFLGFPSPG SADNFLRFGL EGLLLSPTYL SLRELATHAA PLGSYARELA
       810        820        830        840        850        860        870        880
AAGRLYEPAE CFLLSVSVAV GPGTAPPGTP ALPAPAPRSH GPTVRKFAKV ALAAGSPARP PPARSREPDM ETLILTPPPG
       890        900        910        920        930        940        950        960
TAGLDQDGEA GRRAREVAFI HIQRELRLRG VFLRHEFPRV YEQLCEFVEA NRRFTPTTIY PTDRRTGRPF MCMIMAASEP
       970        980
RALDWVASAN LLDDIM
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1901 | 1 | 599.9186 | -47.48 | 3 | 53.6 | 13.3 | 0 | 946-961 | R.TGRPFMCMIMAASEPR.A | |

# Detailed Protein Report

## Protein 441: protein furry homolog [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|117606355 | **Score:** | 29.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 338.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASQQDSGFF | EISIKYLLKS | WSNTSPVGNG | YIKPPVPPAS | GTHREKGPPT | MLPINVDPDS | KPGEYVLKSL | FVNFTTQAER |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KIRIIMAEPL | EKPLTKSLQR | GEDPQFDQVI | SSMSSLSEYC | LPSILRTLFD | WYKRQNGIED | ESHEYRPRTS | NKSKSDEQQR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DYLMERRDLA | IDFIFSLVLI | EVLKQIPLHP | VIDSLIHDVI | NLAFKHFKYK | EGYLGPNTGN | MHIVADLYAE | VIGVLAQAKF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PAVKKKFMAE | LKELRHKEQN | PYVVQSIISL | IMGMKFFRIK | MYPVEDFEAS | LQFMQECAHY | FLEVKDKDIK | HALAGLFVEI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LVPVAAAVKN | EVNVPCLRNF | VESLYDTTLE | LSSRKKHSLA | LYPLVTCLLC | VSQKQLFLNR | WHIFLNNCLS | NLKNKDPKMA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RVALESLYRL | LWVYMIRIKC | ESNTATQSRL | ITIITTLFPK | GSRGVVPRDM | PLNIFVKIIQ | FIAQERLDFA | MKEIIFDFLC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VGKPAKAFSL | NPERMNIGLR | AFLVIADSLQ | QKDGEPPMPV | TGAVLPSGNT | LRVKKTYLSK | TLTEEEAKMI | GMSLYYSQVR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KAVDNILRHL | DKEVGRCMML | TNVQMLNKEP | EDMITGERKP | KIDLFRTCVA | AIPRLLPDGM | SKLELIDLLA | RLSIHMDDEL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RHIAQNSLQG | LLVDFSDWRE | DVLFGFTNFL | LREVNDMHHT | LLDSSLKLLL | QLLTQWKLVI | QTQGKVYEQA | NKIRNSELIA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NGSSHRIQSE | RGPHCSVLHA | VEGFALVLLC | SFQVATRKLS | VLILKEIRAL | FIALGQPEDD | DRPMIDVMDQ | LSSSILESFI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| HVAVSDSATL | PLTHNVDLQW | LVEWNAVLVN | SHYDVKSPSH | VWIFAQSVKD | PWVLCLFSFL | RQENLPKHCP | TALSYAWPYA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| FTRLQSVMPL | VDPNSPINAK | KTSTAGSGDN | YVTLWRNYLI | LCFGVAKPSI | MSPGHLRAST | PEIMATTPDG | TVSYDNKAIG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TPSVGVLLKQ | LVPLMRLESI | EITESLVLGF | GRTNSLVFRE | LVEELHPLMK | EALERRPENK | KRRERRDLLR | LQLLRIFELL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ADAGVISDST | NGALERDTLA | LGALFLEYVD | LTRMLLEAEN | DKEVEILKDI | RAHFSAMVAN | LIQCVPVHHR | RFLFPQQSLR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| HHLFILFSQW | AGPFSIMFTP | LDRYSDRNHQ | ITRYQYCALK | AMSAVLCCGP | VFDNVGLSPD | GYLYKWLDNI | LACQDLRVHQ |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LGCEVVVLLL | ELNPDQINLF | NWAIDRCYTG | SYQLASGCFK | AIATVCGSRN | YPFDIVTLLN | LVLFKASDTN | REIYEISMQL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| MQILEAKLFV | YSKKVAEQRP | GSILYGTHGP | LPPLYSVSLA | LLSCELARMY | PELTLPLFSE | VSQRFPTTHP | NGRQIMLTYL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LPWLHNIELV | DSRLLLPGSS | PSSPEDEVKD | REGDVTASHG | LRGNGWGSPE | ATSLVLNNLM | YMTAKYGDEV | PGPEMENAWN |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ALANNEKWSN | NLRITLQFLI | SLCGVSSDTV | LLPYIKKVAI | YLCRNNTIQT | MEELLFELQQ | TEPVNPIVQH | CDNPPFYRFT |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ASSKASAAAS | GTTSSSNTVV | AGQENFPDAE | ENKILKESDE | RFSNVIRAHT | RLESRYSNSS | GGSYDEDKND | PISPYTGWLL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| TITETKQPQP | LPMPCTGGCW | APLVDYLPET | ITPRGPLHRC | NIAVIFMTEM | VVDHSVREDW | ALHLPLLLHA | VFLGLDHYRP |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| EVFEHSKKLL | LHLLIALSCN | SNFHSIASVL | LQTREMGEAK | TLTVQPAYQP | EYLYTGGFDF | LREDQSSPVP | DSGLSSSSTS |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SSISLGGSSG | NLPQMTQEVE | DVDTAAETDE | KANKLIEFLT | TRAFGPLWCH | EDITPKNQNS | KSAEQLTNFL | RHVVSVFKDS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| KSGFHLEHQL | SEVALQTALA | SSSRHYAGRS | FQIFRALKQP | LSAHALSDLL | SRLVEVIGEH | GDEIQGYVME | ALLTLEAAVD |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| NLSDCLKNSD | LLTVLSRSSS | PDLSSSSKLT | ASRKSTGQLN | MNPGTTSGNT | ATAERSRHQR | SFSVPKKFGV | IDRSSDPPRS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| ATLDRIQACT | QQGLSSKTRS | SSSLKDSLTD | PSHINHPTNL | LATIFWVTVA | LMESDFEFEY | LMALRLLSRL | LAHMPLDKAE |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| NREKLEKLQA | QLKWADFSGL | QQLLLKGFTS | LTTTDLTLQL | FSLLTPVSKI | SMVDASHAIG | FPLNVLCLLP | QLIQHFENPN |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2730 | 1 | 725.3873 | 9.20 | 3 | 65.2 | 13.7 | 2 | 589-606 | K.EPEDMITGERKPKIDLFR.T | |

# Detailed Protein Report

## Protein 442: collagen alpha-2(XI) chain isoform 3 preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|111118968 | **Score:** | 29.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 159.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MERCSRCHRL | LLLLPLVLGL | SAAPGWAGAP | PVDVLRALRF | PSLPDGVRRA | KGICPADVAY | RVARPAQLSA | PTRQLFPGGF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PKDFSLLTVV | RTRPGLQAPL | LTLYSAQGVR | QLGLELGRPV | RFLYEDQTGR | PQPPSQPVFR | GLSLADGKWH | RVAVAVKGQS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VTLIVDCKKR | VTRPLPRSAR | PVLDTHGVII | FGARILDEEV | FEGDVQELAI | VPGVQAAYES | CEQKELECEG | GQRERPQNQQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PHRAQRSPQQ | QPSRLHRPQN | QEPQSQAAHG | PRGLKGEKGE | PAVLEPGMLV | EGPPGPEGPA | GLIGPPGIQG | NPGPVGDPGE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RGPPGRAGLP | GSDGAPGPPG | TSLMLPFRFG | SGGGDKGPVV | AAQEAQAQAI | LQQARLALRG | PPGPMGYTGR | PGPLGQPGSP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GLKGESGDLG | PQGPRGPQGL | TGPPGKAGRR | GRAGADGARG | MPGDPGVKGD | RGFDGLPGLP | GEKGHRGDTG | AQGLPGPPGE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DGERGDDGEI | GPRGLPGESG | PRGLLGPKGP | PGIPGPPGVR | GMDGPQGPKG | SLGPQGEPGP | PGQQGTPGTQ | GLPGPQGAIG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PHGEKGPQGK | PGLPGMPGSD | GPPGHPGKEG | PPGTKGNQGP | SGPQGPLGYP | GPRGVKGVDG | IRGLKGHKGE | KGEDGFPGFK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GDIGVKGDRG | EVGVPGSRGE | DGPEGPKGRT | GPTGDPGPPG | LMGEKGKLGV | PGLPGYPGRQ | GPKGSLGFPG | FPGASGEKGA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RGLSGKSGPR | GERGPTGPRG | QRGPRGATGK | SGAKGTSGGD | GPHGPPGERG | LPGPQGPNGF | PGPKGPPGPP | GKDGLPGHPG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QRGEVGFQGK | TGPPGPPGVV | GPQGAAGETG | PMGERGHPGP | PGPPGEQGLP | GTAGKEGTKG | DPGPPGAPGK | DGPAGLRGFP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GERGLPGTAG | GPGLKGNEGP | SGPPGPAGSP | GERGAAGSGG | PIGPPGRPGP | QGPPGAAGEK | GVPGEKGPIG | PTGRDGVQGP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VGLPGPAGPP | GVAGEDGDKG | EVGDPGQKGT | KGNKGEHGPP | GPPGPIGPVG | QPGAAGADGE | PGARGPQGHF | GAKGDEGTRG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| FNGPPGPIGL | QGLPGPSGEK | GETGDVGPMG | PPGPPGPRGP | AGPNGADGPQ | GPPGGVGNLG | PPGEKGEPGE | SGSPGIQGEP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GVKGPRGERG | EKGESGQPGE | PGPPGPKGPT | GDDGPKGNPG | PVGFPGDPGP | PGEGGPRGQD | GAKGDRGEDG | EPGQPGSPGP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TGENGPPGPL | GKRGPAGSPG | SEGRQGGKGA | KGDPGAIGAP | GKTGPVGPAG | PAGKPGPDGL | RGLPGSVGQQ | GRPGATGQAG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PPGPVGPPGL | PGLRGDAGAK | GEKGHPGLIG | LIGPPGEQGE | KGDRGLPGPQ | GSPGQKGEMG | IPGASGPIGP | GGPPGLPGPA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| GPKGAKGATG | PGGPKGEKGV | QGPPGHPGPP | GEVIQPLPIQ | MPKKTRRSVD | GSRLMQEDEA | IPTGGAPGSP | GGLEEIFGSL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DSLREEIEQM | RRPTGTQDSP | ARTCQDLKLC | HPELPDGEYW | VDPNQGCARD | AFRVFCNFTA | GGETCVTPRD | DVTQFSYVDS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| EGSPVGVVQL | TFLRLLSVSA | HQDVSYPCSG | AARDGPLRLR | GANEDELSPE | TSPYVKEFRD | GCQTQQGRTV | LEVRTPVLEQ |
| 1610 | 1620 | 1630 | | | | | |
| LPVLDASFSD | LGAPPRRGGV | LLGPVCFMG | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 230 | 2 | 575.1791 | -198.73 | 2 | 32.6 | 11.4 | 0 | 1618-1629 | R.GGVLLGPVCFMG.- | |

# Detailed Protein Report

## Protein 443: spindle and kinetochore-associated protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21450832 | **Score:** | 29.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 29.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 12.5 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|88014625 | refseq_human(refseq_human_20140103.fasta) | spindle and kinetochore-associated protein 1 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MASSDLEQLC SHVNEKIGNI KKTLSLRNCG QEPTLKTVLN KIGDEIIVIN ELLNKLELEI QYQEQTNNSL KELCESLEED
        90        100        110        120        130        140        150        160
YKDIEHLKEN VPSHLPQVTV TQSCVKGSDL DPEEPIKVEE PEPVKKPPKE QRSIKEMPFI TCDEFNGVPS YMKSRLTYNQ
       170        180        190        200        210        220        230        240
INDVIKEINK AVISKYKILH QPKKSMNSVT RNLYHRFIDE ETKDTKGRYF IVEADIKEFT TLKADKKFHV LLNILRHCRR
       250        260
LSEVRGGGLT RYVIT
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 72 | 1 | 1069.4912 | -125.31 | 2 | 30.6 | 13.1 | 1 | 37-55 | K.TVLNKIGDEIIVINELLNK.L | |
| 1627 | 3 | 853.3841 | -128.05 | 2 | 50.1 | 16.5 | 2 | 227-239 | K.KFHVLLNILRHCR.R | Carbamidomethyl: 12 |

# Detailed Protein Report

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**Protein 444:** **PREDICTED: uveal autoantigen with coiled-coil domains and ankyrin repeats isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530406156 | **Score:** | 29.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 160.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMNCWFSCTP | KNRHAADWNK | YDDRLMKAAE | RGDVEKVTSI | LAKKGVNPGK | LDVEGRSVFH | VVTSKGNLEC | LNAILIHGVD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ITTSDTAGRN | ALHLAAKYGH | ALCLQKLLQY | NCPTEHADLQ | GRTALHDAAM | ADCPSSIQLL | CDHGASVNAK | DVDGRTPLVL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ATQMSRPTIC | QLLIDRGADV | NSRDKQNRTA | LMLGCEYGCR | DAVEVLIKNG | ADISLLDALG | HDSSYYARIG | DNLDILTLLK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TASENTNKGR | ELWKKGPSLQ | QRNLTHMQDE | VNVKSHQREH | QNIQDLEIEN | EDLKERLRKI | QQEQRILLDK | VNGLQLQLNE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| REKLKSLLAA | KEKQHEESLR | TIEALKNRFK | YFESDHLGSG | SHFSNRKEDM | LLKQGQMYMA | DSQCTSPGIP | AHMQSRSMLR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PLELSLPSQT | SYSENEILKK | ELEAMRTFCE | SAKQDRLKLQ | NELAHKVAEC | KALALECERV | KEDSDEQIKQ | LEDALKDVQK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RMYESEGKVK | QMQTHFLALK | EHLTSEAASG | NHRLTEELKD | QLKDLKVKYE | GASAEVGKLR | NQIKQNEMIV | EEFKRDEGKL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IEENKRLQKE | LSMCEMEREK | KGRKVTEMEG | QAKELSAKLA | LSIPAEKFEN | MKSSLSNEVN | EKAKKLVEME | REHEKSLSEI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RQLKRELENV | KAKLAQHVKP | EEHEQVKSRL | EQKSGELGKK | ITELTLKNQT | LQKEIEKVYL | DNKLLKEQAH | NLTIEMKNHY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VPLKVSEDMK | KSHDAIIDDL | NRKLLDVTQK | YTEKKLEMEK | LLLENDSLSK | DVSRLETVFV | PPEKHEKEII | ALKSNIVELK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KQLSELKKKC | GEDQEKIHAL | TSENTNLKKM | MSNQYVPVKT | HEEVKMTLND | TLAKTNRELL | DVKKKFEDIN | QEFVKIKDKN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EILKRNLENT | QNQIKAEYIS | LAEHEAKMSS | LSQSMRKVQD | SNAEILANYR | KGQEEIVTLH | AEIKAQKKEL | DTIQECIKVK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| YAPIVSFEEC | ERKFKATEKE | LKDQLSEQTQ | KYSVSEEEVK | KNKQENDKLK | KEIFTLQKDL | RDKTVLIEKS | HEMERALSRK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TDELNKQLKD | LSQKYTEVKN | VKEKLVEENA | KQTSEILAVQ | NLLQKQHVPL | EQVEALKKSL | NGTIENLKEE | LKSMQRCYEK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EQQTVTKLHQ | LLENQKNSSV | PLAEHLQIKE | AFEKEVGIIK | ASLREKEEES | QNKMEEVSKL | QSEVQNTKQA | LKKLETREVV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DLSKYKATKS | DLETQISSLN | EKLANLNRKY | EEVCEEVLHA | KKKEISAKDE | KELLHFSIEQ | EIKDQKERCD | KSLTTITELQ |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| RRIQESAKQI | EAKDNKITEL | LNDVERLKQA | LNGLSQLTYT | SGNPTKRQSQ | LIDTLQHQVK | SLEQQLADAD | RQHQEVIAIY |
| 1370 | 1380 | 1390 | 1400 | | | | |
| RTHLLSAAQG | HMDEDVQEAL | LQIIQMRQGL | VC | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1985 | 1 | 599.9122 | -110.16 | 3 | 53.2 | 13.4 | 2 | 959-973 | K.VKYAPIVSFEECERK.F | |

# Detailed Protein Report

**Protein 445:** **cell cycle checkpoint control protein RAD9B isoform 1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|169234617 | **Score:** | 29.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 48.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 7.7 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 0.92 | **CV:** 0.00 % | **No. of Peptides:** 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAMLKCVMS | GSQVKVFGKA | VQALSRISDE | FWLDPSKKGL | ALRCVNSSRS | AYGCVLFSPV | FFQHYQWSAL | VKMSENELDT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TLHLKCKLGM | KSILPIFRCL | NSLERNIEKC | RIFTRSDKCK | VVIQFFYRHG | IKRTHNICFQ | ESQPLQVIFD | KNVCTNTLMI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QPRLLADAIV | LFTSSQEEVT | LAVTPLNFCL | KSSNEESMDL | SNAVHSEMFV | GSDEFDFFQI | GMDTEITFCF | KELKGILTFS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EATHAPISIY | FDFPGKPLAL | SIDDMLVEAN | FILATLADEQ | SRASSPQSLC | LSQKRKRSDL | IEKKAGKNVT | GQALECISKK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AAPRRLYPKE | TLTNISALEN | CGSPAMKRVD | GDVSEVSESS | VSNTEEVPGS | LCLRKFSCMF | FGAVSSDQQE | HFNHPFDSLA |
| 410 | 420 | 430 | | | | | |
| RASDSEEDMN | NVCCRKEFNG | SDAKYFCII | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2570 | 8 | 1044.5429 | 14.94 | 2 | 62.8 | 15.9 | 2 | 1-19 | -.MAAMLKCVMSGSQVKVFGK.A | Carbamidomethyl: 7;<br>Oxidation: 4 | |
| 421 | 1 | 846.3629 | -53.88 | 2 | 35.2 | 13.6 | 2 | 416-429 | R.KEFNGSDAKYFCII.- | Carbamidomethyl: 12 | QU:MU 0.92 |

# Detailed Protein Report

**Protein 446:** **PREDICTED: cadherin EGF LAG seven-pass G-type receptor 2 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578798514 | **Score:** | 29.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 316.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| | | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRSPATGVPL | PTPPPPLLLL | LLLLLPPPLL | GDQVGPCRSL | GSRGRGSSGA | CAPMGWLCPS | SASNLWLYTS | RCRDAGTELT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GHLVPHHDGL | RVWCPESEAH | IPLPPAPEGC | PWSCRLLGIG | GHLSPQGKLT | LPEEHPCLKA | PRLRCQSCKL | AQAPGLRAGE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RSPEESLGGR | RKRNVNTAPQ | FQPPSYQATV | PENQPAGTPV | ASLRAIDPDE | GEAGRLEYTM | DALFDSRSNQ | FFSLDPVTGA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VTTAEELDRE | TKSTHVFRVT | AQDHGMPRRS | ALATLTILVT | DTNDHDPVFE | QQEYKESLRE | NLEVGYEVLT | VRATDGDAPP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NANILYRLLE | GSGGSPSEVF | EIDPRSGVIR | TRGPVDREEV | ESYQLTVEAS | DQGRDPGPRS | TTAAVFLSVE | DDNDNAPQFS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EKRYVVQVRE | DVTPGAPVLR | VTASDRDKGS | NAVVHYSIMS | GNARGQFYLD | AQTGALDVVS | PLDYETTKEY | TLRVRAQDGG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RPPLSNVSGL | VTVQVLDIND | NAPIFVSTPF | QATVLESVPL | GYLVLHVQAI | DADAGDNARL | EYRLAGVGHD | FPFTINNGTG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| WISVAAELDR | EEVDFYSFGV | EARDHGTPAL | TASASVSVTV | LDVNDNNPTF | TQPEYTVRLN | EDAAVGTSVV | TVSAVDRDAH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SVITYQITSG | NTRNRFSITS | QSGGGLVSLA | LPLDYKLERQ | YVLAVTASDG | TRQDTAQIVV | NVTDANTHRP | VFQSSHYTVN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VNEDRPAGTT | VVLISATDED | TGENARITYF | MEDSIPQFRI | DADTGAVTTQ | AELDYEDQVS | YTLAITARDN | GIPQKSDTTY |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LEILVNDVND | NAPQFLRDSY | QGSVYEDVPP | FTSVLQISAT | DRDSGLNGRV | FYTFQGGDDG | DGDFIVESTS | GIVRTLRRLD |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RENVAQYVLR | AYAVDKGMPP | ARTPMEVTVT | VLDVNDNPPV | FEQDEFDVFV | EENSPIGLAV | ARVTATDPDE | GTNAQIMYQI |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VEGNIPEVFQ | LDIFSGELTA | LVDLDYEDRP | EYVLVIQATS | APLVSRATVH | VRLLDRNDNP | PVLGNFEILF | NNYVTNRSSS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| FPGGAIGRVP | AHDPDISDSL | TYSFERGNEL | SLVLLNASTG | ELKLSRALDN | NRPLEAIMSV | LVSDGVHSVT | AQCALRVTII |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TDEMLTHSIT | LRLEDMSPER | FLSPLLGLFI | QAVAATLATP | PDHVVVFNVQ | RDTDAPGGHI | LNVSLSVGQP | PGPGGGPPFL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PSEDLQERLY | LNRSLLTAIS | AQRVLPFDDN | ICLREPCENY | MRCVSVLRFD | SSAPFIASSS | VLFRPIHPVG | GLRCRCPPGF |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TGDYCETEVD | LCYSRPCGPH | GRCRSREGGY | TCLCRDGYTG | EHCEVSARSG | RCTPGVCKNG | GTCVNLLVGG | FKCDCPSGDF |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| EKPYCQVTTR | SFPAHSFITF | RGLRQRFHFT | LALSFATKER | DGLLLYNGRF | NEKHDFVALE | VIQEQVQLTF | SAGESTTTVS |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| PFVPGGVSDG | QWHTVQLKYY | NKPLLGQTGL | PQGPSEQKVA | VVTVDGCDTG | VALRFGSVLG | NYSCAAQGTQ | GGSKKSLDLT |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| GPLLLGGVPD | LPESFPVRMR | QFVGCMRNLQ | VDSRHIDMAD | FIANNGTVPG | CPAKKNVCDS | NTCHNGGTCV | NQWDAFSCEC |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| PLGFGGKSCA | QEMANPQHFL | GSSLVAWHGL | SLPISQPWYL | SLMFRTRQAD | GVLLQAITRG | RSTITLQLRE | GHVMLSVEGT |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| GLQASSLRLE | PGRANDGDWH | HAQLALGASG | GPGHAILSFD | YGQQRAEGNL | GPRLHGLHLS | NITVGGIPGP | AGGVARGFRG |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| CLQGVRVSDT | PEGVNSLDPS | HGESINVEQG | CSLPDPCDSN | PCPANSYCSN | DWDSYSCSCD | PGYYGDNCTN | VCDLNPCEHQ |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| SVCTRKPSAP | HGYTCECPPN | YLGPYCETRI | DQPCPRGWWG | HPTCGPCNCD | VSKGFDPDCN | KTSGECHCKE | NHYRPPGSPT |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| CLLCDCYPTG | SLSRVCDPED | GQCPCKPGVI | GRQCDRCDNP | FAEVTTNGCE | VNYDSCPRAI | EAGIWWPRTR | FGLPAAAPCP |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| KGSFGTAVRH | CDEHRGWLPP | NLFNCTSITF | SELKGFAERL | QRNESGLDSG | RSQQLALLLR | NATQHTAGYF | GSDVKVAYQL |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| ATRLLAHEST | QRGFGLSATQ | DVHFTENLLR | VGSALLDTAN | KRHWELIQQT | EGGTAWLLQH | YEAYASALAQ | NMRHTYLSPF |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2164 | 1 | 937.1664 | 148.30 | 2 | 57.5 | 14.0 | 2 | 129-144 | K.LTLPEEHPCLKAPRLR.C | |
| 1989 | 3 | 572.7550 | -154.40 | 2 | 55.2 | 15.5 | 1 | 1660-1669 | R.GRSTITLQLR.E | |

# Detailed Protein Report

## Protein 447: OTU domain-containing protein 7A [Homo sapiens]

**Accession:** gi|18702331
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 29.5
**MW [kDa]:** 100.6
**pI:** 9.5
**Sequence Coverage [%]:** 4.2
**No. of unique Peptides:** 2

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVSSVLPNPT | SAECWAALLH | DPMTLDMDAV | LSDFVRSTGA | EPGLARDLLE | GKNWDLTAAL | SDYEQLRQVH | TANLPHVFNE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GRGPKQPERE | PQPGHKVERP | CLQRQDDIAQ | EKRLSRGISH | ASSAIVSLAR | SHVASECNNE | QFPLEMPIYT | FQLPDLSVYS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EDFRSFIERD | LIEQATMVAL | EQAGRLNWWS | TVCTSCKRLL | PLATTGDGNC | LLHAASLGMW | GFHDRDLVLR | KALYTMMRTG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AEREALKRRW | RWQQTQQNKE | EEWEREWTEL | LKLASSEPRT | HFSKNGGTGG | GVDNSEDPVY | ESLEEFHVFV | LAHILRRPIV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VVADTMLRDS | GGEAFAPIPF | GGIYLPLEVP | PNRCHCSPLV | LAYDQAHFSA | LVSMEQRDQQ | REQAVIPLTD | SEHKLLPLHF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AVDPGKDWEW | GKDDNDNARL | AHLILSLEAK | LNLLHSYMNV | TWIRIPSETR | APLAQPESPT | ASAGEDVQSL | ADSLDSDRDS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VCSNSNSNNG | KNGKDKEKEK | QRKEKDKTRA | DSVANKLGSF | SKTLGIKLKK | NMGGLGGLVH | GKMGRANSAN | GKNGDSAERG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KEKKAKSRKG | SKEESGASAS | TSPSEKTTPS | PTDKAAGASP | AEKGGGPRGD | AWKYSTDVKL | SLNILRAAMQ | GERKFIFAGL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LLTSHRHQFH | EEMIGYYLTS | AQERFSAEQE | QRRRDAATAA | AAAAAAAAAT | AKRPPRRPET | EGVPVPERAS | PGPPTQLVLK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LKERPSPGPA | AGRAARAAAG | GTASPGGGAR | RASASGPVPG | RSPPAPARQS | VIHVQASGAR | DEACAPAVGA | LRPCATYPQQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NRSLSSQSYS | PARAAALRTV | NTVESLARAV | PGALPGAAGT | AGAAEHKSQT | YTNGFGALRD | GLEFADADAP | TARSNGECGR |
| 890 | 900 | 910 | 920 | 930 | | | |
| GGPGPVQRRC | QRENCAFYGR | AETEHYCSYC | YREELRRRRE | ARGARP | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2690 | 1 | 724.8511 | -130.11 | 2 | 64.7 | 15.6 | 1 | 709-722 | R.ASPGPPTQLVLKLK.E | |
| 41 | 6 | 1068.4771 | -72.42 | 2 | 30.4 | 13.9 | 2 | 737-761 | R.AAAGGTASPGGGARRASASGPVPGR.S | |

# Detailed Protein Report

## Protein 448: transcription elongation factor B polypeptide 2 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|46276893 | **Score:** | 29.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 17.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 15.5 |
| | | **No. of unique Peptides:** | 1 |

```
         10         20         30         40         50         60         70         80
MDVFLMIRRH KTTIFTDAKE SSTVFELKRI VEGILKRPPD EQRLYKDDQL LDDGKTLGEC GFTSQTARPQ APATVGLAFR
         90        100        110        120        130        140        150        160
ADDTFEALCI EPFSSPPELP DVMKPQDSGS SANEQAVHLH VHSQTMAKSR NTSWSQCPGL TACSTREPQD GPTQVHPRWG
        170
L
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2604 | 1 | 913.4894 | 96.33 | 2 | 63.2 | 15.9 | 0 | 131-146 | R.NTSWSQCPGLTACSTR.E | Carbamidomethyl: 7, 13 |

## Protein 449: PREDICTED: protein FAM214A isoform X6 [Homo sapiens]

**Accession:** gi|578827201
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 29.5
**MW [kDa]:** 111.5
**pI:** 9.2
**Sequence Coverage [%]:** 2.3
**No. of unique Peptides:** 2

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578827203 | refseq_human<br>(refseq_human_20140103.fasta) | PREDICTED: protein FAM214A isoform X7 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVEMMLLPDC | CYSDDGPTTE | GIDLNDPAIK | QDALLLERWI | LEPVPRQNGD | RFIEEKTLLL | AVRSFVFFSQ | LSAWLSVSHG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AIPRNILYRI | SAADVDLQWN | FSQTPIEHVF | PVPNVSHNVA | LKVSVQSLPR | QSNYPVLTCS | IHTNIGLYEK | RIQQHKLKTH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QHHNPNEAEQ | CGTNSSQRLC | SKQTWTMAPE | SVLHAKSGPS | PEYTAAVKNI | KLYPGTGSKS | DHGTSQANIL | GFSGIGDIKS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QETSVRTLKS | FSMVDSSISN | RQSFWQSAGE | TNPLIGSLIQ | ERQEIIARIA | QHLIHCDPST | SHVSGRPFNT | QESSSLHSKL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FRVSQENENV | GKGKEAFSMT | FGSPEFSSPE | DTNEGKIRLK | PETPRSETCI | SNDFYSHMPV | GETNPLIGSL | LQERQDVIAR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IAQHLEHIDP | TASHIPRQSF | NMHDSSSVAS | KVFRSSYEDK | NLLKKNKDES | SVSISHTKCS | LLGDISDGKN | LVPNKCFTSF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KNNSKEKCSL | KHQTRNQCQN | NPSEIIQSTY | QETQNKSSSL | STSSILSQHK | ENNLDLTSRF | KEQEMSNGID | KQYSNCTTID |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KQICTNKYKE | KIINENYNPK | FFGNLQSDDS | KKNDSKIKVT | VLEMSEYLNK | YESMSSNKDS | KRPKTCEQNT | QLNSIENYLN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KDNEGFKCKK | SDQLKNEQDK | QEDPTNEKSQ | NYSQRRSIKD | CLSTCEQPKN | TEVLRTTLKH | SNVWRKHNFH | SLDGTSTRAF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HPQTGLPLLS | SPVPQRKTQS | GCFDLDSSLL | HLKSFSSRSP | RPCLNIEDDP | DIHEKPFLSS | SAPPITSLSL | LGNFEESVLN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| YRFDPLGIVD | GFTAEVGASG | AFCPTHLTLP | VEVSFYSVSD | DNAPSPYMGV | ITLESLGKRG | YRVPPSGTIQ | VTLFNPNKTV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VKMFVVIYDL | RDMPANHQTF | LRQRTFSVPV | KQEVKRSVNK | ENIRHTEERL | LRYLIHLRFQ | SSKSGKIYLH | RDVRLLFSRK |
| 970 | 980 | 990 | | | | | |
| SMEVDSGAAY | ELKSYTESPT | NPQFSPRC | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2952 | 1 | 557.9715 | 37.67 | 3 | 65.7 | 10.1 | 1 | 247-261 | R.TLKSFSMVDSSISNR.Q | |
| 1649 | 2 | 480.7758 | 122.24 | 2 | 48.9 | 19.4 | 0 | 661-668 | K.QEDPTNEK.S | |

# Detailed Protein Report

## Protein 450: coagulation factor VIII isoform a precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4503647 | **Score:** | 29.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 266.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.0 |
| | | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQIELSTCFF | LCLLRFCFSA | TRRYYLGAVE | LSWDYMQSDL | GELPVDARFP | PRVPKSFPFN | TSVVYKKTLF | VEFTDHLFNI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AKPRPPWMGL | LGPTIQAEVY | DTVVITLKNM | ASHPVSLHAV | GVSYWKASEG | AEYDDQTSQR | EKEDDKVFPG | GSHTYVWQVL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KENGPMASDP | LCLTYSYLSH | VDLVKDLNSG | LIGALLVCRE | GSLAKEKTQT | LHKFILLFAV | FDEGKSWHSE | TKNSLMQDRD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AASARAWPKM | HTVNGYVNRS | LPGLIGCHRK | SVYWHVIGMG | TTPEVHSIFL | EGHTFLVRNH | RQASLEISPI | TFLTAQTLLM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DLGQFLLFCH | ISSHQHDGME | AYVKVDSCPE | EPQLRMKNNE | EAEDYDDDLT | DSEMDVVRFD | DDNSPSFIQI | RSVAKKHPKT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| WVHYIAAEEE | DWDYAPLVLA | PDDRSYKSQY | LNNGPQRIGR | KYKKVRFMAY | TDETFKTREA | IQHESGILGP | LLYGEVGDTL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LIIFKNQASR | PYNIYPHGIT | DVRPLYSRRL | PKGVKHLKDF | PILPGEIFKY | KWTVTVEDGP | TKSDPRCLTR | YYSSFVNMER |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DLASGLIGPL | LICYKESVDQ | RGNQIMSDKR | NVILFSVFDE | NRSWYLTENI | QRFLPNPAGV | QLEDPEFQAS | NIMHSINGYV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FDSLQLSVCL | HEVAYWYILS | IGAQTDFLSV | FFSGYTFKHK | MVYEDTLTLF | PFSGETVFMS | MENPGLWILG | CHNSDFRNRG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| MTALLKVSSC | DKNTGDYYED | SYEDISAYLL | SKNNAIEPRS | FSQNSRHPST | RQKQFNATTI | PENDIEKTDP | WFAHRTPMPK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IQNVSSSDLL | MLLRQSPTPH | GLSLSDLQEA | KYETFSDDPS | PGAIDSNNSL | SEMTHFRPQL | HHSGDMVFTP | ESGLQLRLNE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KLGTTAATEL | KKLDFKVSST | SNNLISTIPS | DNLAAGTDNT | SSLGPPSMPV | HYDSQLDTTL | FGKKSSPLTE | SGGPLSLSEE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NNDSKLLESG | LMNSQESSWG | KNVSSTESGR | LFKGKRAHGP | ALLTKDNALF | KVSISLLKTN | KTSNNSATNR | KTHIDGPSLL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| IENSPSVWQN | ILESDTEFKK | VTPLIHDRML | MDKNATALRL | NHMSNKTTSS | KNMEMVQQKK | EGPIPPDAQN | PDMSFFKMLF |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LPESARWIQR | THGKNSLNSG | QGPSPKQLVS | LGPEKSVEGQ | NFLSEKNKVV | VGKGEFTKDV | GLKEMVFPSS | RNLFLTNLDN |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LHENNTHNQE | KKIQEEIEKK | ETLIQENVVL | PQIHTVTGTK | NFMKNLFLLS | TRQNVEGSYD | GAYAPVLQDF | RSLNDSTNRT |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KKHTAHFSKK | GEEENLEGLG | NQTKQIVEKY | ACTTRISPNT | SQQNFVTQRS | KRALKQFRLP | LEETELEKRI | IVDDTSTQWS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KNMKHLTPST | LTQIDYNEKE | KGAITQSPLS | DCLTRSHSIP | QANRSPLPIA | KVSSFPSIRP | IYLTRVLFQD | NSSHLPAASY |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| RKKDSGVQES | SHFLQGAKKN | NLSLAILTLE | MTGDQREVGS | LGTSATNSVT | YKKVENTVLP | KPDLPKTSGK | VELLPKVHIY |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| QKDLFPTETS | NGSPGHLDLV | EGSLLQGTEG | AIKWNEANRP | GKVPFLRVAT | ESSAKTPSKL | LDPLAWDNHY | GTQIPKEEWK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| SQEKSPEKTA | FKKKDTILSL | NACESNHAIA | AINEGQNKPE | IEVTWAKQGR | TERLCSQNPP | VLKRHQREIT | RTTLQSDQEE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| IDYDDTISVE | MKKEDFDIYD | EDENQSPRSF | QKKTRHYFIA | AVERLWDYGM | SSSPHVLRNR | AQSGSVPQFK | KVVFQEFTDG |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SFTQPLYRGE | LNEHLGLLGP | YIRAEVEDNI | MVTFRNQASR | PYSFYSSLIS | YEEDQRQGAE | PRKNFVKPNE | TKTYFWKVQH |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| HMAPTKDEFD | CKAWAYFSDV | DLEKDVHSGL | IGPLLVCHTN | TLNPAHGRQV | TVQEFALFFT | IFDETKSWYF | TENMERNCRA |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| PCNIQMEDPT | FKENYRFHAI | NGYIMDTLPG | LVMAQDQRIR | WYLLSMGSNE | NIHSIHFSGH | VFTVRKKEEY | KMALYNLYPG |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| VFETVEMLPS | KAGIWRVECL | IGEHLHAGMS | TLFLVYSNKC | QTPLGMASGH | IRDFQITASG | QYGQWAPKLA | RLHYSGSINA |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| WSTKEPFSWI | KVDLLAPMII | HGIKTQGARQ | KFSSLYISQF | IIMYSLDGKK | WQTYRGNSTG | TLMVFFGNVD | SSGIKHNIFN |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| PPIIARYIRL | HPTHYSIRST | LRMELMGCDL | NSCSMPLGME | SKAISDAQIT | ASSYFTNMFA | TWSPSKARLH | LQGRSNAWRP |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| QVNNPKEWLQ | VDFQKTMKVT | GVTTQGVKSL | LTSMYVKEFL | ISSSQDGHQW | TLFFQNGKVK | VFQGNQDSFT | PVVNSLDPPL |
| 2330 | 2340 | 2350 | 2360 | | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 843 | 1 | 653.3686 | -17.24 | 2 | 40.6 | 10.7 | 2 | 1167-1178 | K.NKVVVGKGEFTK.D | |

# Detailed Protein Report

## Protein 451: PREDICTED: myosin-7B isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578836098 | **Score:** | 29.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 203.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAPSLYGLRS | GCLQGKAPLR | FPAPYICGGG | QRLQRHAAQP | RQPVHADHQF | LATKTGGTLE | DQIIEANPAM | EAFGNAKTLR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NDNSSRFGKF | IRIHFGPSGK | LASADIDSYL | LEKSRVIFQL | PGERSYHVYY | QILSGRKPEL | QDMLLLSMNP | YDYHFCSQGV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ITVDNMNDGE | ELIATDHAMD | ILGFSVDEKC | ACYKIVGALL | HFGNMKFKQK | QREEQAEADG | TESADKAAYL | MGVSSGDLLK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GLLHPRVRVG | NEYVTKGQSV | EQVVFAVGAL | AKATYDRLFR | WLVSRINQTL | DTKLPRQFFI | GVLDIAGFEI | FEFNSFEQLC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| INFTNEKLQQ | FFNQHMFVLE | QEEYKREGID | WVFIDFGLDL | QPCIDLIEKP | LGILSILEEE | CMFPKASDAS | FRAKLYDNHA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GKSPNFQQPR | PDKKRKYQAH | FEVVHYAGVV | PYSIVGWLEK | NKDPLNETVV | PIFQKSQNRL | LATLYENYAG | SCSTEPPKSG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VKEKRKKAAS | FQTVSQLHKE | NLNKLMTNLR | ATQPHFVRCI | VPNENKTPGV | MDAFLVLHQL | RCNGVLEGIR | ICRQGFPNRL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LYTDFRQRYR | ILNPSAIPDD | TFMDSRKATE | KLLGSLDLDH | TQYQFGHTKV | FFKAGLLGVL | EELRDQRLAK | VLTLLQARSR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GRLMRLEYQR | LLGGRDALFT | IQWNIRAFNA | VKNWSWMKLF | FKMKPLLRSA | QAEEELAALR | AELRGLRGAL | AAAEAKRQEL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EETHVSITQE | KNDLALQLQA | EQDNLADAEE | RCHLLIKSKV | QLEGKVKELS | ERLEDEEEVN | ADLAARRRKL | EDECTELKKD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IDDLELTLAK | AEKEKQATEN | KVKNLTEEMA | ALDESVARLT | KEKKALQEAH | QQALGDLQAE | EDRVSALTKA | KLRLEQQVED |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LECSLEQEKK | LRMDTERAKR | KLEGDLKLTQ | ESVADAAQDK | QQLEEKLKKK | DSELSQLSLR | VEDEQLLGAQ | MQKKIKELQA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RAEELEEELE | AERAARARVE | KQRAEAAREL | EELSERLEEA | GGASAGQREG | CRKREAELGR | LRRELEEAAL | RHEATVAALR |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RKQAEGAAEL | GEQVDSLQRV | RQKLEKEKSE | LRMEVDDLAA | NVETLTRAKA | SAEKLCRTYE | DQLSEAKIKV | EELQRQLADA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| STQRGRLQTE | SGELSRLLEE | KECLISQLSR | GKALAAQSLE | ELRRQLEEES | KAKSALAHAV | QALRHDCDLL | REQHEEEAEA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| QAELQRLLSK | ANAEVAQWRS | KYEADAIQRT | EELEEAKKKL | ALRLQEAEEG | VEAANAKCSS | LEKAKLRLQT | ESEDVTLELE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| RATSAAAALD | KKQRHLERAL | EERRRQEEEM | QRELEAAQRE | SRGLGTELFR | LRHGHEEALE | ALETLKRENK | NLQEEISDLT |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| DQVSLSGKSI | QELEKTKKAL | EGEKSEIQAA | LEEAEGALEL | EETKTLRIQL | ELSQVKAEVD | RKLAEKDEEC | ANLRRNHQRA |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| VESLQASLDA | ETRARNEALR | LKKKMEGDLN | DLELQLGHAT | RQATEAQAAT | RLMQAQLKEE | QAGRDEEQRL | AAELHEQAQA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| LERRASLLAA | ELEELRAALE | QGERSRRLAE | QELLEATERL | NLLHSQNTGL | LNQKKKLEAD | LAQLSGEVEE | AAQERREAEE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KAKKAITDAA | MMAEELKKEQ | DTSAHLERMK | KTLEQTVREL | QARLEEAEQA | ALRGGKKQVQ | KLEAKVRELE | AELDAEQKKH |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| AEALKGVRKH | ERRVKELAYQ | AEEDRKNLAR | MQDLVDKLQS | KVKSYKRQFE | EAEQQANTNL | AKYRKAQHEL | DDAEERADMA |
| 1770 | 1780 | 1790 | | | | | |
| ETQANKLRAR | TRDALGPKLS | LSPQHKE | | | | | |

| Cmpd. | No. of | m/z meas. | Δ m/z | z | Rt | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

|  | Cmpds. |  | [ppm] |  | [min] |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|
| 1310 | 1 | 939.8664 | -147.69 | 2 | 46.0 | 16.1 | 1 | 1024-<br>1040 | R.ELEEAALRHEATVAALR.R |  |

# Detailed Protein Report

## Protein 452: regulator of G-protein signaling 10 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4506505 | **Score:** | 29.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 19.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| | | **Sequence Coverage [%]:** | 16.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEHIHDSDGS | SSSSHQSLKS | TAKWAASLEN | LLEDPEGVKR | FREFLKKEFS | EENVLFWLAC | EDFKKMQDKT | QMQEKAKEIY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MTFLSSKASS | QVNVEGQSRL | NEKILEEPHP | LMFQKLQDQI | FNLMKYDSYS | RFLKSDLFLK | HKRTEEEEED | LPDAQTAAKR |
| 170 | | | | | | | |
| ASRIYNT | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2594 | 2 | 1044.5480 | 50.13 | 2 | 63.1 | 15.6 | 2 | 143-160 | K.RTEEEEEDLPDAQTAAKR.A | |

# Detailed Protein Report

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## Protein 453: PREDICTED: nuclear factor 1 X-type isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530414877 | **Score:** | 29.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDEFHPFIEA | LLPHVRAFSY | TWFNLQARKR | KYFKKHEKRM | SKDEERAVKD | ELLGEKPEIK | QKWASRLLAK | LRKDIRPEFR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EDFVLTITGK | KPPCCVLSNP | DQKGKIRRID | CLRQADKVWR | LDLVMVILFK | GIPLESTDGE | RLYKSPQCSN | PGLCVQPHHI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GVTIKELDLY | LAYFVHTPES | GQSDSSNQQG | DADIKPLPNG | HLSFQDCFVT | SGVWNVTELV | RVSQTPVATA | SGPNFSLADL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ESPSYYNINQ | VTLGRRSITS | PPSTSTTKRP | KSIDDSEMES | PVDDVFYPGT | GRSPAAGSSQ | SSGWPNDVDA | GPASLKKSGK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LDFCSALSSQ | GSSPRMAFTH | HPLPVLAGVR | PGSPRATASA | LHFPSTSIIQ | QSSPYFTHPT | IRYHHHHGQD | SLKEFVQFVC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SDGSGQATGQ | PNGSGQGKVP | GSFLLPPPPP | VARPVPLPMP | DSKSTSTAPD | GAALTPPSPS | FATTGASSAN | RFVSIGPRDG |
| 490 | 500 | | | | | | |
| NFLNIPQQSQ | SWFL | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 392 | 1 | 874.3959 | -106.40 | 3 | 34.9 | 13.0 | 0 | 419-443 | K.VPGSFLLPPPPPVARPVPLPMPDSK.S | Oxidation: 21 |

# Detailed Protein Report

## Protein 454: PREDICTED: centrosomal protein KIAA1731 isoform X7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578822447 | **Score:** | 29.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 268.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 0.5 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MERFEKAHVR | GFQAMKKIHL | AQNQEKLMKE | LKQLQQEDLA | RRRQTVAQMP | PQLVELPYKR | SEMKEDWQRE | LEFAFEDMYN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ADRKVKGNLI | LHLEPEPLPT | VTNQIQDEEL | DLSMEQENLG | AAEDLPVTEA | EICSSETDVP | LVMKTQQIPS | KVLFKKLLNK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IRSQKSLWTI | KSMSEDESEM | ITTVSEIESK | APTVESGTIA | SKERTLSSGQ | EQVVESDTLT | IESGPLASED | KPLSCGTNSG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KEQEINETLP | ITTVAQSSVL | LHPQEAAARI | RMSARQKQIM | EIEEQKQKQL | ELLEQIEQQK | LRLETDCFRA | QLEEEKRKKT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QPTGVGCRKS | HHYINHLVGI | APASCPVISD | EDSHRQMIRN | YQHQLLQQNR | LHRQSVETAR | KQLLEYQTML | KGRCPSVSAP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SLITDSVISV | PSWKSERPTA | ISEHWDQGQR | LKLSPNKYQP | IQPIQTSKLE | QDHFQVARQN | HFPQRQVETT | ETLRASDILT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NQALESQEHL | RQFSQTETQQ | RDYKLVPKDS | ETLSRALSHD | RQLISQDARK | ISETFGATTF | QSLESQQLFS | ENSENISYHL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TEPSSFVPLV | PQHSFSSLPV | KVESGKIQEP | FSAMSKSTVS | TSHSIISQMH | DRPLLPSENI | TAQQGNMKAL | QEQLDLQKKV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LQATQEAQEQ | LLLCKQKEVE | QQTGLSVFLP | LVTPDSSALL | PSAKADLGRI | QESSPTKNNI | AVSSDHHVIS | QLQDKRLSLS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QPILSQQNNF | KFLQEQLNIQ | KDSLQARREA | QEVLYVHKQS | ELDRRVCSEQ | AEPSFPFQVA | QHTFTSLPSA | DTKSGKIQEQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| HSSKSEKGLV | SCQSDIPISQ | DGSLSFLQQF | LPLHDSLKLL | QEQLTKQRDT | LQARHEAQVE | LLLHRQRDLG | DSKSGLVSSS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SSPVVVQHSV | ASQASAKAEP | RRIQELYLSE | KENVGPSCHL | IIPTFQDKSL | SFPQHSLAQQ | ENLTILQEQS | QIQRVILGAK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| EGTQEFVHTE | SELEKRISSE | QTGTSSSLSQ | VDESERFQEC | ISIKSDSTIP | LSHPKIPRCQ | ERLLRVSQHM | LPLQDNLEEH |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QAWLDTEKEA | FHFSQKTQEN | TSSEQTGSSS | FIPQLVQLSF | TSLASAESGT | ILEPLFTESE | SKIFSSHLQI | PQLQDRLLRI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SQLIQPQQDN | LKALQEQLAT | QREAIILARQ | EAREELLLHQ | SEWEGRISPE | QVDTSSLPLV | PQHSFASLPL | NESERNQEPC |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SINSDNIVSS | GHSEIPTLPD | GLLGLSHLVL | PQQDNLIALE | EHLHAQTDFL | PSIEKTQKEL | VLSKPCKFEE | KVSSEHFIQS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| HHGDLQALQQ | QLDTQKKAIR | SIQEVQEELL | LQRLSELEKR | VSSEQVCSSS | FVSQVPVADS | ERTQKSFPTK | SNDTLPSSHR |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| EIPRLQDRLL | SLSKPILPQQ | DNMTAQLDAQ | REVMYSYEKP | QEELSLNKQR | KLNKSESAEH | TIPSLFLPKE | TEHSFIPLPF |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| AEAKPKSTCE | LYSSQNEHAA | PPSNPVIPGF | QDRLLSFSQS | VLTQQDNLGL | QKQLDLQREV | LHYSQKAQEK | LLVQRQTALQ |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| QQIQKHEETL | KDFFKDSQIS | KPTVENDLKT | QKMGQLRDWF | PNTQDLAGND | QENIRHADRN | NSDDNHLASE | DTSAKQSGEH |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LEKDLGRRSS | KPPVAKVKCG | LDLNQHELSA | IQEVESPAIG | RTSILGKPGI | YEDRDPLRVS | ISREQSFFGS | PLAHDPFSCL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| QLVGQENVCG | DDYDEAVKLK | ESVVENHAVL | SYAVEEEHAY | LGPTVKPDDK | AKTLSYEPLS | SATVSTGSLL | SYENTDLSLT |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| DPESFSEHMD | DSKQESTTSK | EEETNIISSI | VPSTQDIYQR | QNSSDVHKSL | LPAVDETTCG | HTHFQQMIDK | YINEANLIPE |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| KTDLQELEHI | FPNLHHQLFK | PLEPHPDFDL | SSSSSGISPD | NRDFYQRSDS | SSESHCATGL | SKSTVYFTAL | RRTSMHSSLN |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| TSPNQQPDTN | LAHVGAHSFA | TENIIGGSEQ | CFEQLQPEYS | SQEESQHADL | PSIFSIEARD | SSQGMKNQNY | PSEEHTEILQ |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| NKKKIVHFQL | SIGNLSSVYS | SSDEANVFDQ | LNVQHSTPCG | SNSSECSTKH | QLESRKESMG | FEELSKRGVV | TMLQSQGLIE |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| DNKNETCRVL | DINPQVEETD | SRLCVRTVEM | GTSIQAPYSL | TTQNEKYFEN | SAETDIPKIT | KKLSQLGESE | LFASSGSFSL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 97 | 1 | 608.3115 | -17.30 | 2 | 30.2 | 16.4 | 0 | 749-758 | R.EAQEVLYVHK.Q | |

# Detailed Protein Report

## Protein 455: PREDICTED: nucleobindin-2 isoform X9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578820568 | **Score:** | 29.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| | | **Sequence Coverage [%]:** | 3.8 |
| | | **No. of unique Peptides:** | 2 |

### Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.46 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.06 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MRWRTILLQY CFLLITCLLT ALEAVPIDID KTKVQNIHPV ESAKIEPPDT GLYYDEYLKQ VIDVLETDKH FREKLQKADI
        90        100        110        120        130        140        150        160
EEIKSGRLSK ELDLVSHHVR TKLDELKRQE VGRLRMLIKA KLDSLQDIGM DHQALLKQFD HLNHLNPDKF ESTDLDMLIK
       170        180        190        200        210        220        230        240
AATSDLEHYD KTRHEEFKKY EMMKEHERRE YLKTLNEEKR KEEESKFEEM KKKHENHPKV NHPGSKDQLK EVWEETDGLD
       250        260        270        280        290        300        310        320
PNDFDPKTFF KLHDVNSDGF LDEQELEALF TKELEKVYDP KNEEDDMVEM EEERLRMREH VMNEVDTNKD RLVTLEEFLK
       330        340
ATEKKEFLEP DSWESPSI
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 585 | 1 | 537.7782 | -18.47 | 2 | 37.3 | 11.4 | 2 | 172-179 | K.TRHEEFKK.Y | | QU:MU 1.46<br>WUP:QUP 2.06 |
| 1116 | 1 | 701.1743 | -178.79 | 1 | 44.1 | 17.9 | 0 | 180-184 | K.YEMMK.E | | |

# Detailed Protein Report

**Protein 456:** **PREDICTED: peptide chain release factor 1-like, mitochondrial isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530383831 | **Score:** | 29.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 8.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRSRVLWGAA | RWLWPRRAVG | PARRPLSSGS | PPLEELFTRG | GPLRTFLERQ | AGSEAHLKVR | RPELLAVIKL | LNEKERELRE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TEHLLHDENE | DLRKLAENEI | TLCQKEITQL | KHQIILLLVP | SEETDENDLI | LEVTAGVGGG | LRHASASIGG | SEAYRHMKFE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GGVHRVQRVP | KTEKQGRVHT | STMTVAILPQ | PTEINLVINP | KDLRIDTKRA | SGAGGQHVNT | TDSAVRIVHL | PTGVVSECQQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ERSQLKNKEL | AMTKLRAKLY | SMHLEEEINK | RQNARKIQIG | SKGRSEKIRT | YNFPQNRVTD | HRINKTLHDL | ETFMQGDYLL |
| 330 | 340 | 350 | | | | | |
| DELVQSLKEY | ADYESLVEII | SQKV | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1562 | 1 | 1051.5516 | -26.89 | 2 | 49.2 | 16.6 | 2 | 94-111 | R.KLAENEITLCQKEITQLK.H | |

# Detailed Protein Report

**Protein 457:** **PREDICTED: phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit beta isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530364909 | **Score:** | 29.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 181.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSSTQGNGEH | WKSLESVGIS | RKELAMAEAL | QMEYDALSRL | RHDKEENRAK | QNADPSLISW | DEPGVDFYSK | PAGRRTDLKL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LRGLSGSDPT | LNYNSLSPQE | GPPNHSTSQG | PQPGSDPWPK | GSLSGDYLYI | FDGSDGGVSS | SPGPGDIEGS | CKKLSPPPLP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PRASIWDTPP | LPPRKGSPSS | SKISQPSDIN | TFSLVEQLPG | KLLEHRILEE | EEVLGGGGQG | RLLGSVDYDG | INDAITRLNL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KSTYDAEMLR | DATRGWKEGR | GPLDFSKDTS | GKPVARSKTM | PPQVPPRTYA | SRYGNRKNAT | PGKNRRISAA | PVGSRPHTVA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NGHELFEVSE | ERDEEVAAFC | HMLDILRSGS | DIQDYFLTGY | VWSAVTPSPE | HLGDEVNLKV | TVLCDRLQEA | LTFTCNCSST |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VDLLIYQTLC | YTHDDLRNVD | VGDFVLKPCG | LEEFLQNKHA | LGSHEYIQYC | RKFDIDIRLQ | LMEQKVVRSD | LARTVNDDQS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PSTLNYLVHL | QERPVKQTIS | RQALSLLFDT | YHNEVDAFLL | ADGDFPLKAD | RVVQSVKAIC | NALAAVETPE | ITSALNQLPP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| CPSRMQPKIQ | KDPSVLAVRE | NREKVVEALT | AAILDLVELY | CNTFNADFQT | AVPGSRKHDL | VQEACHFARS | LAFTVYATHR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IPIIWATSYE | DFYLSCSLSH | GGKELCSPLQ | TRRAHFSKYL | FHLIVWDQQI | CFPVQVNRLP | RETLLCATLY | ALPIPPPGSS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SEANKQRRVP | EALGWVTTPL | FNFRQVLTCG | RKLLGLWPAT | QENPSARWSA | PNFHQPDSVI | LQIDFPTSAF | DIKFTSPPGD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KFSPRYEFGS | LREEDQRKLK | DIMQKESLYW | LTDADKKRLW | EKRYYCHSEQ | WTHMNHQDAL | GLLHATFPDQ | EVRRMAVQWI |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GSLSDAELLD | YLPQLVQALK | YECYLDSPLV | RFLLKRAVSD | LRVTHYFFWL | LKDGLKDSQF | SIRYQYLLAA | LLCCCGKGLR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| EEFNRQCWLV | NALAKLAQQV | REAAPSARQG | ILRTGLEEVK | QFFALNGSCR | LPLSPSLLVK | GIVPRDCSYF | NSNAVPLKLS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| FQNVDPLGEN | IRVIFKCGDD | LRQDMLTLQM | IRIMSKIWVQ | EGLDMRMVIF | RCFSTGRGRG | MVEMIPNAET | LRKIQVEHGV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TGSFKDRPLA | DWLQKHNPGE | DEYEKAVENF | IYSCAGCCVA | TYVLGICDRH | NDNIMLKTTG | HMFHIDFGRF | LGHAQMFGNI |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KRDRAPFVFT | SDMAYVINGG | DKPSSRFHDF | VDLCCQAYNL | IRKHTHLFLN | LLGLMLSCGI | PELSDLEDLK | YVYDALRPQD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TEANATTYFT | RLIESSLGSV | ATKLNFFIHN | LAQMKFTGSD | DRLTLSFASR | THTLKSSGRI | SDVFLCRHEK | IFHPNKGYIY |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VVKVMRENTH | EATYIQRTFE | EFQELHNKLR | LLFPSSHLPS | FPSRFVIGRS | RGEAVAERRR | EELNGYIWHL | IHAPPEVAEC |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DLVYTFFHPL | PRDEKAMGTS | PAPKSSDGTW | ARPVGKVGGE | VKLSISYKNN | KLFIMVMHIR | GLQLLQDGND | PDPYVKIYLL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PDPQKTTKRK | TKVARKTCNP | TYNEMLVYDG | IPKGDLQQRE | LQLSVLSEQG | FWENVLLGEV | NIRLRELDLA | QEKTGWFALG |
| 1610 | | | | | | | |
| SRSHGTL | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2067 | 1 | 714.5942 | -120.32 | 3 | 56.2 | 13.5 | 1 | 1227-1243 | R.FHDFVDLCCQAYNLIRK.H | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 458: protein FAM107A isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|6005924 | **Score:** | 29.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 17.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| | | **Sequence Coverage [%]:** | 18.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530371819 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein FAM107A isoform X3 [Homo sapiens] |
| gi\|115583665 | refseq_human (refseq_human_20140103.fasta) | protein FAM107A isoform a [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MYSEIQRERA DIGGLMARPE YREWNPELIK PKKLLNPVKA SRSHQELHRE LLMNHRRGLG VDSKPELQRV LEHRRRNQLI
        90        100        110        120        130        140        150
KKKKEELEAK RLQCPFEQEL LRRQQRLNQL EKPPEKEEDH APEFIKVREN LRRIATLTSE EREL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2090 | 1 | 696.9638 | -136.58 | 3 | 54.5 | 18.1 | 2 | 57-74 | R.RGLGVDSKPELQRVLEHR.R | |

# Detailed Protein Report

## Protein 459: zinc finger protein 469 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|188536004 | **Score:** | 29.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 409.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.9 |
| | | **Sequence Coverage [%]:** | 0.6 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPGERPRGAP | PPTMTGDLQP | RQVASSPGHP | SQPPLEDNTP | ATRTTKGARE | AGGQAQAMEL | PEAQPRQARD | GELKPPSLRG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QAPSSTPGKR | GSPQTPPGRS | PLQAPSRLAG | RAEGSPPQRY | ILGIASSRTK | PTLDETPENP | QLEAAQLPEV | DTPQGPGTGA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PLRPGLPRTE | AQPAAEELGF | HRCFQEPPSS | FTSTNYTSPS | ATPRPPAPGP | PQSRGTSPLQ | PGSYPEYQAS | GADSWPPAAE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NSFPGANFGV | PPAEPEPIPK | GSRPGGSPRG | VSFQFPFPAL | HGASTKPFPA | DVAGHAFTNG | PLVFAFHQPQ | GAWPEEAVGT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GPAYPLPTQP | APSPLPCYQG | QPGGLNRHSD | LSGALSSPGA | AHSAPRPFSD | SLHKSLTKIL | PERPPSAQDG | LGSTRGPPSS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LPQRHFPGQA | YRASGVDTSP | GPPDTELAAP | GPPPARLPQL | WDPTAAPYPT | PPGGPLAATR | SMFFNGQPSP | GQRLCLPQSA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PLPWPQVLPT | ARPSPHGMEM | LSRLPFPAGG | PEWQGGSQGA | LGTAGKTPGP | REKLPAVRSS | QGGSPALFTY | NGMTDPGAQP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LFFGVAQPQV | SPHGTPSLPP | PRVVGASPSE | SPLPSPATNT | AGSTCSSLSP | MSSSPANPSS | EESQLPGPLG | PSAFFHPPTH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PQETGSPFPS | PEPPHSLPTH | YQPEPAKAFP | FPADGLGAEG | AFQCLEETPF | PHEGPEVGRG | GLQGFPRAPP | PYPTHHFSLS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SASLDQLDVL | LTCRQCDRNY | SSLAAFLAHR | QFCGLLLARA | KDGHQRSPGP | PGLPSPPAAP | RVPADAHAGL | LSHAKTFLLA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GDAQAEGKDD | PLRTGFLPSL | AATPFPLPAS | DLDMEDDAKL | DSLITEALNG | MEYQSDNPEI | DSSFIDVFAD | EEPSGPRGPS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SGHPLKSKAG | VTPESKAPPP | LPAATPDPQT | PRPGDRGCPA | RGRPKTRSLG | LAPTEADAPS | QGRQQRRGKQ | LKLFRKDLDS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GGAAEGSGSG | GGGRASGLRP | RRNDGLGERP | PPRPRRPRTQ | APGSRADPAP | RVPRAAALPE | ETRSSRRRRL | PPRKDPRKRK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ARGGAWGKEL | ILKIVQQKNR | LREYDFASES | EEDEQPPPRG | PGFRGRRGRG | EKRKEVELTQ | GPREDEPQKP | RKAARQEAGG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DGAPANPEEP | GGSRPGPGRS | PQARGPSRSL | ETGAAAREGG | PKCADRPSVA | PKDPLQVPTN | TETSEETRPS | LDFPQEAKEP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ETAEESAPDS | TEFTEALRSP | PAACAGEMGA | SPGLLIPEQP | PPSRHDTGTP | KPSGSLANTA | PHGSSPTPGV | GSLLGGPGGT |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| QAPVSHNSKD | PPARQPGEFL | APVANPSSTA | CPKPSVLSSK | ISSFGCDPAG | FNRDPLGVPV | AKKGPQPYSS | PHSELFLGPK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| DLAGCFLEEL | HPKPSARDAP | PASSSCLCQD | GEDAGSLEPQ | LPRSPPGTAE | TEPGRAASPP | TLESSSLFPD | LPVDRFDPPL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| YGSLSANRDS | GLPFACADPP | QKTVPSDPPY | PSFLLLEEVS | PMLPSHFPDL | SGGKVLSKTC | PPERTVVPGA | APSLPGKGSG |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| CSVALMSHLS | EDELEIQKLV | TELESQLQRS | KDTRGAPREL | AEAESVGRVE | LGTGTEPPSQ | RRTCQATVPH | EDTFSAADLT |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| RVGESTAHRE | GAESAVATVE | AVQGRPGGTW | PCPASFHPGH | AALLPCAQED | LVSGAPFSPR | GANFHFQPVQ | KAGASKTGLC |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| QAEGDSRPPQ | DVCLPEPSKQ | PGPQLDAGSL | AKCSPDQELS | FPKNKEAASS | QESEDSLRLL | PCEQRGGFLP | EPGTADQPHR |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| GAPAPEAFGS | PAVHLAPDLA | FQGDGAPPLD | ATWPFGASPS | HAAQGHSAGR | AGGHLHPTAG | RPGFEGNEFA | PAGASSLTAP |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| RGREAWLVPV | PSPACVSNTH | PSRRSQDPAL | SPPIRQLQLP | GPGVAKSKDG | ILGLQELTPA | AQSPPRVNPS | GLEGGTVEGG |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| KVACGPAQGS | PGGVQVTTLP | AVAGHQLGLE | ADGHWGLLGQ | AEKTQGQGTA | NQLQPENGVS | PGGTDNHASV | NASPKTALTG |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| PTEGAVLLEK | CKGSRAAMSL | QEEAEPTPSP | PSPNRESLAL | ALTAAHSRSG | SEGRTPERAS | SPGLNKPLLA | TGDSPAPSVG |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| DLAACAPSPT | SAAHMPCSLG | PLPREDPLTS | PSRAQGGLGG | QLPASPSCRD | PPGPQQLLAC | SPAWAPLEEA | DGVQATTDTG |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2716 | 2 | 715.3661 | -0.43 | 2 | 62.4 | 12.8 | 2 | 3063-3076 | R.RTEEAAGAGRAQGR.G | |

# Detailed Protein Report

## Protein 460: SCO-spondin precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|134031945 | **Score:** | 29.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 547.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 2 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLLPALLFGM | AWALADGRWC | EWTETIRVEE | EVAPRQEDLV | PCASLDHYSR | LGWRLDLPWS | GRSGLTRSPA | PGLCPIYKPP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ETRPAKWNRT | VRTCCPGWGG | AHCTEALAKA | SPEGHCFAMW | QCQLQAGSAN | ASAGSLEECC | ARPWGQSWWD | GSSQACRSCS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SRHLPGSASS | PALLQPLAGA | VGQLWSQHQR | PSATCASWSG | FHYRTFDGRH | YHFLGRCTYL | LAGAADSTWA | VHLTPGDRCP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QPGHCQRVTM | GPEEVLIQAG | NVSVKGQLVP | EGQSWLLHGL | SLQWLGDWLV | LSGGLGVVVR | LDRTGSISIS | VDHELWGQTQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GLCGLYNGWP | EDDFMEPGGG | LAMLAATFGN | SWRLPGSESG | CLDAVEVAQG | CDPLGLIDAD | VEPGHLRAEA | QDVCHQLLEG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PFGQCHAQVS | PAEYHEACLF | AYCAGAMAGS | GQEGRQQAVC | ATFASYVQAC | ARRHIHIRWR | KPGFCERLCP | GGQLYSDCVS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LCPPSCEAVG | QGEEESCREE | CVSGCECPRG | LFWNGTLCVP | AAHCPCYYCR | QRYVPGDTVR | QLCNPCVCRD | GRWHCAQALC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PAECAVGGDG | HYLTFDGRSY | SFWGGQGCRY | SLVQDYVKGQ | LLILLEHGAC | DAGSCLHAIS | VSLEDTHIQL | RDSGAVLVNG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QDVGLPWIGA | EGLSVRRASS | AFLLLRWPGA | QVLWGLSDPV | AYITLDPRHA | HQVQGLCGTF | TQNQQDDFLT | PAGDVETSIA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AFASKFQVAG | KGRCPSEDSA | LLSPCTTHSQ | RHAFAEAACA | ILHSSVFQEC | HRLVDKEPFY | LRCLAAVCGC | DPGSDCLCPV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LSAYARRCAQ | EGASPPWRNQ | TLCPVMCPGG | QEYRECAPAC | GQHCGKPEDC | GELGSCVAGC | NCPLGLLWDP | EGQCVPPSLC |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PCQLGARRYA | PGSATMKECN | RCICQERGLW | NCTARHCPSQ | AFCPRELVYA | PGACLLTCDS | PSANHSCPAG | STDGCVCPPG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TVLLDERCVP | PDLCPCRHSG | QWYLPNATIQ | EDCNVCVCRG | RQWHCTGQRR | SGRCQASGAP | HYVTFDGLAF | TYPGACEYLL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VREASGLFTV | SAQNLPCGAS | GLTCTKALAV | RLEGTVVHML | RGRAVTVNGV | SVTPPKVYTG | PGLSLRRAGL | FLLLSTHLGL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TLLWDGGTRV | LVQLSPQFRG | RVAGLCGDFD | GDASNDLRSR | QGVLEPTAEL | AAHSWRLSPL | CPEPGDLPHP | CTMNTHRAGW |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ARARCGALLQ | PLFTLCHAEV | PPQQHYEWCL | YDACGCDSGG | DCECLCSAIA | TYADECARHG | HHVRWRSQEL | CSLQCEGGQV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| YEACGPTCPP | TCHEQHPEPG | WHCQVVACVE | GCFCPEGTLL | HGGACLEPAS | CPCEWGRNSF | PPGSVLQKDC | GNCTCQEGQW |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| HCGGDGGHCE | ELVPACAEGE | ALCQENGHCV | PHGWLCDNQD | DCGDGSDEEG | CAAPGCGEGQ | MTCSSGHCLP | LALLCDRQDD |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| CGDGTDEPSY | PCPQGLLACA | DGRCLPPALL | CDGHPDCLDA | ADEESCLGQV | TCVPGEVSCV | DGTCLGAIQL | CDGVWDCPDG |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ADEGPGHCPL | PSLPTPPAST | LPGPSPGSLD | TASSPLASAS | PAPPCGPFEF | RCGSGECTPR | GWRCDQEEDC | ADGSDERGCG |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| GPCAPHHAPC | ARGPHCVSPE | QLCDGVRQCP | DGSDEGPDAC | GGLPALGGPN | RTGLPCPEYT | CPNGTCIGFQ | LVCDGQPDCG |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| RPGQVGPSPE | EQGCGAWGPW | SPWGPCSRTC | GPWGQGRSRR | CSPLGLLVLQ | NCPGPEHQSQ | ACFTAACPVD | GEWSTWSPWS |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| VCSEPCRGTM | TRQRQCHSPQ | NGGRTCAALP | GGLHSTRQTK | PCPQDGCPNA | TCSGELMFQP | CAPCPLTCDD | ISGQVTCPPD |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| WPCGSPGCWC | PEGQVLGSEG | WCVWPRQCPC | LVDGARYWPG | QRIKADCQLC | ICQDGRPRRC | RLNPDCAVDC | GWSSWSPWAK |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| CLGPCGSQSI | QWSFRSSNNP | RPSGRGRQCR | GIHRKARRCQ | TEPCEGCEHQ | GQVHRVGERW | HGGPCRVCQC | LHNLTAHCSP |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| YCPLGSCPQG | WVLVEGTGES | CCHCALPGEN | QTVQPMATPA | AAPAPSPQIR | FPLATYILPP | SGDPCYSPLG | LAGLAEGSLH |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| ASSQQLEHPT | QAALLGAPTQ | GPSPQGWHAG | GDAYAKWHTR | PHYLQLDLLQ | PRNLTGILVP | ETGSSNAYAS | SFSLQFSSNG |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1387 | 1 | 927.1161 | 66.38 | 3 | 47.5 | 19.2 | 0 | 2250-2277 | R.GGPCDGVLDCEDGSDEEGCVLLPEGTGR.F | |
| 1393 | 1 | 927.1317 | 74.51 | 3 | 47.0 | 10.1 | 1 | 4052-4077 | R.LCNPMPCEAGCPAGMEVVTCANRCPR.R | Carbamidomethyl: 2 |

# Detailed Protein Report

## Protein 461: leukocyte receptor cluster member 9 [Homo sapiens]

**Accession:** gi|206725452

**Database:** refseq_human(refseq_human_20140103.fasta)

**Database Date:** 2015-11-30

**Score:** 29.2

**MW [kDa]:** 53.1

**pI:** 9.5

**Sequence Coverage [%]:** 8.2

**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGSRPPCGAT | SSARRACQFP | APMAAAREPE | LPQEAPATEP | APPPACRFFL | EGRCRFGARC | RQPHPGAPAP | PGREAQPEAG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AKKPPLRTAA | DVIQRIRWDP | RLDPADFSVG | YVDRFLGVRE | EPFSAFCWDQ | PLAALGPGVL | AVPQHRVRFF | RFHGRLVWDR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ASRTDLVFGS | GSAAGRGPTI | LDAPNTEGAH | GAEGAEWTLA | GTGQEAQAAP | KRGSTRPLCT | GHQEPGVEEP | GELEAAQERA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LGTAADLGTL | APRGRLAGVT | EEALKPTAAT | RTTLLGGKEA | QALGVPGGSA | ETTEAEWGPA | AWPEDKRARL | SVAAPCQPRP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| THFVALMVTE | PGLQAEVTKA | QEYLVHVAPH | CANFLVPSQN | LHLTLALLRL | AGAGEEAAAI | GALRRALLAP | GLNAPPRLSF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RKLVLLGPHV | LCAPPSPTLE | SMAQVLSQRL | EAEGLSTLQS | PGQLHPHLTV | AKVPHGSQVH | LPKLEFTLSQ | EVGCQPLQTL |
| 490 | 500 | 510 | | | | | |
| WLCRIGRTGG | PFQPLAEIRL | E | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1675 | 1 | 1011.7711 | -47.99 | 3 | 51.2 | 10.4 | 1 | 212-239 | K.RGSTRPLCTGHQEPGVEEPGELEAAQER.A | |

# Detailed Protein Report

## Protein 462: rho GTPase-activating protein 42 [Homo sapiens]

**Accession:** gi|221307575
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl, Oxidation

**Score:** 29.2
**MW [kDa]:** 98.5
**pI:** 8.9
**Sequence Coverage [%]:** 2.9
**No. of unique Peptides:** 2

## Quantitation

***QU:MU*** **Median:** 1.65 **CV:** 0.00 % **No. of Peptides:** 1
***WUP:QUP*** **Median:** 0.71 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGLPTLEFSD | SYLDSPDFRE | RLQCHEIELE | RTNKFIKELI | KDGSLLIGAL | RNLSMAVQKF | SQSLQDFQFE | CIGDAETDDE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ISIAQSLKEF | ARLLIAVEEE | RRRLIQNAND | VLIAPLEKFR | KEQIGAAKDG | KKKFDKESEK | YYSILEKHLN | LSAKKKESHL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QEADTQIDRE | HQNFYEASLE | YVFKIQEVQE | KKKFEFVEPL | LSFLQGLFTF | YHEGYELAQE | FAPYKQQLQF | NLQNTRNNFE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| STRQEVERLM | QRMKSANQDY | RPPSQWTMEG | YLYVQEKRPL | GFTWIKHYCT | YDKGSKTFTM | SVSEMKSSGK | MNGLVTSSPE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MFKLKSCIRR | KTDSIDKRFC | FDIEVVERHG | IITLQAFSEA | NRKLWLEAMD | GKEPIYTLPA | IISKKEEMYL | NEAGFNFVRK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CIQAVETRGI | TILGLYRIGG | VNSKVQKLMN | TTFSPKSPPD | IDIDIELWDN | KTITSGLKNY | LRCLAEPLMT | YKLHKDFIIA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VKSDDQNYRV | EAVHALVHKL | PEKNREMLDI | LIKHLVKVSL | HSQQNLMTVS | NLGVIFGPTL | MRAQEETVAA | MMNIKFQNIV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VEILIEHYEK | IFHTAPDPSI | PLPQPQSRSG | SRRTRAICLS | TGSRKPRGRY | TPCLAEPDSD | SYSSSPDSTP | MGSIESLSSH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SSEQNSTTKS | ASCQPREKSG | GIPWIATPSS | SNGQKSLGLW | TTSPESSSRE | DATKTDAESD | CQSVASVTSP | GDVSPPIDLV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KKEPYGLSGL | KRASASSLRS | ISAAEGNKSY | SGSIQSLTSV | GSKETPKASP | NPDLPPKMCR | RLRLDTASSN | GYQRPGSVVA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AKAQLFENVG | SPKPVSSGRQ | AKAMYSCKAE | HSHELSFPQG | AIFSNVYPSV | EPGWLKATYE | GKTGLVPENY | VVFL |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 150 | 1 | 849.3532 | -94.77 | 2 | 31.6 | 11.8 | 1 | 311-325 | K.MNGLVTSSPEMFKLK.S | Oxidation: 11 | WUP:QUP 0.71<br>QU:MU 1.65 |
| 1883 | 2 | 621.2961 | -4.47 | 2 | 53.9 | 17.5 | 0 | 463-472 | R.CLAEPLMTYK.L | Carbamidomethyl: 1;<br>Oxidation: 7 | |

# Detailed Protein Report

## Protein 463: unconventional myosin-Id [Homo sapiens]

**Accession:** gi|51100974
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 29.2
**MW [kDa]:** 116.1
**pI:** 10.0
**Sequence Coverage [%]:** 1.8
**No. of unique Peptides:** 1

## Quantitation

***WUP:QUP*** **Median:** 0.37 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAEQESLEFG | KADFVLMDTV | SMPEFMANLR | LRFEKGRIYT | FIGEVVVSVN | PYKLLNIYGR | DTIEQYKGRE | LYERPPHLFA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IADAAYKAMK | RRSKDTCIVI | SGESGAGKTE | ASKYIMQYIA | AITNPSQRAE | VERVKNMLLK | SNCVLEAFGN | AKTNRNDNSS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RFGKYMDINF | DFKGDPIGGH | INNYLLEKSR | VIVQQPGERS | FHSFYQLLQG | GSEQMLRSLH | LQKSLSSYNY | IHVGAQLKSS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| INDAAEFRVV | ADAMKVIGFK | PEEIQTVYKI | LAAILHLGNL | KFVVDGDTPL | IENGKVVSII | AELLSTKTDM | VEKALLYRTV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ATGRDIIDKQ | HTEQEASYGR | DAFAKAIYER | LFCWIVTRIN | DIIEVKNYDT | TIHGKNTVIG | VLDIYGFEIF | DNNSFEQFCI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NYCNEKLQQL | FIQLVLKQEQ | EEYQREGIPW | KHIDYFNNQI | IVDLVEQQHK | GIIAILDDAC | MNVGKVTDEM | FLEALNSKLG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KHAHFSSRKL | CASDKILEFD | RDFRIRHYAG | DVVYSVIGFI | DKNKDTLFQD | FKRLMYNSSN | PVLKNMWPEG | KLSITEVTKR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PLTAATLFKN | SMIALVDNLA | SKEPYYVRCI | KPNDKKSPQI | FDDERCRHQV | EYLGLLENVR | VRRAGFAFRQ | TYEKFLHRYK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| MISEFTWPNH | DLPSDKEAVK | KLIERCGFQD | DVAYGKTKIF | IRTPRTLFTL | EELRAQMLIR | IVLFLQKVWR | GTLARMRYKR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TKAALTIIRY | YRRYKVKSYI | HEVARRFHGV | KTMRDYGKHV | KWPSPPKVLR | RFEEALQTIF | NRWRASQLIK | SIPASDLPQV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RAKVAAVEML | KGQRADLGLQ | RAWEGNYLAS | KPDTPQTSGT | FVPVANELKR | KDKYMNVLFS | CHVRKVNRFS | KVEDRAIFVT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DRHLYKMDPT | KQYKVMKTIP | LYNLTGLSVS | NGKDQLVVFH | TKDNKDLIVC | LFSKQPTHES | RIGELVGVLV | NHFKSEKRHL |
| 970 | 980 | 990 | 1000 | 1010 | | | |
| QVNVTNPVQC | SLHGKKCTVS | VETRLNQPQP | DFTKNRSGFI | LSVPGN | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2982 | 3 | 729.3741 | -5.85 | 2 | 66.0 | 18.2 | 1 | 985-996 | R.LNQPQPDFTKNR.S | | WUP:QUP 0.37 |

# Detailed Protein Report

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## Protein 464: plakophilin-1 isoform 1a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|53729344 | **Score:** | 29.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 80.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNHSPLKTAL | AYECFQDQDN | STLALPSDQK | MKTGTSGRQR | VQEQVMMTVK | RQKSKSSQSS | TLSHSNRGSM | YDGLADNYNY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GTTSRSSYYS | KFQAGNGSWG | YPIYNGTLKR | EPDNRRFSSY | SQMENWSRHY | PRGSCNTTGA | GSDICFMQKI | KASRSEPDLY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CDPRGTLRKG | TLGSKGQKTT | QNRYSFYSTC | SGQKAIKKCP | VRPPSCASKQ | DPVYIPPISC | NKDLSFGHSR | ASSKICSEDI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ECSGLTIPKA | VQYLSSQDEK | YQAIGAYYIQ | HTCFQDESAK | QQVYQLGGIC | KLVDLLRSPN | QNVQQAAAGA | LRNLVFRSTT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NKLETRRQNG | IREAVSLLRR | TGNAEIQKQL | TGLLWNLSST | DELKEELIAD | ALPVLADRVI | IPFSGWCDGN | SNMSREVVDP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EVFFNATGCL | RNLSSADAGR | QTMRNYSGLI | DSLMAYVQNC | VAASRCDDKS | VENCMCVLHN | LSYRLDAEVP | TRYRQLEYNA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RNAYTEKSST | GCFSNKSDKM | MNNNYDCPLP | EEETNPKGSG | WLYHSDAIRT | YLNLMGKSKK | DATLEACAGA | LQNLTASKGL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MSSGMSQLIG | LKEKGLPQIA | RLLQSGNSDV | VRSGASLLSN | MSRHPLLHRV | MGNQVFPEVT | RLLTSHTGNT | SNSEDILSSA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CYTVRNLMAS | QPQLAKQYFS | SSMLNNIINL | CRSSASPKAA | EAARLLLSDM | WSSKELQGVL | RQQGFDRNML | GTLAGANSLR |
| 730 | | | | | | | |
| NFTSRF | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1592 | 1 | 783.4244 | 89.54 | 2 | 50.1 | 14.5 | 1 | 152-164 | K.ASRSEPDLYCDPR.G | Carbamidomethyl: 10 |

# Detailed Protein Report

## Protein 465: interferon regulatory factor 2-binding protein 2 isoform B [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|116734706 | **Score:** | 29.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.4 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAAVAVAAA | SRRQSCYLCD | LPRMPWAMIW | DFTEPVCRGC | VNYEGADRVE | FVIETARQLK | RAHGCFPEGR | SPPGAAASAA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AKPPPLSAKD | ILLQQQQQLG | HGGPEAAPRA | PQALERYPLA | AAAERPPRLG | SDFGSSRPAA | SLAQPPTPQP | PPVNGILVPN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GFSKLEEPPE | LNRQSPNPRR | GHAVPPTLVP | LMNGSATPLP | TALGLGGRAA | ASLAAVSGTA | AASLGSAQPT | DLGAHKRPAS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VSSSAAVEHE | QREAAAKEKQ | PPPPAHRGPA | DSLSTAAGAA | ELSAEGAGKS | RGSGEQDWVN | RPKTVRDTLL | ALHQHGHSGP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FESKFKKEPA | LTAVARTARK | RKPSPEPEGE | VGPPKINGEA | QPWLSTSTEG | LKIPMTPTSS | FVSPPPPTAS | PHSNRTTPPE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AAQNGQSPMA | ALILVADNAG | GSHASKDANQ | VHSTTRRNSN | SPPSPSSMNQ | RRLGPREVGG | QGAGNTGGLE | PVHPASLPDS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SLATSAPLCC | TLCHERLEDT | HFVQCPSVPS | HKFCFPCSRQ | SIKQQGASGE | VYCPSGEKCP | LVGSNVPWAF | MQGEIATILA |
| 570 | 580 | | | | | | |
| GDVKVKKERD | S | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1850 | 1 | 724.2703 | -144.49 | 2 | 53.0 | 18.8 | 0 | 342-355 | R.KPSPEPEGEVGPPK.I | |
| 2516 | 1 | 715.2357 | -144.98 | 2 | 61.4 | 10.3 | 1 | 513-523 | K.FCFPCSRQSIK.Q | Carbamidomethyl: 2, 5 |

# Detailed Protein Report

## Protein 466: PREDICTED: YLP motif-containing protein 1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530404193 | **Score:** | 29.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 231.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 2 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.46 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.74 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MYPNWGRYGG | SSHYPPPPVP | PPPPVALPEA | SPGPGYSSST | TPAAPSSSGF | MSFREQHLAQ | LQQLQQMHQK | QMQCVLQPHH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LPPPPLPPPP | VMPGGGYGDW | QPPPPPMPPP | PGPALSYQKQ | QQYKHQMLHH | QRDGPPGLVP | MELESPPESP | PVPPGSYMPP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SQSYMPPPQP | PPSYYPPTSS | QPYLPPAQPS | PSQSPPSQSY | LAPTPSYSSS | SSSSQSYLSH | SQSYLPSSQA | SPSRPSQGHS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KSQLLAPPPP | SAPPGNKTTV | QQEPLESGAK | NKSTEQQQAA | PEPDPSTMTP | QEQQQYWYRQ | HLLSLQQRTK | VHLPGHKKGP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VVAKDTPEPV | KEEVTVPATS | QVPESPSSEE | PPLPPPNEEV | PPPLPPEEPQ | SEDPEEDARL | KQLQAAAAHW | QQHQQHRVGF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QYQGIMQKHT | QLQQILQQYQ | QIIQPPPHIQ | TMSVDMQLRH | YEMQQQQFQH | LYQEWEREFQ | LWEEQLHSYP | HKDQLQEYEK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QWKTWQGHMK | ATQSYLQEKV | NSFQNMKNQY | MGNMSMPPPF | VPYSQMPPPL | PTMPPPVLPP | SLPPPVMPPA | LPATVPPPGM |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PPPVMPPSLP | TSVPPPGMPP | SLSSAGPPPV | LPPPSLSSAG | PPPVLPPPSL | SSTAPPPVMP | LPPLSSATPP | PGIPPPGVPQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GIPPQLTAAP | VPPASSSQSS | QVPEKPRPAL | LPTPVSFGSA | PPTTYHPPLQ | SAGPSEQVNS | KAPLSKSALP | YSSFSSDQGL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GESSAAPSQP | ITAVKDMPVR | SGGLLPDPPR | SSYLESPRGP | RFDGPRRFED | LGSRCEGPRP | KGPRFEGNRP | DGPRPRYEGH |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PAEGTKSKWG | MIPRGPASQF | YITPSTSLSP | RQSGPQWKGP | KPAFGQQHQQ | QPKSQAEPLS | GNKEPLADTS | SNQQKNFKMQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SAAFSIAADV | KDVKAAQSNE | NLSDSQQEPP | KSEVSEGPVE | PSNWDQNVQS | METQIDKAQA | VTQPVPLANK | PVPAQSTFPS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KTGGMEGGTA | VATSSLTADN | DFKPVGIGLP | HSENNQDKGL | PRPDNRDNRL | EGNRGNSSSY | RGPGQSRMED | TRDKGLVNRG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RGQAISRGPG | LVKQEDFRDK | MMGRREDSRE | KMNRGEGSRD | RGLVRPGSSR | EKVPGGLQGS | QDRGAAGSRE | RGPPRRAGSQ |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ERGPLRRAGS | RERIPPRRAG | SRERGPPRGP | GSRERGLGRS | DFGRDRGPFR | PEPGDGGEKM | YPYHRDEPPR | APWNHGEERG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| HEEFPLDGRN | APMERERLDD | WDRERYWREC | ERDYQDDTLE | LYNREDRFSA | PPSRSHDGDR | RGPWWDDWER | DQDMDEDYNR |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| EMERDMDRDV | DRISRPMDMY | DRSLDNEWDR | DYGRPLDEQE | SQFRERDIPS | LPPLPPLPPL | PPLDRYRDDR | WREERNREHG |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| YDRDFRDRGE | LRIREYPERG | DTWREKRDYV | PDRMDWERER | LSDRWYPSDV | DRHSPMAEHM | PSSHHSSEMM | GSDASLDSDQ |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GLGGVMVLSQ | RQHEIILKAA | QELKMLREQK | EQLQKMKDFG | SEPQMADHLP | PQESRLQNTS | SRPGMYPPPG | SYRPPPPMGK |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PPGSIVRPSA | PPARSSVPVT | RPPVPIPPPP | PPPPLPPPPP | VIKPQTSAVE | QERWDEDSFY | GLWDTNDEQG | LNSEFKSETA |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| AIPSAPVLPP | PPVHSSIPPP | GPVPMGMPPM | SKPPPVQQTV | DYGHGRDIST | NKVEQIPYGE | RITLRPDPLP | ERSTFETEHA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| GQRDRYDRER | DREPYFDRQS | NVIADHRDFK | RDRETHRDRD | RDRGVIDYDR | DRFDRERRPR | DDRAQSYRDK | KDHSSSRRGG |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| FDRPSYDRKS | DRPVYEGPSM | FGGERRTYPE | ERMPLPAPSL | SHQPPPAPRV | EKKPESKNVD | DILKPPGRES | RPERIVVIMR |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| GLPGSGKTHV | AKLIRDKEVE | FGGPAPRVLS | LDDYFITEVE | KEEKDPDSGK | KVKKKVMEYE | YEAEMEETYR | TSMFKTFKKT |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LDDGFFPFII | LDAINDRVRH | FDQFWSAAKT | KGFEVYLAEM | SADNQTCGKR | NIHGRKLKEI | NKMADHWETA | PRHMMRLDIR |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | |
| SLLQDAAIEE | VEMEDFDANI | EEQKEEKKDA | EEEESELGYI | PKSKWEMDTS | EAKLVCHVEE | V | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 44 | 1 | 767.2360 | -155.99 | 2 | 30.4 | 11.8 | 1 | 1673-1685 | R.STFETEHAGQRDR.Y | | |
| 2835 | 5 | 746.4789 | 26.21 | 1 | 64.1 | 17.2 | 0 | 1835-1840 | R.IVVIMR.G | Oxidation: 5 | WUP:QUP 0.74<br>QU:MU 1.46 |

# Detailed Protein Report

## Protein 467: multidrug resistance protein 3 isoform C [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|9961252 | **Score:** | 29.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 135.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDLEAAKNGT | AWRPTSAEGD | FELGISSKQK | RKKTKTVKMI | GVLTLFRYSD | WQDKLFMSLG | TIMAIAHGSG | LPLMMIVFGE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MTDKFVDTAG | NFSFPVNFSL | SLLNPGKILE | EEMTRYAYYY | SGLGAGVLVA | AYIQVSFWTL | AAGRQIRKIR | QKFFHAILRQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EIGWFDINDT | TELNTRLTDD | ISKISEGIGD | KVGMFFQAVA | TFFAGFIVGF | IRGWKLTLVI | MAISPILGLS | AAVWAKILSA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FSDKELAAYA | KAGAVAEEAL | GAIRTVIAFG | GQNKELERYQ | KHLENAKEIG | IKKAISANIS | MGIAFLLIYA | SYALAFWYGS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TLVISKEYTI | GNAMTVFFSI | LIGAFSVGQA | APCIDAFANA | RGAAYVIFDI | IDNNPKIDSF | SERGHKPDSI | KGNLEFNDVH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FSYPSRANVK | ILKGLNLKVQ | SGQTVALVGS | SGCGKSTTVQ | LIQRLYDPDE | GTINIDGQDI | RNFNVNYLRE | IIGVVSQEPV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LFSTTIAENI | CYGRGNVTMD | EIKKAVKEAN | AYEFIMKLPQ | KFDTLVGERG | AQLSGGQKQR | IAIARALVRN | PKILLLDEAT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SALDTESEAE | VQAALDKARE | GRTTIVIAHR | LSTVRNADVI | AGFEDGVIVE | QGSHSELMKK | EGVYFKLVNM | QTSGSQIQSE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EFELNDEKAA | TRMAPNGWKS | RLFRHSTQKN | LKNSQMCQKS | LDVETDGLEA | NVPPVSFLKV | LKLNKTEWPY | FVVGTVCAIA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NGGLQPAFSV | IFSEIIAIFG | PGDDAVKQQK | CNIFSLIFLF | LGIISFFTFF | LQGFTFGKAG | EILTRRLRSM | AFKAMLRQDM |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SWFDDHKNST | GALSTRLATD | AAQVQGATGT | RLALIAQNIA | NLGTGIIISF | IYGWQLTLLL | LAVVPIIAVS | GIVEMKLLAG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| NAKRDKKELE | AAGKIATEAI | ENIRTVVSLT | QERKFESMYV | EKLYGPYRVF | SAIVFGAVAL | GHASSFAPDY | AKAKLSAAHL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FMLFERQPLI | DSYSEEGLKP | DKFEGNITFN | EVVFNYPTRA | NVPVLQGLSL | EVKKGQTLAL | VGSSGCGKST | VVQLLERFYD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PLAGTVLLDG | QEAKKLNVQW | LRAQLGIVSQ | EPILFDCSIA | ENIAYGDNSR | VVSQDEIVSA | AKAANIHPFI | ETLPHKYETR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| VGDKGTQLSG | GQKQRIAIAR | ALIRQPQILL | LDEATSALDT | ESEKVVQEAL | DKAREGRTCI | VIAHRLSTIQ | NADLIVVFQN |
| 1210 | 1220 | 1230 | 1240 | | | | |
| GRVKEHGTHQ | QLLAQKGIYF | SMVSVQAGTQ | NL | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 408 | 1 | 655.8392 | -137.81 | 2 | 35.1 | 15.6 | 2 | 407-418 | R.ANVKILKGLNLK.V | |
| 439 | 1 | 565.3076 | 0.55 | 2 | 35.1 | 13.4 | 1 | 530-540 | R.GAQLSGGQKQR.I | |

# Detailed Protein Report

## Protein 468: PREDICTED: replication initiator 1 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578814165 | **Score:** | 29.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578814167 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: replication initiator 1 isoform X6 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGIGVSLLLQ | FSLTPGGYRS | VGRSRRCSRG | SIPRNIPKRS | WKKPHPQLCS | LQEEEPMLER | RCRGPLAMGL | AQPRLLSGPS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QESPQTLGKE | SRGLRQQGTS | VAQSGAQAPG | RAHRCAHCRR | HFPGWVALWL | HTRRCQARLP | LPCPECGRRF | RHAPFLALHR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QVHAAATPDL | GFACHLCGQS | FRGWVALVLH | LRAHSAAKRP | IACPKCERRF | WRRKQLRAHL | RRCHPPAPEA | RPFICGNCGR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SFAQWDQLVA | HKRVHVAEAL | EEAAAKALGP | RPRGRPAVTA | PRPGGDAVDR | PFQCACCGKR | FRHKPNLIAH | RRVHTGERPH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QCPECGKRFT | NKPYLTSHRR | IHTGEKPYPC | KECGRRFRHK | PNLLSHSKIH | KRSEGSAQAA | PGPGSPQLPA | GPQESAAEPT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PAVPLKPAQE | PPPGAPPEHP | QDPIEAPPSL | YSCDDCGRSF | RLERFLRAHQ | RQHTGERPFT | CAECGKNFGK | KTHLVAHSRV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HSGERPFACE | ECGRRFSQGS | HLAAHRRDHA | PDRPFVCPDC | GKAFRHKPYL | AAHRRIHTGE | KPYVCPDCGK | AFSQKSNLVS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| HRRIHTGERP | YACPDCDRSF | SQKSNLITHR | KSHIRDGAFC | CAICGQTFDD | EERLLAHQKK | HDV | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1852 | 1 | 897.8615 | -114.49 | 2 | 53.0 | 11.7 | 2 | 193-208 | R.AHSAAKRPIACPKCER.R | Carbamidomethyl: 11 |

# Detailed Protein Report

## Protein 469: ectonucleoside triphosphate diphosphohydrolase 4 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|193083168 | **Score:** | 29.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGRIGISCLF | PASWHFSISP | VGCPRILNTN | LRQIMVISVL | AAAVSLLYFS | VVIIRNKYGR | LTRDKKFQRY | LARVTDIEAT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DTNNPNVNYG | IVVDCGSSGS | RVFVYCWPRH | NGNPHDLLDI | RQMRDKNRKP | VVMKIKPGIS | EFATSPEKVS | DYISPLLNFA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AEHVPRAKHK | ETPLYILCTA | GMRILPESQQ | KAILEDLLTD | IPVHFDFLFS | DSHAEVISGK | QEGVYAWIGI | NFVLGRFEHI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EDDDEAVVEV | NIPGSESSEA | IVRKRTAGIL | DMGGVSTQIA | YEVPKTEEVA | KNLLAEFNLG | CDVHQTEHVY | RVYVATFLGF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GGNAARQRYE | DRIFANTIQK | NRLLGKQTGL | TPDMPYLDPC | LPLDIKDEIQ | QNGQTIYLRG | TGDFDLCRET | IQPFMNKTNE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TQTSLNGVYQ | PPIHFQNSEF | YGFSEFYYCT | EDVLRMGGDY | NAAKFTKAAK | DYCATKWSIL | RERFDRGLYA | SHADLHRLKY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QCFKSAWMFE | VFHRGFSFPV | NYKSLKTALQ | VYDKEVQWTL | GAILYRTRFL | PLRDIQQEAF | RASHTHWRGV | SFVYNHYLFS |
| 570 | 580 | 590 | 600 | 610 | | | |
| GCFLVVLLAI | LLYLLRLRRI | HRRTPRSSSA | AALWMEEGLP | AQNAPGTL | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2772 | 1 | 696.6903 | 49.74 | 3 | 65.0 | 14.8 | 1 | 380-397 | R.GTGDFDLCRETIQPFMNK.T | Oxidation: 16 |

# Detailed Protein Report

## Protein 470: PREDICTED: MDS1 and EVI1 complex locus protein EVI1 isoform X16 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578807160 | **Score:** | 28.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 93.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRSKGRARKL | ATNNECVYGN | YPEIPLEEMP | DADGVASTPS | LNIQEPCSPA | TSSEAFTPKE | GSPYKAPIYI | PDDIPIPAEF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ELRESNMPGA | GLGIWTKRKI | EVGEKFGPYV | GEQRSNLKDP | SYGWEILDEF | YNVKFCIDAS | QPDVGSWLKY | IRFAGCYDQH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NLVACQINDQ | IFYRVVADIA | PGEELLLFMK | SEDYPHETMA | PDIHEERQYR | CEDCDQLFES | KAELADHQKF | PCSTPHSAFS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MVEEDFQQKL | ESENDLQEIH | TIQECKECDQ | VFPDLQSLEK | HMLSHTEERE | YKCDQCPKAF | NWKSNLIRHQ | MSHDSGKHYE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CENCAKQVFT | DPSNLQRHIR | SQHVGARAHA | CPECGKTFAT | SSGLKQHKHI | HSSVKPFICE | VCHKSYTQFS | NLCRHKRMHA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DCRTQIKCKD | CGQMFSTTSS | LNKHRRFCEG | KNHFAAGGFF | GQGISLPGTP | AMDKTSMVNM | SHANPGLADY | FGANRHPAGL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TFPTAPGFSF | SFPGLFPSGL | YHRPPLIPAS | SPVKGLSSTE | QTNKSQSPLM | THPQILPATQ | DILKALSKHP | SVGDNKPVEL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QPERSSEERP | FEKISDQSES | SDLDDVSTPS | GSDLETTSGS | DLESDIESDK | EKFKENGKMF | KDKVSPLQNL | ASINNKKEYS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NHSIFSPSLE | EQTAVSGAVN | DSIKAIASIA | EKYFGSTGLV | GLQDKKVGAL | PYPSMFPLPF | FPAFSQSMYP | FPDRDLRSLP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LKMEPQSPGE | VKKLQKGSSE | SPFDLTTKRK | DEKPLTPVPS | KPPVTPATSQ | DQPLDLSMGS | RSRASGTKLT | EPRKNHVFGG |
| 810 | 820 | 830 | 840 | 850 | | | |
| KKGSNVESRP | ASDGSLQHAR | PTPFFMDPIY | RCQLLKTWQK | S | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2185 | 1 | 1052.4145 | -10.10 | 2 | 57.2 | 11.8 | 1 | 309-326 | R.HQMSHDSGKHYECENCAK.Q | |
| 668 | 2 | 602.8050 | -39.80 | 2 | 37.9 | 17.1 | 1 | 832-840 | R.CQLLKTWQK.S | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 471: PREDICTED: E3 ubiquitin-protein ligase RING2 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530365226 | **Score:** | 28.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 32.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| | | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MCPICLDMLK | NTMTTKECLH | RFCADCIITA | LRSGNKECPT | CRKKLVSKRS | LRPDPNFDAL | ISKIYPSRDE | YEAHQERVLA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RINKHNNQQA | LSHSIEEGLK | IQAMNRLQRG | KKQQIENGSG | AEDNGDSSHC | SNASTHSNQE | AGPSNKRTKT | SDDSGLELDN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NNAAMAIDPV | MDGASEIELV | FRPHPTLMEK | DDSAQTRYIK | TSGNATVDHL | SKYLAVRLAL | EELRSKGESN | QMNLDTASEK |
| 250 | 260 | 270 | 280 | 290 | | | |
| QYTIYIATAS | GQFTVLNGSF | SLELVSEKYW | KVNKPMELYY | APTKEHK | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1896 | 1 | 621.2840 | -141.50 | 1 | 54.1 | 16.2 | 0 | 213-217 | K.YLAVR.L | |

# Detailed Protein Report

## Protein 472: peptidyl-prolyl cis-trans isomerase FKBP5 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4758384 | **Score:** | 28.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 51.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.9 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

***WUP:QUP*** **Median:** 0.99 **CV:** 0.00 % **No. of Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|224809329 | refseq_human (refseq_human_20140103.fasta) | peptidyl-prolyl cis-trans isomerase FKBP5 isoform 1 [Homo sapiens] |
| gi\|224809327 | refseq_human (refseq_human_20140103.fasta) | peptidyl-prolyl cis-trans isomerase FKBP5 isoform 1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTTDEGAKNN | EESPTATVAE | QGEDITSKKD | RGVLKIVKRV | GNGEETPMIG | DKVYVHYKGK | LSNGKKFDSS | HDRNEPFVFS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LGKGQVIKAW | DIGVATMKKG | EICHLLCKPE | YAYGSAGSLP | KIPSNATLFF | EIELLDFKGE | DLFEDGGIIR | RTKRKGEGYS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NPNEGATVEI | HLEGRCGGRM | FDCRDVAFTV | GEGEDHDIPI | GIDKALEKMQ | REEQCILYLG | PRYGFGEAGK | PKFGIEPNAE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LIYEVTLKSF | EKAKESWEMD | TKEKLEQAAI | VKEKGTVYFK | GGKYMQAVIQ | YGKIVSWLEM | EYGLSEKESK | ASESFLLAAF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LNLAMCYLKL | REYTKAVECC | DKALGLDSAN | EKGLYRRGEA | QLLMNEFESA | KGDFEKVLEV | NPQNKAARLQ | ISMCQKKAKE |
| 410 | 420 | 430 | 440 | 450 | 460 | | |
| HNERDRRIYA | NMFKKFAEQD | AKEEANKAMG | KKTSEGVTNE | KGTDSQAMEE | EKPEGHV | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2372 | 1 | 911.8056 | -124.45 | 2 | 57.9 | 13.0 | 1 | 336-352 | K.AVECCDKALGLDSANEK.G | Carbamidomethyl: 4 | WUP:QUP 0.99 |

# Detailed Protein Report

**Protein 473:** **NKAP-like protein [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|56090620 | **Score:** | 28.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| | | **Sequence Coverage [%]:** | 5.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPPVSRSSYS | EDIVGSRRRR | RSSSGSPPSP | QSRCSSWDGC | SRSHSRGREG | LRPPWSELDV | GALYPFSRSG | SRGRLPRFRN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YAFASSWSTS | YSGYRYHRHC | YAEERQSAED | YEKEESHRQR | RLKERERIGE | LGAPEVWGPS | PKFPQLDSDE | HTPVEDEEEV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| THQKSSSSDS | NSEEHRKKKT | SRSRNKKKRK | NKSSKRKHRK | YSDSDSNSES | DTNSDSDDDK | KRVKAKKKKK | KKKHKTKKKK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NKKTKKESSD | SSCKDSEEDL | SEATWMEQPN | VADTMDLIGP | EAPIIHTSQD | EKPLKYGHAL | LPGEGAAMAE | YVKAGKRIPR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RGEIGLTSEE | IGSFECSGYV | MSGSRHRRME | AVRLRKENQI | YSADEKRALA | SFNQEERRKR | ESKILASFRE | MVHKKTKEKD |
| 410 | | | | | | | |
| DK | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1782 | 1 | 938.9355 | -33.28 | 2 | 50.6 | 12.7 | 0 | 296-313 | K.YGHALLPGEGAAMAEYVK.A | |

# Detailed Protein Report

## Protein 474: relA-associated inhibitor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|63003907 | **Score:** | 28.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 89.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|215820635 | refseq_human (refseq_human_20140103.fasta) | relA-associated inhibitor [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDSEAFQSAR | DFLDMNFQSL | AMKHMDLKQM | ELDTAAAKVD | ELTKQLESLW | SDSPAPPGPQ | AGPPSRPPRY | SSSSIPEPFG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SRGSPRKAAT | DGADTPFGRS | ESAPTLHPYS | PLSPKGRPSS | PRTPLYLQPD | AYGSLDRATS | PRPRAFDGAG | SSLGRAPSPR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PGPGPLRQQG | PPTPFDFLGR | AGSPRGSPLA | EGPQAFFPER | GPSPRPPATA | YDAPASAFGS | SLLGSGGSAF | APPLRAQDDL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TLRRRPPKAW | NESDLDVAYE | KKPSQTASYE | RLDVFARPAS | PSLQLLPWRE | SSLDGLGGTG | KDNLTSATLP | RNYKVSPLAS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DRRSDAGSYR | RSLGSAGPSG | TLPRSWQPVS | RIPMPPSSPQ | PRGAPRQRPI | PLSMIFKLQN | AFWEHGASRA | MLPGSPLFTR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| APPPKLQPQP | QPQPQPQSQP | QPQLPPQPQT | QPQTPTPAPQ | HPQQTWPPVN | EGPPKPPTEL | EPEPEIEGLL | TPVLEAGDVD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EGPVARPLSP | TRLQPALPPE | AQSVPELEEV | ARVLAEIPRP | LKRRGSMEQA | PAVALPPTHK | KQYQQIISRL | FHRHGGPGPG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GPEPELSPIT | EGSEARAGPP | APAPPAPIPP | PAPSQSSPPE | QPQSMEMRSV | LRKAGSPRKA | RRARLNPLVL | LLDAALTGEL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EVVQQAVKEM | NDPSQPNEEG | ITALHNAICG | ANYSIVDFLI | TAGANVNSPD | SHGWTPLHCA | ASCNDTVICM | ALVQHGAAIF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ATTLSDGATA | FEKCDPYREG | YADCATYLAD | VEQSMGLMNS | GAVYALWDYS | AEFGDELSFR | EGESVTVLRR | DGPEETDWWW |
| 810 | 820 | 830 | | | | | |
| AALHGQEGYV | PRNYFGLFPR | VKPQRSKV | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 100 | 1 | 1301.5284 | -95.57 | 2 | 31.0 | 12.3 | 1 | 378-400 | K.LQNAFWEHGASRAMLPGSPLFTR.A | Oxidation: 14 |

# Detailed Protein Report

## Protein 475: rho GTPase-activating protein 20 isoform 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|385862212 | **Score:** | 28.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 128.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|385862214 | refseq_human (refseq_human_20140103.fasta) | rho GTPase-activating protein 20 isoform 4 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKTLAERRRS | APSLILDKAL | QKRPTTRDSP | SASVDTCTFL | SSLVCSNRTL | LIDGRAELKR | GLQRQERHLF | LFNDLFVVAK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IKYNNNFKIK | NKIKLTDMWT | ASCVDEVGEG | NTNAMKSFVL | GWPTVNFVAT | FSSPEQKDKW | LSLLQRYINL | EKEKDYPKSI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PLKIFAKDIG | NCAYSKTITV | MNSDTANEVI | NMSLPMLGIT | GSERDYQLWV | NSGKEEAPYP | LIGHEYPYGI | KMSHLRDSAL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LTPGSKDSTT | PFNLQEPFLM | EQLPREMQCQ | FILKPSRLAA | AQQLSDSGHK | TFKRRRSIIN | WAFWRGSSTH | LDNLPSSPTS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PMPGQLFGIS | LPNICENDNL | PKPVLDMLFF | LNQKGPLTKG | IFRQSANVKS | CRELKEKLNS | GVEVHLDCES | IFVIASVLKD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FLRNIPGSIF | SSDLYDHWVS | VMDQGNDEEK | INTVQRLLDQ | LPRANVVLLR | YLFGVLHNIE | QHSSSNQMTA | FNLAVCVAPS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ILWPPASSSP | ELENEFTKKV | SLLIQFLIEN | CLRIFGEEIT | SLFREVSVRC | DTRENASDIS | CFQLNDSSYD | SLENELNEDV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DAPCSDLVKK | LGQGSRSMDS | VLTLSDYDLD | QPEVEGLLTL | SDFDLAHSKD | EDVQMKRPLE | SKPVNILVYT | KIPLRDHARA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PSAMCTPSYL | STAAANAAKS | LRRHRRCSEP | SIDYLDSKLS | YLREFYQKKL | RKSSCDAILS | QKDEDYLKQN | QPLQEEGKTC |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| FKQSLVTGTD | VSKKNATTQN | TKKKSLSGSE | GNHVKLFPKS | KPVAISVASY | SPMSSQDHSK | NQPFDVNTSG | YSPPHTADAL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KGPRTHRRCS | EPNIEDQNRK | LTYLRGIYSK | KQHKTSCEAG | LLHGEEDYLK | RHKSLQMEGQ | KLINQSLVMG | IEVGKSSATN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QNTEKVLPPR | LNLCPRTSYS | SLSSPGTSPS | GSSVSSQDSA | FSQISEHSVF | TPTETSSPID | CTFQAQRKRE | DLSPDFSNAS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| HVSGMPGPSS | GQACSRPAYT | KKDTMEWHSQ | MHSVTLHPST | WLRNGVASLK | NWSLKKKAKA | ARPEEEKIAS | PKGPLEPPPH |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ASGVPEANSL | QEEQKDLPLR | AAEGLSPVQS | AQRCSSSPFQ | DSERHCSSPF | SLVESRLKLC | MKSHEEIEPG | SQSSSGSLPW |
| 1130 | 1140 | 1150 | 1160 | | | | |
| ERASASSWTL | EDATSPDSGP | TVVCDIEDRY | LTKDI | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1952 | 3 | 703.2693 | -86.35 | 2 | 52.8 | 11.2 | 0 | 1085-1096 | R.HCSSPFSLVESR.L | Carbamidomethyl: 2 |

# Detailed Protein Report

## Protein 476: PREDICTED: ninein isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578825856 | **Score:** | 28.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 231.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.8 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDEVEQDQHE | ARLKELFDSF | DTTGTGSLGQ | EELTDLCHML | SLEEVAPVLQ | QTLLQDNLLG | RVHFDQFKEA | LILILSRTLS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NEEHFQEPDC | SLEAQPKYVR | GGKRYGRRSL | PEFQESVEEF | PEVTVIEPLD | EEARPSHIPA | GDCSEHWKTQ | RSEEYEAEGQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LRFWNPDDLN | ASQSGSSPPQ | DWIEEKLQEV | CEDLGITRDG | HLNRKKLVSI | CEQYGLQNVD | GEMLEEVFHN | LDPDGTMSVE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DFFYGLFKNG | KSLTPSASTP | YRQLKRHLSM | QSFDESGRRT | TTSSAMTSTI | GFRVFSCLDD | GMGHASVERI | LDTWQEEGIE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NSQEILKALD | FSLDGNINLT | ELTLALENEL | LVTKNSIHQA | ALASFKAEIR | HLLERVDQVV | REKEKLRSDL | DKAEKLKSLM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ASEVDDHHAA | IERRNEYNLR | KLDEEYKERI | AALKNELRKE | REQILQQAGK | QRLELEQEIE | KAKTEENYIR | DRLALSLKEN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SRLENELLEN | AEKLAEYENL | TNKLQRNLEN | VLAEKFGDLD | PSSAEFFLQE | ERLTQMRNEY | ERQCRVLQDQ | VDELQSELEE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YRAQGRVLRL | PLKNSPSEEV | EANSGGIEPE | HGLGSEECNP | LNMSIEAELV | IEQMKEQHHR | DICCLRLELE | DKVRHYEKQL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DETVVSCKKA | QENMKQRHEN | ETHTLEKQIS | DLKNEIAELQ | GQAAVLKEAH | HEATCRHEEE | KKQLQVKLEE | EKTHLQEKLR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LQHEMELKAR | LTQAQASFER | EREGLQSSAW | TEEKVRGLTQ | ELEQFHQEQL | TSLVEKHTLE | KEELRKELLE | KHQRELQEGR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EKMETECNRR | TSQIEAQFQS | DCQKVTERCE | SALQSLEGRY | RQELKDLQEQ | QREEKSQWEF | EKDELTQECA | EAQELLKETL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KREKTTSLVL | TQEREMLEKT | YKEHLNSMVV | ERQQLLQDLE | DLRNVSETQQ | SLLSDQILEL | KSSHKRELRE | REEVLCQAGA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SEQLASQRLE | RLEMEHDQER | QEMMSKLLAM | ENIHKATCET | ADRERAEMST | EISRLQSKIK | EMQQATSPLS | MLQSGCQVIG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EEEVEGDGAL | SLLQQGEQLL | EENGDVLLSL | QRAHEQAVKE | NVKMATEISR | LQQRLQKLEP | GLVMSSCLDE | PATEFFGNTA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EQTEQFLQQN | RTKQVEGVTR | RHVLSDLEDD | EVRDLGSTGT | SSVQRQEVKI | EESEASVEGF | SELENSEETR | TESWELKNQI |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SQLQEQLMML | CADCDRASEK | KQDLLFDVSV | LKKKLKMLER | IPEASPKYKL | LYEDVSREND | CLQEELRMME | TRYDEALENN |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KELTAEVFRL | QDELKKMEEV | TETFLSLEKS | YDEVKIENEG | LNVLVLRLQG | KIEKLQESVV | QRCDCCLWEA | SLENLEIEPD |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| GNILQLNQTL | EECVPRVRSV | HHVIEECKQE | NQYLEGNTQL | LEKVKAHEIA | WLHGTIQTHQ | ERPRVQNQVI | LEENTTLLGF |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| QDKHFQHQAT | IAELELEKTK | LQELTRKLKE | RVTILVKQKD | VLSHGEKEEE | LKAMMHDLQI | TCSEMQQKVE | LLRYESEKLQ |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| QENSILRNEI | TTLNEEDSIS | NLKLGTLNGS | QEEMWQKTET | VKQENAAVQK | MVENLKKQIS | ELKIKNQQLD | LENTELSQKN |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| SQNQEKLQEL | NQRLTEMLCQ | KEKEPGNSAL | EEREQEKFNL | KEELERCKVQ | SSTLVSSLEA | ELSEVKIQTH | IVQQENHLLK |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| DELEKMKQLH | RCPDLSDFQQ | KISSVLSYNE | KLLKEKEALS | EELNSCVDKL | AKSSLLEHRI | ATMKQEQKSW | EHQSASLKSQ |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| LVASQEKVQN | LEDTVQNVNL | QMSRMKSDLR | VTQQEKEALK | QEVMSLHKQL | QNAGGKSWAP | EIATHPSGLH | NQQKRLSWDK |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| LDHLMNEEQQ | LLWQENERLQ | TMVQNTKAEL | THSREKVRQL | ESNLLPKHQK | HLNPSGTMNP | TEQEKLSLKR | ECDQFQKEQS |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | |
| PANRKVSQMN | SLEQELETIH | LENEGLKKKQ | VKLDEQLMEN | SVVGSSREGC | SSLPEIVCEG | RTFSFNELS | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1578 | 1 | 685.8860 | 27.18 | 2 | 48.0 | 10.3 | 0 | 913-923 | R.QQLLQDLEDLR.N | |

# Detailed Protein Report

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## Protein 477: beta-1,4 N-acetylgalactosaminyltransferase 2 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|227497758 | **Score:** | 28.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.9 |
| | | **Sequence Coverage [%]:** | 4.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.80 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.31 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MFGSMFLQAV FSSPKPELPS PAPGVQKLKL LPEERLRNLF SYDGIWLFPK NQCKCEANKE QGGYNFQDAY GQSDLPAVKA
        90        100        110        120        130        140        150        160
RRQAEFEHFQ RREGLPRPLP LLVQPNLPFG YPVHGVEVMP LHTVPIPGLQ FEGPDAPVYE VTLTASLGTL NTLADVPDSV
       170        180        190        200        210        220        230        240
VQGRGQKQLI ISTSDRKLLK FILQHVTYTS TGYQHQKVDI VSLESRSSVA KFPVTIRHPV IPKLYDPGPE RKLRNLVTIA
       250        260        270        280        290        300        310        320
TKTFLRPHKL MIMLRSIREY YPDLTVIVAD DSQKPLEIKD NHVEYYTMPF GKGWFAGRNL AISQVTTKYV LWVDDDFLFN
       330        340        350        360        370        380        390        400
EETKIEVLVD VLEKTELDVV GGSVLGNVFQ FKLLLEQSEN GACLHKRMGF FQPLDGFPSC VVTSGVVNFF LAHTERLQRV
       410        420        430        440        450        460        470        480
GFDPRLQRVA HSEFFIDGLG TLLVGSCPEV IIGHQSRSPV VDSELAALEK TYNTYRSNTL TRVQFKLALH YFKNHLQCAA
       490
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 26 | 1 | 537.7695 | -77.75 | 2 | 30.0 | 13.9 | 0 | 299-308 | R.NLAISQVTTK.Y | | QU:MU 0.80<br>WUP:QUP 0.31 |

# Detailed Protein Report

**Protein 478:** **PREDICTED: T-complex protein 11-like protein 1 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578820625 | **Score:** | 28.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 36.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 9.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMGTLCAPAR | DEEVKKLKDI | KEIVPLFREI | FSVLDLMKVD | MANFAISSIR | PHLMQQSVEY | ERKKFQEILE | RQPNSLDFVT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QWLEEASEDL | MTQKYKHALP | VGGMAAGSGD | MPRLSPVAVQ | NYAYLKLLKW | DHLQRPFPET | VLMDQSRFHE | LQLQLEQLTI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LGAVLLVTFS | MAAPGISSQA | DFAEKLKMIV | KILLTDMHLP | SFHLKDVLTT | IGEKVCLEVS | SCLSLCGSSP | FTTDKETVLK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GQIQAVASPD | DPIRRIMESR | ILTFLETYLA | SGHQKPLPTV | PGGLSPVQRE | LEEVAIKFAR | LVNYNKMVFC | PYYDAILSKI |
| 330 | | | | | | | |
| LVRS | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 780 | 1 | 541.6146 | -237.37 | 2 | 39.7 | 10.1 | 0 | 1-10 | -.MMGTLCAPAR.D | Oxidation: 1, 2 |

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# Detailed Protein Report

## Protein 479: angiopoietin-related protein 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4757752 | **Score:** | 28.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| | | **Sequence Coverage [%]:** | 7.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530365564 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: angiopoietin-related protein 1 isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKTFTWTLGV | LFFLLVDTGH | CRGGQFKIKK | INQRRYPRAT | DGKEEAKKCA | YTFLVPEQRI | TGPICVNTKG | QDASTIKDMI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TRMDLENLKD | VLSRQKREID | VLQLVVDVDG | NIVNEVKLLR | KESRNMNSRV | TQLYMQLLHE | IIRKRDNSLE | LSQLENKILN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VTTEMLKMAT | RYRELEVKYA | SLTDLVNNQS | VMITLLEEQC | LRIFSRQDTH | VSPPLVQVVP | QHIPNSQQYT | PGLLGGNEIQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RDPGYPRDLM | PPPDLATSPT | KSPFKIPPVT | FINEGPFKDC | QQAKEAGHSV | SGIYMIKPEN | SNGPMQLWCE | NSLDPGGWTV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IQKRTDGSVN | FFRNWENYKK | GFGNIDGEYW | LGLENIYMLS | NQDNYKLLIE | LEDWSDKKVY | AEYSSFRLEP | ESEFYRLRLG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TYQGNAGDSM | MWHNGKQFTT | LDRDKDMYAG | NCAHFHKGGW | WYNACAHSNL | NGVWYRGGHY | RSKHQDGIFW | AEYRGGSYSL |
| 490 | 500 | | | | | | |
| RAVQMMIKPI | D | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2041 | 1 | 1018.3938 | -75.83 | 3 | 55.4 | 17.0 | 0 | 341-366 | K.GFGNIDGEYWLGLENIYMLSNQDNYK.L | |

# Detailed Protein Report

## Protein 480: PREDICTED: protein DBF4 homolog B isoform X7 [Homo sapiens]

**Accession:** gi|578831452
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 28.8
**MW [kDa]:** 48.4
**pI:** 10.4
**Sequence Coverage [%]:** 4.7
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSEPGKGDDC | LELESSMAES | RLRAPDLGVS | RCLGKCQKNS | PGARKHPFSG | KSFYLDLPAG | KNLQFLTGAI | QQLGGVIEGF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LSKEVSYIVS | SRREVKAESS | GKSHRGCPSP | SPSEVRVETS | AMVDPKGSHP | RPSRKPVDSV | PLSRGKELLQ | KAIRNQGSIS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GGGSGGSSSL | LTNARSWGVR | ILHVDEMMMH | VQQLSLASLC | VKKQQPKKPE | GTCPAAESRT | RKVARLKAPF | LKIEDESRKF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RPFHHQFKSF | PEISFLGPKD | ASPFEAPTTL | GSMHHTRESK | DGEPSPRSAA | HTMPRRKKGY | CECCQEAFEE | LHVHLQSAQH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RSFALEAHLY | AEVDRIIAQL | SHSFADIPFQ | AGLPSDPRQG | CGPAAMDRIT | RWCDGTSCKS | HMCECHNPPA | GLAQGLQGAG |
| 410 | 420 | 430 | 440 | 450 | | | |
| LPLSLPSLLY | PVSSGHFLGS | AAWGVVACRG | HAPPSLPRKL | LCPGGHSC | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1527 | 2 | 472.2297 | 42.07 | 2 | 49.3 | 18.1 | 0 | 440-448 | K.LLCPGGHSC.- | Carbamidomethyl: 9 |

# Detailed Protein Report

## Protein 481: PREDICTED: zinc finger protein 675 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530414624 | **Score:** | 28.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578833063 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 675 isoform X6 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MCSHFAQEFW | PEQNIKDSFE | KVTLRRYEKC | GNDNFQLKGC | KSVDECKLHK | GGYNGLNQCL | PTMQSKMFQC | DKYVKVFNKF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SHSDRHKIKH | MENKPFKCKE | CGRSFCMLSH | LTRHERNYTK | VNFCKCEECE | KAVNQSSKLT | KHKRIYTCEK | LYKCQECDRT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FNQFSNLTEY | KKDYAREKPY | KCEECGKAFN | QSSHLTTHKI | IHTGEKPYKC | EECGKAFNQF | SNLTTHKKIH | TGEQPYICEE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CGKAFTQSST | LTTHKRIHTG | EKPYKCEECG | KAFNRSSKLT | EHKNIHTGEQ | PYKCEECGKA | FNRSSNLTEH | RKIHTEEKPY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KCKECGKAFK | HSSALTTHKR | IHTGEKPYKC | EECGKAFNRS | SKLTEHKKLH | TGKKPYKCEE | CGKAFIQSSK | LTEHKKIHSG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EIPYKCEECG | KAFKHSSSLT | THKRIHTGEK | PYKCEECGKA | FSRSSKLTEH | KIIHTGEKPY | KCERCDKAFN | QSANLTKHKK |
| 490 | 500 | | | | | | |
| IHTGEKLQNW | NV | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2266 | 1 | 682.3051 | 5.92 | 3 | 58.8 | 17.1 | 2 | 30-47 | K.CGNDNFQLKGCKSVDECK.L | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 482: PREDICTED: zinc finger protein 646 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530409439 | **Score:** | 28.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 198.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEDTPPSLSC | SDCQRHFPSL | PELSRHRELL | HPSPNQDSEE | ADSIPRPYRC | QQCGRGYRHP | GSLVNHRRTH | ETGLFPCTTC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GKDFSNPMAL | KSHMRTHAPE | GRRRHRPPRP | KEATPHLQGE | TVSTDSWGQR | LGSSEGWENQ | TKHTEETPDC | ESVPDPRAAS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GTWEDLPTRQ | REGLASHPGP | EDGADGWGPS | TNSARAPPLP | IPASSLLSNL | EQYLAESVVN | FTGGQEPTQS | PPAEEERRYK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CSQCGKTYKH | AGSLTNHRQS | HTLGIYPCAI | CFKEFSNLMA | LKNHSRLHAQ | YRPYHCPHCP | RVFRLPRELL | EHQQSHEGER |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QEPRWEEKGM | PTTNGHTDES | SQDQLPSAQM | LNGSAELSTS | GELEDSGLEE | YRPFRCGDCG | RTYRHAGSLI | NHRKSHQTGV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YPCSLCSKQL | FNAAALKNHV | RAHHRPRQGV | GENGQPSVPP | APLLLAETTH | KEEEDPTTTL | DHRPYKCSEC | GRAYRHRGSL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VNHRHSHRTG | EYQCSLCPRK | YPNLMALRNH | VRVHCKAARR | SADIGAEGAP | SHLKVELPPD | PVEAEAAPHT | DQDHVCKHEE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EATDITPAAD | KTAAHICSIC | GLLFEDAESL | ERHGLTHGAG | EKENSRTETT | MSPPRAFACR | DCGKSYRHSG | SLINHRQTHQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TGDFSCGACA | KHFHTMAAMK | NHLRRHSRRR | SRRHRKRAGG | ASGGREAKLL | AAESWTRELE | DNEGLESPQD | PSGESPHGAE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GNLESDGDCL | QAESEGDKCG | LERDETHFQG | DKESGGTGEG | LERKDASLLD | NLDIPGEEGG | GTHFCDSLTG | VDEDQKPATG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QPNSSSHSAN | AVTGWQAGAA | HTCSDCGHSF | PHATGLLSHR | PCHPPGIYQC | SLCPKEFDSL | PALRSHFQNH | RPGEATSAQP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| FLCCLCGMIF | PGRAGYRLHR | RQAHSSSGMT | EGSEEEGEEE | GVAEAAPARS | PPLQLSEAEL | LNQLQREVEA | LDSAGYGHIC |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GCCGQTYDDL | GSLERHHQSQ | SSGTTADKAP | SPLGVAGDAM | EMVVDSVLED | IVNSVSGEGG | DAKSQEGAGT | PLGDSLCIQG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GESLLEAQPR | PFRCNQCGKT | YRHGGSLVNH | RKIHQTGDFL | CPVCSRCYPN | LAAYRNHLRN | HPRCKGSEPQ | VGPIPEAAGS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SELQVGPIPE | GGSNKPQHMA | EEGPGQAEVE | KLQEELKVEP | LEEVARVKEE | VWEETTVKGE | EIEPRLETAE | KGCQTEASSE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| RPFSCEVCGR | SYKHAGSLIN | HRQSHQTGHF | GCQACSKGFS | NLMSLKNHRR | IHADPRRFRC | SECGKAFRLR | KQLASHQRVH |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| MERRGGGGTR | KATREDRPFR | CGQCGRTYRH | AGSLLNHRRS | HETGQYSCPT | CPKTYSNRMA | LKDHQRLHSE | NRRRRAGRSR |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| RTAVRCALCG | RSFPGRGSLE | RHLREHEETE | REPANGQGGL | DGTAASEANL | TGSQGLETQL | GGAEPVPHLE | DGVPRPGERS |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| QSPIRAASSE | APEPLSWGAG | KAGGWPVGGG | LGNHSGGWVP | QFLTRSEEPE | DSVHRSPCHA | GDCQLNGPTL | SHMDSWDNRD |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| NSSQLQPGSH | SSCSQCGKTY | CQSGSLLNHN | TNKTDRHYCL | LCSKEFLNPV | ATKSHSHNHI | DAQTFACPDC | GKAFESHQEL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| ASHLQAHARG | HSQVPAQMEE | ARDPKAGTGE | DQVVLPGQGK | AQEAPSETPR | GPGESVERAR | GGQAVTSMAA | EDKERPFRCT |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| QCGRSYRHAG | SLLNHQKAHT | TGLYPCSLCP | KLLPNLLSLK | NHSRTHTDPK | RHCCSICGKA | FRTAARLEGH | GRVHAPREGP |
| 1770 | 1780 | 1790 | 1800 | 1810 | | | |
| FTCPHCPRHF | RRRISFVQHQ | QQHQEEWTVA | GSGRGHEGSQ | EEEPQWHQ | | | |

| Cmpd. | No. of | m/z meas. | Δ m/z | z | Rt | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

| | Cmpds. | | [ppm] | | [min] | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 1417 | 7 | 1023.6578 | 178.56 | 1 | 47.9 | 16.5 | 0 | 1557-1564 | R.HYCLLCSK.E | Carbamidomethyl: 3 |

# Detailed Protein Report

**Protein 483:** **3-hydroxyisobutyryl-CoA hydrolase, mitochondrial isoform 2 precursor [Homo sapiens]**

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|37594469 | **Score:** | 28.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 11.8 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGQREMWRLM | SRFNAFKRTN | TILHHLRMSK | HTDAAEEVLL | EKKGCTGVIT | LNRPKFLNAL | TLNMIRQIYP | QLKKWEQDPE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TFLIIIKGAG | GKAFCAGGDI | RVISEAEKAK | QKIAPVFFRE | EYMLNNAVGS | CQKPYVALIH | GITMGGGVGL | SVHGQFRVAT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EKCLFAMPET | AIGLFPDVGG | GYFLPRLQGK | LGYFLALTGF | RLKGRDVYRA | GIATHFVDSE | KLAMLEEDLL | ALKSPSKENI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ASVLENYHTE | SKIDRDKSFI | LEEHMDKINS | CFSANTVEEI | IENLQQDGSS | FALEQLKVIN | KMSPTSLKIT | LRQLMEGSSK |
| 330 | 340 |  |  |  |  |  |  |
| TLQEVLTMEY | RLSQACMF |  |  |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2789 | 1 | 863.0890 | -7.69 | 3 | 66.0 | 12.9 | 0 | 163-186 | K.CLFAMPETAIGLFPDVGGGYFLPR.L | Oxidation: 5 |

# Detailed Protein Report

## Protein 484: leucine-rich repeat-containing protein 16A isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|291190783 | **Score:** | 28.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 150.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTEESSDVPR | ELIESIKDVI | GRKIKISVKK | KVKLEVKGDK | VENKVLVLTS | CRAFLVTARI | PTKLELTFSY | LEIHGVVCSK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SAQMIVETEK | CSISMKMASP | EDVSEVLAHI | GTCLRKIFPG | LSPVRIMKKV | SMEPSERLAS | LQALWDSQTV | AEQGPCGGFS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QMYACVCDWL | GFSYREEVQW | DVDTIYLTQD | TRELNLQDFS | HLDHRDLIPI | IAALEYNQWF | TKLSSKDLKL | STDVCEQILR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VVSRSNRLEE | LVLENAGLRT | DFAQKLASAL | AHNPNSGLHT | INLAGNPLED | RGVSSLSIQF | AKLPKGLKHL | NLSKTSLSPK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GVNSLSQSLS | ANPLTASTLV | HLDLSGNVLR | GDDLSHMYNF | LAQPNAIVHL | DLSNTECSLD | MVCGALLRGC | LQYLAVLNLS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RTVFSHRKGK | EVPPSFKQFF | SSSLALMHIN | LSGTKLSPEP | LKALLLGLAC | NHNLKGVSLD | LSNCELRSGG | AQVLEGCIAE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IHNITSLDIS | DNGLESDLST | LIVWLSKNRS | IQHLALGKNF | NNMKSKNLTP | VLDNLVQMIQ | DEESPLQSLS | LADSKLKTEV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TIIINALGSN | TSLTKVDISG | NGMGDMGAKM | LAKALQINTK | LRTVIWDKNN | ITAQGFQDIA | VAMEKNYTLR | FMPIPMYDAS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QALKTNPEKT | EDALQKIENY | LLRNHETRKY | LQEQAYRLQQ | GIVTSTTQQM | IDRICVKVQD | HLNSLRNCGG | DAIQEDLKSA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ERLMRDAKNS | KTLLPNLYHV | GGASWAGASG | LLSSPIQETL | ESMAGEVTRV | VDEQLKALLE | SMVDAAENLC | PNVMKKAHIR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QDLIHASTEK | ISIPRTFVKN | VLLEQSGIDI | LNKISEVKLT | VASFLSDRIV | DEILDALSHC | HHKLADHFSR | RGKTLPQQES |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LEIELAEEKP | VKRSIITVEE | LTEIERLEDL | DTCMMTPKSK | RKSIHSRMLR | PVSRAFEMEF | DLDKALEEVP | IHIEDPPFPS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LRQEKRSSGF | ISELPSEEGK | KLEHFTKLRP | KRNKKQQPTQ | AAVCAANIVS | QDGEQNGLMG | RVDEGVDEFF | TKKVTKMDSK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KWSTRGSESH | ELNEGGDEKK | KRDSRKSSGF | LNLIKSRSKS | ERPPTILMTE | EPSSPKGAVR | SPPVDCPRKD | TKAAEHNGNS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ERIEEIKTPD | SFEESQGEEI | GKVERSDSKS | SPQAGRRYGV | QVMGSGLLAE | MKAKQEKRAA | CAQKKLGNDA | VSQDSSSPAL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SGVERSDGGG | AGLPENRFGL | GTPEKNTKAE | PKAEAGSRSR | SSSSTPTSPK | PLLQSPKPSL | AARPVIPQKP | RTASRPDDIP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DSPSSPKVAL | LPPVLKKVPS | DKERDGQSSP | QPSPRTFSQE | VSRRSWGQQA | QEYQEQKQRS | SSKDGHQGSK | SNDSGEEAEK |
| 1370 | | | | | | | |
| EFIFV | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 843 | 1 | 946.5224 | 65.61 | 3 | 40.1 | 18.7 | 2 | 91-116 | K.CSISMKMASPEDVSEVLAHIGTCLRK.I | Oxidation: 5, 7 |

# Detailed Protein Report

## Protein 485: PREDICTED: 1,5-anhydro-D-fructose reductase isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578818599 | **Score:** | 28.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 22.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 10.7 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MGDIPAVGLS SWKASPGKVT EAVKEAIDAG YRHFDCAYFY HNEREVGAGI RCKIKEGAVR REDLFIATKP PHPEWIMSCS
        90        100        110        120        130        140        150        160
ELSFCLSHPR VQDLPLDESN MVIPSDTDFL DTWEAMEDLV ITGLVKNIGV SNFNHEQLER LLNKPGLRFK PLTNQILIRF
       170        180        190        200
QIQRNVIVIP GSITPSHIKE NIQVCYTLRG NAILRQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1457 | 1 | 960.4393 | -73.19 | 2 | 47.9 | 10.9 | 1 | 180-195 | K.ENIQVCYTLRGNAILR.Q | Carbamidomethyl: 6 |

# Detailed Protein Report

**Protein 486:** **PREDICTED: protein FAM45A isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530393695 | **Score:** | 28.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 7.2 |
| | | **No. of unique Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MLSSDHLSTV EKDTNGEVLW VWCYPSTTAT LRNLLLRKCC LTDENKLLHP FVFGQYRRTW FYITTIEVPD SSILKKVTHF
        90        100        110        120        130        140        150        160
SIVLTAKDFN PEKYAAFTRI LCRMYLKHGS PVKMMESYIA VLTKGICQSE ENGSFLSKDF DARKAYLAGS IKDIVSQFGM
       170        180        190        200        210        220        230        240
ETVILHTALM LKKRIVVYHP KIEAVQEFTR TLPALVWHRQ DWTILHSYVH LNADELEALQ MCTGYVAGFV DLEVSNRPDL
       250        260        270        280        290        300        310        320
YDVFVNLAES EITIAPLAKE AMAMGKLHKE MGQLIVQSAE DPEKSESHVI QDIALKTREI FTNLAPFSEV SADGEKRVLN
       330        340        350
LEALKQKRFP PATENFLYHL AAAEQMLKI
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 837 | 1 | 491.6643 | -76.81 | 2 | 38.9 | 11.9 | 0 | 39-46 | K.CCLTDENK.L | Carbamidomethyl: 1 |
| 2666 | 1 | 973.5093 | -13.80 | 2 | 63.4 | 16.7 | 1 | 77-93 | K.VTHFSIVLTAKDFNPEK.Y | |

# Detailed Protein Report

**Protein 487:** **PREDICTED: FERM and PDZ domain-containing protein 4 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578837988 | **Score:** | 28.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 189.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDTVHPGSHS | WDFCHRTKSS | GWPPPSGTWG | LSQVPPYGWE | MTANRDGRDY | FINHMTQAIP | FDDPRLESCQ | IIPPAPRKVE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MRRDPVLGFG | FVAGSEKPVV | VRSVTPGGPS | EGKLIPGDQI | VMINDEPVSA | APRERVIDLV | RSCKESILLT | VIQPYPSPKS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AFISAAKKAR | LKSNPVKVRF | SEEVIINGQV | SETVKDNSLL | FMPNVLKVYL | ENGQTKSFRF | DCSTSIKDVI | LTLQEKLSIK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GIEHFSLMLE | QRTEGAGTKL | LLLHEQETLT | QVTQRPSSHK | MRCLFRISFV | PKDPIDLLRR | DPVAFEYLYV | QSCNDVVQER |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FGPELKYDIA | LRLAALQMYI | ATVTTKQTQK | ISLKYIEKEW | GLETFLPSAV | LQSMKEKNIK | KALSHLVKAN | QNLVPPGKKQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AEKRSEVTLL | VGPRYGISHV | INTKTNLVAL | LADFSHVNRI | EMFSEEESLV | RVELHVLDVK | PITLLMESSD | AMNLACLTAG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YYRLLVDSRR | SIFNMANKKN | TATQETGPEN | KGKHNLLGPD | WNCIPQMTTF | IGEGEQEAQI | TYIDSKQKTV | EITDSTMCPK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EHRHLYIDNA | YSSDGLNQQL | SQPGEAPCEA | DYRSLAQRSL | LTLSGPETLK | KAQESPRGAK | VSFIFGDFAL | DDGISPPTLG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| YETLLDEGPE | MLEKQRNLYI | GSANDMKGLD | LTPEAEGIQF | VENSVYANIG | DVKSFQAAEG | IEEPLLHDIC | YAENTDDAED |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EDEVSCEEDL | VVGEMNQPAI | LNLSGSSDDI | IDLTSLPPPE | GDDNEDDFLL | RSLNMAIAAP | PPGFRDSSDE | EDSQSQAASF |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PEDKEKGSSL | QNDEIPVSLI | DAVPTSAEGK | CEKGLDNAVV | STLGALEALS | VSEEQQTSDN | SGVAILRAYS | PESSSDSGNE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TNSSEMTESS | ELATAQKQSE | NLSRMFLATH | EGYHPLAEEQ | TEFPASKTPA | GGLPPKSSHA | LAARPATDLP | PKVVPSKQLL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| HSDHMEMEPE | TMETKSVTDY | FSKLHMGSVA | YSCTSKRKSK | LADGEGKAPP | NGNTTGKKQQ | GTKTAEMEEE | ASGKFGTVSS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RDSQHLSTFN | LERTAFRKDS | QRWYVATEGG | MAEKSGLEAA | TGKTFPRASG | LGAREAEGKE | EGAPDGETSD | GSGLGQGDRF |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LTDVTCASSA | KDLDNPEDAD | SSTCDHPSKL | PEADESVARL | CDYHLAKRMS | SLQSEGHFSL | QSSQGSSVDA | GCGTGSSGSA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| CATPVESPLC | PSLGKHLIPD | ASGKGVNYIP | SEERAPGLPN | HGATFKELHP | QTEGMCPRMT | VPALHTAINT | EPLFGTLRDG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| CHRLPKIKET | TALTEPGKER | RGGMPSAWSQ | HPEADPILLP | SNIHSESKVP | IPNQDPNDFS | QANQAYGEAV | SWRPPDLRGG |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| SLRTPPSQKA | LRHSSSILSG | SVDLETFRER | TKGAVSLKCP | GITEAQEASS | ERRAELPLGR | KLTKSFSQSS | MHLSSEGRFH |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KRSPVAHKDS | KLYRTLPLRK | LEGSNWRCRG | PFSYCFLNRG | QDEDGEEEEE | RGEATVQVSC | LYRPQMTQAM | PEPSSPCLAV |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| AIQKQRGELS | RGSVLKVWAE | DLRDPDDLDF | SNLAFDARIA | RINALKESTY | AMPDGFLAAQ | NDANELLCLV | RATKEKREES |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| RPEAYDLTLS | QYKQLLSIES | RQLGSACRKM | AMAEKSPEEM | LLAMTSSFQV | LCCLTEACMR | LVKVVNSETQ | RQEIVGKIDE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | | |
| VVINYICLLK | AAEAATGKNP | GDPNVGLSAR | HSTTMAALVS | TLTRSLKRLL | NK | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 684 | 1 | 460.1264 | -252.38 | 2 | 38.1 | 14.1 | 1 | 1622-1629 | R.QLGSACRK.M | Carbamidomethyl: 6 |

# Detailed Protein Report

## Protein 488: ankyrin repeat and zinc finger domain-containing protein 1 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|109150425 | **Score:** | 28.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 80.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|109150435 | refseq_human (refseq_human_20140103.fasta) | ankyrin repeat and zinc finger domain-containing protein 1 isoform 1 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MSPAPDAAPA PASISLFDLS ADAPVFQGLS LVSHAPGEAL ARAPRTSCSG SGERESPERK LLQGPMDISE KLFCSTCDQT
        90        100        110        120        130        140        150        160
FQNHQEQREH YKLDWHRFNL KQRLKDKPLL SALDFEKQSS TGDLSSISGS EDSDSASEED LQTLDRERAT FEKLSRPPGF
       170        180        190        200        210        220        230        240
YPHRVLFQNA QGQFLYAYRC VLGPHQDPPE EAELLLQNLQ SRGPRDCVVL MAAAGHFAGA IFQGREVVTH KTFHRYTVRA
       250        260        270        280        290        300        310        320
KRGTAQGLRD ARGGPSHSAG ANLRRYNEAT LYKDVRDLLA GPSWAKALEE AGTILLRAPR SGRSLFFGGK GAPLQRGDPR
       330        340        350        360        370        380        390        400
LWDIPLATRR PTFQELQRVL HKLTTLHVYE EDPREAVRLH SPQTHWKTVR EERKKPTEEE IRKICRDEKE ALGQNEESPK
       410        420        430        440        450        460        470        480
QGSGSEGEDG FQVELELVEL TVGTLDLCES EVLPKRRRRK RNKKEKSRDQ EAGAHRTLLQ QTQEEEPSTQ SSQAVAAPLG
       490        500        510        520        530        540        550        560
PLLDEAKAPG QPELWNALLA ACRAGDVGVL KLQLAPSPAD PRVLSLLSAP LGSGGFTLLH AAAAAGRGSV VRLLLEAGAD
       570        580        590        600        610        620        630        640
PTVQDSRARP PYTVAADKST RNEFRRFMEK NPDAYDYNKA QVPGPLTPEM EARQATRKRE QKAARRQREE QQQRQQEQEE
       650        660        670        680        690        700        710        720
REREEQRRFA ALSDREKRAL AAERRLAAQL GAPTSPIPDS AIVNTRRCWS CGASLQGLTP FHYLDFSFCS TRCLQDHRRQ
       730
AGRPSS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 883 | 3 | 529.1891 | -185.79 | 2 | 39.4 | 16.5 | 0 | 277-286 | R.DLLAGPSWAK.A | |

# Detailed Protein Report

## Protein 489: prolow-density lipoprotein receptor-related protein 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|126012562 | **Score:** | 28.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 504.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 0.6 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLTPPLLLLL | PLLSALVAAA | IDAPKTCSPK | QFACRDQITC | ISKGWRCDGE | RDCPDGSDEA | PEICPQSKAQ | RCQPNEHNCL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GTELCVPMSR | LCNGVQDCMD | GSDEGPHCRE | LQGNCSRLGC | QHHCVPTLDG | PTCYCNSSFQ | LQADGKTCKD | FDECSVYGTC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SQLCTNTDGS | FICGCVEGYL | LQPDNRSCKA | KNEPVDRPPV | LLIANSQNIL | ATYLSGAQVS | TITPTSTRQT | TAMDFSYANE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TVCWVHVGDS | AAQTQLKCAR | MPGLKGFVDE | HTINISLSLH | HVEQMAIDWL | TGNFYFVDDI | DDRIFVCNRN | GDTCVTLLDL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ELYNPKGIAL | DPAMGKVFFT | DYGQIPKVER | CDMDGQNRTK | LVDSKIVFPH | GITLDLVSRL | VYWADAYLDY | IEVVDYEGKG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RQTIIQGILI | EHLYGLTVFE | NYLYATNSDN | ANAQQKTSVI | RVNRFNSTEY | QVVTRVDKGG | ALHIYHQRRQ | PRVRSHACEN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DQYGKPGGCS | DICLLANSHK | ARTCRCRSGF | SLGSDGKSCK | KPEHELFLVY | GKGRPGIIRG | MDMGAKVPDE | HMIPIENLMN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PRALDFHAET | GFIYFADTTS | YLIGRQKIDG | TERETILKDG | IHNVEGVAVD | WMGDNLYWTD | DGPKKTISVA | RLEKAAQTRK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TLIEGKMTHP | RAIVVDPLNG | WMYWTDWEED | PKDSRRGRLE | RAWMDGSHRD | IFVTSKTVLW | PNGLSLDIPA | GRLYWVDAFY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DRIETILLNG | TDRKIVYEGP | ELNHAFGLCH | HGNYLFWTEY | RSGSVYRLER | GVGGAPPTVT | LLRSERPPIF | EIRMYDAQQQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QVGTNKCRVN | NGGCSSLCLA | TPGSRQCACA | EDQVLDADGV | TCLANPSYVP | PPQCQPGEFA | CANSRCIQER | WKCDGDNDCL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DNSDEAPALC | HQHTCPSDRF | KCENNRCIPN | RWLCDGDNDC | GNSEDESNAT | CSARTCPPNQ | FSCASGRCIP | ISWTCDLDDD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| CGDRSDESAS | CAYPTCFPLT | QFTCNNGRCI | NINWRCDNDN | DCGDNSDEAG | CSHSCSSTQF | KCNSGRCIPE | HWTCDGDNDC |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GDYSDETHAN | CTNQATRPPG | GCHTDEFQCR | LDGLCIPLRW | RCDGDTDCMD | SSDEKSCEGV | THVCDPSVKF | GCKDSARCIS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KAWVCDGDND | CEDNSDEENC | ESLACRPPSH | PCANNTSVCL | PPDKLCDGND | DCGDGSDEGE | LCDQCSLNNG | GCSHNCSVAP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| GEGIVCSCPL | GMELGPDNHT | CQIQSYCAKH | LKCSQKCDQN | KFSVKCSCYE | GWVLEPDGES | CRSLDPFKPF | IIFSNRHEIR |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| RIDLHKGDYS | VLVPGLRNTI | ALDFHLSQSA | LYWTDVVEDK | IYRGKLLDNG | ALTSFEVVIQ | YGLATPEGLA | VDWIAGNIYW |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VESNLDQIEV | AKLDGTLRTT | LLAGDIEHPR | AIALDPRDGI | LFWTDWDASL | PRIEAASMSG | AGRRTVHRET | GSGGWPNGLT |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| VDYLEKRILW | IDARSDAIYS | ARYDGSGHME | VLRGHEFLSH | PFAVTLYGGE | VYWTDWRTNT | LAKANKWTGH | NVTVVQRTNT |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| QPFDLQVYHP | SRQPMAPNPC | EANGGQGPCS | HLCLINYNRT | VSCACPHLMK | LHKDNTTCYE | FKKFLLYARQ | MEIRGVDLDA |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| PYYNYIISFT | VPDIDNVTVL | DYDAREQRVY | WSDVRTQAIK | RAFINGTGVE | TVVSADLPNA | HGLAVDWVSR | NLFWTSYDTN |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| KKQINVARLD | GSFKNAVVQG | LEQPHGLVVH | PLRGKLYWTD | GDNISMANMD | GSNRTLLFSG | QKGPVGLAID | FPESKLYWIS |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SGNHTINRCN | LDGSGLEVID | AMRSQLGKAT | ALAIMGDKLW | WADQVSEKMG | TCSKADGSGS | VVLRNSTTLV | MHMKVYDESI |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| QLDHKGTNPC | SVNNGDCSQL | CLPTSETTRS | CMCTAGYSLR | SGQQACEGVG | SFLLYSVHEG | IRGIPLDPND | KSDALVPVSG |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| TSLAVGIDFH | AENDTIYWVD | MGLSTISRAK | RDQTWREDVV | TNGIGRVEGI | AVDWIAGNIY | WTDQGFDVIE | VARLNGSFRY |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| VVISQGLDKP | RAITVHPEKG | YLFWTEWGQY | PRIERSRLDG | TERVVLVNVS | ISWPNGISVD | YQDGKLYWCD | ARTDKIERID |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| LETGENREVV | LSSNNMDMFS | VSVFEDFIYW | SDRTHANGSI | KRGSKDNATD | SVPLRTGIGV | QLKDIKVFNR | DRQKGTNVCA |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 87 | 2 | 849.3639 | -63.47 | 2 | 30.0 | 12.9 | 1 | 1560-1573 | R.TVSCACPHLMKLHK.D | Carbamidomethyl: 4, 6; Oxidation: 10 |
| 2236 | 2 | 873.3305 | -116.11 | 2 | 57.8 | 15.6 | 1 | 1952-1966 | R.DQTWREDVVTNGIGR.V | |

# Detailed Protein Report

---

**Protein 490:** **PREDICTED: zinc finger and SCAN domain-containing protein 12 isoform X3 [Homo sapiens]**

**Accession:** gi|578812153
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 28.6
**MW [kDa]:** 65.7
**pI:** 6.2
**Sequence Coverage [%]:** 5.0
**No. of unique Peptides:** 1

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.27 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.85 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASTWAIQAH | MDQDEPLEVK | IEEEKYTTRQ | DWDLRKNNTH | SREVFRQYFR | QFCYQETSGP | REALSRLREL | CHQWLRPETH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TKEQILELLV | LEQFLTILPE | ELQAWVQEQH | PESGEEVVTV | LEDLERELDE | PGEQVSVHTG | EQEMFLQETV | RLRKEGEPSM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SLQSMKAQPK | YESPELESQQ | EQVLDVETGN | EYGNLKQEVS | EEMEPHGKTS | SKFENDMSKS | ARCGETREPE | EITEEPSACS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| REDKQPTCDE | NGVSLTENSD | HTEHQRICPG | EESYGCDDCG | KAFSQHSHLI | EHQRIHTGDR | PYKCEECGKA | FRGRTVLIRH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KIIHTGEKPY | KCNECGKAFG | RWSALNQHQR | LHTGEKHYHC | NDCGKAFSQK | AGLFHHIKIH | TRDKPYQCTQ | CNKSFSRRSI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LTQHQGVHTG | AKPYECNECG | KAFVYNSSLV | SHQEIHHKEK | CYQCKECGKS | FSQSGLIQHQ | RIHTGEKPYK | CDVCEKAFIQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RTSLTEHQRI | HTGERPYKCD | KCGKAFTQRS | VLTEHQRIHT | GERPYKCDEC | GNAFRGITSL | IQHQRIHTGE | KPYQCDECGK |
| 570 | | | | | | | |
| AFRQR | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 224 | 1 | 666.0908 | 127.27 | 3 | 32.5 | 10.0 | 0 | 422-438 | K.AFVYNSSLVSHQEIHHK.E | | WUP:QUP 0.85<br>QU:MU 0.27 |

# Detailed Protein Report

**Protein 491:** **PREDICTED: KN motif and ankyrin repeat domain-containing protein 1 isoform X16 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578816444 | **Score:** | 28.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 122.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.65 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.44 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAHTTKVNGS | ASGKAGDILS | GDQDKEQKDP | YFVETPYGYQ | LDLDFLKYVD | DIQKGNTIKR | LNIQKRRKPS | VPCPEPRTTS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GQQGIWTSTE | SLSSSNSDDN | KQCPNFLIAR | SQVTSTPISK | PPPPLETSLP | FLTIPENRQL | PPPSPQLPKH | NLHVTKTLME |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TRRRLEQERA | TMQMTPGEFR | RPRLASFGGM | GTTSSLPSFV | GSGNHNPAKH | QLQNGYQGNG | DYGSYAPAAP | TTSSMGSSIR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HSPLSSGIST | PVTNVSPMHL | QHIREQMAIA | LKRLKELEEQ | VRTIPVLQVK | ISVLQEEKRQ | LVSQLKNQRA | ASQINVCGVR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KRSYSAGNAS | QLEQLSRARR | SGGELYIDYE | EEEMETVEQS | TQRIKEFRQL | TADMQALEQK | IQDSSCEASS | ELRENGECRS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VAVGAEENMN | DIVVYHRGSR | SCKDAAVGTL | VEMRNCGVSV | TEAMLGVMTE | ADKEIELQQQ | TIESLKEKIY | RLEVQLRETT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HDREMTKLKQ | ELQAAGSRKK | VDKATMAQPL | VFSKVVEAVV | QTRDQMVGSH | MDLVDTCVGT | SVETNSVGIS | CQPECKNKVV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GPELPMNWWI | VKERVEMHDR | CAGRSVEMCD | KSVSVEVSVC | ETGSNTEESV | NDLTLLKTNL | NLKEVRSIGC | GDCSVDVTVC |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SPKECASRGV | NTEAVSQVEA | AVMAVPRTAD | QDTSTDLEQV | HQFTNTETAT | LIESCTNTCL | STLDKQTSTQ | TVETRTVAVG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EGRVKDINSS | TKTRSIGVGT | LLSGHSGFDR | PSAVKTKESG | VGQININDNY | LVGLKMRTIA | CGPPQLTVGL | TASRRSVGVG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DDPVGESLEN | PQPQAPLGMM | TGLDHYIERI | QKLLAEQQTL | LAENYSELAE | AFGEPHSQMG | SLNSQLISTL | SSINSVMKSA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| STEELRNPDF | QKTSLGKITG | NYLGYTCKCG | GLQSGSPLSS | QTSQPEQEVG | TSEGKPISSL | DAFPTQEGTL | SPVNLTDDQI |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| AAGLYACTNN | ESTLKSIMKK | KDGNKDSNGA | KKNLQFVGIN | GGYETTSSDD | SSSDESSSSE | SDDECDVIEY | PLEEEEEEED |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EDTRGMAEGH | HAVNIEGLKS | ARVEDEMQVQ | ECEPEKVEIR | ERYELSEKML | SACNLLKNTI | NDPKALTSKD | MWLNLWKWNL |
| 1130 | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 23 | 1 | 736.0076 | 3.59 | 3 | 30.0 | 11.9 | 1 | 1063-1080 | R.VEDEMQVQECEPEKVEIR.E | Oxidation: 5 | WUP:QUP 0.44<br>QU:MU 1.65 |

# Detailed Protein Report

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**Protein 492:** **PREDICTED: probable threonine--tRNA ligase 2, cytoplasmic isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578826598 | **Score:** | 28.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 82.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 6.5 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAAEALAAEA | VASRLERQEE | DIRWLWSEVE | RLRDEQLNAP | YSCQAEGPCL | TREVAQLRAE | NCDLRHRLCS | LRLCLAEERS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RQATLESAEL | EAAQEAGAQP | PPSQSQDKDM | KKKKMKESEA | DSEVKHQPIF | IKERLKLFEI | LKKDHQLLLA | IYGKKGDTSN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IITVRVADGQ | TVQGEVWKTT | PYQVAAEISQ | ELAESTVIAK | VNGELWDLDR | PLEGDSSLEL | LTFDNEEAQA | VYWHSSAHIL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GEAMELYYGG | HLCYGPPIEN | GFYYDMFIED | RAVSSTELSA | LENICKAIIK | EKQPFERLEV | SKEILLEMFK | YNKFKCRILN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EKVNTATTTV | YRCGPLIDLC | KGPHVRHTGK | IKTIKIFKNS | STYWEGNPEM | ETLQRIYGIS | FPDNKMMRDW | EKFQEEAKNR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DHRKIGKEQE | LFFFHDLSPG | SCFFLPRGAF | IYNTLTDFIR | EEYHKRDFTE | VLSPNMYNSK | LWEASGHWQH | YSENMFTFEI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EKDTFALKPM | NCPGHCLMFA | HRPRSWREMP | IRFADFGVLH | RNELSGTLSG | LTRVRRFQQD | DAHIFCTVEQ | IEEEIKGCLQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FLQSVYSTFG | FSFQLNLSTR | PENFLGEIEM | WNEAEKQLQN | SLMDFGEPWK | MNPGDGAFYG | PKIDIKIKDA | IGRYHQCATI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QLDFQLPIRF | NLTYVSKDGD | DKKRPVIIHR | AILGSVERMI | AILSENYGGK | WYPVNFLKKD | LWLTLTWITV | VH |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2780 | 1 | 849.0600 | -40.11 | 3 | 65.9 | 10.9 | 2 | 1-23 | -.MAAEALAAEAVASRLERQEEDIR.W | Oxidation: 1 |
| 569 | 1 | 689.8555 | -24.02 | 4 | 37.1 | 17.6 | 2 | 627-649 | K.IKDAIGRYHQCATIQLDFQLPIR.F | Carbamidomethyl: 11 |

# Detailed Protein Report

## **Protein 493:** PREDICTED: keratin-associated protein 9-8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578846434 | **Score:** | 28.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 16.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 20.1 |
| | | **No. of unique Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MTHCCSPCCQ PTCCRTTCWK PTTVTTCSST PCCQPSCCVS SCCQPCCRPT CCQNTCCQPI CVTSCCQPSC CSTPCCQPTC
        90        100        110        120        130        140        150        160
CGQTSCGSSC GQSSSCAPVY CRRTCYHPTT VCLPGCLNQS CGSSCCQPCC RPACCETTCC RTTCFQPTCV YSCCQPSCC
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2540 | 1 | 856.9279 | 151.49 | 2 | 62.4 | 10.7 | 0 | 2-15 | M.THCCSPCCQPTCCR.T | Carbamidomethyl: 3, 4, 13 |
| 2119 | 1 | 1044.4110 | 33.02 | 2 | 56.4 | 17.8 | 0 | 142-159 | R.TTCFQPTCVYSCCQPSCC.- | Carbamidomethyl: 3, 8 |

# Detailed Protein Report

**Protein 494:** **ectonucleotide pyrophosphatase/phosphodiesterase family member 2 isoform 3 preproprotein [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|195947389 | **Score:** | 28.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 101.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MARRSSFQSC | QIISLFTFAV | GVNICLGFTA | HRIKRAEGWE | EGPPTVLSDS | PWTNISGSCK | GRCFELQEAG | PPDCRCDNLC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KSYTSCCHDF | DELCLKTARG | WECTKDRCGE | VRNEENACHC | SEDCLARGDC | CTNYQVVCKG | ESHWVDDDCE | EIKAAECPAG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FVRPPLIIFS | VDGFRASYMK | KGSKVMPNIE | KLRSCGTHSP | YMRPVYPTKT | FPNLYTLATG | LYPESHGIVG | NSMYDPVFDA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TFHLRGREKF | NHRWWGGQPL | WITATKQGVK | AGTFFWSVVI | PHERRILTIL | QWLTLPDHER | PSVYAFYSEQ | PDFSGHKYGP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FGPEMTNPLR | EIDKIVGQLM | DGLKQLKLHR | CVNVIFVGDH | GMEDVTCDRT | EFLSNYLTNV | DDITLVPGTL | GRIRSKFSNN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AKYDPKAIIA | NLTCKKPDQH | FKPYLKQHLP | KRLHYANNRR | IEDIHLLVER | RWHVARKPLD | VYKKPSGKCF | FQGDHGFDNK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VNSMQTVFVG | YGSTFKYKTK | VPPFENIELY | NVMCDLLGLK | PAPNNGTHGS | LNHLLRTNTF | RPTMPEEVTR | PNYPGIMYLQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SDFDLGCTCD | DKVEPKNKLD | ELNKRLHTKG | STEAETRKFR | GSRNENKENI | NGNFEPRKER | HLLYGRPAVL | YRTRYDILYH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TDFESGYSEI | FLMPLWTSYT | VSKQAEVSSV | PDHLTSCVRP | DVRVSPSFSQ | NCLAYKNDKQ | MSYGFLFPPY | LSSSPEAKYD |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AFLVTNMVPM | YPAFKRVWNY | FQRVLVKKYA | SERNGVNVIS | GPIFDYDYDG | LHDTEDKIKQ | YVEGSSIPVP | THYYSIITSC |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LDFTQPADKC | DGPLSVSSFI | LPHRPDNEES | CNSSEDESKW | VEELMKMHTA | RVRDIEHLTS | LDFFRKTSRS | YPEILTLKTY |
| 890 | | | | | | | |
| LHTYESEI | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1449 | 1 | 405.2085 | 100.81 | 2 | 48.3 | 16.6 | 0 | 76-81 | R.CDNLCK.S | Carbamidomethyl: 1, 5 |

# Detailed Protein Report

## Protein 495: putative ATP-dependent RNA helicase DHX57 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|39777586 | **Score:** | 28.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 155.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSSVRRKGK | PGKGGGKGSS | RGGRGGRSHA | SKSHGSGGGG | GGGGGGGGGN | RKASSRIWDD | GDDFCIFSES | RRPSRPSNSN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ISKGESRPKW | KPKAKVPLQT | LHMTSENQEK | VKALLRDLQE | QDADAGSERG | LSGEEEDDEP | DCCNDERYWP | AGQEPSLVPD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LDPLEYAGLA | SVEPYVPEFT | VSPFAVQKLS | RYGFNTERCQ | AVLRMCDGDV | GASLEHLLTQ | CFSETFGERM | KISEAVNQIS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LDECMEQRQE | EAFALKSICG | EKFIERIQNR | VWTIGLELEY | LTSRFRKSKP | KESTKNVQEN | SLEICKFYLK | GNCKFGSKCR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FKHEVPPNQI | VGRIERSVDD | SHLNAIEDAS | FLYELEIRFS | KDHKYPYQAP | LVAFYSTNEN | LPLACRLHIS | EFLYDKALTF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AETSEPVVYS | LITLLEEESE | IVKLLTNTHH | KYSDPPVNFL | PVPSRTRINN | PACHKTVIPN | NSFVSNQIPE | VEKASESEES |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DEDDGPAPVI | VENESYVNLK | KKISKRYDWQ | AKSVHAENGK | ICKQFRMKQA | SRQFQSILQE | RQSLPAWEER | ETILNLLRKH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QVVVISGMTG | CGKTTQIPQF | ILDDSLNGPP | EKVANIICTQ | PRRISAISVA | ERVAKERAER | VGLTVGYQIR | LESVKSSATR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LLYCTTGVLL | RRLEGDTALQ | GVSHIIVDEV | HERTEESDFL | LLVLKDIVSQ | RPGLQVILMS | ATLNAELFSD | YFNSCPVITI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PGRTFPVDQF | FLEDAIAVTR | YVLQDGSPYM | RSMKQISKEK | LKARRNRTAF | EEVEEDLRLS | LHLQDQDSVK | DAVPDQQLDF |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KQLLARYKGV | SKSVIKTMSI | MDFEKVNLEL | IEALLEWIVD | GKHSYPPGAI | LVFLPGLAEI | KMLYEQLQSN | SLFNNRRSNR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| CVIHPLHSSL | SSEEQQAVFV | KPPAGVTKII | ISTNIAETSI | TIDDVVYVID | SGKMKEKRYD | ASKGMESLED | TFVSQANALQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RKGRAGRVAS | GVCFHLFTSH | HYNHQLLKQQ | LPEIQRVPLE | QLCLRIKILE | MFSAHNLQSV | FSRLIEPPHT | DSLRASKIRL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RDLGALTPDE | RLTPLGYHLA | SLPVDVRIGK | LMLFGSIFRC | LDPALTIAAS | LAFKSPFVSP | WDKKEEANQK | KLEFAFANSD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| YLALLQAYKG | WQLSTKEGVR | ASYNYCRQNF | LSGRVLQEMA | SLKRQFTELL | SDIGFAREGL | RAREIEKRAQ | GGDGVLDATG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EEANSNAENP | KLISAMLCAA | LYPNVVQVKS | PEGKFQKTST | GAVRMQPKSA | ELKFVTKNDG | YVHIHPSSVN | YQVRHFDSPY |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LLYHEKIKTS | RVFIRDCSMV | SVYPLVLFGG | GQVNVQLQRG | EFVVSLDDGW | IRFVAASHQV | AELVKELRCE | LDQLLQDKIK |
| 1370 | 1380 | 1390 | | | | | |
| NPSIDLCTCP | RGSRIISTIV | KLVTTQ | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1483 | 2 | 699.6611 | -193.23 | 2 | 48.2 | 18.4 | 0 | 33-51 | K.SHGSGGGGGGGGGGGGGNR.K | |

# Detailed Protein Report

## Protein 496: PREDICTED: DNA mismatch repair protein Mlh3 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530403519 | **Score:** | 28.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 143.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MIKCLSVEVQ | AKLRSGLAIS | SLGQCVEELA | LNSIDAEAKC | VAVRVNMETF | QVQVIDNGFG | MGSDDVEKVG | NRYFTSKCHS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VQDLENPRFY | GFRGEALANI | ADMASAVEIS | SKKNRTMKTF | VKLFQSGKAL | KACEADVTRA | SAGTTVTVYN | LFYQLPVRRK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CMDPRLEFEK | VRQRIEALSL | MHPSISFSLR | NDVSGSMVLQ | LPKTKDVCSR | FCQIYGLGKS | QKLREISFKY | KEFELSGYIS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SEAHYNKNMQ | FLFVNKRLVL | RTKLHKLIDF | LLRKESIICK | PKNGPTSRQM | NSSLRHRSTP | ELYGIYVINV | QCQFCEYDVC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MEPAKTLIEF | QNWDTLLFCI | QEGVKMFLKQ | EKLFVELSGE | DIKEFSEDNG | FSLFDATLQK | RVTSDERSNF | QEACNNILDS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YEMFNLQSKA | VKRKTTAENV | NTQSSRDSEA | TRKNTNDAFL | YIYESGGPGH | SKMTEPSLQN | KDSSCSESKM | LEQETIVASE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AGENEKHKKS | FLEHSSLENP | CGTSLEMFLS | PFQTPCHFEE | SGQDLEIWKE | STTVNGMAAN | ILKNNRIQNQ | PKRFKDATEV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GCQPLPFATT | LWGVHSAQTE | KEKKKESSNC | GRRNVFSYGR | VKLCSTGFIT | HVVQNEKTKS | TETEHSFKNY | VRPGPTRAQE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TFGNRTRHSV | ETPDIKDLAS | TLSKESGQLP | NKKNCRTNIS | YGLENEPTAT | YTMFSAFQEG | SKKSQTDCIL | SDTSPSFPWY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RHVSNDSRKT | DKLIGFSKPI | VRKKLSLSSQ | LGSLEKFKRQ | YGKVENPLDT | EVEESNGVTT | NLSLQVEPDI | LLKDKNRLEN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SDVCKITTME | HSDSDSSCQP | ASHILNSEKF | PFSKDEDCLE | QQMPSLRESP | MTLKELSLFN | RKPLDLEKSS | ESLASKLSRL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KGSERETQTM | GMMSRFNELP | NSDSSRKDSK | LCSVLTQDFC | MLFNNKHEKT | ENGVIPTSDS | ATQDNSFNKN | SKTHSNSNTT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ENCVISETPL | VLPYNNSKVT | GKDSDVLIRA | SEQQIGSLDS | PSGMLMNPVE | DATGDQNGIC | FQSEESKARA | CSETEESNTC |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| CSDWQRHFDV | ALGRMVYVNK | MTGLSTFIAP | TEDIQAACTK | DLTTVAVDVV | LENGSQYRCQ | PFRSDLVLPF | LPRARAERTV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| MRQDNRDTVD | DTVSSESLQS | LFSEWDNPVF | ARYPEVAVDV | SSGQAESLAV | KIHNILYPYR | FTKGMIHSMQ | VLQQVDNKFI |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ACLMSTKTEE | NGEAGGNLLV | LVDQHAAHER | IRLEQLIIDS | YEKQQAQGSG | RKKLLSSTLI | PPLEITVTEE | QRRLL |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 964 | 1 | 523.2194 | -171.68 | 2 | 40.4 | 11.9 | 2 | 877-885 | K.LSRLKGSER.E | |

# Detailed Protein Report

## Protein 497: phosphatidylinositol phosphatase PTPRQ precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|222537743 | **Score:** | 28.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 257.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDFLIIFLLL | FIGTSETQVD | VSNVVPGTRY | DITISSISTT | YTSPVTRIVT | TNVTKPGPPV | FLAGERVGSA | GILLSWNTPP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NPNGRIISYI | VKYKEVCPWM | QTVYTQVRSK | PDSLEVLLTN | LNPGTTYEIK | VAAENSAGIG | VFSDPFLFQT | AESAPGKVVN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LTVEAYNASA | VKLIWYLPRQ | PNGKITSFKI | SVKHARSGIV | VKDVSIRVED | ILTGKLPECN | ENSESFLWST | ASPSPTLGRV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TPPSRTTHSS | STLTQNEISS | VWKEPISFVV | THLRPYTTYL | FEVSAATTEA | GYIDSTIVRT | PESVPEGPPQ | NCVTGNITGK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SFSILWDPPT | IVTGKFSYRV | ELYGPSGRIL | DNSTKDLKFA | FTNLTPFTMY | DVYIAAETSA | GTGPKSNISV | FTPPDVPGAV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FDLQLAEVES | TQVRITWKKP | RQPNGIINQY | RVKVLVPETG | IILENTLLTG | NNEYINDPMA | PEIVNIVEPM | VGLYEGSAEM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SSDLHSLATF | IYNSHPDKNF | PARNRAEDQT | SPVVTTRNQY | ITDIAAEQLS | YVIRRLVPFT | EHMISVSAFT | IMGEGPPTVL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SVRTRQQVPS | SIKIINYKNI | SSSSILLYWD | PPEYPNGKIT | HYTIYAMELD | TNRAFQITTI | DNSFLITGLK | KYTKYKMRVA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ASTHVGESSL | SEENDIFVRT | SEDEPESSPQ | DVEVIDVTAD | EIRLKWSPPE | KPNGIIIAYE | VLYKNIDTLY | MKNTSTTDII |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LRNLRPHTLY | NISVRSYTRF | GHGNQVSSLL | SVRTSETVPD | SAPENITYKN | ISSGEIELSF | LPPSSPNGII | QKYTIYLKRS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NGNEERTINT | TSLTQNIKVL | KKYTQYIIEV | SASTLKGEGV | RSAPISILTE | EDAPDSPPQD | FSVKQLSGVT | VKLSWQPPLE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PNGIILYYTV | YVWNRSSLKT | INVTETSLEL | SDLDYNVEYS | AYVTASTRFG | DGKTRSNIIS | FQTPEGAPSD | PPKDVYYANL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SSSSIILFWT | PPSKPNGIIQ | YYSVYYRNTS | GTFMQNFTLH | EVTNDFDNMT | VSTIIDKLTI | FSYYTFWLTA | STSVGNGNKS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SDIIEVYTDQ | DIPEGFVGNL | TYESISSTAI | NVSWVPPAQP | NGLVFYYVSL | ILQQTPRHVR | PPLVTYERSI | YFDNLEKYTD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| YILKITPSTE | KGFSDTYTAQ | LYIKTEEDVP | ETSPIINTFK | NLSSTSVLLS | WDPPVKPNGA | IISYDLTLQG | PNENYSFITS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DNYIILEELS | PFTLYSFFAA | ARTRKGLGPS | SILFFYTDES | VPLAPPQNLT | LINCTSDFVW | LKWSPSPLPG | GIVKVYSFKI |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| HEHETDTIYY | KNISGFKTEA | KLVGLEPVST | YSIRVSAFTK | VGNGNQFSNV | VKFTTQESVP | DVVQNMQCMA | TSWQSVLVKW |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| DPPKKANGII | TQYMVTVERN | STKVSPQDHM | YTFIKLLANT | SYVFKVRAST | SAGEGDESTC | HVSTLPETVP | SVPTNIAFSD |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| VQSTSATLTW | IRPDTILGYF | QNYKITTQLR | AQKCKEWESE | ECVEYQKIQY | LYEAHLTEET | VYGLKKFRWY | RFQVAASTNA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| GYGNASNWIS | TKTLPGPPDG | PPENVHVVAT | SPFSISISWS | EPAVITGPTC | YLIDVKSVDN | DEFNISFIKS | NEENKTIEIK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| DLEIFTRYSV | VITAFTGNIS | AAYVEGKSSA | EMIVTTLESA | PKDPPNNMTF | QKIPDEVTKF | QLTFLPPSQP | NGNIQVYQAL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| VYREDDPTAV | QIHNLSIIQK | TNTFVIAMLE | GLKGGHTYNI | SVYAVNSAGA | GPKVPMRITM | DIKAPARPKT | KPTPIYDATG |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| KLLVTSTTIT | IRMPICYYSD | DHGPIKNVQV | LVTETGAQHD | GNVTKWYDAY | FNKARPYFTN | EGFPNPPCTE | GKTKFSGNEE |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| IYIIGADNAC | MIPGNEDKIC | NGPLKPKKQY | LFKFRATNIM | GQFTDSDYSD | PVKTLGEGLS | ERTVEIILSV | TLCILSIILL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| GTAIFAFARI | RQKQKEGGTY | SPQDAEIIDT | KLKLDQLITV | ADLELKDERL | TRLLSYRKSI | KPISKKSFLQ | HVEELCTNNN |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| LKFQEEFSEL | PKFLQDLSST | DADLPWNRAK | NRFPNIKPYN | NNRVKLIADA | SVPGSDYINA | SYISGYLCPN | EFIATQGPLP |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| GTVGDFWRMV | WETRAKTLVM | LTQCFEKGRI | RCHQYWPEDN | KPVTVFGDIV | ITKLMEDVQI | DWTIRDLKIE | RHGDCMTVRQ |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 13 | 1 | 1002.9641 | -45.61 | 2 | 29.1 | 11.9 | 0 | 30-47 | R.YDITISSISTTYTSPVTR.I | |

# Detailed Protein Report

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**Protein 498:** **zinc finger and SCAN domain-containing protein 32 isoform b [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|32129212 | **Score:** | 28.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 6.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.42 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.51 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578828138 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger and SCAN domain-containing protein 32 isoform X7 [Homo sapiens] |
| gi\|530408311 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger and SCAN domain-containing protein 32 isoform X6 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MRDNRAVSLC | QQEWMCPGPA | QRALYRGATQ | RKDSHVSLAT | GVPWGYEETK | TLLAILSSSQ | FYGKLQTCQQ | NSQIYRAMAE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GLWEQGFLRT | PEQCRTKFKS | LQLSYRKVRR | GRVPEPCIFY | EEMNALSGSW | ASAPPMASDA | VPGQEGSDIE | AGELNHQNGE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PTEVEDGTVD | GADRDEKDFR | NPGQEVRKLD | LPVLFPNRLG | FEFKNEIKKE | NLKWDDSEEV | EINKALQRKS | RGVYWHSELQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KGLESEPTSR | RQCRNSPGES | EEKTPSQEKM | SHQSFCARDK | ACTHILCGKN | CSQSVHSPHK | PALKLEKVSQ | CPECGKTFSR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SSYLVRHQRI | HTGEKPHKCS | ECGKGFSERS | NLTAHLRTHT | GERPYQCGQC | GKSFNQSSSL | IVHQRTHTGE | KPYQCIVCGK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RFNNSSQFSA | HRRIHTGESP | YKCAVCGKIF | NNSSHFSAHR | KTHTGEKPYR | CSHCERGFTK | NSALTRHQTV | HMKAVLSSQE |
| 490 | | | | | | | |
| GRDAL | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 707 | 1 | 647.6537 | -225.58 | 2 | 38.4 | 15.1 | 0 | 402-412 | R.FNNSSQFSAHR.R | | WUP:QUP 0.51<br>QU:MU 2.42 |

# Detailed Protein Report

## Protein 499: PREDICTED: peroxisomal biogenesis factor 5 isoform X9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578822993 | **Score:** | 28.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 63.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.2 |
| | | **Sequence Coverage [%]:** | 4.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDDLLAEMQQ | IEQSNFRQAP | QRAPGVADLA | LSENWAQEFL | AAGDAVDVTQ | DYNETDWSQE | FISEVTDPLS | VSPARWAEEY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LEQSEEKLWL | GEPEGTATDR | WYDEYHPEED | LQHTASDFVA | KVDDPKLANS | EWPVCVSVPQ | FLKFVRQIGE | GQVSLESGAG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SGRAQAEQWA | AEFIQQQGTS | DAWVDQFTRP | VNTSALDMEF | ERAKSAIESD | VDFWDKLQAE | LEEMAKRDAE | AHPWLSDYDD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LTSATYDKGY | QFEEENPLRD | HPQPFEEGLR | RLQEGDLPNA | VLLFEAAVQQ | DPKHMEAWQY | LGTTQAENEQ | ELLAISALRR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CLELKPDNQT | ALMALAVSFT | NESLQRQACE | TLRDWLRYTP | AYAHLVTPAE | EGAGGAGLGP | SKRILGSLLS | DSLFLEVKEL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FLAAVRLDPT | SIDPDVQCGL | GVLFNLSGEY | DKAVDCFTAA | LSVRPNDYLL | WNKLGATLAN | GNQSEEAVAA | YRRALELQPG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YIRSRYNLGI | SCINLGAHRE | AVEHFLEALN | MQRKSRGPRG | EGGAMSENIW | STLRLALSML | GQSDAYGAAD | ARDLSTLLTM |
| 570 | | | | | | | |
| FGLPQ | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 438 | 1 | 718.3578 | -29.07 | 2 | 34.0 | 11.2 | 0 | 553-565 | R.DLSTLLTMFGLPQ.- | |

# Detailed Protein Report

**Protein 500:** **proto-oncogene vav isoform 3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|384551649 | **Score:** | 28.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 94.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MELWRQCTHW | LIQCRVLPPS | HRVTWDGAQV | CELAQALRDG | VLLCQLLNNL | LPHAINLREV | NLRPQMSQFL | CLKNIRTFLS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TCCEKFGLKR | SELFEAFDLF | DVQDFGKVIY | TLSALSWTPI | AQNRGIMPFP | TEEESVGDED | IYSGLSDQID | DTVEEDEDLY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DCVENEEAEG | DEIYEDLMRS | EPVSMPHFLK | PLQRFLKPQD | IEIIFINIED | LLRVHTHFLK | EMKEALGTPG | AANLYQVFIK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YKERFLVYGR | YCSQVESASK | HLDRVAAARE | DVQMKLEECS | QRANNGRFTL | RDLLMVPMQR | VLKYHLLLQE | LVKHTQEAME |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KENLRLALDA | MRDLAQCVNE | VKRDNETLRQ | ITNFQLSIEN | LDQSLAHYGR | PKIDGELKIT | SVERRSKMDR | YAFLLDKALL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ICKRRGDSYD | LKDFVNLHSF | QVRDDSSGDR | DNKKWSHMFL | LIEDQGAQGY | ELFFKTRELK | KKWMEQFEMA | ISNIYPENAT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ANGHDFQMFS | FEETTSCKAC | QMLLRGTFYQ | GYRCHRCRAS | AHKECLGRVP | PCGRHGQDFP | GTMKKDKLHR | RAQDKKRNEL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GLPKMEVFQE | YYGLPPPPGA | IGPFLRLNPG | DIVELTKAEA | EQNWWEGRNT | STNEIGWFPC | NRVKPYVHGP | PQDLSVHLWY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AGPMERAGAE | SILANRSDGT | FLVRQRVKDA | AEFAISIKYN | VEVKHIKIMT | AEGLYRITEK | KAFRGLTELV | EFYQQNSLKD |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CFKSLDTTLQ | FPFKEPEKRT | ISRPAVGSTK | YFGTAKARYD | FCARDRSELS | LKEGDIIKIL | NKKGQQGWWR | GEIYGRVGWF |
| 810 | 820 | | | | | | |
| PANYVEEDYS | EYC | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2147 | 1 | 788.3156 | -165.74 | 2 | 56.7 | 13.2 | 2 | 665-678 | R.QRVKDAAEFAISIK.Y | |

# Detailed Protein Report

**Protein 501:** **sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|148886654 | **Score:** | 28.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 389.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| | | **Sequence Coverage [%]:** | 0.7 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 2.04 | **CV:** 0.00 % | **No. of Peptides:** 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWPRLAFCCW | GLALVSGWAT | FQQMSPSRNF | SFRLFPETAP | GAPGSIPAPP | APGDEAAGSR | VERLGQAFRR | RVRLLRELSE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RLELVFLVDD | SSSVGEVNFR | SELMFVRKLL | SDFPVVPTAT | RVAIVTFSSK | NYVVPRVDYI | STRRARQHKC | ALLLQEIPAI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SYRGGGTYTK | GAFQQAAQIL | LHARENSTKV | VFLITDGYSN | GGDPRPIAAS | LRDSGVEIFT | FGIWQGNIRE | LNDMASTPKE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EHCYLLHSFE | EFEALARRAL | HEDLPSGSFI | QDDMVHCSYL | CDEGKDCCDR | MGSCKCGTHT | GHFECICEKG | YYGKGLQYEC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TACPSGTYKP | EGSPGGISSC | IPCPDENHTS | PPGSTSPEDC | VCREGYRASG | QTCELVHCPA | LKPPENGYFI | QNTCNNHFNA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ACGVRCHPGF | DLVGSSIILC | LPNGLWSGSE | SYCRVRTCPH | LRQPKHGHIS | CSTREMLYKT | TCLVACDEGY | RLEGSDKLTC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QGNSQWDGPE | PRCVERHCST | FQMPKDVIIS | PHNCGKQPAK | FGTICYVSCR | QGFILSGVKE | MLRCTTSGKW | NVGVQAAVCK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DVEAPQINCP | KDIEAKTLEQ | QDSANVTWQI | PTAKDNSGEK | VSVHVHPAFT | PPYLFPIGDV | AIVYTATDLS | GNQASCIFHI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KVIDAEPPVI | DWCRSPPPVQ | VSEKVHAASW | DEPQFSDNSG | AELVITRSHT | QGDLFPQGET | IVQYTATDPS | GNNRTCDIHI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VIKGSPCEIP | FTPVNGDFIC | TPDNTGVNCT | LTCLEGYDFT | EGSTDKYYCA | YEDGVWKPTY | TTEWPDCAKK | RFANHGFKSF |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EMFYKAARCD | DTDLMKKFSE | AFETTLGKMV | PSFCSDAEDI | DCRLEENLTK | KYCLEYNYDY | ENGFAIGPGG | WGAANRLDYS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| YDDFLDTVQE | TATSIGNAKS | SRIKRSAPLS | DYKIKLIFNI | TASVPLPDER | NDTLEWENQQ | RLLQTLETIT | NKLKRTLNKD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PMYSFQLASE | ILIADSNSLE | TKKASPFCRP | GSVLRGRMCV | NCPLGTYYNL | EHFTCESCRI | GSYQDEEGQL | ECKLCPSGMY |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TEYIHSRNIS | DCKAQCKQGT | YSYSGLETCE | SCPLGTYQPK | FGSRSCLSCP | ENTSTVKRGA | VNISACGVPC | PEGKFSRSGL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| MPCHPCPRDY | YQPNAGKAFC | LACPFYGTTP | FAGSRSITEC | SSFSSTFSAA | EESVVPPASL | GHIKKRHEIS | SQVFHECFFN |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PCHNSGTCQQ | LGRGYVCLCP | LGYTGLKCET | DIDECSPLPC | LNNGVCKDLV | GEFICECPSG | YTGQRCEENI | NECSSSPCLN |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KGICVDGVAG | YRCTCVKGFV | GLHCETEVNE | CQSNPCLNNA | VCEDQVGGFL | CKCPPGFLGT | RCGKNVDECL | SQPCKNGATC |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KDGANSFRCL | CAAGFTGSHC | ELNINECQSN | PCRNQATCVD | ELNSYSCKCQ | PGFSGKRCET | EQSTGFNLDF | EVSGIYGYVM |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LDGMLPSLHA | LTCTFWMKSS | DDMNYGTPIS | YAVDNGSDNT | LLLTDYNGWV | LYVNGREKIT | NCPSVNDGRW | HHIAITWTSA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| NGIWKVYIDG | KLSDGGAGLS | VGLPIPGGGA | LVLGQEQDKK | GEGFSPAESF | VGSISQLNLW | DYVLSPQQVK | SLATSCPEEL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| SKGNVLAWPD | FLSGIVGKVK | IDSKSIFCSD | CPRLGGSVPH | LRTASEDLKP | GSKVNLFCDP | GFQLVGNPVQ | YCLNQGQWTQ |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| PLPHCERISC | GVPPPLENGF | HSADDFYAGS | TVTYQCNNGY | YLLGDSRMFC | TDNGSWNGVS | PSCLDVDECA | VGSDCSEHAS |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| CLNVDGSYIC | SCVPPYTGDG | KNCAEPIKCK | APGNPENGHS | SGEIYTVGAE | VTFSCQEGYQ | LMGVTKITCL | ESGEWNHLIP |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| YCKAVSCGKP | AIPENGCIEE | LAFTFGSKVT | YRCNKGYTLA | GDKESSCLAN | SSWSHSPPVC | EPVKCSSPEN | INNGKYILSG |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LTYLSTASYS | CDTGYSLQGP | SIIECTASGI | WDRAPPACHL | VFCGEPPAIK | DAVITGNNFT | FRNTVTYTCK | EGYTLAGLDT |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| IECLADGKWS | RSDQQCLAVS | CDEPPIVDHA | SPETAHRLFG | DIAFYYCSDG | YSLADNSQLL | CNAQGKWVPP | EGQDMPRCIA |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| HFCEKPPSVS | YSILESVSKA | KFAAGSVVSF | KCMEGFVLNT | SAKIECMRGG | QWNPSPMSIQ | CIPVRCGEPP | SIMNGYASGS |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2764 | 2 | 639.3642 | -0.12 | 2 | 63.1 | 17.4 | 2 | 903-913 | R.IKRSAPLSDYK.I | | |
| 281 | 1 | 743.8595 | -21.15 | 2 | 33.5 | 10.8 | 0 | 1214-1227 | R.GYVCLCPLGYTGLK.C | | QU:MU 2.04 |

# Detailed Protein Report

## Protein 502: PREDICTED: protein NLRC5 isoform X13 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578829278 | **Score:** | 28.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 152.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDPVGLQLGN | KNLWSCLVRL | LTKDPEWLNA | KMKFFLPNTD | LDSRNETLDP | EQRVILQLNK | LHVQGSDTWQ | SFIHCVCMQL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EVPLDLEVLL | LSTFGYDDGF | TSQLGAEGKS | QPESQLHHGL | KRPHQSCGSS | PRRKQCKKQQ | LELAKKYLQL | LRTSAQQRYR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SQIPGSGQPH | AFHQVYVPPI | LRRATASLDT | PEGAIMGDVK | VEDGADVSIS | DLFNTRVNKG | PRVTVLLGKA | GMGKTTLAHR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LCQKWAEGHL | NCFQALFLFE | FRQLNLITRF | LTPSELLFDL | YLSPESDHDT | VFQYLEKNAD | QVLLIFDGLD | EALQPMGPDG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PGPVLTLFSH | LCNGTLLPGC | RVMATSRPGK | LPACLPAEAA | MVHMLGFDGP | RVEEYVNHFF | SAQPSREGAL | VELQTNGRLR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SLCAVPALCQ | VACLCLHHLL | PDHAPGQSVA | LLPNMTQLYM | QMVLALSPPG | HLPTSSLLDL | GEVALRGLET | GKVIFYAKDI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| APPLIAFGAT | HSLLTSFCVC | TGPGHQQTGY | AFTHLSLQEF | LAALHLMASP | KVNKDTLTQY | VTLHSRWVQR | TKARLGLSDH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LPTFLAGLAS | CTCRPFLSHL | AQGNEDCVGA | KQAAVVQVLK | KLATRKLTGP | KVVELCHCVD | ETQEPELASL | TAQSLPYQLP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FHNFPLTCTD | LATLTNILEH | REAPIHLDFD | GCPLEPHCPE | ALVGCGQIEN | LSFKSRKCGD | AFAEALSRSL | PTMGRLQMLG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LAGSKITARG | ISHLVKALPL | CPQLKEVSFR | DNQLSDQVVL | NIVEVLPHLP | RLRKLDLSSN | SICVSTLLCL | ARVAVTCPTV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RMLQAREADL | IFLLSPPTET | TAELQRAPDL | QESDGQRKGA | QSRSLTLRLQ | KCQLQVHDAE | ALIALLQEGP | HLEEVDLSGN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QLEDEGCRLM | AEAASQLHIA | RKLDLSNNGL | SVAGVHCVLR | AVSACWTLAE | LHISLQHKTV | IFMFAQEPEE | QKGPQERAAF |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LDSLMLQMPS | ELPLSSRRMR | LTHCGLQEKH | LEQLCKALGG | SCHLGHLHLD | FSGNALGDEG | AARLAQLLPG | LGALQSLNLS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ENGLSLDAVL | GLVRCFSTLQ | WLFRLDISFE | SQHILLRGDK | TSRDMWATGS | LPDFPAAAKF | LGFRQRCIPR | SLCLSECPLE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PPSLTRLCAT | LKDCPGPLEL | QLSCEFLSDQ | SLETLLDCLP | QLPQLSLLQL | SQTGLSPKSP | FLLANTLSLC | PRVKKVDLRS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LHHATLHFRS | NEEEEGVCCG | RFTGCSLSQE | HVESLCWLLS | KCKDLSQVDL | SANLLGDSGL | RCLLECLPQV | PISGLLDLSH |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| NSISQESALY | LLETLPSCPR | VREASVNLGS | EQSFRIHFSR | EDQAGKTLRL | SECSFRPEHV | SRLATGLSKS | LQLTELTLTQ |
| 1370 | 1380 | 1390 | | | | | |
| CCLGQKQLAI | LLSLVGRPAG | LFSLS | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1152 | 1 | 983.1542 | 145.88 | 2 | 44.5 | 13.7 | 0 | 775-792 | K.LDLSSNSICVSTLLCLAR.V | Carbamidomethyl: 15 |

# Detailed Protein Report

## Protein 503: DNA repair and recombination protein RAD54B isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|6912622 | **Score:** | 28.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 102.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRRSAAPSQL | QGNSFKKPKF | IPPGRSNPGL | NEEITKLNPD | IKLFEGVAIN | NTFLPSQNDL | RICSLNLPSE | ESTREINNRD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NCSGKYCFEA | PTLATLDPPH | TVHSAPKEVA | VSKEQEEKSD | SLVKYFSVVW | CKPSKKKHKK | WEGDAVLIVK | GKSFILKNLE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GKDIGRGIGY | KFKELEKIEE | GQTLMICGKE | IEVMGVISPD | DFSSGRCFQL | GGGSTAISHS | SQVARKCFSN | PFKSVCKPSS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KENRQNDFQN | CKPRHDPYTP | NSLVMPRPDK | NHQWVFNKNC | FPLVDVVIDP | YLVYHLRPHQ | KEGIIFLYEC | VMGMRMNGRC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GAILADEMGL | GKTLQCISLI | WTLQCQGPYG | GKPVIKKTLI | VTPGSLVNNW | KKEFQKWLGS | ERIKIFTVDQ | DHKVEEFIKS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IFYSVLIISY | EMLLRSLDQI | KNIKFDLLIC | DEGHRLKNSA | IKTTTALISL | SCEKRIILTG | TPIQNDLQEF | FALIDFVNPG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ILGSLSSYRK | IYEEPIILSR | EPSASEEEKE | LGERRAAELT | CLTGLFILRR | TQEIINKYLP | PKIENVVFCR | PGALQIELYR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KLLNSQVVRF | CLQGLLENSP | HLICIGALKK | LCNHPCLLFN | SIKEKECSST | CDKNEEKSLY | KGLLSVFPAD | YNPLLFTEKE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SGKLQVLSKL | LAVIHELRPT | EKVVLVSNYT | QTLNILQEVC | KRHGYAYTRL | DGQTPISQRQ | QIVDGFNSQH | SSFFIFLLSS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KAGGVGLNLI | GGSHLILYDI | DWNPATDIQA | MSRVWRDGQK | YPVHIYRLLT | TGTIEEKIYQ | RQISKQGLCG | AVVDLTKTSE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| HIQFSVEELK | NLFTLHESSD | CVTHDLLDCE | CTGEEVHTGD | SLEKFIVSRD | CQLGPHHQKS | NSLKPLSMSQ | LKQWKHFSGD |
| 890 | 900 | 910 | 920 | | | | |
| HLNLTDPFLE | RITENVSFIF | QNITTQATGT | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 920 | 1 | 945.9532 | -58.91 | 2 | 39.9 | 10.3 | 1 | 860-875 | K.SNSLKPLSMSQLKQWK.H | Oxidation: 9 |

# Detailed Protein Report

## Protein 504: PREDICTED: serine/threonine-protein kinase MRCK beta isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530404963 | **Score:** | 28.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 169.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSAKVRLKKL | EQLLLDGPWR | NESALSVETL | LDVLVCLYTE | CSHSALRRDK | YVAEFLEWAK | PFTQLVKEMQ | LHREDFEIIK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VIGRGAFGEV | AVVKMKNTER | IYAMKILNKW | EMLKRAETAC | FREERDVLVN | GDCQWITALH | YAFQDENHLY | LVMDYYVGGD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLTLLSKFED | KLPEDMARFY | IGEMVLAIDS | IHQLHYVHRD | IKPDNVLLDV | NGHIRLADFG | SCLKMNDDGT | VQSSVAVGTP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DYISPEILQA | MEDGMGKYGP | ECDWWSLGVC | MYEMLYGETP | FYAESLVETY | GKIMNHEERF | QFPSHVTDVS | EEAKDLIQRL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ICSRERRLGQ | NGIEDFKKHA | FFEGLNWENI | RNLEAPYIPD | VSSPSDTSNF | DVDDDVLRNT | EILPPGSHTG | FSGLHLPFIG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FTFTTESCFS | DRGSLKSIMQ | SNTLTKDEDV | QRDLEHSLQM | EAYERRIRRL | EQEKLELSRK | LQESTQTVQS | LHGSSRALSN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SNRDKEIKKL | NEEIERLKNK | IADSNRLERQ | LEDTVALRQE | REDSTQRLRG | LEKQHRVVRQ | EKEELHKQLV | EASERLKSQA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KELKDAHQQR | KLALQEFSEL | NERMAELRAQ | KQKVSRQLRD | KEEEMEVATQ | KVDAMRQEMR | RAEKLRKELE | AQLDDAVAEA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SKERKLREHS | ENFCKQMESE | LEALKVKQGG | RGAGATLEHQ | QEISKIKSEL | EKKVLFYEEE | LVRREASHVL | EVKNVKKEVH |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DSESHQLALQ | KEILMLKDKL | EKSKRERHNE | MEEAVGTIKD | KYERERAMLF | DENKKLTAEN | EKLCSFVDKL | TAQNRQLEDE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LQDLAAKKES | VAHWEAQIAE | IIQWVSDEKD | ARGYLQALAS | KMTEELEALR | SSSLGSRTLD | PLWKVRRSQK | LDMSARLELQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SALEAEIRAK | QLVQEELRKV | KDANLTLESK | LKDSEAKNRE | LLEEMEILKK | KMEEKFRADT | GLKLPDFQDS | IFEYFNTAPL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| AHDLTFRDSL | SSSSASSLLA | FWEETSSASE | QETQAPKPEA | SPSMSVAASE | QQEDMARPPQ | RPSAVPLPTT | QALALAGPKP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KAHQFSIKSF | SSPTQCSHCT | SLMVGLIRQG | YACEVCSFAC | HVSCKDGAPQ | VCPIPPEQSK | RPLGVDVQRG | IGTAYKGHVK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| VPKPTGVKKG | WQRAYAVVCD | CKLFLYDLPE | GKSTQPGVIA | SQVLDLRDDE | FSVSSVLASD | VIHATRRDIP | CIFRVTASLL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| GAPSKTSSLL | ILTENENEKR | KWVGILEGLQ | SILHKNRLRN | QVVHVPLEAY | DSSLPLIKAI | LTAAIVDADR | IAVGLEEGLY |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VIEVTRDVIV | RAADCKKVHQ | IELAPREKIV | ILLCGRNHHV | HLYPWSSLDG | AEGSFDIKLP | ETKGCQLMAT | ATLKRNSGTC |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LFVAVKRLIL | CYEIQRTKPF | HRKFNEIVAP | GSVQCLAVLR | DRLCVGYPSG | FCLLSIQGDG | QPLNLVNPND | PSLAFLSQQS |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | | |
| FDALCAVELE | SEEYLLCFSH | MGLYVDPQGR | RARAQELMWP | AAPVACKEKS | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 413 | 1 | 946.2338 | -157.99 | 2 | 34.8 | 16.0 | 0 | 1069-1085 | R.QGYACEVCSFACHVSCK.D | Carbamidomethyl: 16 |

# Detailed Protein Report

**Protein 505:** **sodium/hydrogen exchanger 9B1 isoform 2 [Homo sapiens]**

**Accession:** gi|154937338
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 28.1
**MW [kDa]:** 52.2
**pI:** 9.5
**Sequence Coverage [%]:** 4.4
**No. of unique Peptides:** 2

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MHTTESKNEH | LEDENFQTST | TPQSLIDPNN | TAHEETKTVL | SDTEEIKPQT | KKETYISCPL | RGVLNVIITN | GVILFVIWCM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TWSILGSEAL | PGGNLFGLFI | IFYSAIIGGK | ILQLIRIPLV | PPLPPLLGML | LAGFTIRNVP | FINEHVHVPN | TWSSILRSIA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LTIILIRAGL | GLDPQALRHL | KVVCFRLAVG | PCLMEASAAA | VFSHFIMKFP | WQWAFLLGFV | LGAVSPAVVV | PYMMVLQENG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YGVEEGIPTL | LMAASSMDDI | LAITGFNTCL | SIVFSSGGIL | NNAIASIRNV | CISLLAGIVL | GFFVRYFPSE | DQKKLTLKRG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FLVLTMCVSA | VLGSQRIGLH | GSGGLCTLVL | SFIAGTKWSQ | EKMKVQKIIT | TVWDIFQPLL | FGLVGAEVSV | SSLESNIVGI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SVATLSLALC | VRILTTYLLM | CFAGFSFKEK | IFIALAWMPK | ATVQINQAIL | LLFLLREEWT | NCKVAKKCEY | TKERQ |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2206 | 1 | 682.1436 | 141.92 | 3 | 58.0 | 11.6 | 0 | 337-357 | R.IGLHGSGGLCTLVLSFIAGTK.W | |
| 2202 | 1 | 701.1391 | 121.39 | 3 | 57.9 | 16.6 | 0 | 337-357 | R.IGLHGSGGLCTLVLSFIAGTK.W | Carbamidomethyl: 10 |

# Detailed Protein Report

## Protein 506: centrosomal protein of 170 kDa protein B isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|326319990 | **Score:** | 28.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 163.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| | | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.10 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.87 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRIPDQKYVT | LKLNDVIRFG | YDSNMYVLER | VQHRVPEEAL | KHEKYTSQLQ | VSVKGLAPKR | SEALPEHTPY | CEASNPRPEK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GDRRPGTEAA | SYRTPLYGQP | SWWGEDDGST | LPDAQRQGEP | YPERPKGPVQ | QDGELHGFRA | PAEPQGCSFR | REPSYFEIPT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KETPQPSQPP | EVPAHEMPTK | DAEAGGGGAA | PVVQSHASFT | IEFDDCSPGK | MKIKDHITKF | SLRQRRPPGK | EATPGEMVSA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ETKVADWLVQ | NDPSLLHRVG | PGDDRHSTKS | DLPVHTRTLK | GHKHEDGTQS | DSEDPLAKAA | SAAGVPLEAS | GEQVRLQRQI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KRDPQELLHN | QQAFVIEFFD | EDTPRKKRSQ | SFTHSPSGDP | KADKRRGPTP | ADRDRPSVPA | PVQAGGRSSG | PQRAGSLKRE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KTEERLGSPS | PASRTPARPF | GSVGRRSRLA | QDFMAQCLRE | SSPAARPSPE | KVPPVLPAPL | TPHGTSPVGP | PTPPPAPTDP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QLTKARKQEE | DDSLSDAGTY | TIETEAQDTE | VEEARKMIDQ | VFGVLESPEL | SRASSATFRP | VIRGDRDESD | DGGVAQRMAL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LQEFASRPLG | AAPQAEHQGL | PVPGSPGGQK | WVSRWASLAD | SYSDPGLTED | GLGRRGGEPE | GSLPVRMRRR | LPQLPSERAD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SPAGPESSRR | SGPGPPELDS | EQPSRLFGQE | ELDPDSLSDA | SGSDGGRGPE | PGVEPQDSRR | RSPQEGPTWS | RGRRSPRAPG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EPTPASFFIG | DQNGDAVLSR | KPLAAPGDGE | GLGQTAQPSP | PARDGVYVSA | NGRMVIQLRP | GRSPEPDGPA | PAFLRQESFT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KEPASGPPAP | GKPPHISSHP | LLQDLAATRA | ARMDFHSQDT | HLILKETETA | LAALEARLLS | NSVDAECEGG | STPRPPEDAL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SGDSDVDTAS | TVSLRSGKSG | PSPTTPQPLR | AQKEMSPSPP | AAQDPGGTAL | VSAREQSSER | QHHPLGPTDM | GRGEPVRRSA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| IRRGHRPRGS | LDWPSEERGP | VLAHLPSSDV | MASNHETPEA | TGAGRLGSRR | KPAAPPPSPA | AREEQSRSSA | SSQKGPQALT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RSNSLSTPRP | TRASRLRRAR | LGDASDTEAA | DGERGSLGNP | EPVGRPAAEQ | AKKLSRLDIL | AMPRKRAGSF | TGTSDPEAAP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ARTSFSGRSV | ELCCASRKPT | MAEARAVSRK | AANTATTTGP | RQPFSRARSG | SARYTSNTRR | RQQGSDYTST | SEEEYGSRHG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SPKHTRSHTS | TATQTPRAGS | SSRARSRAPG | PRDTDDDEEE | PDPYGFIVQT | AEIAEIARLS | QTLVKDVAIL | AQEIHDVAGD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| GDTLGSSEPA | HSASLSNMPS | TPASTISARE | ELVQRIPEAS | LNFQKVPPGS | LNSRDFDQNM | NDSCEDALAN | KTRPRNREEV |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| IFDNLMLNPV | SQLSQAIREN | TEHLAEKMKI | LFQNTGRAWE | DLEARINAEN | EVPILKTSNK | EISSILKELR | RVQKQLEVIN |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| AIVDPSGSLD | LLTGNRSLAS | SAQPGLGKGR | VAAQSPPSPA | SAEALLPALP | LRNFPQRASC | GPPSLPDPTF | LPDAERFLI |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1914 | 1 | 909.8535 | -115.14 | 2 | 54.3 | 13.0 | 2 | 1105-1122 | R.KRAGSFTGTSDPEAAPAR.T | | QU:MU 1.10<br>WUP:QUP 0.87 |

# Detailed Protein Report

## Protein 507: zinc finger protein Aiolos isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|38045959 | **Score:** | 28.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 51.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEDIQTNAEL | KSTQEQSVPA | ESAAVLNDYS | LTKSHEMENV | DSGEGPANED | EDIGDDSMKV | KDEYSERDEN | VLKSEPMGNA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EEPEIPYSYS | REYNEYENIK | LERHVVSFDS | SRPTSGKMNC | DVCGLSCISF | NVLMVHKRSH | TVEKPYKCEF | CGRSYKQRSS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LEEHKERCRT | FLQSTDPGDT | ASAEARHIKA | EMGSERALVL | DRLASNVAKR | KSSMPQKFIG | EKRHCFDVNY | NSSYMYEKES |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ELIQTRMMDQ | AINNAISYLG | AEALRPLVQT | PPAPTSEMVP | VISSMYPIAL | TRAEMSNGAP | QELEKKSIHL | PEKSVPSERG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LSPNNSGHDS | TDTDSNHEER | QNHIYQQNHM | VLSRARNGMP | LLKEVPRSYE | LLKPPPICPR | DSVKVINKEG | EVMDVYRCDH |
| 410 | 420 | 430 | 440 | 450 | 460 | | |
| CRVLFLDYVM | FTIHMGCHGF | RDPFECNMCG | YRSHDRYEFS | SHIARGEHRA | LLK | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 278 | 1 | 998.9505 | -27.17 | 2 | 33.5 | 14.8 | 2 | 138-153 | K.RSHTVEKPYKCEFCGR.S | Carbamidomethyl: 11 |

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# Detailed Protein Report

## Protein 508: PREDICTED: SNW domain-containing protein 1 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530403266 | **Score:** | 28.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 65.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 6.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.04 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.32 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MALTSFLPAP | TQLSQDQLEA | EEKARSQRSR | QTSLVSSRRE | PPPYGYRKGW | IPRLLEDFGD | GGAFPEIHVA | QYPLDMGRKK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KMSNALAIQV | DSEGKIKYDA | IARQGQSKDK | VIYSKYTDLV | PKEVMNADDP | DLQRPDEEAI | KEITEKTRVA | LEKSVSQKVA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AAMPVRAADK | LAPAQYIRYT | PSQQGVAFNS | GAKQRVIRMV | EMQKDPMEPP | RFKINKKIPR | GPPSPPAPVM | HSPSRKMTVK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EQQEWKIPPC | ISNWKNAKGY | TIPLDKRLAA | DGRGLQTVHI | NENFAKLAEA | LYIADRKARE | AVEMRAQVER | KMAQKEKEKH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EEKLREMAQK | ARERRAGIKT | HVEKEDGEAR | ERDEIRHDRR | KERQHDRNLS | RAAPDKRSKL | QRNENRDISE | VIALGVPNPR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TSNEVQYDQR | LFNQSKGMDS | GFAGGEDEIY | NVYDQAWRGG | KDMAQSIYRP | SKNLDKDMYG | DDLEARIKTN | RCQAIQLNFS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VYTGESKVVH | SFFSFSLDLF | PTRSFLVQTV | DREAEKDQCS | LRKILLVWTS | FWKKPNSMVA | LKDPQIAAAP | RNTSMKARRG |
| 570 | 580 | | | | | | |
| GRNRHRSLQS | E | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2282 | 1 | 863.8185 | -157.42 | 2 | 56.9 | 13.4 | 2 | 543-558 | K.DPQIAAAPRNTSMKAR.R | | QU:MU 1.04<br>WUP:QUP 0.32 |

# Detailed Protein Report

## Protein 509: tetratricopeptide repeat protein 37 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|7662078 | **Score:** | 28.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 175.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.1 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSKEVKTAL | KSARDAIRNK | EYKEALKHCK | TVLKQEKNNY | NAWVFIGVAA | AELEQPDQAQ | SAYKKAAELE | PDQLLAWQGL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ANLYEKYNHI | NAKDDLPGVY | QKLLDLYESV | DKQKWCDVCK | KLVDLYYQEK | KHLEVARTWH | KLIKTRQEQG | AENEELHQLW |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RKLTQFLAES | TEDQNNETQQ | LLFTAFENAL | GLSDKIPSED | HQVLYRHFIQ | SLSKFPHESA | RLKKACEGMI | NIYPTVQYPL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EVLCLHLIES | GNLTDEGQQY | CCRLVEMDSK | SGPGLIGLGI | KALQDKKYED | AVRNLTEGLK | ESPVCTSGWY | HLAEAQVKMH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RPKEAVLSCS | QALKIVDNLG | ASGNSLYQRN | LCLHLKAEAL | IKLSDYDSSE | EAIRTLDQIS | DADNIPGLLV | LKSLAYRNKG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SFDEAAKIME | DLLSSYPDLA | EVHALEALIH | FTKKDYLQAE | KCFQRALEKD | TEVAEYHYQL | GLTYWFMGEE | TRKDKTKALT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HFLKAARLDT | YMGKVFCYLG | HYYRDVVGDK | NRARGCYRKA | FELDDTDAES | GAAAVDLSVE | LEDMEMALAI | LTTVTQKASA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GTAKWAWLRR | GLYYLKAGQH | SQAVADLQAA | LRADPKDFNC | WESLGEAYLS | RGGYTTALKS | FTKASELNPE | SIYSVFKVAA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IQQILGKYKE | AVAQYQMIIK | KKEDYVPALK | GLGECHLMMA | KAALVDYLDG | KAVDYIEKAL | EYFTCALQHR | ADVSCLWKLA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GDACTCLYAV | APSKVNVHVL | GVLLGQKEGK | QVLKKNELLH | LGGRCYGRAL | KLMSTSNTWC | DLGINYYRQA | QHLAETGSNM |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NDLKELLEKS | LHCLKKAVRL | DSNNHLYWNA | LGVVACYSGI | GNYALAQHCF | IKSIQSEQIN | AVAWTNLGVL | YLTNENIEQA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| HEAFKMAQSL | DPSYLMCWIG | QALIAEAVGS | YDTMDLFRHT | TELNMHTEGA | LGYAYWVCTT | LQDKSNRETE | LYQYNILQMN |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| AIPAAQVILN | KYVERIQNYA | PAFTMLGYLN | EHLQLKKEAA | NAYQRAILLL | QTAEDQDTYN | VAIRNYGRLL | CSTGEYDKAI |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QAFKSTPLEV | LEDIIGFALA | LFMKGLYKES | SKAYERALSI | VESEQDKAHI | LTALAITEYK | QGKTDVAKTL | LFKCSILKEP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TTESLQALCA | LGLAMQDATL | SKAALNELLK | HIKHKDSNYQ | RCLLTSAIYA | LQGRSVAVQK | QISKAVHSNP | GDPALWSLLS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| RVVAQYAQRN | AKGGVVAGNV | AHILDSNHGK | KALLYTAVNQ | LAMGSSSAED | EKNTALKTIQ | KAALLSPGDP | AIWAGLMAAC |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| HADDKLALVN | NTQPKRIDLY | LALLSAVSAS | IKDEKFFENY | NQSLEKWSLS | QAVTGLIDTG | RISEAETLCT | KNLKSNPDQP |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| AVILLLRQVQ | CKPLLESQKP | LPDAVLEELQ | KTVMSNSTSV | PAWQWLAHVY | QSQGMMRAAE | MCYRKSLQLA | SQRGSWSGKL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SSLLRLALLA | LKVCMANISN | DHWPSLVQEA | TTEALKLCFC | PLAVLLQALL | QFKRKMGARE | TRRLLERVVY | QPGYPKSIAS |
| 1530 | 1540 | 1550 | 1560 | 1570 | | | |
| TARWYLLRHL | YAKDDYELID | VLVNNAKTHG | DTRALELNQR | LSSQ | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2200 | 1 | 899.4081 | -76.29 | 2 | 55.9 | 13.7 | 1 | 319-334 | K.MHRPKEAVLSCSQALK.I | |
| 728 | 1 | 705.9560 | -25.50 | 2 | 37.6 | 14.3 | 1 | 1440-<br>1452 | K.LSSLLRLALLALK.V | |

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# Detailed Protein Report

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**Protein 510:** **PREDICTED: huntingtin-interacting protein 1-related protein isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530401786 | **Score:** | 28.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 118.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 1.07 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEARFSPINQ | ILPWCRQDLA | ISISKAINTQ | EAPVKEKHAR | RIILGTHHEK | GAFTFWSYAI | GLPLPSSSIL | SWKFCHVLHK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VLRDGHPNVL | HDCQRYRSNI | REIGDLWGHL | HDRYGQLVNV | YTKLLLTKIS | FHLKHPQFPA | GLEVTDEVLE | KAAGTDVNNI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FQLTVEMFDY | MDCELKLSES | VFRQLNTAIA | VSQMSSGQCR | LAPLIQVIQD | CSHLYHYTVK | LLFKLHSCLP | ADTLQGHRDR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FHEQFHSLRN | FFRRASDMLY | FKRLIQIPRL | PEGPPNFLRA | SALAEHIKPV | VVIPEEAPED | EEPENLIEIS | TGPPAGEPVV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VADLFDQTFG | PPNGSVKDDR | TSVPRDLQIE | SLKREVEMLR | SELEKIKLEA | QRYIAQLKSQ | VNALEGELEE | QRKQKQKALV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DNEQLRHELA | QLRAAQLEGE | RSQGLREEAE | RKASATEARY | NKLKEKHSEL | VHVHAELLRK | NADTAKQLTV | TQQSQEEVAR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VKEQLAFQVE | QVKRESELKL | EEKSDQLEKL | KRELEAKAGE | LARAQEALSH | TEQSKSELSS | RLDTLSAEKD | ALSGAVRQRE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ADLLAAQSLV | RETEAALSRE | QQRSSQEQGE | LQGRLAERES | QEQGLRQRLL | DEQFAVLRGA | AAEAAGILQD | AVSKLDDPLH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LRCTSSPDYL | VSRAQEALDA | VSTLEEGHAQ | YLTSLADASA | LVAALTRFSH | LAADTIINGG | ATSHLAPTDP | ADRLIDTCRE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CGARALELMG | QLQDQQALRH | MQASLVRTPL | QGILQLGQEL | KPKSLDVRQE | ELGAVVDKEM | AATSAAIEDA | VRRIEDMMNQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ARHASSGVKL | EVNERILNSC | TDLMKAIRLL | VTTSTSLQKE | IVESGRGAAT | QQEFYAKNSR | WTEGLISASK | AVGWGATQLV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EAADKVVLHT | GKYEELIVCS | HEIAASTAQL | VAASKVKANK | HSPHLSRLQE | CSRTVNERAA | NVVASTKSGQ | EQIEDRDTMD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FSGLSLIKLK | KQEMETQVRV | LELEKTLEAE | RMRLGELRKQ | HYVLAGASGS | PGEEVAIRPS | TAPRSVTTKK | PPLAQKPSVA |
| 1050 | 1060 | 1070 | | | | | |
| PRQDHQLDKK | DGIYPAQLVN | Y | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 662 | 1 | 593.6995 | -211.24 | 2 | 38.3 | 11.3 | 1 | 513-523 | R.ELEAKAGELAR.A | | QU:MU 1.07 |

# Detailed Protein Report

## Protein 511: contactin-associated protein-like 4 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|148664242 | **Score:** | 28.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 137.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWNYDCDDPL | VSALPQASFS | SSSELSSSHG | PGFARLNRRD | GAGGWSPLVS | NKYQWLQIDL | GERMEVTAVA | TQGGYGSSNW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VTSYLLMFSD | SGWNWKQYRQ | EDSIWGFSGN | ANADSVVYYR | LQPSIKARFL | RFIPLEWNPK | GRIGMRIEVF | GCAYRSEVVD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LDGKSSLLYR | FDQKSLSPIK | DIISLKFKTM | QSDGILLHRE | GPNGDHITLQ | LRRARLFLLI | NSGEAKLPST | STLVNLTLGS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LLDDQHWHSV | LIQRLGKQVN | FTVDEHRHHF | HARGEFNLMN | LDYEGNVSFS | CSQPQSMPVT | FLSSRSYLAL | PDFSGEEEVS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ATFQFRTWNK | AGLLLFSELQ | LISGGILLFL | SDGKLKSNLY | QPGKLPSDIT | AGVELNDGQW | HSVSLSAKKN | HLSVAVDGQM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ASAAPLLGPE | QIYSGGTYYF | GGCPDKSFGS | KCKSPLGGFQ | GCMRLISISG | KVVDLISVQQ | GSLGNFSDLQ | IDSCGISDRC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LPNYCEHGGE | CSQSWSTFHC | NCTNTGYRGA | TCHNSIYEQS | CEAYKHRGNT | SGFYYIDSDG | SGPLEPFLLY | CNMTETAWTI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IQHNGSDLTR | VRNTNPENPY | AGFFEYVASM | EQLQATINRA | EHCEQEFTYY | CKKSRLVNKQ | DGTPLSWWVG | RTNETQTYWG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GSSPDLQKCT | CGLEGNCIDS | QYYCNCDADR | NEWTNDTGLL | AYKEHLPVTK | IVITDTGRLH | SEAAYKLGPL | LCQGDRSFWN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SASFDTEASY | LHFPTFHGEL | SADVSFFFKT | TASSGVFLEN | LGIADFIRIE | LRSPTVVTFS | FDVGNGPFEI | SVQSPTHFND |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NQWHHVRVER | NMKEASLQVD | QLTPKTQPAP | ADGHVLLQLN | SQLFVGGTAT | RQRGFLGCIR | SLQLNGMTLD | LEERAQVTPE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VQPGCRGHCS | SYGKLCRNGG | KCRERPIGFF | CDCTFSAYTG | PFCSNEISAY | FGSGSSVIYN | FQENYLLSKN | SSSHAASFHG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DMKLSREMIK | FSFRTTRTPS | LLLFVSSFYK | EYLSVIIAKN | GSLQIRYKLN | KYQEPDVVNF | DFKNMADGQL | HHIMINREEG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VVFIEIDDNR | RRQVHLSSGT | EFSAVKSLVL | GRILEHSDVD | QDTALAGAQG | FTGCLSAVQL | SHVAPLKAAL | HPSHPDPVTV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TGHVTESSCM | AQPGTDATSR | ERTHSFADHS | GTIDDREPLA | NAIKSDSAVI | GGLIAVVIFI | LLCITAIAVR | IYQQKRLYKR |
| 1210 | 1220 | 1230 | 1240 | | | | |
| SEAKRSENVD | SAEAVLKSEL | NIQNAVNENQ | KEYFF | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2542 | 1 | 715.3361 | -67.84 | 2 | 61.7 | 15.1 | 2 | 964-974 | K.LSREMIKFSFR.T | Oxidation: 5 |
| 1571 | 1 | 1061.1650 | -10.98 | 3 | 49.3 | 12.9 | 1 | 1024-1050 | K.NMADGQLHHIMINREEGVVFIEIDDNR.R | Oxidation: 2 |

# Detailed Protein Report

**Protein 512:** **PREDICTED: synaptojanin-2 isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530384175 | **Score:** | 27.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 122.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.9 |
| | | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNCLDCLDRT | NTVQSFIALE | VLHLQLKTLG | LSSKPIVDRF | VESFKAMWSL | NGHSLSKVFT | GSRALEGKAK | VGKLKDGARS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MSRTIQSNFF | DGVKQEAIKL | LLVGDVYGEE | VADKGGMLLD | STALLVTPRI | LKAMTERQSE | FTNFKRIRIA | MGTWNVNGGK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QFRSNVLRTA | ELTDWLLDSP | QLSGATDSQD | DSSPADIFAV | GFEEMVELSA | GNIVNASTTN | KKMWGEQLQK | AISRSHRYIL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LTSAQLVGVC | LYIFVRPYHV | PFIRDVAIDT | VKTGMGGKAG | NKGAVGIRFQ | FHSTSFCFIC | SHLTAGQSQV | KERNEDYKEI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TQKLCFPMGR | NVFSHDYVFW | CGDFNYRIDL | TYEEVFYFVK | RQDWKKLLEF | DQLQLQKSSG | KIFKDFHEGA | INFGPTYKYD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VGSAAYDTSD | KCRTPAWTDR | VLWWRKKHPF | DKTAGELNLL | DSDLDVDTKV | RHTWSPGALQ | YYGRAELQAS | DHRPVLAIVE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VEVQEVDVGA | RERVFQEVSS | FQGPLDATVV | VNLQSPTLEE | KNEFPEDLRT | ELMQTLGSYG | TIVLVRINQG | QMLVTFADSH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SALSVLDVDG | MKVKGRAVKI | RPKTKDWLKG | LREEIIRKRD | SMAPVSPTAN | SCLLEENFDF | TSLDYESEGD | ILEDDEDYLV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DEFNQPGVSD | SELGGDDLSD | VPGPTALAPP | SKSPALTKKK | QHPTYKDDAD | LVELKRELEA | VGEFRHRSPS | RSLSVPNRPR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PPQPPQRPPP | PTGLMVKKSA | SDASISSGTH | GQYSILQTAR | LLPGAPQQPP | KARTGISKPY | NVKQIKTTNA | QEAEAAIRCL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LEARGGASEE | ALSAVAPRDL | EASSEPEPTP | GAAKPETPQA | PPLLPRRPPP | RVPAIKKPTL | RRTGKPLSPE | EQFEQQTVHF |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TIGPPETSVE | APPVVTAPRV | PPVPKPRTFQ | PGKAAERPSH | RKPASDEAPP | GAGASVPPPL | EAPPLVPKVP | PRRKKSAPAA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FHLQVLQSNS | QLLQGLTYNS | SDSPSGHPPA | AGTVFPQGDF | LSTSSATSPD | SDGTKAMKPE | AAPLLGDYQD | PFWNLLHHPK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LLNNTWLSKS | SDPLDSGTRS | PKRDPIDPVS | AGASAAKAEL | PPDHEHKTLG | HWVTISDQEK | RTALQVFDPL | AKT |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1895 | 1 | 643.2981 | -123.24 | 2 | 54.1 | 16.3 | 0 | 28-39 | K.TLGLSSKPIVDR.F | |

# Detailed Protein Report

## Protein 513: myosin-2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|153791586 | **Score:** | 27.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 222.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|153792663 | refseq_human (refseq_human_20140103.fasta) | myosin-2 [Homo sapiens] |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSDSELAVF | GEAAPFLRKS | ERERIEAQNR | PFDAKTSVFV | AEPKESFVKG | TIQSREGGKV | TVKTEGGATL | TVKDDQVFPM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NPPKYDKIED | MAMMTHLHEP | AVLYNLKERY | AAWMIYTYSG | LFCVTVNPYK | WLPVYKPEVV | TAYRGKKRQE | APPHIFSISD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NAYQFMLTDR | ENQSILITGE | SGAGKTVNTK | RVIQYFATIA | VTGEKKKEEI | TSGKIQGTLE | DQIISANPLL | EAFGNAKTVR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NDNSSRFGKF | IRIHFGTTGK | LASADIETYL | LEKSRVVFQL | KAERSYHIFY | QITSNKKPEL | IEMLLITTNP | YDYPFVSQGE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ISVASIDDQE | ELMATDSAID | ILGFTNEEKV | SIYKLTGAVM | HYGNLKFKQK | QREEQAEPDG | TEVADKAAYL | QSLNSADLLK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ALCYPRVKVG | NEYVTKGQTV | EQVSNAVGAL | AKAVYEKMFL | WMVARINQQL | DTKQPRQYFI | GVLDIAGFEI | FDFNSLEQLC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| INFTNEKLQQ | FFNHHMFVLE | QEEYKKEGIE | WTFIDFGMDL | AACIELIEKP | MGIFSILEEE | CMFPKATDTS | FKNKLYDQHL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GKSANFQKPK | VVKGKAEAHF | ALIHYAGVVD | YNITGWLEKN | KDPLNETVVG | LYQKSAMKTL | AQLFSGAQTA | EGEGAGGGAK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KGGKKKGSSF | QTVSALFREN | LNKLMTNLRS | THPHFVRCII | PNETKTPGAM | EHELVLHQLR | CNGVLEGIRI | CRKGFPSRIL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YADFKQRYKV | LNASAIPEGQ | FIDSKKASEK | LLASIDIDHT | QYKFGHTKVF | FKAGLLGLLE | EMRDDKLAQL | ITRTQARCRG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FLARVEYQRM | VERREAIFCI | QYNIRSFMNV | KHWPWMKLFF | KIKPLLKSAE | TEKEMATMKE | EFQKIKDELA | KSEAKRKELE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EKMVTLLKEK | NDLQLQVQAE | AEGLADAEER | CDQLIKTKIQ | LEAKIKEVTE | RAEDEEEINA | ELTAKKRKLE | DECSELKKDI |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DDLELTLAKV | EKEKHATENK | VKNLTEEMAG | LDETIAKLTK | EKKALQEAHQ | QTLDDLQAEE | DKVNTLTKAK | IKLEQQVDDL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EGSLEQEKKL | RMDLERAKRK | LEGDLKLAQE | SIMDIENEKQ | QLDEKLKKKE | FEISNLQSKI | EDEQALGIQL | QKKIKELQAR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| IEELEEEIEA | ERASRAKAEK | QRSDLSRELE | EISERLEEAG | GATSAQIEMN | KKREAEFQKM | RRDLEEATLQ | HEATAATLRK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KHADSVAELG | EQIDNLQRVK | QKLEKEKSEM | KMEIDDLASN | VETVSKAKGN | LEKMCRTLED | QLSELKSKEE | EQQRLINDLT |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| AQRGRLQTES | GEFSRQLDEK | EALVSQLSRG | KQAFTQQIEE | LKRQLEEEIK | AKNALAHALQ | SSRHDCDLLR | EQYEEEQESK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| AELQRALSKA | NTEVAQWRTK | YETDAIQRTE | ELEEAKKKLA | QRLQAAEEHV | EAVNAKCASL | EKTKQRLQNE | VEDLMLDVER |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| TNAACAALDK | KQRNFDKILA | EWKQKCEETH | AELEASQKEA | RSLGTELFKI | KNAYEESLDQ | LETLKRENKN | LQQEISDLTE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| QIAEGGKRIH | ELEKIKKQVE | QEKCELQAAL | EEAEASLEHE | EGKILRIQLE | LNQVKSEVDR | KIAEKDEEID | QLKRNHIRIV |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| ESMQSTLDAE | IRSRNDAIRL | KKKMEGDLNE | MEIQLNHANR | MAAEALRNYR | NTQGILKDTQ | IHLDDALRSQ | EDLKEQLAMV |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| ERRANLLQAE | IEELRATLEQ | TERSRKIAEQ | ELLDASERVQ | LLHTQNTSLI | NTKKKLETDI | SQMQGEMEDI | LQEARNAEEK |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| AKKAITDAAM | MAEELKKEQD | TSAHLERMKK | NMEQTVKDLQ | LRLDEAEQLA | LKGGKKQIQK | LEARVRELEG | EVESEQKRNA |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| EAVKGLRKHE | RRVKELTYQT | EEDRKNILRL | QDLVDKLQAK | VKSYKRQAEE | AEEQSNTNLA | KFRKLQHELE | EAEERADIAE |
| 1930 | 1940 | 1950 | | | | | |
| SQVNKLRVKS | REVHTKVISE | E | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2807 | 1 | 714.6776 | 11.25 | 3 | 66.4 | 12.9 | 1 | 1228-1246 | K.SEMKMEIDDLASNVETVSK.A | Oxidation: 3 |

# Detailed Protein Report

**Protein 514:** **PREDICTED: nuclear receptor subfamily 1 group D member 2 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530373510 | **Score:** | 27.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.35 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MEVNAGGVIA YISSSSSASS PASCHSEGSE NSFQSSSSSV PSSPNSSNSD TNGNPKNGDL ANIEGILKND RIDCSMKTSK
        90        100        110        120        130        140        150        160
SSAPGMTKSH SGVTKFSGMV LLCKVCGDVA SGFHYGVHAC EGCKGFFRRS IQQNIQYKKC LKNENCSIMR MNRNRCQQCR
       170        180        190        200        210        220        230        240
FKKCLSVGMS RDAVRFGRIP KREKQRMLIE MQSAMKTMMN SQFSGHLQND TLVEHHEQTA LPAQEQLRPK PQLEQENIKS
       250        260        270        280        290        300        310        320
SSPPSSDFAK EEVIGMVTRA HKDTFMYNQE QQENSAESMQ PQRGERIPKN MEQYNLNHDH CGNGLSSHFP CSESQQHLNG
       330        340        350        360        370        380        390        400
QFKGRNIMHY PNGHAICIAN GHCMNFSNAY TQRVCDRVPI DGFSQNENKN SYLCNTGGRM HLYSVHIQPK FHQKQQYHTI
       410
SSLNHEVL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 80 | 1 | 877.8666 | -76.26 | 2 | 30.7 | 12.1 | 2 | 183-196 | R.EKQRMLIEMQSAMK.T | Oxidation: 9, 13 | WUP:QUP 0.35 |

# Detailed Protein Report

## Protein 515: ephrin type-A receptor 7 isoform 2 precursor [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|568599847 | **Score:** | 27.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 111.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
|  |  | **Sequence Coverage [%]:** | 3.5 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVFQTRYPSW | IILCYIWLLR | FAHTGEAQAA | KEVLLLDSKA | QQTELEWISS | PPNGWEEISG | LDENYTPIRT | YQVCQVMEPN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QNNWLRTNWI | SKGNAQRIFV | ELKFTLRDCN | SLPGVLGTCK | ETFNLYYYET | DYDTGRNIRE | NLYVKIDTIA | ADESFTQGDL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GERKMKLNTE | VREIGPLSKK | GFYLAFQDVG | ACIALVSVKV | YYKKCWSIIE | NLAIFPDTVT | GSEFSSLVEV | RGTCVSSAEE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EAENAPRMHC | SAEGEWLVPI | GKCICKAGYQ | QKGDTCEPCG | RGFYKSSSQD | LQCSRCPTHS | FSDKEGSSRC | ECEDGYYRAP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SDPPYVACTR | PPSAPQNLIF | NINQTTVSLE | WSPPADNGGR | NDVTYRILCK | RCSWEQGECV | PCGSNIGYMP | QQTGLEDNYV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TVMDLLAHAN | YTFEVEAVNG | VSDLSRSQRL | FAAVSITTGQ | AAPSQVSGVM | KERVLQRSVE | LSWQEPEHPN | GVITEYEIKY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YEKDQRERTY | STVKTKSTSA | SINNLKPGTV | YVFQIRAFTA | AGYGNYSPRL | DVATLEEATA | TAVSSEQNPV | IIIAVVAVAG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TIILVFMVFG | FIIGRRHCGY | SKADQEGDEE | LYFHFKFPGT | KTYIDPETYE | DPNRAVHQFA | KELDASCIKI | ERVIGAGEFG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EVCSGRLKLP | GKRDVAVAIK | TLKVGYTEKQ | RRDFLCEASI | MGQFDHPNVV | HLEGVVTRGK | PVMIVIEFME | NGALDAFLRK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HDGQFTVIQL | VGMLRGIAAG | MRYLADMGYV | HRDLAARNIL | VNSNLVCKVS | DFGLSRVIED | DPEAVYTTTG | GKIPVRWTAP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EAIQYRKFTS | ASDVWSYGIV | MWEVMSYGER | PYWDMSNQDV | IKAIEEGYRL | PAPMDCPAGL | HQLMLDCWQK | ERAERPKFEQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| IVGILDKMIR | NPNSLKTPLG | TCSRPISPLL | DQNTPDFTTF | CSVGEWLQAI | KMERYKDNFT | AAGYNSLESV | ARMTIEDVMS |
| 970 | 980 | 990 | 1000 |  |  |  |  |
| LGITLVGHQK | KIMSSIQTMR | AQMLHLHGTG | IQV |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1992 | 1 | 857.8267 | -91.44 | 2 | 55.3 | 11.3 | 0 | 937-952 | K.DNFTAAGYNSLESVAR.M |  |

# Detailed Protein Report

## Protein 516: PREDICTED: protein 4.1 isoform X29 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578798602 | **Score:** | 27.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 90.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MHCKVSLLDD | TVYECVVEKH | AKGQDLLKRV | CEHLNLLEED | YFGLAIWDNA | TSKTWLDSAK | EIKKQVRGVP | WNFTFNVKFY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PPDPAQLTED | ITRYYLCLQL | RQDIVAGRLP | CSFATLALLG | SYTIQSELGD | YDPELHGVDY | VSDFKLAPNQ | TKELEEKVME |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LHKSYRSMTP | AQADLEFLEN | AKKLSMYGVD | LHKAKDLEGV | DIILGVCSSG | LLVYKDKLRI | NRFPWPKVLK | ISYKRSSFFI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KIRPGEQEQY | ESTIGFKLPS | YRAAKKLWKV | CVEHHTFFRL | TSTDTIPKSK | FLALGSKFRY | SGRTQAQTRQ | ASALIDRPAP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HFERTASKRA | SRSLDGAAAV | DSADRSPRPT | SAPAITQGQV | AEGGVLDASA | KKTVVPKAQK | ETVKAEVKKE | DEPPEQAEPE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PTEAWKVEKT | HIEVTVPTSN | GDQTQKLAEK | TEDLIRMRKK | KRERLDGENI | YIRHSNLMLE | DLDKSQEEIK | KHHASISELK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KNFMESVPEP | RPSEWDKRLS | THSPFRTLNI | NGQIPTGEGV | KKTSVLPSER | KSINGIRTEE | VAVVTKGPST | NPDSEWEGPK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HSVVPSKSQM | TTSSESLQSF | AFGSLSISSK | ETEEKEEGAA | GYLDIKEMPR | GPTGGCIGVE | EQASALKFSV | TPASCQLQPG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VKKAESSEEH | VTPGEPPGKQ | NGSFLDFHVG | NQFPTLIRSF | QPPLVKTQTV | TISDNANAVK | SEIPTKDVPI | VHTETKTITY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EAAQTDDNSG | DLDPGVLLTA | QTITSETPSS | TTTTQITKTV | KGGISETRIE | KRIVITGDAD | IDHDQVLVQA | IKEAKEQHPD |
| 810 | 820 | | | | | | |
| MSVTKVVVHQ | ETEIADE | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1704 | 1 | 682.2585 | -109.76 | 3 | 51.6 | 12.4 | 1 | 454-470 | R.HSNLMLEDLDKSQEEIK.K | Oxidation: 5 |
| 100 | 1 | 565.6045 | -3.81 | 3 | 31.2 | 15.5 | 1 | 596-610 | K.EEGAAGYLDIKEMPR.G | Oxidation: 13 |

# Detailed Protein Report

## Protein 517: mucin-2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|557129045 | **Score:** | 27.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 539.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 0.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.72 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.63 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGLPLARLAA | VCLALSLAGG | SELQTEGRTR | NHGHNVCSTW | GNFHYKTFDG | DVFRFPGPCD | YNFASDCRGS | YKEFAVHLKR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GPGQAEAPAG | VESILLTIKD | DTIYLTRHLA | VLNGAVVSTP | HYSPGLLIEK | SDAYTKVYSR | AGLTLMWNRE | DALMLELDTK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FRNHTCGLCG | DYNGLQSYSE | FLSDGVLFSP | LEFGNMQKIN | QPDVVCEDPE | EEVAPASCSE | HRAECERLLT | AEAFADCQDL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VPLEPYLRAC | QQDRCRCPGG | DTCVCSTVAE | FSRQCSHAGG | RPGNWRTATL | CPKTCPGNLV | YLESGSPCMD | TCSHLEVSSL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CEEHRMDGCF | CPEGTVYDDI | GDSGCVPVSQ | CHCRLHGHLY | TPGQEITNDC | EQCVCNAGRW | VCKDLPCPGT | CALEGGSHIT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TFDGKTYTFH | GDCYYVLAKG | DHNDSYALLG | ELAPCGSTDK | QTCLKTVVLL | ADKKKNVVVF | KSDGSVLLNE | LQVNLPHVTA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SFSVFRPSSY | HIMVSMAIGV | RLQVQLAPVM | QLFVTLDQAS | QGQVQGLCGN | FNGLEGDDFK | TASGLVEATG | AGFANTWKAQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| STCHDKLDWL | DDPCSLNIES | ANYAEHWCSL | LKKTETPFGR | CHSAVDPAEY | YKRCKYDTCN | CQNNEDCLCA | ALSSYARACT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AKGVMLWGWR | EHVCNKDVGS | CPNSQVFLYN | LTTCQQTCRS | LSEADSHCLE | GFAPVDGCGC | PDHTFLDEKG | RCVPLAKCSC |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YHRGLYLEAG | DVVVRQEERC | VCRDGRLHCR | QIRLIGQSCT | APKIHMDCSN | LTALATSKPR | ALSCQTLAAG | YYHTECVSGC |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VCPDGLMDDG | RGGCVVEKEC | PCVHNNDLYS | SGAKIKVDCN | TCTCKRGRWV | CTQAVCHGTC | SIYGSGHYIT | FDGKYYDFDG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| HCSYVAVQDY | CGQNSSLGSF | SIITENVPCG | TTGVTCSKAI | KIFMGRTELK | LEDKHRVVIQ | RDEGHHVAYT | TREVGQYLVV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ESSTGIIVIW | DKRTTVFIKL | APSYKGTVCG | LCGNFDHRSN | NDFTTRDHMV | VSSELDFGNS | WKEAPTCPDV | STNPEPCSLN |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PHRRSWAEKQ | CSILKSSVFS | ICHSKVDPKP | FYEACVHDSC | SCDTGGDCEC | FCSAVASYAQ | ECTKEGACVF | WRTPDLCPIF |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| CDYYNPPHEC | EWHYEPCGNR | SFETCRTING | IHSNISVSYL | EGCYPRCPKD | RPIYEEDLKK | CVTADKCGCY | VEDTHYPPGA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SVPTEETCKS | CVCTNSSQVV | CRPEEGKILN | QTQDGAFCYW | EICGPNGTVE | KHFNICSITT | RPSTLTTFTT | ITLPTTPTTF |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TTTTTTTTPT | SSTVLSTTPK | LCCLWSDWIN | EDHPSSGSDD | GDRETFDGVC | GAPEDIECRS | VKDPHLSLEQ | LGQKVQCDVS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VGFICKNEDQ | FGNGPFGLCY | DYKIRVNCCW | PMDKCITTPS | PPTTTPSPPP | TSTTTLPPTT | TPSPPTTTTT | TPPPTTTPSP |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| PITTTTTPPP | TTTPSPPIST | TTTPPPTTTP | SPPTTTPSPP | TTTPSPPTTT | TTTPPPTTTP | SPPTTTPITP | PASTTTLPPT |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| TTPSPPTTTT | TTPPPTTTPS | PPTTTPITPP | TSTTTLPPTT | TPSPPPTTTT | TPPPTTTPSP | PTTTTPSPPT | ITTTTPPPTT |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| TPSPPTTTTT | TPPPTTTPSP | PTTTPITPPT | STTTLPPTTT | PSPPPTTTTT | PPPTTTPSPP | TTTTPSPPIT | TTTTPPPTTT |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| PSSPITTTPS | PPTTTMTTPS | PTTTPSSPIT | TTTTPSSTTT | PSPPPTTMTT | PSPTTTPSPP | TTTMTTLPPT | TTSSPLTTTP |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| LPPSITPPTF | SPFSTTTPTT | PCVPLCNWTG | WLDSGKPNFH | KPGGDTELIG | DVCGPGWAAN | ISCRATMYPD | VPIGQLGQTV |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| VCDVSVGLIC | KNEDQKPGGV | IPMAFCLNYE | INVQCCECVT | QPTTMTTTTT | ENPTPPTTTP | ITTTTTVTPT | PTPTGTQTPT |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| TTPITTTTTV | TPTPTPTGTQ | TPTTTPITTT | TTVTPTPTPT | GTQTPTTTPI | TTTTTVTPTP | TPTGTQTPTT | TPITTTTTVT |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| PTPTPTGTQT | PTTTPITTTT | TVTPTPTPTG | TQTPTTTPIT | TTTTVTPTPT | PTGTQTPTTT | PITTTTTVTP | TPTPTGTQTP |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| TTTPITTTTT | VTPTPTPTGT | QTPTTTPITT | TTTVTPTPTP | TGTQTPTTTP | ITTTTTVTPT | PTPTGTQTPT | TTPITTTTTV |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| TPTPTPTGTQ | TPTTTPITTT | TTVTPTPTPT | GTQTPTTTPI | TTTTTVTPTP | TPTGTQTPTT | TPITTTTTVT | PTPTPTGTQT |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| PTTTPITTTT | TVTPTPTPTG | TQTPTTTPIT | TTTTVTPTPT | PTGTQTPTTT | PITTTTTVTP | TPTPTGTQTP | TTTPITTTTT |
| 2330 | 2340 | 2350 | 2360 | 2370 | 2380 | 2390 | 2400 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2127 | 3 | 937.3845 | -87.61 | 2 | 56.5 | 16.1 | 0 | 764-780 | K.IHMDCSNLTALATSKPR.A | Oxidation: 3 | WUP:QUP 1.63<br>QU:MU 0.72 |

# Detailed Protein Report

**Protein 518:** **PREDICTED: von Willebrand factor A domain-containing protein 5B1 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578798398 | **Score:** | 27.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 102.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MPHVLIEKGD MTLGEFDQHL KGRTDFIKGM KKKSRAERKT EIIRKRLHKD IPHHSVIMLN FCPDLQSVQP CLRKAHGEFI
        90        100        110        120        130        140        150        160
FLIDRSSSMS GISMHRVKDA MLVALKSLMP ACLFNIIGFG STFKSLFPSS QTYSEDSLAM ACDDIQRMKA DMGGTNILSP
       170        180        190        200        210        220        230        240
LKWVIRQPVH RGHPRLLFVI TDGAVNNTGK VLELVRNHAF STRCYSFGIG PNVCHRLVKG LASVSEGSAE LLMEGERLQP
       250        260        270        280        290        300        310        320
KMVKSLKKAM APVLSDVTVE WIFPETTEVL VSPVSASSLF PGERLVGYGI VCDASLHISN PRSDKRRRYS MLHSQESGSS
       330        340        350        360        370        380        390        400
VFYHSQDDGP GLEGGDCAKN SGAPFILGQA KNARLASGDS TTKHDLNLSQ RRRAYSTNQI TNHKPLPRAT MASDPMPAAK
       410        420        430        440        450        460        470        480
RYPLRKARLQ DLTNQTSLDV QRWQIDLQPL LNSGQDLNQG PKLRGPGARR PSLLPQGCQP FLPWGQETQA WSPVRERTSD
       490        500        510        520        530        540        550        560
SRSPGDLEPS HHPSAFETET SSDWDPPAES QERASPSRPA TPAPVLGKAL VKGLHDSQRL QWEVSFELGT PGPERGGAQD
       570        580        590        600        610        620        630        640
ADLWSETFHH LAARAIIRDF EQLAEREGEI EQGSNRRYQV SALHTSKACN IISKYTAFVP VDVSKSRYLP TVVEYPNSGA
       650        660        670        680        690        700        710        720
ALRMLGSRAL AQQWRGTSSG FGRPQTMLGE DSAPGNDMEA SPTALFSEAR SPGREKHGAS EGPQRSLATN TLSSMKASEN
       730        740        750        760        770        780        790        800
LFGSWLNLNK SRLLTRAAKG FLSKPLIKAV ESTSGNQSFD YIPLVSLQLA SGAFLLNEAF CEATHIPMEK LKWTSPFTCH
       810        820        830        840        850        860        870        880
RVSLTTRPSE SKTPSPQLCT SSPPRHPSCD SFSLEPLAKG KLGLEPRAVV EHTGKLWATV VGLAWLEHSS ASYFTEWELV
       890        900        910        920        930        940
AAKANSWLEQ QEVPEGRTQG TLKAAARQLF VLLRHWDENL EFNMLCYNPN YV
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1946 | 1 | 745.7827 | -91.37 | 2 | 54.7 | 12.0 | 0 | 9-21 | K.GDMTLGEFDQHLK.G | |

# Detailed Protein Report

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**Protein 519:** **glyoxalase domain-containing protein 4 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|217330598 | **Score:** | 27.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 33.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 8.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.22 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.40 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MAARRALHFV FKVGNRFQTA RFYRDVLGMK VLRHEEFEEG CKAACNGPYD GKWSKTMVGF GPEDDHFVAE LTYNYGVGDY
        90        100        110        120        130        140        150        160
KLGNDFMGIT LASSQAVSNA RKLEWPLTEV AEGVFETEAP GGYKFYLQNR SLPQSDPVLK VTLAVSDLQK SLNYWCNLLG
       170        180        190        200        210        220        230        240
MKIYEKDEEK QRALLGYADN QCKLELQGVK GGVDHAAAFG RIAFSCPQKE LPDLEDLMKR ENQKILTPLV SLDTPGKATV
       250        260        270        280        290        300
QVVILADPDG HEICFVGDEA FRELSKMDPE GSKLLDDAMA ADKSDEWFAK HNKPKASG
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1097 | 1 | 631.1089 | 141.12 | 3 | 42.0 | 17.0 | 2 | 6-21 | R.ALHFVFKVGNRFQTAR.F | | WUP:QUP 1.40<br>QU:MU 0.22 |

# Detailed Protein Report

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**Protein 520:** **PREDICTED: T-lymphoma invasion and metastasis-inducing protein 1 isoform X4 [Homo sapiens]**

**Accession:** gi|530419050
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 27.6
**MW [kDa]:** 161.7
**pI:** 6.4
**Sequence Coverage [%]:** 2.1
**No. of unique Peptides:** 1

## Quantitation

***QU:MU*** **Median:** 4.76 **CV:** 0.00 % **No. of Peptides:** 1
***WUP:QUP*** **Median:** 0.17 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGNAESQHVE | HEFYGEKHAS | LGRKHTSRSL | RLSHKTRRTR | HASSGKVIHR | NSEVSTRSSS | TPSIPQSLAE | NGLEPFSQDG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TLEDFGSPIW | VDRVDMGLRP | VSYTDSSVTP | SVDSSIVLTA | ASVQSMPDTE | ESRLYGDDAT | YLAEGGRRQH | SYTSNGPTFM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ETASFKKKRS | KSADIWREDS | LEFSLSDLSQ | EHLTSNEEIL | GSAEEKDCEE | ARGMETRASP | RQLSTCQRAN | SLGDLYAQKN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SGVTANGGPG | SKFAGYCRNL | VSDIPNLANH | KMPPAAAEET | PPYSNYNTLP | CRKSHCLSEG | ATNPQISHSN | SMQGRRAKTT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QDVNAGEGSE | FADSGIEGAT | TDTDLLSRRS | NATNSSYSPT | TGRAFVGSDS | GSSSTGDAAR | QGVYENFRRE | LEMSTTNSES |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LEEAGSAHSD | EQSSGTLSSP | GQSDILLTAA | QGTVRKAGAL | AVKNFLVHKK | NKKVESATRR | KWKHYWVSLK | GCTLFFYESD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GRSGIDHNSI | PKHAVWVENS | IVQAVPEHPK | KDFVFCLSNS | LGDAFLFQTT | SQTELENWIT | AIHSACATAV | ARHHHKEDTL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RLLKSEIKKL | EQKIDMDEKM | KKMGEMQLSS | VTDSKKKKTI | LDQIFVWEQN | LEQFQMDLFR | FRCYLASLQG | GELPNPKRLL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AFASRPTKVA | MGRLGIFSVS | SFHALVAART | GETGVRRRTQ | AMSRSASKRR | SRFSSLWGLD | TTSKKKQGRP | SINQVFGEGT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EAVKKSLEGI | FDDIVPDGKR | EKEVVLPNVH | QHNPDCDIWV | HEYFTPSWFC | LPNNQPALTV | VRPGDTARDT | LELICKTHQL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DHSAHYLRLK | FLIENKMQLY | VPQPEEDIYE | LLYKEIEICP | KVTQSIHIEK | SDTAADTYGF | SLSSVEEDGI | RRLYVNSVKE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TGLASKKGLK | AGDEILEINN | RAADALNSSM | LKDFLSQPSL | GLLVRTYPEL | EEGVELLESP | PHRVDGPADL | GESPLAFLTS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NPGHSLCSEQ | GSSAETAPEE | TEGPDLESSD | ETDHSSKSTE | QVAAFCRSLH | EMNPSDQSPS | PQDSTGPQLA | TMRQLSDADK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LRKVICELLE | TERTYVKDLN | CLMERYLKPL | QKETFLTQDE | LDVLFGNLTE | MVEFQVEFLK | TLEDGVRLVP | DLEKLEKVDQ |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| FKKVLFSLGG | SFLYYADRFK | LYSAFCASHT | KVPKVLVKAK | TDTAFKAFLD | AQNPKQQHSS | TLESYLIKPI | QRILKYPLLL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| RELFALTDAE | SEEHYHLDVA | IKTMNKVASH | INEMQKIHEE | FGAVFDQLIA | EQTGEKKEVA | DLSMGDLLLH | TTVIWLNPPA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SLGKWKKEPE | LAAFVFKTAV | VLVYKDGSKQ | KKKLVGSHRL | SIYEDWDPFR | FRHMIPTEAL | QVRALASADA | EANAVCEIVH |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VKSESEGRPE | RVFHLCCSSP | ESRKDFLKAV | HSILRDKHRR | QLLKTESLPS | SQQYVPFGGK | RLCALKGARP | AMSRAGTVGI |
| 1450 | 1460 | | | | | | |
| RTFKIPVTPT | PQ | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 44 | 2 | 750.8174 | -45.94 | 2 | 30.3 | 15.2 | 0 | 134-147 | R.LYGDDATYLAEGGR.R | | WUP:QUP 0.17<br>QU:MU 4.76 |

# Detailed Protein Report

## Protein 521: ataxin-7-like protein 3 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|149588534 | **Score:** | 27.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 6.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKMEEMSLSG | LDNSKLEAIA | QEIYADLVED | SCLGFCFEVH | RAVKCGYFFL | DDTDPDSMKD | FEIVDQPGLD | IFGQVFNQWK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SKECVCPNCS | RSIAASRFAP | HLEKCLGMGR | NSSRIANRRI | ANSNNMNKSE | SDQEDNDDIN | DNDWSYGSEK | KAKKRKSDKN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PNSPRRSKSL | KHKNGELSNS | DPFKYNNSTG | ISYETLGPEE | LRSLLTTQCG | VISEHTKKMC | TRSLRCPQHT | DEQRRTVRIY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FLGPSAVLPE | VESSLDNDSF | DMTDSQALIS | RLQWDGSSDL | SPSDSGSSKT | SENQGWGLGT | NSSESRKTKK | KKSHLSLVGT |
| 330 | 340 | 350 | | | | | |
| ASGLGSNKKK | KPKPPAPPTP | SIYDDIN | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 631 | 1 | 766.4842 | 137.27 | 2 | 37.4 | 10.7 | 1 | 98-110 | R.FAPHLEKCLGMGR.N | Carbamidomethyl: 8;<br>Oxidation: 11 |

# Detailed Protein Report

## Protein 522: PREDICTED: E3 ubiquitin-protein ligase UBR5 isoform X7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530389115 | **Score:** | 27.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 200.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMRRSLRAAG | LGRHEAGASS | SDHQDPVSPP | IAPPSWVPDP | PAMDPDGDID | FILAPAVGSL | TTAATGTGQG | PSTSTIPGPS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TEPSVVESKD | RKANAHFILK | LLCDSVVLQP | YLRELLSAKD | ARGMTPFMSA | VSGRAYPAAI | TILETAQKIA | KAEISSSEKE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EDVFMGMVCP | SGTNPDDSPL | YVLCCNDTCS | FTWTGAEHIN | QDIFECRTCG | LLESLCCCTE | CARVCHKGHD | CKLKRTSPTA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YCDCWEKCKC | KTLIAGQKSA | RLDLLYRLLT | ATNLVTLPNS | RGEHLLLFLV | QTVARQTVEH | CQYRPPRIRE | DRNRKTASPE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DSDMPDHDLE | PPRFAQLALE | RVLQDWNALK | SMIMFGSQEN | KDPLSASSRI | GHLLPEEQVY | LNQQSGTIRL | DCFTHCLIVK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CTADILLLDT | LLGTLVKELQ | NKYTPGRREE | AIAVTMRFLR | SVARVFVILS | VEMASSKKKN | NFIPQPIGKC | KRVFQALLPY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AVEELCNVAE | SLIVPVRMGI | ARPTAPFTLA | STSIDAMQGS | EELFSVEPLP | PRPSSDQSSS | SSQSQSSYII | RNPQQRRISQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SQPVRGRDEE | QDDIVSADVE | EVEVVEGVAG | EEDHHDEQEE | HGEENAEAEG | QHDEHDEDGS | DMELDLLAAA | ETESDSESNH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SNQDNASGRR | SVVTAATAGS | EAGASSVPAF | FSEDDSQSND | SSDSDSSSSQ | SDDIEQETFM | LDEPLERTTN | SSHANGAAQA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PRSMQWAVRN | TQHQRAASTA | PSSTSTPAAS | SAGLIYIDPS | NLRRSGTIST | SAAAAAAALE | ASNASSYLTS | ASSLARAYSI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VIRQISDLMG | LIPKYNHLVY | SQIPAAVKLT | YQDAVNLQNY | VEEKLIPTWN | WMVSIMDSTE | AQLRYGSALA | SAGDPGHPNH |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PLHASQNSAR | RERMTAREEA | SLRTLEGRRR | ATLLSARQGM | MSARGDFLNY | ALSLMRSHND | EHSDVLPVLD | VCSLKHVAYV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FQALIYWIKA | MNQQTTLDTP | QLERKRTREL | LELGIDNEDS | EHENDDDTNQ | SATLNDKDDD | SLPAETGQNH | PFFRRSDSMT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| FLGCIPPNPF | EVPLAEAIPL | ADQPHLLQPN | ARKEDLFGRP | SQGLYSSSAS | SGKCLMEVTV | DRNCLEVLPT | KMSYAANLKN |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| VMNMQNRQKK | EGEEQPVLPE | ETESSKPGPS | AHDLAAQLKS | SLLAEIGLTE | SEGPPLTSFR | PQCSFMGMVI | SHDMLLGRWR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LSLELFGRVF | MEDVGAEPGS | ILTELGGFEV | KESKFRREME | KLRNQQSRDL | SLEVKVDRDR | DLLIQQTMRQ | LNNHFGRRCA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TTPMAVHRVK | VTFKDEPGEG | SGVARSFYTA | IAQAFLSNEK | LPNLECIQNA | NKGTHTSLMQ | RLRNRGERDR | EREREREMRR |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| SSGLRAGSRR | DRDRDFRRQL | SIDTRPFRPA | SEGNPSDDPE | PLPAHRQALG | ERLYPRVQAM | QPAFASKITG | MLLELSPAQL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LLLLASEDSL | RARVDEAMEL | IIAHGRENGA | DSILDLGLVD | SSEKVQQENR | KRHGSSRSVV | DMDLDDTDDG | DDNAPLFYQP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| GKRGFYTPRP | GKNTEARLNC | FRNIGRILGL | CLLQNELCPI | TLNRHVIKVL | LGRKVNWHDF | AFFDPVMYES | LRQLILASQS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| SDADAVFSAM | DLAFAIDLCK | EEGGGQVELI | PNGVNIPVTP | QNVYEYVRKY | AEHRMLVVAE | QPLHAMRKGL | LDVLPKNSLE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| DLTAEDFRLL | VNGCGEVNVQ | MLISFTSFND | ESGENAEKLL | QFKRWFWSIV | EKMSMTERQD | LVYFWTSSPS | LPASEEGFQP |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | | |
| MPSITIRPPD | DQHLPTANTC | ISRLYVPLYS | SKQILKQKLL | LAIKTKNFGF | V | | |

| Cmpd. | No. of | m/z meas. | Δ m/z | z | Rt | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

|  | Cmpds. |  | [ppm] |  | [min] |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|
| 2795 | 1 | 958.9896 | 49.22 | 2 | 65.4 | 17.4 | 1 | 1112-<br>1127 | K.MSYAANLKNVMNMQNR.Q | Oxidation: 11, 13 |

# Detailed Protein Report

**Protein 523:** **EGF domain-specific O-linked N-acetylglucosamine transferase isoform a precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|522838254 | **Score:** | 27.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 62.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.7 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578805996 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: EGF domain-specific O-linked N-acetylglucosamine transferase isoform X3 [Homo sapiens] |
| gi\|530373685 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: EGF domain-specific O-linked N-acetylglucosamine transferase isoform X2 [Homo sapiens] |
| gi\|530373683 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: EGF domain-specific O-linked N-acetylglucosamine transferase isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLMLFVFGVL | LHEVSLSGQN | EAPPNTHSIP | GEPLYNYASI | RLPEEHIPFF | LHNNRHIATV | CRKDSLCPYK | KHLEKLKYCW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GYEKSCKPEF | RFGYPVCSYV | DMGWTDTLES | AEDIFWKQAD | FGYARERLEE | MHVLCQPKET | SDSSLVCSRY | LQYCRATNLY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LDLRNIKRNH | DRFKEDFFQS | GEIGGHCKLD | IRTLTSEGQR | KSPLQSWFAE | LQSYTQLNFR | PIEDAKCDIV | IEKPTYFMKL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DAGVNMYHHF | CDFINLYITQ | HVNNSFSTDV | YIVMWDTSSY | GYGDLFSDTW | NAFTDYDVIH | LKTYDSKRVC | FKEAVFSLLP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RMRYGLFYNT | PLISGCQNTG | LFRAFAQHVL | HRLNITQEGP | KDGKIRVTIL | ARSTEYRKIL | NQNELVNALK | TVSTFEVQIV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DYKYRELGFL | DQLRITHNTD | IFIGMHGAGL | THLLFLPDWA | AVFELYNCED | ERCYLDLARL | RGVHYITWRR | QNKVFPQDKG |
| 490 | 500 | 510 | 520 | 530 | | | |
| HHPTLGEHPK | FTNYSFDVEE | FMYLVLQAAD | HVLQHPKWPF | KKKHDEL | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 674 | 1 | 698.6888 | 27.74 | 3 | 38.4 | 13.0 | 2 | 76-91 | K.LKYCWGYEKSCKPEFR.F | Carbamidomethyl: 11 |

# Detailed Protein Report

**Protein 524:** **cytoskeleton-associated protein 2 isoform 3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|557878731 | **Score:** | 27.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 71.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLSSRDQRVV | TSEDQVQEGT | KVLKLKTKMA | DKENMKRPAE | SKNNTVVGKH | CIPLKPSNEL | TNSTVVIDTH | KPKDSNQTPH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LLLTEDDPQS | QHMTLSQAFH | LKNNSKKKQM | TTEKQKQDAN | MPKKPVLGSY | RGQIVQSKIN | SFRKPLQVKD | ESSAATKKLS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ATIPKATKPQ | PVNTSSVTVK | SNRSSNMTAT | TKFVSTTSQN | TQLVRPPIRS | HHSNTRDTVK | QGISRTSANV | TIRKGPHEKE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LLQSKTALSS | VKTSSSQGII | RNKTLSRSIA | SEVIARPASL | SNDKLMEKSE | PVDQRRHTAG | KAIVDSRSAQ | PKETSEERKA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RLSEWKAGKG | RVLKRPPNSV | VTQHEPAGQN | EKPVGSFWTT | MAEEDEQRLF | TEKVNNTFSE | CLNLINEGCP | KEDILVTLND |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LIKNIPDAKK | LVKYWICLAL | IEPITSPIEN | IIAIYEKAIL | AGAQPIEEMR | HTIVDILTMK | SQEKANLGEN | MEKSCASKEE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VKEVSIEDTG | VDVDPEKLEM | ESKLHRNLLF | QDCEKEQDNK | TKDPTHDVKT | PNTETRTSCL | IKYNVSTTPY | LQSVKKKVQF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DGTNSAFKEL | KFLTPVRRSR | RLQEKTSKLP | DMLKDHYPCV | SSLEQLTELG | RETDAFVCRP | NAALCRVYYE | ADTT |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2617 | 1 | 732.5346 | 128.71 | 1 | 63.5 | 10.7 | 0 | 572-577 | K.FLTPVR.R | |

# Detailed Protein Report

## Protein 525: long-chain-fatty-acid--CoA ligase 1 isoform d [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|557878742 | **Score:** | 27.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 58.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.6 |
| | | **Sequence Coverage [%]:** | 5.1 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MVIVPLYDTL | GNEAITYIVN | KAELSLVFVD | KPEKAKLLLE | GVENKLIPGL | KIIVVMDAYG | SELVERGQRC | GVEVTSMKAM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EDLGRANRRK | PKPPAPEDLA | VICFTSGTTG | NPKGAMVTHR | NIVSDCSAFV | KATENTVNPC | PDDTLISFLP | LAHMFERVVE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CVMLCHGAKI | GFFQGDIRLL | MDDLKVLQPT | VFPVVPRLLN | RMFDRIFGQA | NTTLKRWLLD | FASKRKEAEL | RSGIIRNNSL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| WDRLIFHKVQ | SSLGGRVRLM | VTGAAPVSAT | VLTFLRAALG | CQFYEGYGQT | ECTAGCCLTM | PGDWTAGHVG | APMPCNLIKL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VDVEEMNYMA | AEGEGEVCVK | GPNVFQGYLK | DPAKTAEALD | KDGWLHTGDI | GKWLPNGTLK | IIDRKKHIFK | LAQGEYIAPE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KIENIYMRSE | PVAQVFVHGE | SLQAFLIAIV | VPDVETLCSW | AQKRGFEGSF | EELCRNKDVK | KAILEDMVRL | GKDSGLKPFE |
| 490 | 500 | 510 | 520 | 530 | | | |
| QVKGITLHPE | LFSIDNGLLT | PTMKAKRPEL | RNYFRSQIDD | LYSTIKV | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2760 | 1 | 848.9242 | -91.80 | 2 | 64.9 | 14.2 | 2 | 244-258 | R.LIFHKVQSSLGGRVR.L | |
| 2516 | 1 | 715.3738 | 61.15 | 2 | 62.0 | 13.4 | 1 | 444-455 | K.RGFEGSFEELCR.N | |

# Detailed Protein Report

## Protein 526: PREDICTED: nucleoprotein TPR isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530365345 | **Score:** | 27.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 274.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| | | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 0.29 | **CV:** 0.00 % | **No. of Peptides:** 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPSSGSVSRS | RQRGRSMASR | GFDGSRRGSL | RRAGAREPPS | EVIEAAAQAS | GSCWSSPFFS | ASTPSAAATG | VPGPTDMAAV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LQQVLERTEL | NKLPKSVQNK | LEKFLADQQS | EIDGLKGRHE | KFKVESEQQY | FEIEKRLSHS | QERLVNETRE | CQSLRLELEK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LNNQLKALTE | KNKELEIAQD | RNIAIQSQFT | RTKEELEAEK | RDLIRTNERL | SQELEYLTED | VKRLNEKLKE | SNTTKGELQL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KLDELQASDV | SVKYREKRLE | QEKELLHSQN | TWLNTELKTK | TDELLALGRE | KGNEILELKC | NLENKKEEVS | RLEEQMNGLK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TSNEHLQKHV | EDLLTKLKEA | KEQQASMEEK | FHNELNAHIK | LSNLYKSAAD | DSEAKSNELT | RAVEELHKLL | KEAGEANKAI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QDHLLEVEQS | KDQMEKEMLE | KIGRLEKELE | NANDLLSATK | RKGAILSEEE | LAAMSPTAAA | VAKIVKPGMK | LTELYNAYVE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TQDQLLLEKL | ENKRINKYLD | EIVKEVEAKA | PILKRQREEY | ERAQKAVASL | SVKLEQAMKE | IQRLQEDTDK | ANKQSSVLER |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DNRRMEIQVK | DLSQQIRVLL | MELEEARGNH | VIRDEEVSSA | DISSSSEVIS | QHLVSYRNIE | ELQQQNQRLL | VALRELGETR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EREEQETTSS | KITELQLKLE | SALTELEQLR | KSRQHQMQLV | DSIVRQRDMY | RILLSQTTGV | AIPLHASSLD | DVSLASTPKR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PSTSQTVSTP | APVPVIESTE | AIEAKAALKQ | LQEIFENYKK | EKAENEKIQN | EQLEKLQEQV | TDLRSQNTKI | STQLDFASKR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| YEMLQDNVEG | YRREITSLHE | RNQKLTATTQ | KQEQIINTMT | QDLRGANEKL | AVAEVRAENL | KKEKEMLKLS | EVRLSQQRES |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LLAEQRGQNL | LLTNLQTIQG | ILERSETETK | QRLSSQIEKL | EHEISHLKKK | LENEVEQRHT | LTRNLDVQLL | DTKRQLDTET |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NLHLNTKELL | KNAQKEIATL | KQHLSNMEVQ | VASQSSQRTG | KGQPSNKEDV | DDLVSQLRQT | EEQVNDLKER | LKTSTSNVEQ |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| YQAMVTSLEE | SLNKEKQVTE | EVRKNIEVRL | KESAEFQTQL | EKKLMEVEKE | KQELQDDKRR | AIESMEQQLS | ELKKTLSSVQ |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| NEVQEALQRA | STALSNEQQA | RRDCQEQAKI | AVEAQNKYER | ELMLHAADVE | ALQAAKEQVS | KMASVRQHLE | ETTQKAESQL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LECKASWEER | ERMLKDEVSK | CVCRCEDLEK | QNRLLHDQIE | KLSDKVVASV | KEGVQGPLNV | SLSEEGKSQE | QILEILRFIR |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| REKEIAETRF | EVAQVESLRY | RQRVELLERE | LQELQDSLNA | EREKVQVTAK | TMAQHEELMK | KTETMNVVME | TNKMLREEKE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| RLEQDLQQMQ | AKVRKLELDI | LPLQEANAEL | SEKSGMLQAE | KKLLEEDVKR | WKARNQHLVS | QQKDPDTEEY | RKLLSEKEVH |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| TKRIQQLTEE | IGRLKAEIAR | SNASLTNNQN | LIQSLKEDLN | KVRTEKETIQ | KDLDAKIIDI | QEKVKTITQV | KKIGRRYKTQ |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| YEELKAQQDK | VMETSAQSSG | DHQEQHVSVQ | EMQELKETLN | QAETKSKSLE | SQVENLQKTL | SEKETEARNL | QEQTVQLQSE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LSRLRQDLQD | RTTQEEQLRQ | QITEKEEKTR | KAIVAAKSKI | AHLAGVKDQL | TKENEELKQR | NGALDQQKDE | LDVRITALKS |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| QYEGRISRLE | RELREHQERH | LEQRDEPQEP | SNKVPEQQRQ | ITLKTTPASG | ERGIASTSDP | PTANIKPTPV | VSTPSKVTAA |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| AMAGNKSTPR | ASIRPMVTPA | TVTNPTTTPT | ATVMPTTQVE | SQEAMQSEGP | VEHVPVFGST | SGSVRSTSPN | VQPSISQPIL |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| TVQQQTQATA | FVQPTQQSHP | QIEPANQELS | SNIVEVVQSS | PVERPSTSTA | VFGTVSATPS | SSLPKRTREE | EEDSTIEASD |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| QVSDDTVEMP | LPKKLKSVTP | VGTEEEVMAE | ESTDGEVETQ | VYNQDSQDSI | GEGVTQGDYT | PMEDSEETSQ | SLQIDLGPLQ |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| SDQQTTTSSQ | DGQGKGDDVI | VIDSDDEEED | DDENDGEHED | YEEDEEDDDD | DEDDTGMGDE | GEDSNEGTGS | ADGNDGYEAD |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| DAEGGDGTDP | GTETEESMGG | GEGNHRAADS | QNSGEGNTGA | AESSFSQEVS | REQQPSSASE | RQAPRAPQSP | RRPPHPLPPR |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| LTIHAPPQEL | GPPVQRIQMT | RRQSVGRGLQ | LTPGIGGMQQ | HFFDDEDRTV | PSTPTLVVPH | RTDGFAEAIH | SPQVAGVPRF |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| RFGPPEDMPQ | TSSSHSDLGQ | LASQGGLGMY | ETPLFLAHEE | ESGGRSVPTT | PLQVAAPVTV | FTESTTSDAS | EHASQSVPMV |
| 2330 | 2340 | 2350 | 2360 | 2370 | 2380 | 2390 | 2400 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1647 | 1 | 524.8144 | 75.03 | 2 | 50.8 | 12.8 | 2 | 12-20 | R.QRGRSMASR.G |  | QU:MU 0.29 |

# Detailed Protein Report

## Protein 527: PREDICTED: pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530424571 | **Score:** | 27.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 136.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.31 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.51 | **CV:** | 37.25 % | **No. of Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGDTSEDASI | HRLEGTDLDC | QVGGLICKSK | SAASEQHVFK | APAPRPSLLG | LDLLASLKRR | EREEKDDGED | KKKSKVSSYK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DWEESKDDQK | DAEEEGGDQA | GQNIRKDRHY | RSARVETPSH | PGGVSEEFWE | RSRQRERERR | EHGVYASSKE | EKDWKKEKSR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DRDYDRKRDR | DAATPSRSTW | EEEDSGYGSS | RRSQWESPSP | TPSYRDSERS | HRLSTRDRDR | SVRGKYSDDT | PLPTPSYKYN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EWADDRRHLG | STPRLSRGRG | RREEGEEGIS | FDTEEERQQW | EDDQRQADRD | WYMMDEGYDE | FHNPLAYSSE | DYVRRREQHL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HKQKQKRISA | QRRQINEDNE | RWETNRMLTS | GVVHRLEVDE | DFEEDNAAKV | HLMVHNLVPP | FLDGRIVFTK | QPEPVIPVKD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ATSDLAIIAR | KGSQTVRKHR | EQKERKKAQH | KHWELAGTKL | GDIMGVKKEE | EPDKAVTEDG | KVDYRTEQKF | ADHMKRKSEA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SSEFAKKKSI | LEQRQYLPIF | AVQQELLTII | RDNSIVIVVG | ETGSGKTTQL | TQYLHEDGYT | DYGMIGCTQP | RRVAAMSVAK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RVSEEMGGNL | GEEVGYAIRF | EDCTSENTLI | KYMTDGILLR | ESLREADLDH | YSAIIMDEAH | ERSLNTDVLF | GLLREVVARR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SDLKLIVTSA | TMDAEKFAAF | FGNVPIFHIP | GRTFPVDILF | SKTPQEDYVE | AAVKQSLQVH | LSGAPGDILI | FMPGQEDIEV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TSDQIVEHLE | ELENAPALAV | LPIYSQLPSD | LQAKIFQKAP | DGVRKCIVAT | NIAETSLTVD | GIMFVIDSGY | CKLKVFNPRI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GMDALQIYPI | SQANANQRSG | RAGRTGPGQC | FRLYTQSAYK | NELLTTTVPE | IQRTNLANVV | LLLKSLGVQD | LLQFHFMDPP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PEDNMLNSMY | QLWILGALDN | TGGLTSTGRL | MVEFPLDPAL | SKMLIVSCDM | GCSSEILLIV | SMLSVPAIFY | RPKGREEESD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QIREKFAVPE | SDHLTYLNVY | LQWKNNNYST | IWCNDHFIHA | KAMRKVREVR | AQLKDIMVQQ | RMSLASCGTD | WDIVRKCICA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AYFHQAAKLK | GIGEYVNIRT | GMPCHLHPTS | SLFGMGYTPD | YIVYHELVMT | TKEYMQCVTA | VDGEWLAELG | PMFYSVKQAG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KSRQENRRRA | KEEASAMEEE | MALAEEQLRA | RRQEQEKRSP | LGSVRSTKIY | TPGRKEQGEP | MTPRRTPARF | GL |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 145 | 1 | 896.4035 | -68.20 | 3 | 31.5 | 16.8 | 2 | 800-824 | R. IGMDALQIYPISQANANQRSGRAG T | | QU:MU 2.31<br>WUP:QUP 0.73 |
| 1651 | 1 | 720.3147 | -23.44 | 2 | 50.9 | 10.7 | 0 | 1037-1048 | K.CICAAYFHQAAK.L | Carbamidomethyl: 1, 3 | WUP:QUP 0.35 |

# Detailed Protein Report

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**Protein 528:** **retinoblastoma-associated protein [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|108773787 | **Score:** | 27.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 106.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.9 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPPKTPRKTA | ATAAAAAAEP | PAPPPPPPPE | EDPEQDSGPE | DLPLVRLEFE | ETEEPDFTAL | CQKLKIPDHV | RERAWLTWEK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VSSVDGVLGG | YIQKKKELWG | ICIFIAAVDL | DEMSFTFTEL | QKNIEISVHK | FFNLLKEIDT | STKVDNAMSR | LLKKYDVLFA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LFSKLERTCE | LIYLTQPSSS | ISTEINSALV | LKVSWITFLL | AKGEVLQMED | DLVISFQLML | CVLDYFIKLS | PPMLLKEPYK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TAVIPINGSP | RTPRRGQNRS | ARIAKQLEND | TRIIEVLCKE | HECNIDEVKN | VYFKNFIPFM | NSLGLVTSNG | LPEVENLSKR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YEEIYLKNKD | LDARLFLDHD | KTLQTDSIDS | FETQRTPRKS | NLDEEVNVIP | PHTPVRTVMN | TIQQLMMILN | SASDQPSENL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ISYFNNCTVN | PKESILKRVK | DIGYIFKEKF | AKAVGQGCVE | IGSQRYKLGV | RLYYRVMESM | LKSEEERLSI | QNFSKLLNDN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IFHMSLLACA | LEVVMATYSR | STSQNLDSGT | DLSFPWILNV | LNLKAFDFYK | VIESFIKAEG | NLTREMIKHL | ERCEHRIMES |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LAWLSDSPLF | DLIKQSKDRE | GPTDHLESAC | PLNLPLQNNH | TAADMYLSPV | RSPKKKGSTT | RVNSTANAET | QATSAFQTQK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PLKSTSLSLF | YKKVYRLAYL | RLNTLCERLL | SEHPELEHII | WTLFQHTLQN | EYELMRDRHL | DQIMMCSMYG | ICKVKNIDLK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| FKIIVTAYKD | LPHAVQETFK | RVLIKEEEYD | SIIVFYNSVF | MQRLKTNILQ | YASTRPPTLS | PIPHIPRSPY | KFPSSPLRIP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GGNIYISPLK | SPYKISEGLP | TPTKMTPRSR | ILVSIGESFG | TSEKFQKINQ | MVCNSDRVLK | RSAEGSNPPK | PLKKLRFDIE |
| 890 | 900 | 910 | 920 | 930 | | | |
| GSDEADGSKH | LPGESKFQQK | LAEMTSTRTR | MQKQKMNDSM | DTSNKEEK | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2018 | 1 | 1044.9422 | -30.44 | 2 | 55.6 | 16.6 | 1 | 699-715 | R.HLDQIMMCSMYGICKVK.N | Carbamidomethyl: 14;<br>Oxidation: 6, 10 |

# Detailed Protein Report

## Protein 529: metastasis-associated in colon cancer protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|157502191 | **Score:** | 27.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 96.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| | | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.50 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLITERKHFR | SGRIAQSMSE | ANLIDMEAGK | LSKSCNITEC | QDPDLLHNWP | DAFTLRGNNA | SKVANPFWNQ | LSASNPFLDD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ITQLRNNRKR | NNISILKEDP | FLFCREIENG | NSFDSSGDEL | DVHQLLRQTS | SRNSGRSKSV | SELLDILDDT | AHAHQSIHNS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DQILLHDLEW | LKNDREAYKM | AWLSQRQLAR | SCLDLNTISQ | SPGWAQTQLA | EVTIACKVNH | QGGSVQLPES | DITVHVPQGH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VAVGEFQEVS | LRAFLDPPHM | LNHDLSCTVS | PLLEIMLGNL | NTMEALLLEM | KIGAEVRKDP | FSQVMTEMVC | LHSLGKEGPF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KVLSNCYIYK | DTIQVKLIDL | SQVMYLVVAA | QAKALPSPAA | TIWDYIHKTT | SIGIYGPKYI | HPSFTVVLTV | CGHNYMPGQL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TISDIKKGGK | NISPVVFQLW | GKQSFLLDKP | QDLSISIFSC | DPDFEVKTEG | ERKEIKQKQL | EAGEVVHQQF | LFSLVEHREM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HLFDFCVQVE | PPNGEPVAQF | SITTPDPTPN | LKRLSNLPGY | LQKKEEIKSA | PLSPKILVKY | PTFQDKTLNF | SNYGVTLKAV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LRQSKIDYFL | EYFKGDTIAL | LGEGKVKAIG | QSKVKEWYVG | VLRGKIGLVH | CKNVKVISKE | QVMFMSDSVF | TTRNLLEQIV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LPLKKLTYIY | SVVLTLVSEK | VYDWKVLADV | LGYSHLSLED | FDQIQADKES | EKVSYVIKKL | KEDCHTERNT | RKFLYELIVA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LLKMDCQELV | ARLIQEAAVL | TSAVKLGKGW | RELAEKLVRL | TKQQMEAYEI | PHRGNTGDVA | VEMMWKPAYD | FLYTWSAHYG |
| 810 | 820 | 830 | 840 | 850 | 860 | | |
| NNYRDVLQDL | QSALDRMKNP | VTKHWRELTG | VLILVNSLEV | LRVTAFSTSE | EV | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2511 | 1 | 841.8162 | -157.28 | 2 | 61.3 | 16.7 | 0 | 354-368 | K.ALPSPAATIWDYIHK.T | | WUP:QUP 0.50 |

# Detailed Protein Report

## Protein 530: ephrin type-A receptor 3 isoform b precursor [Homo sapiens]

**Accession:** gi|32967314
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 27.5
**MW [kDa]:** 60.9
**pI:** 5.5
**Sequence Coverage [%]:** 3.0
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDCQLSILLL | LSCSVLDSFG | ELIPQPSNEV | NLLDSKTIQG | ELGWISYPSH | GWEEISGVDE | HYTPIRTYQV | CNVMDHSQNN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| WLRTNWVPRN | SAQKIYVELK | FTLRDCNSIP | LVLGTCKETF | NLYYMESDDD | HGVKFREHQF | TKIDTIAADE | SFTQMDLGDR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ILKLNTEIRE | VGPVNKKGFY | LAFQDVGACV | ALVSVRVYFK | KCPFTVKNLA | MFPDTVPMDS | QSLVEVRGSC | VNNSKEEDPP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RMYCSTEGEW | LVPIGKCSCN | AGYEERGFMC | QACRPGFYKA | LDGNMKCAKC | PPHSSTQEDG | SMNCRCENNY | FRADKDPPSM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ACTRPPSSPR | NVISNINETS | VILDWSWPLD | TGGRKDVTFN | IICKKCGWNI | KQCEPCSPNV | RFLPRQFGLT | NTTVTVTDLL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AHTNYTFEID | AVNGVSELSS | PPRQFAAVSI | TTNQAAPSPV | LTIKKDRTSR | NSISLSWQEP | EHPNGIILDY | EVKYYEKQEQ |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| ETSYTILRAR | GTNVTISSLK | PDTIYVFQIR | ARTAAGYGTN | SRKFEFETSP | DCMYYFNAV | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2832 | 2 | 945.9883 | 67.92 | 2 | 64.0 | 16.1 | 1 | 366-381 | K.CGWNIKQCEPCSPNVR.F | Carbamidomethyl: 8 |

# Detailed Protein Report

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**Protein 531:** **PREDICTED: delta and Notch-like epidermal growth factor-related receptor isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530371157 | **Score:** | 27.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 73.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.9 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQPRRAQAPG | AQLLPALALL | LLLLGAGPRG | SSLANPVPAA | PLSAPGPCAA | QPCRNGGVCT | SRPEPDPQHP | APAGEPGYSC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TCPAGISGAN | CQLVADPCAS | NPCHHGNCSS | SSSSSSDGYL | CICNEGYEGP | NCEQALPSLP | ATGWTESMAP | RQLQPVPATQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EPDKILPRSQ | ATVTLPTWQP | KTGQKVVEMK | WDQVEVIPDI | ACGNASSNSS | AGGRLVSFEV | PQNTSVKIRQ | DATASLILLW |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KVTATGFQQC | SLIDGRSVTP | LQASGGLVLL | EEMLALGNNH | FIGFVNDSVT | KSIVALRLTL | VVKVSTCVPG | ESHANDLECS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GKGKCTTKPS | EATFSCTCEE | QYVGTFCEEY | DACQRKPCQN | NASCIDANEK | QDGSNFTCVC | LPGYTGELCQ | SKIDYCILDP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CRNGATCISS | LSGFTCQCPE | GYFGSACEEK | VDPCASSPCQ | NNGTCYVDGV | HFTCNCSPGF | TGPTCAQLID | FCALSPCAHG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TCRSVGTSYK | CLCDPGTHCE | LYKDPCANVS | CLNGATCDSD | GLNGTCICAP | GFTGEECDID | INECDSNPCH | HGGSCLDQPN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GYNCHCPHGW | VGANCEIHLQ | WKSGHMAESL | TNMPRHSLYI | IIGALCVAFI | LMLIILIVGI | CRISRIEYQG | SSRPAYEEFY |
| 650 | 660 | 670 | 680 | 690 | 700 | | |
| NCRSIDSEFS | NAIASIRHAR | FGKKSRPAMY | DVSPIAYEDY | SPDDKPLVTL | IKTKDL | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2308 | 1 | 1002.6780 | 75.60 | 3 | 59.3 | 12.4 | 2 | 1-29 | -.MQPRRAQAPGAQLLPALALLLLLLGAGPR.G | |
| 1231 | 1 | 1023.8326 | -111.10 | 2 | 45.5 | 15.1 | 0 | 304-322 | K.VSTCVPGESHANDLECSGK.G | Carbamidomethyl: 4, 16 |

# Detailed Protein Report

## Protein 532: protein dopey-2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|45827701 | **Score:** | 27.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 258.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578836735 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein dopey-2 isoform X1 [Homo sapiens] |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDPEEQELLN | DYRYRSYSSV | IEKALRNFES | SSEWADLISS | LGKLNKALQS | NLRYSLLPRR | LLISKRLAQC | LHPALPSGVH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LKALETYEII | FKIVGTKWLA | KDLFLYSCGL | FPLLAHAAVS | VRPVLLTLYE | KYFLPLQKLL | LPSLQAFIVG | LLPGLEEGSE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ISDRTDALLL | RLSLVVGKEV | FYTALWGSVL | ASPSIRLPAS | VFVVGHINRD | APGREQKYML | GTNHQLTVKS | LRASLLDSNV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LVQRNNLEIV | LFFFPFYTCL | DSNERAIPLL | RSDIVRILSA | ATQTLLRRDM | SLNRRLYAWL | LGSDIKGNTV | VPESEISNSY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EDQSSYFFEK | YSKDLLVEGL | AEILHQKFID | ADVEERHHAY | LKPFRVLISL | LDKPEIGPQV | VGNLFLEVIR | AFYSYCRDAL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GSDLKLSYTQ | SGNSLISAIK | ENRNASEIVK | TVNLLITSLS | TDFLWDYMTR | CFEECFRPVK | QRYSVRNSVS | PPPTVSELCA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LLVFLLDVIP | LELYSEVQTQ | YLPQVLGCLV | QPLAEDMEAL | SLPELTHALK | TCFKVLSKVQ | MPPSYLDTES | TSGTSSPVKG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ENGKIILETK | AVIPGDEDAS | FPPLKSEDSG | IGLSASSPEL | SEHLRVPRVS | LERDDVWKKG | GSMQRTFLCI | QELIANFASK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NIFGVQLTAS | GEESKSEEPA | GKRDRDGTQS | LAANDSSRKN | SWEPKPITVP | QFKQMLSDLF | TARGSPFKTK | SSESPSSSPS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SPARKNGGEW | DVEKVVIDLG | GSREERREAF | AAACHLLLDC | ATFPVYLSEE | ETEQLCATLF | QLPGAGDSSF | PSWLKSLMTI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| CCCVTDCYLQ | NVAISTLLEV | INHSQSLALV | IEDKMKRYKS | SGHNPFFGKL | QMVTVPPIAP | GILKVIAEKT | DFYQRVARVL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| WNQLNKETRE | HHVTCVELFY | RLHCLAPTAN | ICEDIICHAL | LDPDKGTRLE | ALFRFSVIWH | LTREIQGSRV | TSHNRSFDRS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LFVVLDSLAC | TDGAIGAAAQ | GWLVRALSLG | DVARILEPVL | LLLLQPKTQR | TSIHCLKQEN | SADDLHRWFN | RKKTSFREAC |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AVPEPQESGS | EEHLPLSQFT | TVDREAIWAE | VEKEPEKYPL | RGELSEEELP | YYVELPDRTA | HGAPDSSEHT | ESADTSSCHT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DSENTSSFSS | PSHDLQELSN | EENCCAPIPM | GGRAYPKRSA | LLAAFQSESF | KAGAKLSLVR | VDSDKTQASE | SFSSDEEADL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ELQALTTSRL | LKQQRERQEA | VEALFKHILL | YLQPYDSRRV | LYAFSVLEAV | LKTNPKEFIE | AVSRTSMDTS | STAHLNLISN |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LLARHQEALI | GQSFYGKLQT | QVPNVCPHSL | LLELLTYLCL | SFLRSYYPCY | LKVSHRDILG | NRDVQVKSVE | VLIRIMMQLV |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| SVAKSSEGKN | VEFIHSLLQR | CKVQEFVLLS | LSASMYTSQK | RYGLATAHHG | RALPEDSLFE | ESLINLGQDQ | IWSEHPLQIE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LLKLLQVLIV | LEHHLGRAHE | EAENQPDLSR | EWQRALNFQQ | AISALQYVQP | HPLTSQGLLV | SAVVRGLQPA | YGYGMHPAWV |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| SLVTHSLPYF | GKSLGWTVTP | FVVQICKNLD | DLVKQYESES | VKLSVSTTSK | RENISPDYPL | TLLEGLTTIS | HFCLLEQANQ |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| NKKTMAAGDP | ANLRNARNAI | LEELPRTVNT | MALLWNVLRK | EETQKRPVDL | LGATKGSSSV | YFKTTKTIRQ | KILDFLNPLT |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| AHLGVQLTAA | VAAVWSRKKA | QRHSKMKIIP | TASASQLTLV | DLVCALSTLQ | TDTLLHLVKE | VVKRPPQVKG | GDEKSPLVDI |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| PVLQFCYAFL | QRLPVPALQE | NFSSLLGVLK | ESVQLNLAPP | GYFLLLSMLN | DFVTRTPNLE | NKKDQKDLQE | ITQKILEAVG |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| NIAGSSLEQT | SWLSRNLEVK | AQPQASLEES | DAEEDLYDAA | AASAMVSSSA | PSVYSVQALS | LLAEVLASLL | DMVYRSDEKE |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| KAVPLISRLL | YYVFPYLRNH | SAYNAPSFRA | GAQLLSSLSG | YAYTKRAWRK | EVLELFLDPA | FFQMDTSCVH | WKSIIDHLLT |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| HEKTMFKDLM | NMQSSSLKLF | SSFEQKAMLL | KRQAFAVFSG | ELDQYHLYLP | LIQERLTDNL | RVGQTSIVAA | QMFLFFRVLL |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| LRISPQHLTS | LWPIMVSELI | QTFTQLEEDL | KDEDESLRST | NKVNRTKVSV | PDANGPSVGE | IPQSELILYL | SACKFLDTAL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| SFPPDKMPLF | QIYRWAFIPE | VDTEGPAFLS | DVEENHQECK | PHTVRILELL | KLKFGEISSS | DEITMKSEFP | LLRQHSVSSI |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | | |
| RQLMPFFMTL | NGAFKTQRQL | PADSPGTPFL | DFPVTDSPRI | LKQLEECIEY | DFLEHPEC | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1889 | 1 | 673.7777 | -150.29 | 2 | 54.0 | 16.1 | 0 | 1929-1938 | R.LLYYVFPYLR.N | |

# Detailed Protein Report

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**Protein 533:** **PREDICTED: peroxidasin-like protein isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530388290 | **Score:** | 27.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 95.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MCGSEFFWPC CDQHVSYSHG KPHTSSDLLA QFHYPRDPLI VEMARAGEIF EHTLQLIRER VKQGLTVDLE GKEFRYNDLV
        90        100        110        120        130        140        150        160
SPRSLSLIAN LSGCTARRPL PNCSNRCFHA KYRAHDGTCN NLQQPTWGAA LTAFARLLQP AYRDGIRAPR GLGLPVGSRQ
       170        180        190        200        210        220        230        240
PLPPPRLVAT VWARAAAVTP DHSYTRMLMH WGWFLEHDLD HTVPALSTAR FSDGRPCSSV CTNDPPCFPM NTRHADPRGT
       250        260        270        280        290        300        310        320
HAPCMLFARS SPACASGRPS ATVDSVYARE QINQQTAYID GSNVYGSSER ESQALRDPSV PRGLLKTGFP WPPSGKPLLP
       330        340        350        360        370        380        390        400
FSTGPPTECA RQEQESPCFL AGDHRANEHL ALAAMHTLWF REHNRMATEL SALNPHWEGN TVYQEARKIV GAELQHITYS
       410        420        430        440        450        460        470        480
HWLPKVLGDP GTRMLRGYRG YNPNVNAGII NSFATAAFRF GHTLINPILY RLNATLGEIS EGHLPFHKAL FSPSRIIKEG
       490        500        510        520        530        540        550        560
GIDPVLRGLF GVAAKWRAPS YLLSPELTQR LFSAAYSAAV DSAATIIQRG RDHGIPPYVD FRVFCNLTSV KNFEDLQNEI
       570        580        590        600        610        620        630        640
KDSEIRQKLR KLYGSPGDID LWPALMVEDL IPGTRVGPTL MCLFVTQFQR LRDGDRFWYE NPGVFTPAQL TQLKQASLSR
       650        660        670        680        690        700        710        720
VLCDNGDSIQ QVQADVFVKA EYPQDYLNCS EIPKVDLRVW QDCCADCRSR GQFRAVTQES QKKRSAQYSY PVDKDMELSH
       730        740        750        760        770        780        790        800
LRSRQQDKIY VGEDARNVTV LAKTKFSQDF STFAAEIQET ITALREQINK LEARLRQAGC TDVRGVPRKA EERWMKEDCT
       810        820        830        840        850
HCICESGQVT CVVEICPPAP CPSPELVKGT CCPVCRDRGM PSDSPEKR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1949 | 1 | 656.8239 | 117.11 | 2 | 54.8 | 14.5 | 0 | 679-688 | R.VWQDCCADCR.S | Carbamidomethyl: 5, 9 |

# Detailed Protein Report

**Protein 534:** **PREDICTED: zinc finger protein 449 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530422388 | **Score:** | 27.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 32.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 1.24 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
METMYPFIVT LEGNALQGPI LQKDYVQLEN QWETPPEDLQ TDLAKLVDQQ NPTLGETPEN SNLEEPLNPK PHKKKSPGEK
        90        100        110        120        130        140        150        160
PHRCPQCGKC FARKSQLTGH QRIHSGEEPH KCPECGKRFL RSSDLYRHQR LHTGERPYEC TVCKKRFTRR SHLIGHQRTH
       170        180        190        200        210        220        230        240
SEEETYKCLE CGKSFCHGSS LKRHLKTHTG EKPHRCHNCG KSFSRLTALT LHQRTHTEER PFKCNYCGKS FRQRPSLVIH
       250        260        270        280
LRIHTGEKPY KCTHCSKSFR QRAGLIMHQV THFRGLI
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2275 | 1 | 1130.5320 | 8.03 | 2 | 58.9 | 12.4 | 2 | 215-232 | R.THTEERPFKCNYCGKSFR.Q | Carbamidomethyl: 10 | WUP:QUP 1.24 |

# Detailed Protein Report

## Protein 535: PREDICTED: AP-3 complex subunit beta-2 isoform X2 [Homo sapiens]

**Accession:** gi|578827454
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 27.4
**MW [kDa]:** 114.4
**pI:** 5.4
**Sequence Coverage [%]:** 2.0
**No. of unique Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578827456 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: AP-3 complex subunit beta-2 isoform X3 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MLDTNKDSLK LEAMKRIVAM IARGKNASDL FPAVVKNVAC KNIEVKKLVY VYLVRYAEEQ QDLALLSIST FQRGLKDPNQ

        90        100        110        120        130        140        150        160
LIRASALRVL SSIRVPIIVP IMMLAIKEAA SDMSPYVRKT AAHAIPKLYS LDSDQKDQLI EVIEKLLADK TTLVAGSVVM

       170        180        190        200        210        220        230        240
AFEEVCPERI DLIHKNYRKL CNLLIDVEEW GQVVIISMLT RYARTQFLSP TQNESLLEEN AEKAFYGSEE DEAKGAGSEE

       250        260        270        280        290        300        310        320
TAAAAAPSRK PYVMDPDHRL LLRNTKPLLQ SRSAAVVMAV AQLYFHLAPK AEVGVIAKAL VRLLRSHSEV QYVVLQNVAT

       330        340        350        360        370        380        390        400
MSIKRRGMFE PYLKSFYIRS TDPTQIKILK LEVLTNLANE TNIPTVLREF QTYIRSMDKD FVAATIQAIG RCATNIGRVR

       410        420        430        440        450        460        470        480
DTCLNGLVQL LSNRDELVVA ESVVVIKKLL QMQPAQHGEI IKHLAKLTDN IQVPMARASI LWLIGEYCEH VPRIAPDVLR

       490        500        510        520        530        540        550        560
KMAKSFTAEE DIVKLQVINL AAKLYLTNSK QTKLLTQYVL SLAKYDQNYD IRDRARFTRQ LIVPSEQGGA LSRHAKKLFL

       570        580        590        600        610        620        630        640
APKPAPVLES SFKDRDHFQL GSLSHLLNAK ATGYQELPDW PEEAPDPSVR NVEVPEWTKC SNREKRKEKE KPFYSDSEGE

       650        660        670        680        690        700        710        720
SGPTESADSD PESESESDSK SSSESGSGES SSESDNEDQD EDEEKGRGSE SEQSEEDGKR KTKKKVPERK GEASSSDEGS

       730        740        750        760        770        780        790        800
DSSSSSSESE MTSESEEEQL EPASWSRKTP PSSKSAPATK EISLLDLEDF TPPSVQPVSP PAIVSTSLAA DLEGLTLTDS

       810        820        830        840        850        860        870        880
TLVPSLLSPV SGVGRQELLH RVAGEGLAVD YTFSRQPFSG DPHMVSVHIH FSNSSDTPIK GLHVGTPKLP AGISIQEFPE

       890        900        910        920        930        940        950        960
IESLAPGESA TAVMGINFCD STQAANFQLC TQTRQFYVSI QPPVGELMAP VFMSENEFKK EQGKLMGMNE ITEKLMLPDT

       970        980        990       1000       1010       1020       1030       1040
CRSDHIVVQK VTATANLGRV PCGTSDEYRF AGRTLTGGSL VLLTLDARPA GAAQLTVNSE KMVIGTMLVK DVIQALTQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1596 | 1 | 677.3556 | 42.21 | 2 | 50.2 | 10.6 | 1 | 108-119 | K.EAASDMSPYVRK.T | |

# Detailed Protein Report

## Protein 536: serine/threonine-protein kinase MRCK gamma [Homo sapiens]

**Accession:** gi|156766068
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 27.4
**MW [kDa]:** 172.4
**pI:** 5.9
**Sequence Coverage [%]:** 1.9
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MERRLRALEQ | LARGEAGGCP | GLDGLLDLLL | ALHHELSSGP | LRRERSVAQF | LSWASPFVSK | VKELRLQRDD | FEILKVIGRG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AFGEVTVVRQ | RDTGQIFAMK | MLHKWEMLKR | AETACFREER | DVLVKGDSRW | VTTLHYAFQD | EEYLYLVMDY | YAGGDLLTLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SRFEDRLPPE | LAQFYLAEMV | LAIHSLHQLG | YVHRDVKPDN | VLLDVNGHIR | LADFGSCLRL | NTNGMVDSSV | AVGTPDYISP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EILQAMEEGK | GHYGPQCDWW | SLGVCAYELL | FGETPFYAES | LVETYGKIMN | HEDHLQFPPD | VPDVPASAQD | LIRQLLCRQE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ERLGRGGLDD | FRNHPFFEGV | DWERLASSTA | PYIPELRGPM | DTSNFDVDDD | TLNHPGTLPP | PSHGAFSGHH | LPFVGFTYTS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GSHSPESSSE | AWAALERKLQ | CLEQEKVELS | RKHQEALHAP | TDHRELEQLR | KEVQTLRDRL | PEMLRDKASL | SQTDGPPAGS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PGQDSDLRQE | LDRLHRELAE | GRAGLQAQEQ | ELCRAQGQQE | ELLQRLQEAQ | EREAATASQT | RALSSQLEEA | RAAQRELEAQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VSSLSRQVTQ | LQGQWEQRLE | ESSQAKTIHT | ASETNGMGPP | EGGPQEAQLR | KEVAALREQL | EQAHSHRPSG | KEEALCQLQE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ENRRLSREQE | RLEAELAQEQ | ESKQRLEGER | RETESNWEAQ | LADILSWVND | EKVSRGYLQA | LATKMAEELE | SLRNVGTQTL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PARPLDHQWK | ARRLQKMEAS | ARLELQSALE | AEIRAKQGLQ | ERLTQVQEAQ | LQAERRLQEA | EKQSQALQQE | LAMLREELRA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RGPVDTKPSN | SLIPFLSFRS | SEKDSAKDPG | ISGEATRHGG | EPDLRPEGRR | SLRMGAVFPR | APTANTASTE | GLPAKPGSHT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LRPRSFPSPT | KCLRCTSLML | GLGRQGLGCD | ACGYFCHTTC | APQAPPCPVP | PDLLRTALGV | HPETGTGTAY | EGFLSVPRPS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GVRRGWQRVF | AALSDSRLLL | FDAPDLRLSP | PSGALLQVLD | LRDPQFSATP | VLASDVIHAQ | SRDLPRIFRV | TTSQLAVPPT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TCTVLLLAES | EGERERWLQV | LGELQRLLLD | ARPRPRPVYT | LKEAYDNGLP | LLPHTLCAAI | LDQDRLALGT | EEGLFVIHLR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SNDIFQVGEC | RRVQQLTLSP | SAGLLVVLCG | RGPSVRLFAL | AELENIEVAG | AKIPESRGCQ | VLAAGSILQA | RTPVLCVAVK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| RQVLCYQLGP | GPGPWQRRIR | ELQAPATVQS | LGLLGDRLCV | GAAGGFALYP | LLNEAAPLAL | GAGLVPEELP | PSRGGLGEAL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| GAVELSLSEF | LLLFTTAGIY | VDGAGRKSRG | HELLWPAAPM | GWGYAAPYLT | VFSENSIDVF | DVRRAEWVQT | VPLKKVRPLN |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PEGSLFLYGT | EKVRLTYLRN | QLAEKDEFDI | PDLTDNSRRQ | LFRTKSKRRF | FFRVSEEQQK | QQRREMLKDP | FVRSKLISPP |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| TNFNHLVHVG | PANGRPGARD | KSPAPEEKGR | VARGSGPQRP | HSFSEALRRP | ASMGSEGLGG | DADPMKRKPW | TSLSSESVSC |
| 1530 | 1540 | 1550 | 1560 | | | | |
| PQGSLSPATS | LMQVSERPRS | LPLSPELESS | P | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2153 | 1 | 974.3330 | -124.42 | 2 | 55.3 | 15.2 | 1 | 1489-1507 | R.RPASMGSEGLGGDADPMKR.K | Oxidation: 5 |

# Detailed Protein Report

## Protein 537: tubulin-specific chaperone E isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|568215736 | **Score:** | 27.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 64.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.1 |
| | | **Sequence Coverage [%]:** | 5.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSDTLTADVI | GRRVEVNGEH | ATVRFAGVVP | PVAGPWLGVE | WDNPERGKHD | GSHEGTVYFK | CRHPTGGSFI | RPNKVNFGTD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FLTAIKNRYV | LEDGPEEDRK | EQIVTIGNKP | VETIGFDSIM | KQQSQLSKLQ | EVSLRNCAVS | CAGEKGGVAE | ACPNIRKVDL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SKNLLSSWDE | VIHIADQLRH | LEVLNVSENK | LKFPSGSVLT | GTLSVLKVLV | LNQTGITWAE | AHAQCGGSRH | GLDMQKDASK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FVDLCVLQKC | STSNCIISAK | DHTSMRMNVA | KVLRCVAGCP | GLEELYLESN | NIFISERPTD | VLQTVKLLDL | SSNQLIDENQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LYLIAHLPRL | EQLILSDTGI | SSLHFPDAGI | GCKTSMFPSL | KYLVVNDNQI | SQWSFFNELE | KLPSLRALSC | LRNPLTKEDK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EAETARLLII | ASIGQLKTLN | KCEILPEERR | RAELDYRKAF | GNEWKQAGGH | KDPEKNRLSE | EFLTAHPRYQ | FLCLKYGAPE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DWELKTQQPL | MLKNQLLTLK | IKYPHQLDQK | VLEKQLPGSM | TIQKVKGLLS | RLLKVPVSDL | LLSYESPKKP | GREIELENDL |
| 570 | 580 | | | | | | |
| KSLQFYSVEN | GDCLLVRW | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1805 | 1 | 781.2970 | -97.72 | 2 | 52.9 | 10.5 | 1 | 47-60 | R.GKHDGSHEGTVYFK.C | |

# Detailed Protein Report

## Protein 538: PREDICTED: synaptotagmin-7 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530397573 | **Score:** | 27.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 68.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| | | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.55 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.74 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MYRDPEAASP | GAPSRDVLLV | SAIITVSLSV | TVVLCGLCHW | CQRKLGKRYK | NSLETVGTPD | SGRGRSEKKA | INDLDRDFWN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NNESTVQQKW | SSYPPKEFIL | NISPYAPYGD | PRLSLNFEDS | TLSTATTLES | IPSSTGEPKC | QRPRTLMRQQ | SLQQPLSQHQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RGRQPSQPTT | SQSLGQLQAH | MASAPGPNPR | AYGRGQARQG | TSAGSKYRAA | GGRSRSNPGS | WDHVVGQIRN | RGLDMKSFLE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GRMVVLSLVL | GLSEQDDFAN | IPDLQNPGTQ | QNQNAQGDKR | LPAGGKAVNT | APVPGQTPHD | ESDRRTEPRS | SVSDLVNSLT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SEMLMLSPGS | EEDEAHEGCS | RENLGRIQFS | VGYNFQESTL | TVKIMKAQEL | PAKDFSGTSD | PFVKIYLLPD | KKHKLETKVK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RKNLNPHWNE | TFLFEGFPYE | KVVQRILYLQ | VLDYDRFSRN | DPIGEVSIPL | NKVDLTQMQT | FWKDLKPCSD | GSGSRGELLL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SLCYNPSANS | IIVNIIKARN | LKAMDIGGTS | DPYVKVWLMY | KDKRVEKKKT | VTMKRNLNPI | FNESFAFDIP | TEKLRETTII |
| 570 | 580 | 590 | 600 | 610 | 620 | | |
| ITVMDKDKLS | RNDVIGKIYL | SWKSGPGEVK | HWKDMIARPR | QPVAQWHQLK | A | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 285 | 1 | 733.8676 | -12.20 | 2 | 33.5 | 11.8 | 2 | 195-208 | R.GQARQGTSAGSKYR.A | | QU:MU 1.55<br>WUP:QUP 1.74 |
| 2844 | 1 | 655.3688 | 27.19 | 2 | 66.0 | 15.5 | 1 | 591-600 | K.HWKDMIARPR.Q | | |

# Detailed Protein Report

## Protein 539: pyrroline-5-carboxylate reductase 2 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|410991931 | **Score:** | 27.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 25.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 8.5 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSVGFIGAGQ LAYALARGFT AAGILSAHKI IASSPEMNLP TVSALRKMGV NLTRSNKETV KHSDVLFLAV KPHIIPFILD

        90        100        110        120        130        140        150        160
EIGADVQARH IVVSCAAGVT ISSVEKAFMA LDALADGGVK MGLPRRLAIQ LGAQALLGAA KMLLDSEQHP CQLKDNVCSP

       170        180        190        200        210        220        230        240
GGATIHALHF LESGGFRSLL INAVEASCIR TRELQSMADQ EKISPAALKK TLLDRVKLES PTVSTLTPSS PGKLLTRSLA

       250
LGGKKD
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 325 | 1 | 1074.4954 | -137.82 | 2 | 34.1 | 27.3 | 2 | 121-141 | K.MGLPRRLAIQLGAQALLGAAK.M | |

# Detailed Protein Report

## Protein 540: chloride anion exchanger [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4557535 | **Score:** | 27.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 84.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578813973 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: chloride anion exchanger isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MIEPFGNQYI | VARPVYSTNA | FEENHKKTGR | HHKTFLDHLK | VCCSCSPQKA | KRIVLSLFPI | ASWLPAYRLK | EWLLSDIVSG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ISTGIVAVLQ | GLAFALLVDI | PPVYGLYASF | FPAIIYLFFG | TSRHISVGPF | PILSMMVGLA | VSGAVSKAVP | DRNATTLGLP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NNSNNSSLLD | DERVRVAAAA | SVTVLSGIIQ | LAFGILRIGF | VVIYLSESLI | SGFTTAAAVH | VLVSQLKFIF | QLTVPSHTDP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VSIFKVLYSV | FSQIEKTNIA | DLVTALIVLL | VVSIVKEINQ | RFKDKLPVPI | PIEFIMTVIA | AGVSYGCDFK | NRFKVAVVGD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MNPGFQPPIT | PDVETFQNTV | GDCFGIAMVA | FAVAFSVASV | YSLKYDYPLD | GNQELIALGL | GNIVCGVFRG | FAGSTALSRS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AVQESTGGKT | QIAGLIGAII | VLIVVLAIGF | LLAPLQKSVL | AALALGNLKG | MLMQFAEIGR | LWRKDKYDCL | IWIMTFIFTI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VLGLGLGLAA | SVAFQLLTIV | FRTQFPKCST | LANIGRTNIY | KNKKDYYDMY | EPEGVKIFRC | PSPIYFANIG | FFRRKLIDAV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GFSPLRILRK | RNKALRKIRK | LQKQGLLQVT | PKGFICTVDT | IKDSDEELDN | NQIEVLDQPI | NTTDLPFHID | WNDDLPLNIE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VPKISLHSLI | LDFSAVSFLD | VSSVRGLKSI | LQEFIRIKVD | VYIVGTDDDF | IEKLNRYEFF | DGEVKSSIFF | LTIHDAVLHI |
| 730 | 740 | 750 | 760 | 770 | | | |
| LMKKDYSTSK | FNPSQEKDGK | IDFTINTNGG | LRNRVYEVPV | ETKF | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2677 | 1 | 862.3965 | -52.92 | 2 | 64.6 | 13.5 | 1 | 450-463 | K.GMLMQFAEIGRLWR.K | Oxidation: 4 |

# Detailed Protein Report

## Protein 541: TBC1 domain family member 22A isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|546231127 | **Score:** | 27.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 50.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 5.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASDGARKQF | WKRSNSKLPG | SLLRSTAKMP | TTPVKAKRVS | TFQEFESNTS | DAWDAGEDDD | ELLAMAAESL | NSEVVMETAN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RVLRNHSQRQ | GRPTLQEGPG | LQQKPRPEAE | PPSPPSGDLR | LVKSVSESHT | SCPAEELRRL | SWSGIPKPVR | PMTWKLLSGY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LPANVDRRPA | TLQRKQKEYF | AFIEHYYDSR | NDEVHQDTYR | QIHIDIPRMS | PEALILQPKV | TEIFERILFI | WAIRHPASGY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VQGINDLVTP | FFVVFICEYI | EAEEVDTVDV | SGVPAEVLCN | IEADTYWCMS | KLLDGIQDNY | TFAQPGIQMK | VKMLEELVSR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IDEQVHRHLD | QHEVRYLQFA | FRWMNNLLMR | EVPLRCTIRL | WDTYQSEPDG | FSHFHLYVCA | AFLVRWRKEI | LEEKDFQELL |
| 410 | 420 | 430 | 440 | | | | |
| LFLQNLPTAH | WDDEDISLLL | AEAYRLKFAF | ADAPNHYKK | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1413 | 1 | 816.3918 | 26.50 | 2 | 47.3 | 12.4 | 0 | 124-138 | K.SVSESHTSCPAEELR.R | |

# Detailed Protein Report

## Protein 542: dynein heavy chain 12, axonemal isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|194440727 | **Score:** | 27.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 356.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***WUP:QUP*** | **Median:** | 1.30 | **CV:** | 0.00 % | **No. of Peptides:** | 1 | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSDANKAAIA | AEKEALNLKL | PPIVHLPENI | GVDTPTQSKL | LKYRRSKEQQ | QKINQLVIDG | AKRNLDRTLG | KRTPLLPPPD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YPQTMTSEMK | KKGFNYIYMK | QCVESSPLVP | IQQEWLDHML | RLIPESLKEG | KEREELLESL | INEVSSDFEN | SMKRYLVQSV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LVKPPVKSLE | DEGGPLPESP | VGLDYSNPWH | SSYVQARNQI | FSNLHIIHPT | MKMLLDLGYT | TFADTVLLDF | TGIRAKGPID |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CESLKTDLSI | QTRNAEEKIM | NTWYPKVINL | FTKKEALEGV | KPEKLDAFYS | CVSTLMSNQL | KDLLRRTVEG | FVKLFDPKDQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QRLPIFKIEL | TFDDDKMEFY | PTFQDLEDNV | LSLVERIAEA | LQNVQTIPSW | LSGTSTPVNL | DTELPEHVLH | WAVDTLKAAV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HRNLEGARKH | YETYVEKYNW | LLDGTAVENI | ETFQTEDHTF | DEYTEFIEKF | LSLASEIMLL | PQWIHYTMVR | LDCEDLKTGL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TNKAKAFANI | LLNDIASKYR | KENECICSEF | EAIKEHALKV | PETTEEMMDL | ISYVEKARTV | GIEELILRIQ | ESKRQMSYFL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DVFLFPQEDL | ALNATVLMWP | RKINPIFDEN | DELIENAKHK | KENELMAKRE | KLILEIEKES | RRMEEFTEFA | ELERMQQYVT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DVRQLQKRIQ | ESEEAVQFIN | KEEELFKWEL | TKYPELDKLK | VNIEPYQKFF | NFVLKWQRSE | KRWMDGGFLD | LNGESMEADV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EEFSREIFKT | LKFFQTKLKK | ELQEKRKAAR | KRSLEEEKIE | EEPKDNATIT | MCRMRARHWK | QISEIVGYDL | TPDSGTTLRK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VLKLNLTPYL | EQFEVISAGA | SKEFSLEKAM | NTMIGTWEDI | AFHISLYRDT | GVCILSSVDE | IQAILDDQII | KTQTMRGSPF |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| IKPFEHEIKA | WEDRLIRIQE | TIDEWLKVQA | QWLYLEPIFC | SEDIMQQMPE | EGRQFQTVDR | HWRDIMKFCA | KDPKVLAATS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LTGLLEKLQN | CNELLEKIMK | GLNAYLEKKR | LFFPRFFFLS | NDEMLEILSE | TKDPLRVQPH | LKKCFEGIAK | LEFLPNLDIK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AMYSSEGERV | ELIALISTSA | ARGAVEKWLI | QVEDLMLRSV | HDVIAAARLA | YPESARRDWV | REWPGQVVLC | ISQMFWTSET |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QEVISGGTEG | LKKYYKELQN | QLNEIVELVR | GKLSKQTRTT | LGALVTIDVH | ARDVVMDMIK | MGVSHDTDFL | WLAQLRYYWE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| NENARVRIIN | CNVKYAYEYL | GNSPRLVITP | LTDRCYRTLI | GAFYLNLGGA | PEGPAGTGKT | ETTKDLAKAL | AVQCVVFNCS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DGLDYLAMGK | FFKGLASSGA | WACFDEFNRI | ELEVLSVVAQ | QILCIQRAIQ | QKLVVFVFEG | TELKLNPNCF | VAITMNPGYA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| GRSELPDNLK | VLFRTVAMMV | PNYALIAEIS | LYSYGFLNAR | PLSVKIVMTY | RLCSEQLSSQ | FHYDYGMRAV | KAVLVAAGNL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KLKYPNENED | ILLLRSIKDV | NEPKFLSHDI | PLFNGITSDL | FPGIKLPEAD | YHEFLECAHE | ACNVHNLQPV | KFFLEKIIQT |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| YEMMIVRHGF | MLVGEPFAAK | TKVLHVLADT | LTLMNEHGYG | EEEKVIYRTV | NPKSITMGQL | FGQFDPVSHE | WTDGIVANTF |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| REFALSETPD | RKWVVFDGPI | DTLWIESMNT | VLDDNKKLCL | MSGEIIQMSP | QMSLIFETMD | LSQASPATVS | RCGMIYLEPS |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| QLGWEPLVSS | WLNSLKGPLC | EPEYQALLRG | LFAWLIPPSL | NQRVELFQLN | YLYTTIVSKI | LKILITFRIS | NYFKYVPLKT |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| QCTFIKFFLH | QQACFIFSLI | WSIGGSCDTD | GRRVFDTFIR | LIILGKDDEN | PVPDSVGKWE | CPFDEKGLVY | DYMYELKNKG |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| RWVHWNELIK | NTNLGDKQIK | IQDIIVPTMD | TIRYTFLMDL | SITYAKPLLF | VGPTGTGKSV | YVKDKLMNHL | EKDQYFPFYI |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| NLSARTSANQ | VQNIIMARLD | KRRKGVFGPP | MGKKCIIFID | DMNMPALEKY | GAQPPIELLR | QFFDCGHWYD | LKDTSKITLV |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| DIELIAAMGP | PGGGRNPVTP | RCIRHFNICS | INSFSDETMV | RIFSSIVAFY | LRTHEFPPEY | FVIGNQIVNG | TMEIYKQSVE |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| NLLPTPTKSH | YTFNLRDFSR | VIRGCLLIER | DAVANKHTMI | RLFVHEVLRV | FYDRLINDDD | RRWLFQLTKT | VIKDHFKESF |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2090 | 1 | 1159.8674 | -54.47 | 3 | 56.0 | 10.4 | 2 | 1512-1540 | K.<br>FFLEKIIQTYEMMIVRHGFMLVGE<br>T | Oxidation: 12, 20 | |
| 1721 | 1 | 646.7566 | -109.88 | 2 | 51.8 | 16.9 | 1 | 1602-1612 | R.EFALSETPDRK.W | | WUP:QUP 1.30 |

# Detailed Protein Report

## Protein 543: kalirin isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4504335 | **Score:** | 27.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 192.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.55 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.02 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTDRFWDQWY | LWYLRLLRLL | DRGSFRNDGL | KASDVLPILK | EKVAFVSGGR | DKRGGPILTF | PARSNHDRIR | QEDLRKLVTY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LASVPSEDVC | KRGFTVIIDM | RGSKWDLIKP | LLKTLQEAFP | AEIHVALIIK | PDNFWQKQKT | NFGSSKFIFE | TSMVSVEGLT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KLVDPSQLTE | EFDGSLDYNH | EEWIELRLSL | EEFFNSAVHL | LSRLEDLQEM | LARKEFPVDV | EGSRRLIDEH | TQLKKKVLKA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PVEELDREGQ | RLLQCIRCSD | GFSGRNCIPG | SADFQSLVPK | ITSLLDKLHS | TRQHLHQMWH | VRKLKLDQCF | QLRLFEQDAE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KMFDWISHNK | ELFLQSHTEI | GVSYQYALDL | QTQHNHFAMN | SMNAYVNINR | IMSVASRLSE | AGHYASQQIK | QISTQLDQEW |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KSFAAALDER | STILAMSAVF | HQKAEQFLSG | VDAWCKMCSE | GGLPSEMQDL | ELAIHHHQTL | YEQVTQAYTE | VSQDGKALLD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VLQRPLSPGN | SESLTATANY | SKAVHQVLDV | VHEVLHHQRR | LESIWQHRKV | RLHQRLQLCV | FQQDVQQVLD | WIENHGEAFL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SKHTGVGKSL | HRARALQKRH | DDFEEVAQNT | YTNADKLLEA | AEQLAQTGEC | DPEEIYKAAR | HLEVRIQDFV | RRVEQRKLLL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DMSVSFHTHT | KELWTWMEDL | QKEMLEDVCA | DSVDAVQELI | KQFQQQTAT | LDATLNVIKE | GEDLIQQLRS | APPSLGEPSE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ARDSAVSNNK | TPHSSSISHI | ESVLQQLDDA | QVQMEELFHE | RKIKLDIFLQ | LRIFEQYTIE | VTAELDAWNE | DLLRQMNDFN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TEDLTLAEQR | LQRHTERKLA | MNNMTFEVIQ | QGQDLHQYIT | EVQASGIELI | CEKDIDLAAQ | VQELLEFLHE | KQHELELNAE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QTHKRLEQCL | QLRHLQAEVK | QVLGWIRNGE | SMLNASLVNA | SSLSEAEQLQ | REHEQFQLAI | ESLFHATSLQ | KTHQSALQVQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QKAEVLLQAG | HYDADAIREC | AEKVALHWQQ | LMLKMEDRLK | LVNASVAFYK | TSEQVCSVLE | SLEQEYRRDE | DWCGGRDKLG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PAAEIDHVIP | LISKHLEQKE | AFLKACTLAR | RNAEVFLKYI | HRNNVSMPSV | ASHTRGPEQQ | VKAILSELLQ | RENRVLHFWT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LKKRRLDQCQ | QYVVFERSAK | QALDWIQETG | EFYLSTHTST | GETTEETQEL | LKEYGEFRVP | AKQTKEKVKL | LIQLADSFVE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KGHIHATEIR | KWVTTVDKHY | RDFSLRMGKY | RYSLEKALGV | NTEDNKDLEL | DIIPASLSDR | EVKLRDANHE | VNEEKRKSAR |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KKEFIMAELL | QTEKAYVRDL | HECLETYLWE | MTSGVEEIPP | GILNKEHIIF | GNIQEIYDFH | NNIFLKELEK | YEQLPEDVGH |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| CFVTWADKFQ | MYVTYCKNKP | DSNQLILEHA | GTFFDEIQQR | HGLANSISSY | LIKPVQRITK | YQLLLKELLT | CCEEGKGELK |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DGLEVMLSVP | KKANDAMHVS | MLEGFDENLD | VQGELILQDA | FQVWDPKSLI | RKGRERHLFL | FEISLVFSKE | IKDSSGHTKY |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| VYKNKLLTSE | LGVTEHVEGD | PCKFALWSGR | TPSSDNKTVL | KASNIETKQE | WIKNIREVIQ | ERIIHLKGAL | KEPLQLPKTP |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | |
| AKQRNNSKRD | GVEDIDSQGD | GSSQPDTISI | ASRTSQNTVD | SDKDGNLVPR | WHLGPGDPFS | TYV | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 599 | 1 | 562.7645 | 22.71 | 2 | 37.5 | 10.4 | 0 | 1427-1436 | K.ELLTCCEEGK.G | | QU:MU 1.55<br>WUP:QUP 1.02 |

# Detailed Protein Report

## Protein 544: Krueppel-like factor 12 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21071074 | **Score:** | 27.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 44.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.6 |
| | | **Sequence Coverage [%]:** | 8.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578824739 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: Krueppel-like factor 12 isoform X3 [Homo sapiens] |
| gi\|530402087 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: Krueppel-like factor 12 isoform X2 [Homo sapiens] |
| gi\|530402085 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: Krueppel-like factor 12 isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MNIHMKRKTI | KNINTFENRM | LMLDGMPAVR | VKTELLESEQ | GSPNVHNYPD | MEAVPLLLNN | VKGEPPEDSL | SVDHFQTQTE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PVDLSINKAR | TSPTAVSSSP | VSMTASASSP | SSTSTSSSSS | SRLASSPTVI | TSVSSASSSS | TVLTPGPLVA | SASGVGGQQF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LHIIHPVPPS | SPMNLQSNKL | SHVHRIPVVV | QSVPVVYTAV | RSPGNVNNTI | VVPLLEDGRG | HGKAQMDPRG | LSPRQSKSDS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DDDDLPNVTL | DSVNETGSTA | LSIARAVQEV | HPSPVSRVRG | NRMNNQKFPC | SISPFSIEST | RRQRRSESPD | SRKRRIHRCD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FEGCNKVYTK | SSHLKAHRRT | HTGEKPYKCT | WEGCTWKFAR | SDELTRHYRK | HTGVKPFKCA | DCDRSFSRSD | HLALHRRRHM |
| 410 | | | | | | | |
| LV | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1218 | 1 | 758.4479 | 56.96 | 3 | 44.8 | 16.1 | 1 | 202-223 | R.SPGNVNNTIVVPLLEDGRGHGK.A | |

# Detailed Protein Report

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**Protein 545:** very long-chain specific acyl-CoA dehydrogenase, mitochondrial isoform 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|76496475 | **Score:** | 27.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 68.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 6.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQAARMAASL | GRQLLRLGGG | SSRLTALLGQ | PRPGPARRPY | AGGAAQESKS | FAVGMFKGQL | TTDQVFPYPS | VLNEEQTQFL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KELVEPVSRF | FEEVNDPAKN | DALEMVEETT | WQGLKELGAF | GLQVPSELGG | VGLCNTQYAR | LVEIVGMHDL | GVGITLGAHQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SIGFKGILLF | GTKAQKEKYL | PKLASGETVA | AFCLTEPSSG | SDAASIRTSA | VPSPCGKYYT | LNGSKLWISN | GGLADIFTVF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AKTPVTDPAT | GAVKEKITAF | VVERGFGGIT | HGPPEKKMGI | KASNTAEVFF | DGVRVPSENV | LGEVGSGFKV | AMHILNNGRF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GMAAALAGTM | RGIIAKAVDH | ATNRTQFGEK | IHNFGLIQEK | LARMVMLQYV | TESMAYMVSA | NMDQGATDFQ | IEAAISKIFG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SEAAWKVTDE | CIQIMGGMGF | MKEPGVERVL | RDLRIFRIFE | GTNDILRLFV | ALQGCMDKGK | ELSGLGSALK | NPFGNAGLLL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GEAGKQLRRR | AGLGSGLSLS | GLVHPELSRS | GELAVRALEQ | FATVVEAKLI | KHKKGIVNEQ | FLLQRLADGA | IDLYAMVVVL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SRASRSLSEG | HPTAQHEKML | CDTWCIEAAA | RIREGMAALQ | SDPWQQELYR | NFKSISKALV | ERGGVVTSNP | LGF |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1617 | 2 | 1051.5420 | 13.25 | 2 | 50.0 | 13.5 | 1 | 38-57 | R.RPYAGGAAQESKSFAVGMFK.G | |

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# Detailed Protein Report

## Protein 546: transient receptor potential cation channel subfamily M member 3 isoform d [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|154091318 | **Score:** | 27.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 176.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MYVRVSFDTK | PDLLLHLMTK | EWQLELPKLL | ISVHGGLQNF | ELQPKLKQVF | GKGLIKAAMT | TGAWIFTGGV | NTGVIRHVGD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ALKDHASKSR | GKICTIGIAP | WGIVENQEDL | IGRDVVRPYQ | TMSNPMSKLT | VLNSMHSHFI | LADNGTTGKY | GAEVKLRRQL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EKHISLQKIN | TRIGQGVPVV | ALIVEGGPNV | ISIVLEYLRD | TPPVPVVVCD | GSGRASDILA | FGHKYSEEGG | LINESLRDQL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LVTIQKTFTY | TRTQAQHLFI | ILMECMKKKE | LITVFRMGSE | GHQDIDLAIL | TALLKGANAS | APDQLSLALA | WNRVDIARSQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IFIYGQQWPV | GSLEQAMLDA | LVLDRVDFVK | LLIENGVSMH | RFLTISRLEE | LYNTRHGPSN | TLYHLVRDVK | KGNLPPDYRI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SLIDIGLVIE | YLMGGAYRCN | YTRKRFRTLY | HNLFGPKRDD | IPLRRGRKTT | KKREEEVDID | LDDPEINHFP | FPFHELMVWA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VLMKRQKMAL | FFWQHGEEAM | AKALVACKLC | KAMAHEASEN | DMVDDISQEL | NHNSRDFGQL | AVELLDQSYK | QDEQLAMKLL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TYELKNWSNA | TCLQLAVAAK | HRDFIAHTCS | QMLLTDMWMG | RLRMRKNSGL | KVILGILLPP | SILSLEFKNK | DDMPYMSQAQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EIHLQEKEAE | EPEKPTKEKE | EEDMELTAML | GRNNGESSRK | KDEEEVQSKH | RLIPLGRKIY | EFYNAPIVKF | WFYTLAYIGY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LMLFNYIVLV | KMERWPSTQE | WIVISYIFTL | GIEKMREILM | SEPGKLLQKV | KVWLQEYWNV | TDLIAILLFS | VGMILRLQDQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PFRSDGRVIY | CVNIIYWYIR | LLDIFGVNKY | LGPYVMMIGK | MMIDMMYFVI | IMLVVLMSFG | VARQAILFPN | EEPSWKLAKN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| IFYMPYWMIY | GEVFADQIDP | PCGQNETRED | GKIIQLPPCK | TGAWIVPAIM | ACYLLVANIL | LVNLLIAVFN | NTFFEVKSIS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NQVWKFQRYQ | LIMTFHERPV | LPPPLIIFSH | MTMIFQHLCC | RWRKHESDPD | ERDYGLKLFI | TDDELKKVHD | FEEQCIEEYF |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| REKDDRFNSS | NDERIRVTSE | RVENMSMRLE | EVNEREHSMK | ASLQTVDIRL | AQLEDLIGRM | ATALERLTGL | ERAESNKIRS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RTSSDCTDAA | YIVRQSSFNS | QEGNTFKLQE | SIDPAGEETM | SPTSPTLMPR | MRSHSFYSVN | MKDKGGIEKL | ESIFKERSLS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LHRATSSHSV | AKEPKAPAAP | ANTLAIVPDS | RRPSSCIDIY | VSAMDELHCD | IDPLDNSVNI | LGLGEPSFST | PVPSTAPSSS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| AYATLAPTDR | PPSRSIDFED | ITSMDTRSFS | SDYTHLPECQ | NPWDSEPPMY | HTIERSKSSR | YLATTPFLLE | EAPIVKSHSF |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| MFSPSRSYYA | NFGVPVKTAE | YTSITDCIDT | RCVNAPQAIA | DRAAFPGGLG | DKVEDLTCCH | PEREAELSHP | SSDSEENEAK |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GRRATIAISS | QEGDNSERTL | SNNITVPKIE | RANSYSAEEP | SAPYAHTRKS | FSISDKLDRQ | RNTASLRNPF | QRSKSSKPEG |
| 1530 | 1540 | 1550 | | | | | |
| RGDSLSMRRL | SRTSAFQSFE | SKHN | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2053 | 1 | 575.2161 | -129.75 | 3 | 55.6 | 15.5 | 2 | 1055-1068 | R.IRVTSERVENMSMR.L | Oxidation: 11 |

# Detailed Protein Report

## Protein 547: deoxyribonuclease gamma isoform 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|375151549 | **Score:** | 27.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 9.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.28 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.55 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSRELAPLLL LLLSIHSALA MRICSFNVRS FGESKQEDKN AMDVIVKVIK RCDIILVMEI KDSNNRICPI LMEKLNREKL
        90        100        110        120        130        140        150        160
VSVKRSYHYH DYQDGDADVF SREPFVVWFQ SPHTAVKDFV IIPLHTTPET SVKEIDELVE VYTDVKHRWK AENFIFMGDF
       170        180        190        200        210        220        230        240
NAGCSYVPKK AWKNIRLRTD PRFVWLIGDQ EDTTVKKSTN CAYDRIVLRG QEIVSSVVPK SNSVFDFQKA YKLTEEEALD
       250        260        270        280
VSDHFPVEFK LQSSRAFTNS KKSVTLRKKT KSKRS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2460 | 1 | 873.4565 | -23.34 | 2 | 59.0 | 11.5 | 2 | 36-50 | K.QEDKNAMDVIVKVIK.R | Oxidation: 7 | QU:MU 1.28<br>WUP:QUP 1.55 |

# Detailed Protein Report

**Protein 548:** **PREDICTED: rab11 family-interacting protein 4 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530411171 | **Score:** | 27.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 67.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSPQLDTKSP | SAHAGLPATG | GGGAAPSTGA | QKCERQRRGR | DCSCASGLPA | ASPRAADPRP | LASAPLPGSG | PRMRTPPALG |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| SQGSEVTGPT | FADGELIPRE | PGFFPEDEEE | AMTLAPPEGP | QELYTDSPME | STQSLEGSVG | SPAEKDGGLG | GLFLPEDKSL |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| VHTPSMTTSD | LSTHSTTSLI | SNEEQFEDYG | EGDDVDCAPS | SPCPDDETRT | NVYSDLGSSV | SSSAGQTPRK | MRHVYNSELL |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| DVYCSQCCKK | INLLNDLEAR | LKNLKANSPN | RKISSTAFGR | QLMHSSNFSS | SNGSTEDLFR | DSIDSCDNDI | TEKVSFLEKK |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| VTELENDSLT | NGDLKSKLKQ | ENTQLVHRVH | ELEEMVKDQE | TTAEQALEEE | ARRHREAYGK | LEREKATEVE | LLNARVQQLE |
| **410** | **420** | **430** | **440** | **450** | **460** | **470** | **480** |
| EENTELRTTV | TRLKSQTEKL | DEERQRMSDR | LEDTSLRLKD | EMDLYKRMMD | KLRQNRLEFQ | KEREATQELI | EDLRKELEHL |
| **490** | **500** | **510** | **520** | **530** | **540** | **550** | **560** |
| QMYKLDCERP | GRGRSASSGL | GEFNARAREV | ELEHEVKRLK | QENYKLRDQN | DDLNGQILSL | SLYEAKNLFA | AQTKAQSLAA |
| **570** | **580** | **590** | **600** | **610** | | | |
| EIDTASRDEL | MEALKEQEEI | NFRLRQYMDK | IILAILDHNP | SILEIKH | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1981 | 1 | 696.2626 | -62.02 | 2 | 54.7 | 16.3 | 0 | 41-54 | R.DCSCASGLPAASPR.A | Carbamidomethyl: 2 |

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# Detailed Protein Report

## Protein 549: sterol 26-hydroxylase, mitochondrial precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4503211 | **Score:** | 27.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 60.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 5.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAALGCARLR | WALRGAGRGL | CPHGARAKAA | IPAALPSDKA | TGAPGAGPGV | RRRQRSLEEI | PRLGQLRFFF | QLFVQGYALQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LHQLQVLYKA | KYGPMWMSYL | GPQMHVNLAS | APLLEQVMRQ | EGKYPVRNDM | ELWKEHRDQH | DLTYGPFTTE | GHHWYQLRQA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LNQRLLKPAE | AALYTDAFNE | VIDDFMTRLD | QLRAESASGN | QVSDMAQLFY | YFALEAICYI | LFEKRIGCLQ | RSIPEDTVTF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VRSIGLMFQN | SLYATFLPKW | TRPVLPFWKR | YLDGWNAIFS | FGKKLIDEKL | EDMEAQLQAA | GPDGIQVSGY | LHFLLASGQL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SPREAMGSLP | ELLMAGVDTT | SNTLTWALYH | LSKDPEIQEA | LHEEVVGVVP | AGQVPQHKDF | AHMPLLKAVL | KETLRLYPVV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PTNSRIIEKE | IEVDGFLFPK | NTQFVFCHYV | VSRDPTAFSE | PESFQPHRWL | RNSQPATPRI | QHPFGSVPFG | YGVRACLGRR |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| IAELEMQLLL | ARLIQKYKVV | LAPETGELKS | VARIVLVPNK | KVGLQFLQRQ | C | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2189 | 1 | 937.1073 | 154.72 | 2 | 57.8 | 12.8 | 2 | 124-137 | K.YPVRNDMELWKEHR.D | |

# Detailed Protein Report

## Protein 550: proline dehydrogenase 1, mitochondrial isoform 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|304766736 | **Score:** | 27.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 67.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.8 |
| | | **Sequence Coverage [%]:** | 4.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MALRRALPAL | RPCIPRFVPL | STAPASREQP | AAGPAAVPGG | GSATAVRPPV | PAVDFGNAQE | AYRSRRTWEL | ARSLLVLRLC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AWPALLARHE | QLLYVSRKLL | GQRLFNKLMK | MTFYGHFVAG | EDQESIQPLL | RHYRAFGVSA | ILDYGVEEDL | SPEEAEHKEM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ESCTSAAERD | GSGTNKRDKQ | YQAHRAFGDR | RNGVISARTY | FYANEAKCDS | HMETFLRCIE | ASGRVSDDGF | IAIKLTALGR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PQFLLQFSEV | LAKWRCFFHQ | MAVEQGQAGL | AAMDTKLEVA | VLQESVAKLG | IASRAEIEDW | FTAETLGVSG | TMDLLDWSSL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IDSRTKLSKH | LVVPNAQTGQ | LEPLLSRFTE | EEELQMTRML | QRMDVLAKKA | TEMGVRLMVD | AEQTYFQPAI | SRLTLEMQRK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FNVEKPLIFN | TYQCYLKDAY | DNVTLDVELA | RREGWCFGAK | LVRGAYLAQE | RARAAEIGYE | DPINPTYEAT | NAMYHRCLDY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VLEELKHNAK | AKVMVASHNE | DTVRFALRRM | EELGLHPADH | QVYFGQLLGM | CDQISFPLGQ | AGYPVYKYVP | YGPVMEVLPY |
| 570 | 580 | 590 | 600 | 610 | | | |
| LSRRALENSS | LMKGTHRERQ | LLWLELLRRL | RTGNLFHRPA | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1081 | 1 | 851.8806 | -166.32 | 2 | 43.6 | 11.8 | 2 | 2-16 | M.ALRRALPALRPCIPR.F | |

# Detailed Protein Report

## Protein 551: tyrosine-protein phosphatase non-receptor type 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4506295 | **Score:** | 27.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 105.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MTSRFRLPAG RTYNVRASEL ARDRQHTEVV CNILLLDNTV QAFKVNKHDQ GQVLLDVVFK HLDLTEQDYF GLQLADDSTD
        90        100        110        120        130        140        150        160
NPRWLDPNKP IRKQLKRGSP YSLNFRVKFF VSDPNKLQEE YTRYQYFLQI KQDILTGRLP CPSNTAALLA SFAVQSELGD
       170        180        190        200        210        220        230        240
YDQSENLSGY LSDYSFIPNQ PQDFEKEIAK LHQQHIGLSP AEAEFNYLNT ARTLELYGVE FHYARDQSNN EIMIGVMSGG
       250        260        270        280        290        300        310        320
ILIYKNRVRM NTFPWLKIVK ISFKCKQFFI QLRKELHESR ETLLGFNMVN YRACKNLWKA CVEHHTFFRL DRPLPPQKNF
       330        340        350        360        370        380        390        400
FAHYFTLGSK FRYCGRTEVQ SVQYGKEKAN KDRVFARSPS KPLARKLMDW EVVSRNSISD DRLETQSLPS RSPPGTPNHR
       410        420        430        440        450        460        470        480
NSTFTQEGTR LRPSSVGHLV DHMVHTSPSE VFVNQRSPSS TQANSIVLES SPSQETPGDG KPPALPPKQS KKNSWNQIHY
       490        500        510        520        530        540        550        560
SHSQQDLESH INETFDIPSS PEKPTPNGGI PHDNLVLIRM KPDENGRFGF NVKGGYDQKM PVIVSRVAPG TPADLCVPRL
       570        580        590        600        610        620        630        640
NEGDQVVLIN GRDIAEHTHD QVVLFIKASC ERHSGELMLL VRPNAVYDVV EEKLENEPDF QYIPEKAPLD SVHQDDHSLR
       650        660        670        680        690        700        710        720
ESMIQLAEGL ITGTVLTQFD QLYRKKPGMT MSCAKLPQNI SKNRYRDISP YDATRVILKG NEDYINANYI NMEIPSSSII
       730        740        750        760        770        780        790        800
NQYIACQGPL PHTCTDFWQM TWEQGSSMVV MLTTQVERGR VKCHQYWPEP TGSSSYGCYQ VTCHSEEGNT AYIFRKMTLF
       810        820        830        840        850        860        870        880
NQEKNESRPL TQIQYIAWPD HGVPDDSSDF LDFVCHVRNK RAGKEEPVVV HCSAGIGRTG VLITMETAMC LIECNQPVYP
       890        900        910        920        930
LDIVRTMRDQ RAMMIQTPSQ YRFVCEAILK VYEEGFVKPL TTSTNK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 702 | 1 | 733.4640 | 133.70 | 3 | 38.8 | 14.9 | 0 | 226-245 | R.DQSNNEIMIGVMSGGILIYK.N | Oxidation: 12 |
| 2736 | 1 | 694.8753 | -23.24 | 2 | 64.6 | 12.1 | 2 | 676-686 | K.LPQNISKNRYR.D | |

# Detailed Protein Report

## Protein 552: coiled-coil domain-containing protein lobo homolog isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|574584573 | **Score:** | 27.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 96.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEVLREKVEE | EEEAEREEAA | EWAEWARMEK | MMRPVEVRKE | EITLKQETLR | DLEKKLSEIQ | ITVSAELPAF | TKDTIDISKL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PISYKTNTPK | EEHLLQVADN | FSRQYSHLCP | DRVPLFLHPL | NECEVPKFVS | TTLRPTLMPY | PELYNWDSCA | QFVSDFLTMV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PLPDPLKPTI | KKEEKVLPKK | YTIKPPRDLC | SRFEQEQEVK | KQQEIRAQEK | KRLREEEERL | MEAEKAKPDA | LHGLRVHSWV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LVLSGKREVP | ENFFIDPFTG | HSYSTQDEHF | LGIESLWNHK | NYWINMQDCW | NCCKDLIFDL | GDPVRWEYML | LGTDKSQLSL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TEEDDSGIND | EDDVENLGKE | DEDKSFDMPH | SWVEQIEISP | EAFETRCPNG | KKVIQYKRAK | LEKWAPYLNS | NGLVSRLTTY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EDLQCTNILE | IKEWYQNRED | MLELKHINKT | TDLKTDYFKP | GHPQALRVHS | YKSMQPEMDR | VIEFYETARV | DGLMKREETP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RTMTEYYQGR | PDFLSYRHAS | FGPRVKKLTL | SSAESNPRPI | VKITERFFRN | PAKPAEEDVA | ERVFLVAEER | IQLRYHCRED |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HITASKREFL | RRTEVDSKGN | KIIMTPDMCI | SFEVEPMEHT | KKLLYQYEAM | MHLKREEKLS | RHQVWESELE | VLEILKLREE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EEAAHTLTIS | IYDTKRNEKS | KEYREAMERM | MHEEHLRQVE | TQLDYLAPFL | AQLPPGEKLT | CWQAVRLKDE | CLSDFKQRLI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NKANLIQARF | EKETQELQKK | QQWYQENQVT | LTPEDEDLYL | SYCSQAMFRI | RILEQRLNRH | KELAPLKYLA | LEEKLYKDPR |
| 810 | | | | | | | |
| LGELQKIFA | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1516 | 1 | 513.1182 | -169.11 | 2 | 48.6 | 13.7 | 0 | 453-460 | K.SMQPEMDR.V | Oxidation: 2, 6 |

# Detailed Protein Report

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## Protein 553: tubby-related protein 4 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|55953100 | **Score:** | 27.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 168.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.3 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***WUP:QUP*** | **Median:** | 0.72 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530383880 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: tubby-related protein 4 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MYAAVEHGPV | LCSDSNILCL | SWKGRVPKSE | KEKPVCRRRY | YEEGWLATGN | GRGVVGVTFT | SSHCRRDRST | PQRINFNLRG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HNSEVVLVRW | NEPYQKLATC | DADGGIFVWI | QYEGRWSVEL | VNDRGAQVSD | FTWSHDGTQA | LISYRDGFVL | VGSVSGQRHW |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SSEINLESQI | TCGIWTPDDQ | QVLFGTADGQ | VIVMDCHGRM | LAHVLLHESD | GVLGMSWNYP | IFLVEDSSES | DTDSDDYAPP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QDGPAAYPIP | VQNIKPLLTV | SFTSGDISLM | NNYDDLSPTV | IRSGLKEVVA | QWCTQGDLLA | VAGMERQTQL | GELPNGPLLK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SAMVKFYNVR | GEHIFTLDTL | VQRPIISICW | GHRDSRLLMA | SGPALYVVRV | EHRVSSLQLL | CQQAIASTLR | EDKDVSKLTL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PPRLCSYLST | AFIPTIKPPI | PDPNNMRDFV | SYPSAGNERL | HCTMKRTEDD | PEVGGPCYTL | YLEYLGGLVP | ILKGRRISKL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RPEFVIMDPR | TDSKPDEIYG | NSLISTVIDS | CNCSDSSDIE | LSDDWAAKKS | PKISRASKSP | KLPRISIEAR | KSPKLPRAAQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ELSRSPRLPL | RKPSVGSPSL | TRREFPFEDI | TQHNYLAQVT | SNIWGTKFKI | VGLAAFLPTN | LGAVIYKTSL | LHLQPRQMTI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| YLPEVRKISM | DYINLPVFNP | NVFSEDEDDL | PVTGASGVPE | NSPPCTVNIP | IAPIHSSAQA | MSPTQSIGLV | QSLLANQNVQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LDVLTNQTTA | VGTAEHAGDS | ATQYPVSNRY | SNPGQVIFGS | VEMGRIIQNP | PPLSLPPPPQ | GPMQLSTVGH | GDRDHEHLQK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SAKALRPTPQ | LAAEGDAVVF | SAPQEVQVTK | INPPPPYPGT | IPAAPTTAAP | PPPLPPPQPP | VDVCLKKGDF | SLYPTSVHYQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TPLGYERITT | FDSSGNVEEV | CRPRTRMLCS | QNTYTLPGPG | SSATLRLTAT | EKKVPQPCSS | ATLNRLTVPR | YSIPTGDPPP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| YPEIASQLAQ | GRGAAQRSDN | SLIHATLRRN | NREATLKMAQ | LADSPRAPLQ | PLAKSKGGPG | GVVTQLPARP | PPALYTCSQC |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SGTGPSSQPG | ASLAHTASAS | PLASQSSYSL | LSPPDSARDR | TDYVNSAFTE | DEALSQHCQL | EKPLRHPPLP | EAAVTLKRPP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PYQWDPMLGE | DVWVPQERTA | QTSGPNPLKL | SSLMLSQGQH | LDVSRLPFIS | PKSPASPTAT | FQTGYGMGVP | YPGSYNNPPL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PGVQAPCSPK | DALSPTQFAQ | QEPAVVLQPL | YPPSLSYCTL | PPMYPGSSTC | SSLQLPPVAL | HPWSSYSACP | PMQNPQGTLP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PKPHLVVEKP | LVSPPPADLQ | SHLGTEVMVE | TADNFQEVLS | LTESPVPQRT | EKFGKKNRKR | LDSRAEEGSV | QAITEGKVKK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| EARTLSDFNS | LISSPHLGRE | KKKVKSQKDQ | LKSKKLNKTN | EFQDSSESEP | ELFISGDELM | NQSQGSRKGW | KSKRSPRAAG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ELEEAKCRRA | SEKEDGRLGS | QGFVYVMANK | QPLWNEATQV | YQLDFGGRVT | QESAKNFQIE | LEGRQVMQFG | RIDGSAYILD |
| 1530 | 1540 | 1550 | | | | | |
| FQYPFSAVQA | FAVALANVTQ | RLK | | | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2366 | 1 | 649.2906 | -70.12 | 3 | 60.0 | 16.8 | 2 | 1340-1357 | K.RLDSRAEEGSVQAITEGK.V |  | WUP:QUP 0.72 |

# Detailed Protein Report

**Protein 554:** **PREDICTED: transmembrane channel-like protein 8 isoform X4 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578830481 | **Score:** | 26.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLLPRSVSSE | RAPGVPEPEE | LWEAEMERLR | GSGTPVRGLP | YAMMDKRLIW | QLREPAGVQT | LRWQRWQRRR | QTVERRLREA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AQRLARGLGL | WEGALYEIGG | LFGTGIRSYF | TFLRFLLLLN | LLSLLLTASF | VLLPLVWLRP | PDPGPTLNLT | LQCPGSRQSP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PGVLRFHNQL | WHVLTGRAFT | NTYLFYGAYR | VGPESSSVYS | IRLAYLLSPL | ACLLLCFCGT | LRRMVKGLPQ | KTLLGQGYQA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PLSAKVFSSW | DFCIRVQEAA | TIKKHEISNE | FKVELEEGRR | FQLMQQQTRA | QTACRLLSYL | RVNVLNGLLV | VGAISAIFWA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TKYSQDNKEV | SGVPVSAAPV | PAPWGHRPGQ | LPGSPAVHIS | GPAGELPSQH | GGQPHSDLVR | GAEAGQLGDV | LRLPGSDHTV |
| 410 | | | | | | | |
| HWQRQEQL | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1031 | 1 | 598.1512 | -245.53 | 2 | 43.0 | 26.9 | 0 | 281-289 | R.FQLMQQQTR.A | Oxidation: 4 |

# Detailed Protein Report

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## Protein 555: E3 ubiquitin-protein ligase UHRF1 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|115430235 | **Score:** | 26.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 89.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWIQVRTMDG | RQTHTVDSLS | RLTKVEELRR | KIQELFHVEP | GLQRLFYRGK | QMEDGHTLFD | YEVRLNDTIQ | LLVRQSLVLP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HSTKERDSEL | SDTDSGCCLG | QSESDKSSTH | GEAAAETDSR | PADEDMWDET | ELGLYKVNEY | VDARDTNMGA | WFEAQVVRVT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RKAPSRDEPC | SSTSRPALEE | DVIYHVKYDD | YPENGVVQMN | SRDVRARART | IIKWQDLEVG | QVVMLNYNPD | NPKERGFWYD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AEISRKRETR | TARELYANVV | LGDDSLNDCR | IIFVDEVFKI | ERPGEGSPMV | DNPMRRKSGP | SCKHCKDDVN | RLCRVCACHL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CGGRQDPDKQ | LMCDECDMAF | HIYCLDPPLS | SVPSEDEWYC | PECRNDASEV | VLAGERLRES | KKKAKMASAT | SSSQRDWGKG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MACVGRTKEC | TIVPSNHYGP | IPGIPVGTMW | RFRVQVSESG | VHRPHVAGIH | GRSNDGAYSL | VLAGGYEDDV | DHGNFFTYTG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SGGRDLSGNK | RTAEQSCDQK | LTNTNRALAL | NCFAPINDQE | GAEAKDWRSG | KPVRVVRNVK | GGKNSKYAPA | EGNRYDGIYK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VVKYWPEKGK | SGFLVWRYLL | RRDDDEPGPW | TKEGKDRIKK | LGLTMQYPEG | YLEALANRER | EKENSKREEE | EQQEGGFASP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RTGKGKWKRK | SAGGGPSRAG | SPRRTSKKTK | VEPYSLTAQQ | SSLIREDKSN | AKLWNEVLAS | LKDRPASGSP | FQLFLSKVEE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TFQCICCQEL | VFRPITTVCQ | HNVCKDCLDR | SFRAQVFSCP | ACRYDLGRSY | AMQVNQPLQT | VLNQLFPGYG | NGR |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2815 | 2 | 626.8578 | 121.32 | 2 | 63.8 | 11.9 | 1 | 396-406 | R.DWGKGMACVGR.T | Carbamidomethyl: 8;<br>Oxidation: 6 |
| 2699 | 1 | 973.4997 | 26.66 | 2 | 64.8 | 15.0 | 2 | 544-560 | K.NSKYAPAEGNRYDGIYK.V | |

# Detailed Protein Report

**Protein 556:** **PREDICTED: core histone macro-H2A.1 isoform X3 [Homo sapiens]**

**Accession:** gi|530380257

**Database:** refseq_human(refseq_human_20140103.fasta)

**Database Date:** 2015-11-30

**Score:** 26.9

**MW [kDa]:** 39.0

**pI:** 10.3

**Sequence Coverage [%]:** 9.0

**No. of unique Peptides:** 2

```
         10         20         30         40         50         60         70         80
MSSRGGKKKS TKTSRSAKAG VIFPVGRMLR YIKKGHPKYR IGVGAPVYMA AVLEYLTAEI LELAGNAARD NKKGRVTPRH
         90        100        110        120        130        140        150        160
ILLAVANDEE LNQLLKGVTI ASGGVLPNIH PELLAKKRGS KGKLEAIITP PPAKKAKSPS QKKPVSKKAG GKKGARKSKK
        170        180        190        200        210        220        230        240
QGEVSKAASA DSTTEGTPAD GFTVLSTKSL FLGQKLQVVQ ADIASIDSDA VVHPTNTDFY IGGEVGNTLE KKGGKEFVEA
        250        260        270        280        290        300        310        320
VLELRKKNGP LEVAGAAVSA GHGLPAKFVI HCNSPVWGAD KCEELLEKTV KNCLALADDK KLKSIAFPSI GSGRNGFPKQ
        330        340        350        360        370
TAAQLILKAI SSYFVSTMSS SIKTVYFVLF DSESIGIYVQ EMAKLDAN
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2553 | 1 | 639.3415 | -83.77 | 2 | 61.9 | 15.2 | 1 | 124-135 | K.LEAIITPPPAKK.A | |
| 2834 | 1 | 806.4289 | 45.18 | 3 | 65.9 | 11.7 | 1 | 268-288 | K.FVIHCNSPVWGADKCEELLEK.T | |

# Detailed Protein Report

## Protein 557: PREDICTED: LIM domain only protein 7 isoform X22 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530402379 | **Score:** | 26.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 147.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

*QU:MU* **Median:** 2.64 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEGLEEAEAN | CSVAFAEAQR | WVEAVTEKNF | ETKDFRASLE | NGVLLCDLIN | KLKPGVIKKI | NRLSTPIAGL | DNINVFLKAC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EQIGLKEAQL | FHPGDLQDLS | NRVTVKQEET | DRRVKNVLIT | LYWLGRKAQS | NPYYNGPHLN | LKAFENLLGQ | ALTKALEDSS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FLKRSGRDSG | YGDIWCPERG | EFLAPPRHHK | REDSFESLDS | LGSRSLTSCS | SDITLRGGRE | GFESDTDSEF | TFKMQDYNKD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DMSYRRISAV | EPKTALPFNR | FLPNKSRQPS | YVPAPLRKKK | PDKHEDNRRS | WASPVYTEAD | GTFSRLFQKI | YGENGSKSMS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DVSAEDVQNL | RQLRYEEMQK | IKSQLKEQDQ | KWQDDLAKWK | DRRKSYTSDL | QKKKEEREEI | EKQALEKSKR | SSKTFKEMLQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DRESQNQKST | VPSRRRMYSF | DDVLEEGKRP | PTMTVSEASY | QSERVEEKGA | TYPSEIPKED | STTFAKREDR | VTTEIQLPSQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SPVEEQSPAS | LSSLRSRSTQ | MESTRVSASL | PRSYRKTDTV | RLTSVVTPRP | FGSQTRGISS | LPRSYTMDDA | WKYNGDVEDI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KRTPNNVVST | PAPSPDASQL | ASSLSSQKEV | AATEEDVTRL | PSPTSPFSSL | SQDQAATSKA | TLSSTSGLDL | MSESGEGEIS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PQREVSRSQD | QFSDMRISIN | QTPGKSLDFG | FTIKWDIPGI | FVASVEAGSP | AEFSQLQVDD | EIIAINNTKF | SYNDSKEWEE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AMAKAQETGH | LVMDVRRYGK | AGSPETKWID | ATSGIYNSEK | SSNLSVTTDF | SESLQSSNIE | SKEINGIHDE | SNAFESKASE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SISLKNLKRR | SQFFEQGSSD | SVVPDLPVPT | ISAPSRWVWD | QEEERKRQER | WQKEQDRLLQ | EKYQREQEKL | REEWQRAKQE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| AERENSKYLD | EELMVLSSNS | MSLTTREPSL | ATWEATWSEG | SKSSDREGTR | AGEEERRQPQ | EEVVHEDQGK | KPQDQLVIER |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ERKWEQQLQE | EQEQKRLQAE | AEEQKRPAEE | QKRQAEIERE | TSVRIYQYRR | PVDSYDIPKT | EEASSGFLPG | DRNKSRSTTE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LDDYSTNKNG | NNKYLDQIGN | MTSSQRRSKK | EQVPSGAELE | RQQILQEMRK | RTPLHNDNSW | IRQRSASVNK | EPVSLPGIMR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RGESLDNLDS | PRSNSWRQPP | WLNQPTGFYA | SSSVQDFSRP | PPQLVSTSNR | AYMRNPSSSV | PPPSAGSVKT | STTGVATTQS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PTPRSHSPSA | SQSGSQLRNR | SVSGKRICSY | CNNILGKGAA | MIIESLGLCY | HLHCFKCVAC | ECDLGGSSSG | AEVRIRNHQL |
| 1290 | 1300 | | | | | | |
| YCNDCYLRFK | SGRPTAM | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 51 | 1 | 857.9018 | -103.42 | 2 | 29.6 | 11.0 | 0 | 63-78 | R.LSTPIAGLDNINVFLK.A | | |
| 1358 | 1 | 955.9298 | -2.00 | 2 | 46.6 | 15.9 | 2 | 164-179 | K.RSGRDSGYGDIWCPER.G | Carbamidomethyl: 13 | QU:MU 2.64 |

# Detailed Protein Report

## Protein 558: PREDICTED: dedicator of cytokinesis protein 7 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530363514 | **Score:** | 26.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 209.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAERRAFAQK | ISRTVAAEVR | KQISGQYSGS | PQLLKNLNIV | GNISHHTTVP | LTEAVDPVDL | EDYLITHPLA | VDSGPLRDLI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EFPPDDIEVV | YSPRDCRTLV | SAVPEESEMD | PHVRDCIRSY | TEDWAIVIRK | YHKLGTGFNP | NTLDKQKERQ | KGLPKQVFES |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DEAPDGNSYQ | DDQDDLKRRS | MSIDDTPRGS | WACSIFDLKN | SLPDALLPNL | LDRTPNEEID | RQNDDQRKSN | RHKELFALHP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SPDEEEPIER | LSVPDIPKEH | FGQRLLVKCL | SLKFEIEIEP | IFASLALYDV | KEKKKISENF | YFDLNSEQMK | GLLRPHVPPA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AITTLARSAI | FSITYPSQDV | FLVIKLEKVL | QQGDIGECAE | PYMIFKEADA | TKNKEKLEKL | KSQADQFCQR | LGKYRMPFAW |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TAIHLMNIVS | SAGSLERDST | EVEISTGERK | GSWSERRNSS | IVGRRSLERT | TSGDDACNLT | SFRPATLTVT | NFFKQEGDRL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SDEDLYKFLA | DMRRPSSVLR | RLRPITAQLK | IDISPAPENP | HYCLTPELLQ | VKLYPDSRVR | PTREILEFPA | RDVYVPNTTY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RNLLYIYPQS | LNFANRQGSA | RNITVKVQFM | YGEDPSNAMP | VIFGKSSCSE | FSKEAYTAVV | YHNRSPDFHE | EIKVKLPATL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TDHHHLLFTF | YHVSCQQKQN | TPLETPVGYT | WIPMLQNGRL | KTGQFCLPVS | LEKPPQAYSV | LSPEVPLPGM | KWVDNHKGVF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NVEVVAVSSI | HTQDPYLDKF | FALVNALDEH | LFPVRIGDMR | IMENNLENEL | KSSISALNSS | QLEPVVRFLH | LLLDKLILLV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IRPPVIAGQI | VNLGQASFEA | MASIINRLHK | NLEGNHDQHG | RNSLLASYIH | YVFRLPNTYP | NSSSPGPGGL | GGSVHYATMA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RSAVRPASLN | LNRSRSLSNS | NPDISGTPTS | PDDEVRSIIG | SKGLDRSNSW | VNTGGPKAAP | WGSNPSPSAE | STQAMDRSCN |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RMSSHTETSS | FLQTLTGRLP | TKKLFHEELA | LQWVVCSGSV | RESALQQAWF | FFELMVKSMV | HHLYFNDKLE | APRKSRFPER |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| FMDDIAALVS | TIASDIVSRF | QKDTEMVERL | NTSLAFFLND | LLSVMDRGFV | FSLIKSCYKQ | VSSKLYSLPN | PSVLVSLRLD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| FLRIICSHEH | YVTLNLPCSL | LTPPASPSPS | VSSATSQSSG | FSTNVQDQKI | ANMFELSVPF | RQQHYLAGLV | LTELAVILDP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DAEGLFGLHK | KVINMVHNLL | SSHDSDPRYS | DPQIKARVAM | LYLPLIGIIM | ETVPQLYDFT | ETHNQRGRPI | CIATDDYESE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SGSMISQTVA | MAIAGTSVPQ | LTRPGSFLLT | STSGRQHTTF | SAESSRSLLI | CLLWVLKNAD | ETVLQKWFTD | LSVLQLNRLL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| DLLYLCVSCF | EYKGKKVFER | MNSLTFKKSK | DMRAKLEEAI | LGSIGARQEM | VRRSRGQLER | SPSGSAFGSQ | ENLRWRKDMT |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| HWRQNTEKLD | KSRAEIEHEA | LIDGNLATEA | NLIILDTLEI | VVQTVSVTES | KESILGGVLK | VLLHSMACNQ | SAVYLQHCFA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| TQRALVSKFP | ELLFEEETEQ | CADLCLRLLR | HCSSSIGTIR | SHASASLYLL | MRQNFEIGNN | FARVKMQVTM | SLSSLVGTSQ |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| NFNEEFLRRS | LKTILTYAEE | DLELRETTFP | DQVQDLVFNL | HMILSDTVKM | KEHQEDPEML | IDLMYRIAKG | YQTSPDLRLT |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| WLQNMAGKHS | ERSNHAEAAQ | CLVHSAALVA | EYLSMLEDRK | YLPVGCVTFQ | NISSNVLEES | AVSDDVVSPD | EEGICSGKYF |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| TESGLVGLLE | QAAASFSMAG | MYEAVNEVYK | VLIPIHEANR | DAKKLSTIHG | KLQEAFSKIV | HQSTGWEFYL | VYIFLFDSMK |
| 1850 | 1860 | | | | | | |
| TSVILFFLKA | MFPS | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 122 | 1 | 879.4101 | -14.16 | 3 | 30.5 | 16.1 | 0 | 1501-1523 | K.VLLHSMACNQSAVYLQHCFATQR.A | Oxidation: 6 |

# Detailed Protein Report

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**Protein 559:** **cation channel sperm-associated protein subunit beta precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|51339295 | **Score:** | 26.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 126.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.92 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MESPLIYVSV LLLNIFEFSS GIVYNKDDTE KRFACSNKGF PQENEIIKLY LFLENLKIQC FFQTENEIAS KAMLSVFTSG
        90        100        110        120        130        140        150        160
GLAPSLGIMN STYNGIFHFN LTLFSDRILW LVDIPRENIT QSTDIAAVEE WLVRITLHHG LNIYATEGTL LDVIREPILQ
       170        180        190        200        210        220        230        240
WTPGDVIPES EISKLYPHVV DLKVTKCPCA NDVALLGFIV DTIVDGVYIG ITFGGFWHDY DTTWFNMTQT IYSQLQEEYE
       250        260        270        280        290        300        310        320
DLSLVDMVLT NHFLVILTSL GLFVSEDLRY PSRHSLSFSR ADFCGFERVD YVKGKLWYNE RCFANREHFE VDYVTVTFER
       330        340        350        360        370        380        390        400
NRTLSESSSC FYSQEPFLEW VPCLPHIFKG IKIFPTVLTF LVDQERGTGV YLFYNKVRKT AIASVSTLRN NEPNSQSKFP
       410        420        430        440        450        460        470        480
IFRFPSSFSS PVGMVFHPRS HFLYAYGNQI WLSVDGGNTF QLIANFHDDI IKKTFHSFYT SAITFVSQRG KVYSTKAGMG
       490        500        510        520        530        540        550        560
RYSAVGSVTE RIFTLYYDHL GFLHKLTLGR FEASGPPTAF GNSRNLFGQP PDMGFETALA PQHTSLDEII FFAYVPENEP
       570        580        590        600        610        620        630        640
QETIYSKKFG NIHYGKVIHS GKTGRAYIRK VLQHTTPKGF LSSVIAEMKE PFGLEEVNES SCLSSSLLIN KAGNVYKLTL
       650        660        670        680        690        700        710        720
DSQVVQALFE DTDIEKTVVL PGYSSFLITS ILDNKNALAI ATMPESAPNN MTFLKSTWFL YNFGQRNGRT WKIYSKPCNY
       730        740        750        760        770        780        790        800
WFQHDDSPSL NIVKYIDLGN SYVLKAKVIR NAKGFRMLEI PLLTVFVGNP NLLEVTAEVT FDDTDSYVIT ISAASKVLHQ
       810        820        830        840        850        860        870        880
GSTSLAFIMW SASTECFVTT MVPTLKSSCS YLRSMHHIPS KFIPFEDWIS GVHKDSQGFN LIKTLPINYR PPSNMGIAIP
       890        900        910        920        930        940        950        960
LTDNFYHADP SKPIPRNMFH MSKKTGKFKQ CANVSTREEC NCTKDQKFSH AVAFSDCREK VPRFKFPITQ YPVSLEIINE
       970        980        990       1000       1010       1020       1030       1040
DGRVPLQSPY LVTVTEVNMR HNWKLKHTVP ENIKRMKQLV EPILGAAVYN PSGLNLSIKG SELFHFRVTV ISGVTFCNLI
      1050       1060       1070       1080       1090       1100       1110       1120
EEFQIYVDEA PLPFPGHTLI AVATAVVLGG LIFIAFMFQL QGIHPWRTFQ RWIRRNQEKF SSISLSELIH RSKSEE
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2126 | 1 | 1051.4446 | -118.59 | 2 | 56.4 | 11.5 | 1 | 591-609 | K.VLQHTTPKGFLSSVIAEMK.E | Oxidation: 18 | QU:MU 0.92 |

BRUKER

# Detailed Protein Report

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## Protein 560: coiled-coil domain-containing protein 80 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|41152074 | **Score:** | 26.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 108.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.45 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.23 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|41152076 | refseq_human (refseq_human_20140103.fasta) | coiled-coil domain-containing protein 80 precursor [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTWRMGPRFT | MLLAMWLVCG | SEPHPHATIR | GSHGGRKVPL | VSPDSSRPAR | FLRHTGRSRG | IERSTLEEPN | LQPLQRRRSV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PVLRLARPTE | PPARSDINGA | AVRPEQRPAA | RGSPREMIRD | EGSSARSRML | RFPSGSSSPN | ILASFAGKNR | VWVISAPHAS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EGYYRLMMSL | LKDDVYCELA | ERHIQQIVLF | HQAGEEGGKV | RRITSEGQIL | EQPLDPSLIP | KLMSFLKLEK | GKFGMVLLKK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TLQVEERYPY | PVRLEAMYEV | IDQGPIRRIE | KIRQKGFVQK | CKASGVEGQV | VAEGNDGGGG | AGRPSLGSEK | KKEDPRRAQV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PPTRESRVKV | LRKLAATAPA | LPQPPSTPRA | TTLPPAPATT | VTRSTSRAVT | VAARPMTTTA | FPTTQRPWTP | SPSHRPPTTT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EVITARRPSV | SENLYPPSRK | DQHRERPQTT | RRPSKATSLE | SFTNAPPTTI | SEPSTRAAGP | GRFRDNRMDR | REHGHRDPNV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VPGPPKPAKE | KPPKKKAQDK | ILSNEYEEKY | DLSRPTASQL | EDELQVGNVP | LKKAKESKKH | EKLEKPEKEK | KKKMKNENAD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KLLKSEKQMK | KSEKKSKQEK | EKSKKKKGGK | TEQDGYQKPT | NKHFTQSPKK | SVADLLGSFE | GKRRLLLITA | PKAENNMYVQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QRDEYLESFC | KMATRKISVI | TIFGPVNNST | MKIDHFQLDN | EKPMRVVDDE | DLVDQRLISE | LRKEYGMTYN | DFFMVLTDVD |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LRVKQYYEVP | ITMKSVFDLI | DTFQSRIKDM | EKQKKEGIVC | KEDKKQSLEN | FLSRFRWRRR | LLVISAPNDE | DWAYSQQLSA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LSGQACNFGL | RHITILKLLG | VGEEVGGVLE | LFPINGSSVV | EREDVPAHLV | KDIRNYFQVS | PEYFSMLLVG | KDGNVKSWYP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SPMWSMVIVY | DLIDSMQLRR | QEMAIQQSLG | MRCPEDEYAG | YGYHSYHQGY | QDGYQDDYRH | HESYHHGYPY | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1362 | 5 | 698.8981 | 6.72 | 2 | 46.7 | 13.9 | 0 | 350-363 | R.ATTLPPAPATTVTR.S | | WUP:QUP 1.23<br>QU:MU 1.45 |
| 1645 | 1 | 1062.1080 | -81.53 | 3 | 50.3 | 12.9 | 2 | 697-722 | R.LISELRKEYGMTYNDFFMVLTDVDV | Oxidation: 18 | |

# Detailed Protein Report

## Protein 561: pleckstrin homology domain-containing family G member 1 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|71274148 | **Score:** | 26.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 155.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.7 |
|  |  | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578812862 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: pleckstrin homology domain-containing family G member 1 isoform X7 [Homo sapiens] |
| gi\|578812859 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: pleckstrin homology domain-containing family G member 1 isoform X6 [Homo sapiens] |
| gi\|530383900 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: pleckstrin homology domain-containing family G member 1 isoform X4 [Homo sapiens] |
| gi\|530383898 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: pleckstrin homology domain-containing family G member 1 isoform X3 [Homo sapiens] |
| gi\|530383896 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: pleckstrin homology domain-containing family G member 1 isoform X2 [Homo sapiens] |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MELSDSDRPV | SFGSTSSSAS | SRDSHGSFGS | RMTLVSNSHM | GLFNQDKEVG | AIKLELIPAR | PFSSSELQRD | NPATGQQNAD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EGSERPPRAQ | WRVDSNGAPK | TIADSATSPK | LLYVDRVVQE | ILETERTYVQ | DLKSIVEDYL | DCIRDQTKLP | LGTEERSALF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GNIQDIYHFN | SELLQDLENC | ENDPVAIAEC | FVSKSEEFHI | YTQYCTNYPR | SVAVLTECMR | NKILAKFFRE | RQETLKHSLP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LGSYLLKPVQ | RILKYHLLLH | EIENHLDKDT | EGYDVVLDAI | DTMQRVAWHI | NDMKRKHEHA | VRLQEIQSLL | TNWKGPDLTS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YGELVLEGTF | RIQRAKNERT | LFLFDKLLLI | TKKRDDTFTY | KAHILCGNLM | LVEVIPKEPL | SFSVFHYKNP | KLQHTVQAKS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QQDKRLWVLH | LKRLILENHA | AKIPAKAKQA | ILEMDAIHHP | GFCYSPEGGT | KALFGSKEGS | APYRLRRKSE | PSSRSHKVLK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TSETAQDIQK | VSREEGSPQL | SSARPSPAQR | NSQPSSSTMI | SVLRAGGALR | NIWTDHQIRQ | ALFPSRRSPQ | ENEDDEDDYQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MFVPSFSSSD | LNSTRLCEDS | TSSRPCSWHM | GQMESTETSS | SGHRIVRRAS | SAGESNTCPP | EIGTSDRTRE | LQNSPKTEGQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EEMTPFGSSI | ELTIDDIDHV | YDNISYEDLK | LMVAKREEAE | STPSKSARDS | VRPKSTPELA | FTKRQAGHSK | GSLYAQTDGT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LSGGEASSQS | THELQAVEEN | IYDTIGLPDP | PSLGFKCSSL | KRAKRSTFLG | LEADFVCCDS | LRPFVSQDSL | QLSEDEAPYH |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QATPDHGYLS | LLYDSPSGNL | SMPHKPVSDK | LSEEVDEIWN | DLENYIKKNE | DKARDRLLAA | FPVSKDDVPD | RLHAESTPEL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SRDVGRSVST | LSLPESQALL | TPVKSRAGRA | SRANCPFEED | LISKEGSFMS | LNRLSLASEM | PLMDNPYDLA | NSGLSQTDPE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NPDLGMEATD | KTKSRVFMMA | RQYSQKIKKA | NQLLKVKSLE | LEQPPASQHQ | KSMHKDLAAI | LEEKKQGGPA | IGARIAEYSQ |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LYDQIVFRES | PLKIQKDGWA | SPQESSLLRS | VSPSQVHHGS | GDWLLHSTYS | NGELADFCLP | PEQDLRSRYP | TFEINTKSTP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RQLSAACSVP | SLQTSDPLPG | SVQRCSVVVS | QPNKENWCQD | HLYNSLGRKG | ISAKSQPYHR | SQSSSSVLIN | KSMDSINYPS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DVGKQQLLSL | HRSSRCESHQ | DLLPDIADSH | QQGTEKLSDL | TLQDSQKVVV | VNRNLPLNAQ | IATQNYFSNF | KETDGDEDDY |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VEIKSEEDES | ELELSHNRRR | KSDSKFVDAD | FSDNVCSGNT | LHSLNSPRTP | KKPVNSKLGL | SPYLTPYNDS | DKLNDYLWRG |
| 1370 | 1380 | 1390 |  |  |  |  |  |
| PSPNQQNIVQ | SLREKFQCLS | SSSFA |  |  |  |  |  |

| Cmpd. | No. of | m/z meas. | Δ m/z | z | Rt | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

| | Cmpds. | | [ppm] | | [min] | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 2063 | 1 | 697.5833 | -140.16 | 3 | 56.2 | 11.8 | 1 | 998-1015 | K.SLELEQPPASQHQKSMHK.D | Oxidation: 16 |

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# Detailed Protein Report

## Protein 562: PREDICTED: collagen alpha-2(I) chain-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578803403 | **Score:** | 26.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.4 |
| | | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKNRRPGTPS | HRDSWVPFRP | TPHTPYTLWR | CALARAILSQ | CMYFLAGFLT | ENREGGELGD | VRVWSKSLPP | TTSCTSRRED |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ELSAPLQAAG | AASPPRWLSG | SGLRESGRRA | RRLPTFPKHN | PGKFRLREGD | GAVGRGGDEN | RGRRFQPGSS | SHTQRLPLTA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RGGGVNGGIP | TASRGRRLLG | EAAPRRSRRS | GGARSPESHI | RAGSESGRPP | IRLGGAGQHR | AVRSAAAGQG | LRLSAAPPPG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RRRPPSALPA | SPLSAAARSP | PASPRSPAVS | SPSVVCVCAR | ARAHGSVWGN | RKFCRLGEQY | GKSEPRRQRW | RAGEAARGRS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GGRVSRGAGT | PRGTPGCGGA | GLDARAGGRG | WPWMGPAGPR | ISRGPCGQHC | LLEPGMGEWR | GPCCPRGLGT | LPLPTPTRAA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AGRSSLRSSG | PSVTLSRDAV | IHGGGGGGRG | RDKHGSGEVL | NSVLLSCLSL | GTFSPLGSVL | DFAGCENLLT | SESSVEPRLG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LWSAYFLQSD | CSCLRWSLSV | PLWGTSALIS | ALTAAVRAAG | KWGAPSGGRV | AVSLLISSVT | FKLSLEATAA | AGHVRRALGC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| WGKISSAGSR | DRAGGRRGTA | PRPRLGTWEG | RAGALGPGAR | PSWDTREDGG | GEEVGSAAGE | LGIMQMGKEN | LRPRPSAKSS |
| 650 | 660 | 670 | | | | | |
| LGICRYCGHV | MEGSGKYGLI | F | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 195 | 1 | 572.8054 | 9.14 | 2 | 32.4 | 16.7 | 2 | 312-323 | R.AGEAARGRSGGR.V | |

# Detailed Protein Report

## Protein 563: PREDICTED: dynamin-binding protein isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578819186 | **Score:** | 26.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 172.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| | | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEAGSVVRAI | FDFCPSVSEE | LPLFVGDIIE | VLAVVDEFWL | LGKKEDVTGQ | FPSSFVEIVT | IPSLKEGERL | FVCICEFTSQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ELDNLPLHRG | DLVILDGIPT | AGWLQGRSCW | GARGFFPSSC | VRELCLSSQS | RQWHSQSALF | QIPEYSMGQA | RALMGLSAQL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DEELDFREGD | VITIIGVPEP | GWFEGELEGR | RGIFPEGFVE | LLGPLRTVDE | SVSSGNQDDC | IVNGEVDTPV | GEEEIGPDED |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EEEPGTYGVA | LYRFQALEPN | ELDFEVGDKI | RILATLEDGW | LEGSLKGRTG | IFPYRFVKLC | PDTRVEETMA | LPQEGSLARI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PETSLDCLEN | TLGVEEQRHE | TSDHEAEEPD | CIISEAPTSP | LGHLTSEYDT | DRNSYQDEDT | AGGPPRSPGV | EWEMPLATDS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PTSDPTEVVN | GISSQPQVPF | HPNLQKSQYY | STVGGSHPHS | EQYPDLLPLE | ARTRDYASLP | PKRMYSQLKT | LQKPVLPLYR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GSSVSASRVV | KPRQSSPQLH | NLASYTKKHH | TSSVYSISER | LEMKPGPQAQ | GLVMEAATHS | QGDGSTDLDS | KLTQQLIEFE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KSLAGPGTEP | DKILRHFSIM | DFNSEKDIVR | GSSKLITEQE | LPERRKALRP | PPPRPCTPVS | TSPHLLVDQN | LKPAPPLVVR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PSRPAPLPPS | AQQRTNAVSP | KLLSRHRPTC | ETLEKEGPGH | MGRSLDQTSP | CPLVLVRIEE | MERDLDMYSR | AQEELNLMLE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EKQDESSRAE | TLEDLKFCES | NIESLNMELQ | QLREMTLLSS | QSSSLVAPSG | SVSAENPEQR | MLEKRAKVIE | ELLQTERDYI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RDLEMCIERI | MVPMQQAQVP | NIDFEGLFGN | MQMVIKVSKQ | LLAALEISDA | VGPVFLGHRD | ELEGTYKIYC | QNHDEAIALL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EIYEKDEKIQ | KHLQDSLADL | KSLYNEWGCT | NYINLGSFLI | KPVQRVMRYP | LLLMELLNST | PESHPDKVPL | TNAVLAVKEI |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NVNINEYKRR | KDLVLKYRKG | DEDSLMEKIS | KLNIHSIIKK | SNRVSSHLKH | LTGFAPQIKD | EVFEETEKNF | RMQERLIKSF |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| IRDLSLYLQH | IRKERTERLV | ISPLNQLLSM | FTGPHKLVQK | RFDKLLDFYN | CTERAEKLKD | KKTLEELQSA | RNNYEALNAQ |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LLDELPKFHQ | YAQGLFTNCV | HGYAEAHCDF | VHQALEQLKP | LLSLLKVAGR | EGNLIAIFHE | EHSRVLQQLQ | VFTFFPESLP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ATKKPFERKT | IDRQSARKPL | LGLPSYMLQS | EELRASLLAR | YPPEKLFQAE | RNFNAAQDLD | VSLLEGDLVG | VIKKKDPMGS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| QNRWLIDNGV | TKGFVYSSFL | KPYNPRRSHS | DASVGSHSST | ESEHGSSSPR | FPRQNSGSTL | TFNPSSMAVS | FTSGSCQKQP |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| QDASPPPKEC | DQGTLSASLN | PSNSESSPSR | CPSDPDSTSQ | PRSGDSADVA | RDVKQPTATP | RSYRNFRHPE | IVGYSVPGRN |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GQSQDLVKGC | ARTAQAPEDR | STEPDGSEAE | GNQVYFAVYT | FKARNPNELS | VSANQKLKIL | EFKDVTGNTE | WWLAEVNGKK |
| 1530 | 1540 | | | | | | |
| GYVPSNYIRK | TEYT | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2669 | 1 | 995.0095 | -40.18 | 2 | 63.5 | 15.5 | 2 | 1235-1251 | R.ASLLARYPPEKLFQAER.N | |

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# Detailed Protein Report

## Protein 564: sialate O-acetylesterase isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|321267600 | **Score:** | 26.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVLQKEPAGA | VIWGFGTPGA | TVTVTLRQGQ | ETIMKKVTSV | KAHSDTWMVV | LDPMKPGGPF | EVMAQQTLEK | INFTLRVHDV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LFGDVWLCSG | QSNMQMTVLQ | IFNATRELSN | TAAYQSVRIL | SVSPIQAEQE | LEDLVAVDLQ | WSKPTSENLG | HGYFKYMSAV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CWLFGRHLYD | TLQYPIGLIA | SSWGGTPIEA | WSSGRSLKAC | GVPKQGSIPY | DSVTGPSKHS | VLWNAMIHPL | CNMTLKGVVW |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YQGESNINYN | TDLYNCTFPA | LIEDWRETFH | RGSQGQTERF | FPFGLVQLSS | DLSKKSSDDG | FPQIRWHQTA | DFGYVPNPKM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PNTFMAVAMD | LCDRDSPFGS | IHPRDKQTVA | YRLHLGARAL | AYGEKNLTFE | GPLPEKIELL | AHKGLLNLTY | YQQIQVQKKD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NKIFEISCCS | DHRCKWLPAS | MNTVSTQSLT | LAIDSCHGTV | VALRYAWTTW | PCEYKQCPLY | HPSSALPAPP | FIAFITDQGP |
| 490 | | | | | | | |
| GHQSNVAK | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 693 | 1 | 1035.0409 | 84.42 | 2 | 38.6 | 14.9 | 2 | 400-415 | K.DNKIFEISCCSDHRCK.W | Carbamidomethyl: 9, 10, 15 |

# Detailed Protein Report

## Protein 565: PREDICTED: RAD51-associated protein 2 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530367071 | **Score:** | 26.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 132.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.1 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAELRKPTSS | LTPPEDPDSQ | PPSSKRLCLE | EPGGVFKAGW | RLPLVPRLSE | AEKVWELSPR | PFKGLLVSTN | AIFDNSTDSC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VEKSVSGKQI | CNLKCSNLKF | QMSSCLQSPP | SQSPDSDLRA | SGRSEAGLHD | REAFSVHRSN | SSKAGVSQLL | PSTSIHDIHG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IRNENRKQQF | VQGRDNVHKE | NPFLDVTFYK | ETKSPFHEIK | NRCKANSVVP | SNKRENNISS | SVLKISKSQN | QPSLEIAKPS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YFRDSGTISV | PQFPMDLNSK | MSSVYLKEIA | KKKNDKKEAY | VRDFTNIYWS | QNRPDVKKQK | LQNDKKTVEA | ENIFSKCYEN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DYPSLSSQNT | CKRKDLISSN | YCNCSSIQCN | VRDSRKNFAI | LENANWEEAE | CLDSYVLTRL | EKSQNWDCNV | RHILRRNRGN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CWIINNCKTK | CENMKKTEEK | WNWLLLLEID | LLSKEDYHCA | KVINAYEEQS | KLLVREILGS | QTALITTVWL | NGKGENDNTL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QLRYNTTQKV | FHVNNPFESF | IIEIFYFHKS | ISGNKKDNSI | LTCCNILKCK | KQIGIIGIQN | LITRNMNTNI | KNGILSIYLQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DSVSEPLDIL | LKTNIAFLLN | NFDSLTRIEN | DFELEEECIF | KCMLYLKYPK | NIVENHTAYL | VKILTSSRLL | EDNMKPMLKK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RKLFRTEQVF | EKSKKKLINS | FSMTTQNTGF | PIFETYEKIP | LLMDFDDMDE | ISLIREITCQ | NMSCPQQVVN | VENWAHYNSS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TVKAHGNSCP | QFIQNNRGYI | NENFYEVNMH | SQDLNMERKQ | GHNKISNFDC | EHIFEDLCNV | RQQAIPASHN | IIHNEETHTT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SITQVLNFWN | LLSEIEEKKY | DLILKEEVKV | TAESLTNSCQ | VHKDTKIEKE | EKDSFFPMDD | MFSVQSVSLI | SKEVNVEENK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| YVNQNYVTNT | NEYESILPER | EIANSKDFHR | KNDSALYINH | QFETGLSEGN | DECFQDLAAK | YLSTEALTIV | KDFEMKRKFD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LVLEELRMFH | EISRENELLS | TVETNNGQEN | YFGENDAEKV | KMEIEKDLKM | VVVNKIRASS | SFHDTIAGPN | MGKSHQSLFK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| WKTVPNNGEQ | EVPNESCYPS | RSEEELLYST | SEKDCETPLP | KRPAFLPDEC | KEEFNYLLRG | GSHFPHGISR | VRPLKTCSRP |
| 1130 | 1140 | 1150 | 1160 | | | | |
| IRIGLSRKAR | IKQLHPYLKQ | MCYGNLKENF | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1446 | 1 | 698.8871 | -14.31 | 2 | 47.7 | 15.2 | 2 | 261-272 | K.MSSVYLKEIAKK.K | |

# Detailed Protein Report

**Protein 566:** **complexin-3 precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|71725345 | **Score:** | 26.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 17.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 19.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MAFMVKTMVG GQLKNLTGSL GGGEDKGDGD KSAAEAQGMS REEYEEYQKQ LVEEKMERDA QFTQRKAERA TLRSHFRDKY
        90        100        110        120        130        140        150        160
RLPKNETDES QIQMAGGDVE LPRELAKMIE EDTEEEEEKA SVLGQLASLP GLNLGSLKDK AQATLGDLKQ SAEKCHVM
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1306 | 1 | 721.2739 | -148.07 | 2 | 45.9 | 11.1 | 1 | 2-14 | M.AFMVKTMVGGQLK.N | Oxidation: 3, 7 |

# Detailed Protein Report

**Protein 567:** **metallothionein-1G [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|10835230 | **Score:** | 26.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 6.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 70.5 |
| | | **No. of unique Peptides:** | 1 |

```
         10         20         30         40         50         60         70
MDPNCSCAAG VSCTCASSCK CKECKCTSCK KSCCSCCPVG CAKCAQGCIC KGASEKCSCC A
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1987 | 2 | 862.6346 | -31.70 | 3 | 53.2 | 13.2 | 2 | 1-25 | -.MDPNCSCAAGVSCTCASSCKCKECK.C | Carbamidomethyl: 7 |

# Detailed Protein Report

## Protein 568: death-inducer obliterator 1 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|301129165 | **Score:** | 26.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 243.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.9 |
| | | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 0.74 | **CV:** 0.00 % | **No. of Peptides:** 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|301129170 | refseq_human (refseq_human_20140103.fasta) | death-inducer obliterator 1 isoform c [Homo sapiens] |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDDKGDPSNE | EAPKAIKPTS | KEFRKTWGFR | RTTIAKREGA | GDAEADPLEP | PPPQQQLGLS | LRRSGRQPKR | TERVEQFLTI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ARRRGRRSMP | VSLEDSGEPT | SCPATDAETA | SEGSVESASE | TRSGPQSAST | AVKERPASSE | KVKGGDDHDD | TSDSDSDGLT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LKELQNRLRR | KREQEPTERP | LKGIQSRLRK | KRREEGPAET | VGSEASDTVE | GVLPSKQEPE | NDQGVVSQAG | KDDRESKLEG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KAAQDIKDEE | PGDLGRPKPE | CEGYDPNALY | CICRQPHNNR | FMICCDRCEE | WFHGDCVGIS | EARGRLLERN | GEDYICPNCT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ILQVQDETHS | ETADQQEAKW | RPGDADGTDC | TSIGTIEQKS | SEDQGIKGRI | EKAANPSGKK | KLKIFQPVIE | APGASKCIGP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GCCHVAQPDS | VYCSNDCILK | HAAATMKFLS | SGKEQKPKPK | EKMKMKPEKP | SLPKCGAQAG | IKISSVHKRP | APEKKETTVK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KAVVVPARSE | ALGKEAACES | STPSWASDHN | YNAVKPEKTA | APSPSLLYKS | TKEDRRSEEK | AAAMAASKKT | APPGSAVGKQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PAPRNLVPKK | SSFANVAAAT | PAIKKPPSGF | KGTIPKRPWL | SATPSSGASA | ARQAGPAPAA | ATAASKKFPG | SAALVGAVRK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PVVPSVPMAS | PAPGRLGAMS | AAPSQPNSQI | RQNIRRSLKE | ILWKRVNDSD | DLIMTENEVG | KIALHIEKEM | FNLFQVTDNR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YKSKYRSIMF | NLKDPKNQGL | FHRVLREEIS | LAKLVRLKPE | ELVSKELSTW | KERPARSVME | SRTKLHNESK | KTAPRQEAIP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DLEDSPPVSD | SEEQQESARA | VPEKSTAPLL | DVFSSMLKDT | TSQHRAHLFD | LNCKICTGQV | PSAEDEPAPK | KQKLSASVKK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EDLKSKHDSS | APDPAPDSAD | EVMPEAVPEV | ASEPGLESAS | HPNVDRTYFP | GPPGDGHPEP | SPLEDLSPCP | ASCGSGVVTT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VTVSGRDPRT | APSSSCTAVA | SAASRPDSTH | MVEARQDVPK | PVLTSVMVPK | SILAKPSSSP | DPRYLSVPPS | PNISTSESRS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PPEGDTTLFL | SRLSTIWKGF | INMQSVAKFV | TKAYPVSGCF | DYLSEDLPDT | IHIGGRIAPK | TVWDYVGKLK | SSVSKELCLI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RFHPATEEEE | VAYISLYSYF | SSRGRFGVVA | NNNRHVKDLY | LIPLSAQDPV | PSKLLPFEGP | GLESPRPNII | LGLVICQKIK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| RPANSGELDK | MDEKRTRLQP | EEADVPAYPK | VATVPQSEKK | PSKYPLCSAD | AAVSTTPPGS | PPPPPPLPEP | PVLKVLSSLK |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PAAPSPATAA | TTAAAASTAA | SSTASSASKT | ASPLEHILQT | LFGKKKSFDP | SAREPPGSTA | GLPQEPKTTA | EDGVPAPPLL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| DPIVQQFGQF | SKDKALEEEE | DDRPYDPEEE | YDPERAFDTQ | LVERGRRHEV | ERAPEAAAAE | REEVAYDPED | ETILEEAKVT |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| VDDLPNRMCA | DVRRNSVERP | AEPVAGAATP | SLVEQQKMLE | ELNKQIEEQK | RQLEEQEEAL | RQQRAAVGVS | MAHFSVSDAL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| MSPPPKSSLP | KAELFQQEQQ | SADKPASLPP | ASQASNHRDP | RQARRLATET | GEGEGEPLSR | LSARGAQGAL | PERDASRGGL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| VGQAPMPVPE | EKEPASSPWA | SGEKPPAGSE | QDGWKAEPGE | GTRPATVGDS | SARPARRVLL | PTPPCGALQP | GFPLQHDGER |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| DPFTCPGFAS | QDKALGSAQY | EDPRNLHSAG | RSSSPAGETE | GDREPQARPG | EGTAPLPPPG | QKVGGSQPPF | QGQREPGPHA |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| LGMSGLHGPN | FPGPRGPAPP | FPEENIASND | GPRGPPPARF | GAQKGPIPSL | FSGQHGPPPY | GDSRGPSPSY | LGGPRGVAPS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| QFEERKDPHG | EKREFQDAPY | NEVTGAPAQF | EGTEQAPFLG | SRGGAPFQFG | GQRRPLLSQL | KGPRGGPPPS | QFGGQRGPPP |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| GHFVGPRGPH | PSQFETARGP | HPNQFEGPRG | QAPNFMPGPR | GIQPQQFEDQ | RVHSPPRFTN | QRAPAPLQFG | GLRGSAPFSE |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| KNEQTPSRFH | FQGQAPQVMK | PGPRPLLELP | SHPPQHRKDR | WEEAGPPSAL | SSSAPGQGPE | ADGQWASADF | REGKGHEYRN |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| QTFEGRQRER | FDVGPKEKPL | EEPDAQGRAS | EDRRRERERG | RNWSRERDWD | RPREWDRHRD | KDSSRDWDRN | RERSANRDRE |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 411 | 1 | 701.3611 | 72.76 | 2 | 35.1 | 11.7 | 1 | 2-14 | M.DDKGDPSNEEAPK.A |  | QU:MU 0.74 |

# Detailed Protein Report

## Protein 569: cullin-associated NEDD8-dissociated protein 2 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|112420977 | **Score:** | 26.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 122.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSTAAFHISS | LLEKMTSSDK | DFRFMATSDL | MSELQKDSIQ | LDEDSERKVV | KMLLRLLEDK | NGEVQNLAVK | WLGVPLGAFH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ASLLHCLLPQ | LSSPRLAVRK | RAVGALGHLA | AACSTDLFVE | LADHLLDRLP | GPRVPTSPTA | IRTLIQCLGS | VGRQAGHRLG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AHLDRLVPLV | EDFCNLDDDE | LRESCLQAFE | AFLRKCPKEM | GPHVPNVTSL | CLQYIKHDPN | YNYDSDEDEE | QMETEDSEFS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EQESEDEYSD | DDDMSWKVRR | AAAKCIAALI | SSRPDLLPDF | HCTLAPVLIR | RFKEREENVK | ADVFTAYIVL | LRQTQPPKGW |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LEAMEEPTQT | GSNLHMLRGQ | VPLVVKALQR | QLKDRSVRAR | QGCFSLLTEL | AGVLPGSLAE | HMPVLVSGII | FSLADRSSSS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TIRMDALAFL | QGLLGTEPAE | AFHPHLPILL | PPVMACVADS | FYKIAAEALV | VLQELVRALW | PLHRPRMLDP | EPYVGEMSAV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TLARLRATDL | DQEVKERAIS | CMGHLVGHLG | DRLGDDLEPT | LLLLLDRLRN | EITRLPAIKA | LTLVAVSPLQ | LDLQPILAEA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LHILASFLRK | NQRALRLATL | AALDALAQSQ | GLSLPPSAVQ | AVLAELPALV | NESDMHVAQL | AVDFLATVTQ | AQPASLVEVS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GPVLSELLRL | LRSPLLPAGV | LAAAEGFLQA | LVGTRPPCVD | YAKLISLLTA | PVYEQAVDGG | PGLHKQVFHS | LARCVAALSA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ACPQEAASTA | SRLVCDARSP | HSSTGVKVLA | FLSLAEVGQV | AGPGHQRELK | AVLLEALGSP | SEDVRAAASY | ALGRVGAGSL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PDFLPFLLEQ | IEAEPRRQYL | LLHSLREALG | AAQPDSLKPY | AEDIWALLFQ | RCEGAEEGTR | GVVAECIGKL | VLVNPSFLLP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RLRKQLAAGR | PHTRSTVITA | VKFLISDQPH | PIDPLLKSFI | AVHNKPSLVR | DLLDDILPLL | YQETKIRRDL | IREVEMGPFK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| HTVDDGLDVR | KAAFECMYSL | LESCLGQLDI | CEFLNHVEDG | LKDHYDIRML | TFIMVARLAT | LCPAPVLQRV | DRLIEPLRAT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| CTAKVKAGSV | KQEFEKQDEL | KRSAMRAVAA | LLTIPEVGKS | PIMADFSSQI | RSNPELAALF | ESIQKDSASA | PSTDSMELS |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1132 | 1 | 701.3400 | -16.93 | 3 | 44.3 | 12.1 | 0 | 199-216 | K.EMGPHVPNVTSLCLQYIK.H | Carbamidomethyl: 13;<br>Oxidation: 2 |
| 2247 | 1 | 1017.5903 | -9.72 | 2 | 58.5 | 14.5 | 2 | 884-902 | R.KQLAAGRPHTRSTVITAVK.F | |

# Detailed Protein Report

**Protein 570:** **1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-1 isoform c [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|195972873 | **Score:** | 26.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 114.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.72 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MADLEVYKNL | SPEKVERCMS | VMQSGTQMIK | LKRGTKGLVR | LFYLDEHRTR | LRWRPSRKSE | KAKILIDSIY | KVTEGRQSEI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FHRQAEGNFD | PSCCFTIYHG | NHMESLDLIT | SNPEEARTWI | TGLKYLMAGI | SDEDSLAKRQ | RTHDQWVKQT | FEEADKNGDG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLNIEEIHQL | MHKLNVNLPR | RKVRQMFQEA | DTDENQGTLT | FEEFCVFYKM | MSLRRDLYLL | LLSYSDKKDH | LTVEELAQFL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KVEQKMNNVT | TDYCLDIIKK | FEVSEENKVK | NVLGIEGFTN | FMRSPACDIF | NPLHHEVYQD | MDQPLCNYYI | ASSHNTYLTG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DQLLSQSKVD | MYARVLQEGC | RCVEVDCWDG | PDGEPVVHHG | YTLTSKILFR | DVVETINKHA | FVKNEFPVIL | SIENHCSIQQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QRKIAQYLKG | IFGDKLDLSS | VDTGECKQLP | SPQSLKGKIL | VKGKKLPYHL | GDDAEEGEVS | DEDSADEIED | ECKFKLHYSN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GTTEHQVESF | IRKKLESLLK | ESQIRDKEDP | DSFTVRALLK | ATHEGLNAHL | KQSPDVKESG | KKSHGRSLMT | NFGKHKKTTK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SRSKSYSTDD | EEDTQQSTGK | EGGQLYRLGR | RRKTMKLCRE | LSDLVVYTNS | VAAQDIVDDG | TTGNVLSFSE | TRAHQVVQQK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SEQFMIYNQK | QLTRIYPSAY | RIDSSNFNPL | PYWNAGCQLV | ALNYQSEGRM | MQLNRAKFKA | NGNCGYVLKP | QQMCKGTFNP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| FSGDPLPANP | KKQLILKVIS | GQQLPKPPDS | MFGDRGEIID | PFVEVEIIGL | PVDCCKDQTR | VVDDNGFNPV | WEETLTFTVH |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| MPEIALVRFL | VWDHDPIGRD | FVGQRTVTFS | SLVPGYRHVY | LEGLTEASIF | VHITINEIYG | KWSPLILNPS | YTILHFLGAT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KNRQLQGLKG | LFNKNPRHSS | SENNSHYVRK | RSIGDRILRR | TASAPAKGRK | KSKMGFQEMV | EIKDSVSEAT | RDQDGVLRRT |
| 970 | 980 | 990 | 1000 | 1010 | | | |
| TRSLQARPVS | MPVDRNLLGA | LSLPVSETAK | DIEGKENSLV | QI | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2076 | 1 | 649.2852 | -47.07 | 3 | 54.3 | 10.8 | 2 | 18-33 | R.CMSVMQSGTQMIKLKR.G | Carbamidomethyl: 1;<br>Oxidation: 2, 5, 11 | WUP:QUP 0.72 |

# Detailed Protein Report

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## Protein 571: teashirt homolog 2 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|301171536 | **Score:** | 26.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 114.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.5 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 1.12 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMAAALLHYT | GYAQEEQLKE | EEEIKEEEEE | EDSGSVAQLQ | GGNDTGTDEE | LETGPEQKGC | FSYQNSPGSH | LSNQDAENES |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LLSDASDQVS | DIKSVCGRDA | SDKKAHTHVR | LPNEAHNCMD | KMTAVYANIL | SDSYWSGLGL | GFKLSNSERR | NCDTRNGSNK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SDFDWHQDAL | SKSLQQNLPS | RSVSKPSLFS | SVQLYRQSSK | MCGTVFTGAS | RFRCRQCSAA | YDTLVELTVH | MNETGHYQDD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NRKKDKLRPT | SYSKPRKRAF | QDMDKEDAQK | VLKCMFCGDS | FDSLQDLSVH | MIKTKHYQKV | PLKEPVPTIS | SKMVTPAKKR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VFDVNRPCSP | DSTTGSFADS | FSSQKNANLQ | LSSNNRYGYQ | NGASYTWQFE | ACKSQILKCM | ECGSSHDTLQ | QLTTHMMVTG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HFLKVTSSAS | KKGKQLVLDP | LAVEKMQSLS | EAPNSDSLAP | KPSSNSASDC | TASTTELKKE | SKKERPEETS | KDEKVVKSED |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YEDPLQKPLD | PTIKYQYLRE | EDLEDGSKGG | GDILKSLENT | VTTAINKAQN | GAPSWSAYPS | IHAAYQLSEG | TKPPLPMGSQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VLQIRPNLTN | KLRPIAPKWK | VMPLVSMPTH | LAPYTQVKKE | SEDKDEAVKE | CGKESPHEEA | SSFSHSEGDS | FRKSETPPEA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KKTELGPLKE | EEKLMKEGSE | KEKPQPLEPT | SALSNGCALA | NHAPALPCIN | PLSALQSVLN | NHLGKATEPL | RSPSCSSPSS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| STISMFHKSN | LNVMDKPVLS | PASTRSASVS | RRYLFENSDQ | PIDLTKSKSK | KAESSQAQSC | MSPPQKHALS | DIADMVKVLP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KATTPKPASS | SRVPPMKLEM | DVRRFEDVSS | EVSTLHKRKG | RQSNWNPQHL | LILQAQFASS | LFQTSEGKYL | LSDLGPQERM |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QISKFTGLSM | TTISHWLANV | KYQLRKTGGT | KFLKNMDKGH | PIFYCSDCAS | QFRTPSTYIS | HLESHLGFQM | KDMTRLSVDQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QSKVEQEISR | VSSAQRSPET | IAAEEDTDSK | FKCKLCCRTF | VSKHAVKLHL | SKTHSKSPEH | HSQFVTDVDE | E |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 50 | 1 | 645.8133 | -54.63 | 2 | 29.6 | 11.6 | 0 | 516-527 | K.SLENTVTTAINK.A | | QU:MU 1.12 |

# Detailed Protein Report

## Protein 572: von Willebrand factor A domain-containing protein 8 isoform b precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|57863273 | **Score:** | 26.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 116.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQSRLLLLGA | PGGHGGPASR | RMRLLLRQVV | QRRPGGDRQR | PEVRLLHAGS | GADTGDTVNI | GDVSYKLKIP | KNPELVPQNY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ISDSLAQSVV | QHLRWIMQKD | LLGQDVFLIG | PPGPLRRSIA | MQYLELTKRE | VEYIALSRDT | TETDLKQRRE | IRAGTAFYID |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QCAVRAATEG | RTLILEGLEK | AERNVLPVLN | NLLENREMQL | EDGRFLMSAE | RYDKLLRDHT | KKELDSWKIV | RVSENFRVIA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LGLPVPRYSG | NPLDPPLRSR | FQARDIYYLP | FKDQLKLLYS | IGANVSAEKV | SQLLSFATTL | CSQESSTLGL | PDFPLDSLAA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AVQILDSFPM | MPIKHAIQWL | YPYSILLGHE | GKMAVEGVLK | RFELQDSGSS | LLPKEIVKVE | KMMENHVSQA | SVTIRIADKE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VTIKVPAGTR | LLSQPCASDR | FIQTLSHKQL | QAEMMQSHMV | KDICLIGGKG | CGKTVIAKNF | ADTLGYNIEP | IMLYQDMTAR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DLLQQRYTLP | NGDTAWRSSP | LVNAALEGKL | VLLDGIHRVN | AGTLAVLQRL | IHDRELSLYD | GSRLLREDRY | MRLKEELQLS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DEQLQKRSIF | PIHPSFRIIA | LAEPPVIGST | AHQWLGPEFL | TMFFFHYMKP | LVKSEEIQVI | KEKVPNVPQE | ALDKLLSFTH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KLRETQDPTA | QSLAASLSTR | QLLRISRRLS | QYPNENLHSA | VTKACLSRFL | PSLARSALEK | NLADATIEIN | TDDNLEPELK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DYKCEVTSGT | LRIGAVSAPI | YNAHEKMKVP | DVLFYDNIQH | VIVMEDMLKD | FLLGEHLLLV | GNQGVGKNKI | VDRFLHLLNR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PREYIQLHRD | TTVQTLTLQP | SVKDGLIVYE | DSPLVKAVKL | GHILVVDEAD | KAPTNVTCIL | KTLVENGEMI | LADGRRIVAN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SANVNGRENV | VVIHPDFRMI | VLANRPGFPF | LGNDFFGTLG | DIFSCHAVDN | PKPHSELEML | RQYGPNVPEP | ILQKLVAAFG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ELRSLADQGI | INYPYSTREV | VNIVKHLQKF | PTEGLSSVVR | NVFDFDSYNN | DMREILINTL | HKYGIPIGAK | PTSVQLAKE |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2188 | 1 | 958.6176 | 79.28 | 2 | 55.7 | 10.0 | 2 | 5-23 | R.LLLLGAPGGHGGPASRRMR.L | |

# Detailed Protein Report

## Protein 573: PREDICTED: microtubule-associated serine/threonine-protein kinase 4 isoform X12 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578810348 | **Score:** | 26.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 247.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRPRSRSLSP | GRSPACCDHE | IIMMNHVYKE | RFPKATAQME | ERLKEIITSY | SPDNVLPLAD | GVLSFTHHQI | IELARDCLDK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SHQGLITSRY | FLELQHKLDK | LLQEAHDRSE | SGELAFIKQL | VRKILIVIAR | PARLLECLEF | DPEEFYYLLE | AAEGHAKEGQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GIKTDIPRYI | ISQLGLNKDP | LEEMAHLGNY | DSGTAETPET | DESVSSSNAS | LKLRRKPRES | DFETIKLISN | GAYGAVYFVR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HKESRQRFAM | KKINKQNLIL | RNQIQQAFVE | RDILTFAENP | FVVSMYCSFE | TRRHLCMVME | YVEGGDCATL | MKNMGPLPVD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MARMYFAETV | LALEYLHNYG | IVHRDLKPDN | LLVTSMGHIK | LTDFGLSKVG | LMSMTTNLYE | GHIEKDAREF | LDKQVCGTPE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YIAPEVILRQ | GYGKPVDWWA | MGIILYEFLV | GCVPFFGDTP | EELFGQVISD | EINWPEKDEA | PPPDAQDLIT | LLLRQNPLER |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LGTGGAYEVK | QHRFFRSLDW | NSLLRQKAEF | IPQLESEDDT | SYFDTRSEKY | HHMETEEEDD | TNDEDFNVEI | RQFSSCSHRF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SKVFSSIDRI | TQNSAEEKED | SVDKTKSTTL | PSTETLSWSS | EYSEMQQLST | SNSSDTESNR | HKLSSGLLPK | LAISTEGEQD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EAASCPGDPH | EEPGKPALPP | EECAQEEPEV | TTPASTISSS | TLSVGSFSEH | LDQINGRSEC | VDSTDNSSKP | SSEPASHMAR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QRLESTEKKK | ISGKVTKSLS | ASALSLMIPG | DMFAVSPLGS | PMSPHSLSSD | PSSSRDSSPS | RDSSAASASP | HQPIVIHSSG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KNYGFTIRAI | RVYVGDSDIY | TVHHIVWNVE | EGSPACQAGL | KAGDLITHIN | GEPVHGLVHT | EVIELLLKSG | NKVSITTTPF |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ENTSIKTGPA | RRNSYKSRMV | RRSKKSKKKE | SLERRRSLFK | KLAKQPSPLL | HTSRSFSCLN | RSLSSGESLP | GSPTHSLSPR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SPTPSYRSTP | DFPSGTNSSQ | SSSPSSSAPN | SPAGSGHIRP | STLHGLAPKL | GGQRYRSGRR | KSAGNIPLSP | LARTPSPTPQ |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PTSPQRSPSP | LLGHSLGNSK | IAQAFPSKMH | SPPTIVRHIV | RPKSAEPPRS | PLLKRVQSEE | KLSPSYGSDK | KHLCSRKHSL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EVTQEEVQRE | QSQREAPLQS | LDENVCDVPP | LSRARPVEQG | CLKRPVSRKV | GRQESVDDLD | RDKLKAKVVV | KKADGFPEKQ |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ESHQKSHGPG | SDLENFALFK | LEEREKKVYP | KAVERSSTFE | NKASMQEAPP | LGSLLKDALH | KQASVRASEG | AMSDGRVPAE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| HRQGGGDFRR | APAPGTLQDG | LCHSLDRGIS | GKGEGTEKSS | QAKELLRCEK | LDSKLANIDY | LRKKMSLEDK | EDNLCPVLKP |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KMTAGSHECL | PGNPVRPTGG | QQEPPPASES | RAFVSSTHAA | QMSAVSFVPL | KALTGRVDSG | TEKPGLVAPE | SPVRKSPSEY |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KLEGRSVSCL | KPIEGTLDIA | LLSGPQASKT | ELPSPESAQS | PSPSGDVRAS | VPPVLPSSSG | KKNDTTSARE | LSPSSLKMNK |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| SYLLEPWFLP | PSRGLQNSPA | VSLPDPEFKR | DRKGPHPTAR | SPGTVMESNP | QQREGSSPKH | QDHTTDPKLL | TCLGQNLHSP |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| DLARPRCPLP | PEASPSREKP | GLRESSERGP | PTARSERSAA | RADTCREPSM | ELCFPETAKT | SDNSKNLLSV | GRTHPDFYTQ |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| TQAMEKAWAP | GGKTNHKDGP | GEARPPPRDN | SSLHSAGIPC | EKELGKVRRG | VEPKPEALLA | RRSLQPPGIE | SEKSEKLSSF |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| PSLQKDGAKE | PERKEQPLQR | HPSSIPPPPL | TAKDLSSPAA | RQHCSSPSHA | SGREPGAKPS | TAEPSSSPQD | PPKPVAAHSE |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| SSSHKPRPGP | DPGPPKTKHP | DRSLSSQKPS | VGATKGKEPA | TQSLGGSSRE | GKGHSKSGPD | VFPATPGSQN | KASDGIGQGE |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| GGPSVPLHTD | RAPLDAKPQP | TSGGRPLEVL | EKPVHLPRPG | HPGPSEPADQ | KLSAVGEKQT | LSPKHPKPST | VKDCPTLCKQ |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| TDNRQTDKSP | SQPAANTDRR | AEGKKCTEAL | YAPAEGDKLE | AGLSFVHSEN | RLKGAERPAA | GVGKGFPEAR | GKGPGPQKPP |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| TEADKPNGMK | RSPSATGQSS | FRSTALPEKS | LSCSSSFPET | RAGVREASAA | SSDTSSAKAA | GGMLELPAPS | NRDHRKAQPA |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2513 | 1 | 694.6522 | -36.12 | 3 | 59.7 | 10.7 | 0 | 1135-1153 | R.EAPLQSLDENVCDVPPLSR.A | |

# Detailed Protein Report

**Protein 574:** **sushi domain-containing protein 1 isoform 3 precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|544063419 | **Score:** | 26.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 80.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MGRGPWDAGP SRRLLPLLLL LGLARGAAGA PGPDGLDVCA TCHEHATCQQ REGKKICICN YGFVGNGRTQ CVDKNECQFG
        90        100        110        120        130        140        150        160
ATLVCGNHTS CHNTPGGFYC ICLEGYRATN NNKTFIPNDG TFCTDIDECE VSGLCRHGGR CVNTHGSFEC YCMDGYLPRN
       170        180        190        200        210        220        230        240
GPEPFHPTTD ATSCTEIDCG TPPEVPDGYI IGNYTSSLGS QVRYACREGF FSVPEDTVSS CTGLGTWESP KLHCQEINCG
       250        260        270        280        290        300        310        320
NPPEMRHAIL VGNHSSRLGG VARYVCQEGF ESPGGKITSV CTEKGTWRES TLTCTEILTK INDVSLFNDT CVRWQINSRR
       330        340        350        360        370        380        390        400
INPKISYVIS IKGQRLDPME SVREETVNLT TDSRTPEVCL ALYPGTNYTV NISTAPPRRS MPAVIGFQTA EVDLLEDDGS
       410        420        430        440        450        460        470        480
FNISIFNETC LKLNRRSRKV GSEHMYQFTV LGQRWYLANF SHATSFNFTT REQVPVVCLD LYPTTDYTVN VTLLRSPKRH
       490        500        510        520        530        540        550        560
SVQITIATPP AVKQTISNIS GFNETCLRWR SIKTADMEEM YLFHIWGQRW YQKEFAQEMT FNISSSSRDP EVCLDLRPGT
       570        580        590        600        610        620        630        640
NYNVSLRALS SELPVVISLT TQITEPPLPE VEFFTVHRGP LPRLRLRKAK EKNGPISSYQ VLVLPLALQS TFSCDSEGAS
       650        660        670        680        690        700        710        720
SFFSNASDAD GYVAAELLAK DVPDDAMEIP IGDRLYYGEY YNAPLKRGSD YCIILRITSE WNKIRHSCCC RWRVLDWVPW
       730
LL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 893 | 1 | 736.8280 | -19.37 | 2 | 41.2 | 11.4 | 0 | 56-68 | K.ICICNYGFVGNGR.T | Carbamidomethyl: 4 |

# Detailed Protein Report

## Protein 575: PREDICTED: coiled-coil domain-containing protein 111 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578808887 | **Score:** | 26.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 58.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.8 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.36 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.06 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MNRKWEAKLK QIEERASHYE RKPLSSVYRP RLSKPEEPPS IWRLFHRQAQ AFNFVKSCKE DVHVFALECK VGDGQRIYLV

        90        100        110        120        130        140        150        160
TTYAEFWFYY KSRKNLLHCY EVIPENAVCK LYFDLEFNKP ANPGADGKKM VALLIEYVCK ALQELYGVNC SAEDVLNLDS

       170        180        190        200        210        220        230        240
STDEKFSRHL IFQLHDVAFK DNIHVGNFLR KILQPALDLL GSEDDDSAPE TTGHGFPHFS EAPARQGFSF NKMFTEKATE

       250        260        270        280        290        300        310        320
ESWTSNSKKL ERLGSAEQSS PDLSFLVVKN NMGEKHLFVD LGVYTRNRNF RLYKSSKIGK RVALEVTEDN KFFPIQSKDV

       330        340        350        360        370        380        390        400
SDEYQYFLSS LVSNVRFSDT LRILTCEPSQ NKQKGVGYFN SIGTSVETIE GFQCSPYPEV DHFVLSLVNK DGIKGGIRRW

       410        420        430        440        450        460        470        480
NYFFPEELLV YDICKYRWCE NIGRAHKSNN IMILVDLKNE VWYQKCHDPV CKAENFKSDC FPLPAEVCLL FLFKELDCPL

       490        500        510
VKKLNPPLLF RRGVLKSMCT EL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1088 | 1 | 540.6458 | -238.97 | 2 | 43.2 | 12.3 | 1 | 493-502 | R.GVLKSMCTEL.- | | QU:MU 2.36<br>WUP:QUP 0.06 |

# Detailed Protein Report

## Protein 576: ubiquitin carboxyl-terminal hydrolase 12 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|301500675 | **Score:** | 26.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 42.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 7.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEILMTVSKF | ASICTMGANA | SALEKEIGPE | QFPVNEHYFG | LVNFGNTCYC | NSVLQALYFC | RPFREKVLAY | KSQPRKKESL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LTCLADLFHS | IATQKKKVGV | IPPKKFITRL | RKENELFDNY | MQQDAHEFLN | YLLNTIADIL | QEERKQEKQN | GRLPNGNIDN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ENNNSTPDPT | WVHEIFQGTL | TNETRCLTCE | TISSKDEDFL | DLSVDVEQNT | SITHCLRGFS | NTETLCSEYK | YYCEECRSKQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EAHKRMKVKK | LPMILALHLK | RFKYMDQLHR | YTKLSYRVVF | PLELRLFNTS | GDATNPDRMY | DLVAVVVHCG | SGPNRGHYIA |
| 330 | 340 | 350 | 360 | 370 | 380 | | |
| IVKSHDFWLL | FDDDIVEKID | AQAIEEFYGL | TSDISKNSES | GYILFYQSRD | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 620 | 1 | 647.6390 | -191.68 | 2 | 36.2 | 14.2 | 1 | 231-239 | K.YYCEECRSK.Q | Carbamidomethyl: 3, 6 |

# Detailed Protein Report

**Protein 577:** **PREDICTED: RING finger protein 32 isoform X5 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578813915 | **Score:** | 26.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 9.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLKNKGHSSK | KDNLAVNAVA | LQDHILHDLQ | LRNLSVADHS | KTQVQKKENK | SLKRDTKAII | DTGLKKTTQC | PKLEDSEKEY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VLDPKPPPLT | LAQKLGLIGP | PPPPLSSDEW | EKVKQRSLLQ | GDSVQPCPIC | KEEFELRPQV | LLSCSHVFHK | ACLQAFEKFT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NKKTCPLCRK | NQYQTRVIHD | GARLFRIKCV | TRIQAYWRGC | VVRKWYRNLR | KTVPPTDAKL | RKKFFEKKTQ | DWKPA |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 428 | 1 | 862.8357 | -97.27 | 2 | 35.3 | 14.1 | 2 | 164-176 | K.TCPLCRKNQYQTR.V | Carbamidomethyl: 2, 5 |

# Detailed Protein Report

**Protein 578:** **PREDICTED: putative Polycomb group protein ASXL2 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578802980 | **Score:** | 26.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 125.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.8 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKRTKCADID | VETPDSILVN | TNLRALINKH | TFSVLPGDCQ | QRLLLLLPEV | DRQVGPDGLM | KLNGSALNNE | FFTSAAQGWK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ERLSEGEFTP | EMQVRIRQEI | EKEKKVEPWK | EQFFESYYGQ | SSGLSLEDSK | KLTASPSDPK | VKKTPAEQPK | SMPVSEASLI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RIVPVVSQSE | CKEEALQMSS | PGRKEECESQ | GEVQPNFSTS | SEPLLSSALN | THELSSILPI | KCPKDEDLLE | QKPVTSAEQE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SEKNHLTTAS | NYNKSESQES | LVTSPSKPKS | PGVEKPIVKP | TAGAGPQETN | MKEPLATLVD | QSPESLKRKS | SLTQEEAPVS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WEKRPRVTEN | RQHQQPFQVS | PQPFLNRGDR | IQVRKVPPLK | IPVSRISPMP | FHPSQVSPRA | RFPVSITSPN | RTGARTLADI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KAKAQLVKAQ | RAAAAAAAAA | AAAASVGGTI | PGPGPGGGQG | PGEGGEGQTA | RGGSPGSDRV | SETGKGPTLE | LAGTGSRGGT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RELLPCGPET | QPQSETKTTP | SQAQPHSVSG | AQLQQTPPVP | PTPAVSGACT | SVPSPAHIEK | LDNEKLNPTR | ATATVASVSH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PQGPSSCRQE | KAPSPTGPAL | ISGASPVHCA | ADGTVELKAG | PSKNIPNPSA | SSKTDASVPV | AVTPSPLTSL | LTTATLEKLP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VPQVSATTAP | AGSAPPSSTL | PAASSLKTPG | TSLNMNGPTL | RPTSSIPANN | PLVTQLLQGK | DVPMEQILPK | PLTKVEMKTV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PLTAKEERGM | GALIATNTTE | NSTREEVNER | QSHPATQQQL | GKTLQSKQLP | QVPRPLQLFS | AKELRDSSID | THQYHEGLSK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ATQDQILQTL | IQRVRRQNLL | SVVPPSQFNF | AHSGFQLEDI | STSQRFMLGF | AGRRTSKPAM | AGHYLLNIST | YGRGSESFRR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| THSVNPEDRF | CLSSPTEALK | MGYTDCKNAT | GESSSSKEDD | TDEESTGDEQ | ESVTVKEEPQ | VSQSAGKGDT | SSGPHSRETL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| STSDCLASKN | VKAEIPLNEQ | TTLSKENYLF | TRGQTFDEKT | LARDLIQAAQ | KQMAHAVRGK | AIRSSPELFS | STVLPLPADS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PTHQPLLLPP | LQTPKLYGSP | TQIGPSYRGM | INVSTSSDMD | HNSAVPGSQV | SSNVGDVMSF | SVTVTTIPAS | QAMNPSSHGQ |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | | |
| TIPVQAFSEE | NSIEGTPSKC | YCRLKAMIMC | KGCGAFCHDD | CIGPSKLCVS | CLVVR | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 326 | 1 | 761.7364 | -167.46 | 2 | 34.1 | 10.4 | 0 | 83-95 | R.LSEGEFTPEMQVR.I | |

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# Detailed Protein Report

## Protein 579: PREDICTED: inositol 1,4,5-trisphosphate receptor type 2 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578822836 | **Score:** | 26.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 212.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTEKMSSFLY | IGDIVSLYAE | GSVNGFISTL | GLVDDRCVVH | PEAGDLANPP | KKFRDCLFKV | CPMNRYSAQK | QYWKAKQAKQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GNHTEAALLK | KLQHAAELEQ | KQNESENKKL | LGEIVKYSNV | IQLLHIKSNK | YLTVNKRLPA | LLEKNAMRVS | LDAAGNEGSW |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FYIHPFWKLR | SEGDNIVVGD | KVVLMPVNAG | QPLHASNIEL | LDNPGCKEVN | AVNCNTSWKI | TLFMKYSSYR | EDVLKGGDVV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RLFHAEQEKF | LTCDEYEKKQ | HIFLRTTLRQ | SATSATSSKA | LWEIEVVHHD | PCRGGAGQWN | SLFRFKHLAT | GNYLAAELNP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DYRDAQNEGK | NVRDGVPPTS | KKKRQAGEKI | MYTLVSVPHG | NDIASLFELD | ATTLQRADCL | VPRNSYVRLR | HLCTNTWVTS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TSIPIDTDEE | RPVMLKIGTC | QTKEDKEAFA | IVSVPLSEVR | DLDFANDANK | VLATTVKKLE | NGTITQNERR | FVTKLLEDLI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FFVADVPNNG | QEVLDVVITK | PNRERQKLMR | EQNILAQVFG | ILKAPFKEKA | GEGSMLRLED | LGDQRYAPYK | YMLRLCYRVL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RHSQQDYRKN | QEYIAKNFCV | MQSQIGYDIL | AEDTITALLH | NNRKLLEKHI | TAKEIETFVS | LLRRNREPRF | LDYLSDLCVS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NTTAIPVTQE | LICKFMLSPG | NADILIQTKV | VSMQADNPME | SSILSDDIDD | EEVWLYWIDS | NKEPHGKAIR | HLAQEAKEGT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KADLEVLTYY | RYQLNLFARM | CLDRQYLAIN | QISTQLSVDL | ILRCVSDESL | PFDLRASFCR | LMLHMHVDRD | PQESVVPVRY |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ARLWTEIPTK | ITIHEYDSIT | DSSRNDMKRK | FALTMEFVEE | YLKEVVNQPF | PFGDKEKNKL | TFEVVHLARN | LIYFGFYSFS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ELLRLTRTLL | AILDIVQAPM | SSYFERLSKF | QDGGNNVMRT | IHGVGEMMTQ | MVLSRGSIFP | MSVPDVPPSI | HPSKQGSPTE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| HEDVTVMDTK | LKIIEILQFI | LSVRLDYRIS | YMLSIYKKEF | GEDNDNAETS | ASGSPDTLLP | SAIVPDIDEI | AAQAETMFAG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RKEKNPVQLD | DEGGRTFLRV | LIHLIMHDYP | PLLSGALQLL | FKHFSQRAEV | LQAFKQVQLL | VSNQDVDNYK | QIKADLDQLR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LTVEKSELWV | EKSSNYENGE | IGESQVKGGE | EPIEESNILS | PVQDGTKKPQ | IDSNKSNNYR | IVKEILIRLS | KLCVQNKKCR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| NQHQRLLKNM | GAHSVVLDLL | QIPYEKNDEK | MNEVMNLAHT | FLQNFCRGNP | QNQVLLHKHL | NLFLTPGLLE | AETMRHIFMN |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| NYHLCNEISE | RVVQHFVHCI | ETHGRHVEYL | RFLQTIVKAD | GKYVKKCQDM | VMTELINGGE | DVLIFYNDRA | SFPILLHMMC |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| SERDRGDESG | PLAYHITLVE | LLAACTEGKN | VYTEIKCNSL | LPLDDIVRVV | THDDCIPEVK | IAYVNFVNHC | YVDTEVEMKE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| IYTSNHIWKL | FENFLVDMAR | VCNTTTDRKH | ADIFLEKCVT | ESIMNIVSGF | FNSPFSDNST | SLQTHQPVFI | QLLQSAFRIY |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| NCTWPNPAQK | ASVESCIRTL | AEVAKNRGIA | IPVDLDSQVN | TLFMKSHSNM | VQRAAMGWRL | SARSGPRFKE | ALGGPAWDYR |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| NIIEKLQDVV | ASLEHQFSPM | MQAEFSVLVD | VLYSPELLFP | EGSDARIRCG | AFMSKLINHT | KKLMEKEEKL | CIKILQTLRE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| MLEKKDSFVE | EGNTLRKILL | NRYFKGDYSI | GVNGHLSGAY | SKTAQVGGSF | SGQDSDKMGI | SMSDIQCLLD | KEGASELVID |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| VIVNTKNDRI | FSEGIFLGIA | LLEGGNTQTQ | YSFYQQLHEQ | KKSEKFFKVL | YDRMKAAQKE | IRSTVTVNTI | DLGNKKRDDD |
| 1850 | 1860 | 1870 | | | | | |
| NELMTSGPRM | REFWSWGDPK | TALQD | | | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 725 | 1 | 771.2336 | -342.03 | 1 | 39.0 | 11.8 | 0 | 110-116 | K.LLGEIVK.Y | |
| 1690 | 4 | 648.2368 | -188.91 | 2 | 51.4 | 14.8 | 2 | 1199-1208 | K.CRNQHQRLLK.N | |

# Detailed Protein Report

## Protein 580: zinc finger protein 570 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21389599 | **Score:** | 26.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 62.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 7.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAVGLLKAMY | QELVTFRDVA | VDFSQEEWDC | LDSSQRHLYS | NVMLENYRIL | VSLGLCFSKP | SVILLLEQGK | APWMVKRELT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KGLCSGWEPI | CETEELTPKQ | DFYEEHQSQK | IIETLTSYNL | EYSSLREEWK | CEGYFERQPG | NQKACFKEEI | ITHEEPLFDE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| REQEYKSWGS | FHQNPLLCTQ | KIIPKEEKVH | KHDTQKRSFK | KNLMAIKPKS | VCAEKKLLKC | NDCEKVFSQS | SSLTLHQRIH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TGEKPYKCIE | CGKAFSQRSN | LVQHQRIHTG | EKPYECKECR | KAFSQNAHLV | QHLRVHTGEK | PYECKVCRKA | FSQFAYLAQH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QRVHTGEKPY | ECIECGKAFS | NRSSIAQHQR | VHTGEKPYEC | NVCGKAFSLR | AYLTVHQRIH | TGERPYECKE | CGKAFSQNSH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LAQHQRIHTG | EKPYKCQECR | KAFSQIAYLA | QHQRVHTGEK | PYECIECGKA | FSNDSSLTQH | QRVHTGEKPY | ECTVCGKAFS |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| YCGSLAQHQR | IHTGERPYEC | KECKKTFRQH | AHLAHHQRIH | IGESLSPPNP | VNHQVL | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 17 | 1 | 1103.4962 | -28.67 | 2 | 29.9 | 11.4 | 1 | 144-161 | K.ACFKEEIITHEEPLFDER.E | |

# Detailed Protein Report

## Protein 581: cyclic nucleotide-gated cation channel beta-1 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|554790418 | **Score:** | 26.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 139.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| | | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.40 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.56 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLGWVQRVLP | QPPGTPRKTK | MQEEEEVEPE | PEMEAEVEPE | PNPEEAETES | ESMPPEESFK | EEEVAVADPS | PQETKEAALT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| STISLRAQGA | EISEMNSPSR | RVLTWLMKGV | EKVIPQPVHS | ITEDPAQILG | HGSTGDTGCT | DEPNEALEAQ | DTRPGLRLLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WLEQNLERVL | PQPPKSSEVW | RDEPAVATAP | PGRPQEMGPK | LQARETPSLP | TPIPLQPKEE | PKEAPAPEPQ | PGSQAQTSSL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PPTRDPARLV | AWVLHRLEMA | LPQPVLHGKI | GEQEPDSPGI | CDVQTISILP | GGQVEPDLVL | EEVEPPWEDA | HQDVSTSPQG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TEVVPAYEEE | NKAVEKMPRE | LSRIEEEKED | EEEEEEEEEE | EEEEEVTEVL | LDSCVVSQVG | VGQSEEDGTR | PQSTSDQKLW |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EEVGEEAKKE | AEEKAKEEAE | EVAEEEAEKE | PQDWAETKEE | PEAEAEAASS | GVPATKQHPE | VQVEDTDADS | CPLMAEENPP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| STVLPPPSPA | KSDTLIVPSS | ASGTHRKKLP | SEDDEAEELK | ALSPAESPVV | AWSDPTTPKD | TDGQDRAAST | ASTNSAIIND |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RLQELVKLFK | ERTEKVKEKL | IDPDVTSDEE | SPKPSPAKKA | PEPAPDTKPA | EAEPVEEEHY | CDMLCCKFKH | RPWKKYQFPQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SIDPLTNLMY | VLWLFFVVMA | WNWNCWLIPV | RWAFPYQTPD | NIHHWLLMDY | LCDLIYFLDI | TVFQTRLQFV | RGGDIITDKK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DMRNNYLKSR | RFKMDLLSLL | PLDFLYLKVG | VNPLLRLPRC | LKYMAFFEFN | SRLESILSKA | YVYRVIRTTA | YLLYSLHLNS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| CLYYWASAYQ | GLGSTHWVYD | GVGNSYIRCY | YFAVKTLITI | GGLPDPKTLF | EIVFQLLNYF | TGVFAFSVMI | GQMRDVVGAA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TAGQTYYRSC | MDSTVKYMNF | YKIPKSVQNR | VKTWYEYTWH | SQGMLDESEL | MVQLPDKMRL | DLAIDVNYNI | VSKVALFQGC |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DRQMIFDMLK | RLRSVVYLPN | DYVCKKGEIG | REMYIIQAGQ | VQVLGGPDGK | SVLVTLKAGS | VFGEISLLAV | GGGNRRTANV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VAHGFTNLFI | LDKKDLNEIL | VHYPESQKLL | RKKARRMLRS | NNKPKEEKSV | LILPPRAGTP | KLFNAALAMT | GKMGGKGAKG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GKLAHLRARL | KELAALEAAA | KQQELVEQAK | SSQDVKGEEG | SAAPDQHTHP | KEAATDPPAP | RTPPEPPGSP | PSSPPPASLG |
| 1210 | 1220 | 1230 | 1240 | 1250 | | | |
| RPEGEEEGPA | EPEEHSVRIC | MSPGPEPGEQ | ILSVKMPEER | EEKAE | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1888 | 3 | 612.7759 | -142.99 | 2 | 54.0 | 15.4 | 0 | 836-847 | K.TLITIGGLPDPK.T | | QU:MU 0.40<br>WUP:QUP 2.56 |
| 1512 | 1 | 851.5801 | 69.44 | 1 | 48.6 | 11.1 | 1 | 1120-1127 | K.GGKLAHLR.A | | |

# Detailed Protein Report

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**Protein 582:** **PREDICTED: alpha-N-acetylneuraminide alpha-2,8-sialyltransferase isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530399363 | **Score:** | 26.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 23.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.8 |
| | | **Sequence Coverage [%]:** | 13.2 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSPCGRARRQ | TSRGAMAVLA | WKFPRTRLPM | GASALCVVVL | CWLYIFPVYR | LPNEKEIVQG | VLQQGTAWRR | NQTAARAFRK |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| QMEDCCDPAH | LFAMTKMNSP | MGKSMWYDGE | FLYSFTIDNS | TYSLFPQATP | FQLPLKKCAV | VGNGGILKKS | GCGRQIDEAN |
| **170** | **180** | **190** | **200** | **210** | | | |
| FVMRCNLPPL | SSEYTKDVGS | KSQLVTANPS | IIRQRDFTAV | ERVKK | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 550 | 1 | 581.8032 | -38.57 | 2 | 36.9 | 10.8 | 2 | 71-80 | R.NQTAARAFRK.Q | |

# Detailed Protein Report

## Protein 583: RNA 3'-terminal phosphate cyclase isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|195927044 | **Score:** | 26.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 7.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 1.59 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAGPRVEVDG | SIMEGGGQIL | RVSTALSCLL | GLPLRVQKIR | AGRSTPGLSS | GGWKSKIKVL | TRPQHLSGLE | MIRDLCDGQL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EGAEIGSTEI | TFTPEKIKGG | IHTADTKTAG | SVCLLMQVSM | PCVLFAASPS | ELHLKGGTNA | EMAPQIDYTV | MVFKPIVEKF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GFIFNCDIKT | RGYYPKGGGE | VIVRMSPVKQ | LNPINLTERG | CVTKIYGRAF | VAGVLPFKVA | KDMAAAAVRC | IRKEIRDLYV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NIQPVQEPKD | QAFGNGNGII | IIAETSTGCL | FAGSSLGKRG | VNADKVGIEA | AEMLLANLRH | GGTVDEYLQD | QLIVFMALAN |
| 330 | 340 | 350 | 360 | 370 | 380 | | |
| GVSRIKTGPV | TLHTQTAIHF | AEQIAKAKFI | VKKSEDEEDA | AKDTYIIECQ | GIGMTNPNL | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2681 | 1 | 559.7841 | -33.68 | 2 | 64.6 | 11.9 | 1 | 219-229 | K.VAKDMAAAAVR.C | Oxidation: 5 | WUP:QUP 1.59 |

# Detailed Protein Report

## Protein 584: PREDICTED: DNA polymerase zeta catalytic subunit isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530383948 | **Score:** | 26.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 301.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 0.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFSVRIVTAD | YYMASPLQGL | DTCQSPLTQA | PVKKVPVVRV | FGATPAGQKT | CLHLHGIFPY | LYVPYDGYGQ | QPESYLSQMA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FSIDRALNVA | LGNPSSTAQH | VFKVSLVSGM | PFYGYHEKER | HFMKIYLYNP | TMVKRICELL | QSGAIMNKFY | QPHEAHIPYL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LQLFIDYNLY | GMNLINLAAV | KFRKARRKSN | TLHATGSCKN | HLSGNSLADT | LFRWEQDEIP | SSLILEGVEP | QSTCELEVDA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VAADILNRLD | IEAQIGGNPG | LQAIWEDEKQ | RRRNRNETSQ | MSQPESQDHR | FVPATESEKK | FQKRLQEILK | QNDFSVTLSG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SVDYSDGSQE | FSAELTLHSE | VLSPEMLQCT | PANMVEVHKD | KESSKGHTRH | KVEEALINEE | AILNLMENSQ | TFQPLTQRLS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ESPVFMDSSP | DEALVHLLAG | LESDGYRGER | NRMPSPCRSF | GNNKYPQNSD | DEENEPQIEK | EEMELSLVMS | QRWDSNIEEH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CAKKRSLCRN | THRSSTEDDD | SSSGEEMEWS | DNSLLLASLS | IPQLDGTADE | NSDNPLNNEN | SRTHSSVIAT | SKLSVKPSIF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HKDAATLEPS | SSAKITFQCK | HTSALSSHVL | NKEDLIEDLS | QTNKNTEKGL | DNSVTSFTNE | STYSMKYPGS | LSSTVHSENS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HKENSKKEIL | PVSSCESSIF | DYEEDIPSVT | RQVPSRKYTN | IRKIEKDSPF | IHMHRHPNEN | TLGKNSFNFS | DLNHSKNKVS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SEGNEKGNST | ALSSLFPSSF | TENCELLSCS | GENRTMVHSL | NSTADESGLN | KLKIRYEEFQ | EHKTEKPSLS | QQAAHYMFFP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SVVLSNCLTR | PQKLSPVTYK | LQPGNKPSRL | KLNKRKLAGH | QETSTKSSET | GSTKDNFIQN | NPCNSNPEKD | NALASDLTKT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TRGAFENKTP | TDGFIDCHFG | DGTLETEQSF | GLYGNKYTLR | AKRKVNYETE | DSESSFVTHN | SKISLPHPME | IGESLDGTLK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SRKRRKMSKK | LPPVIIKYII | INRFRGRKNM | LVKLGKIDSK | EKQVILTEEK | MELYKKLAPL | KDFWPKVPDS | PATKYPIYPL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TPKKSHRRKS | KHKSAKKKTG | KQQRTNNENI | KRTLSFRKKR | SHAILSPPSP | SYNAETEDCD | LNYSDVMSKL | GFLSERSTSP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| INSSPPRCWS | PTDPRAEEIM | AAAEKEAMLF | KGPNVYKKTV | NSRIGKTSRA | RAQIKKSKAK | LANPSIVTKK | RNKRNQTNKL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VDDGKKKPRA | KQKTNEKGTS | RKHTTLKDEK | IKSQSGAEVK | FVLKHQNVSE | FASSSGGSQL | LFKQKDMPLM | GSAVDHPLSA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SLPTGINAQQ | KLSGCFSSFL | ESKKSVDLQT | FPSSRDDLHP | SVVCNSIGPG | VSKINVQRPH | NQSAMFTLKE | STLIQKNIFD |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LSNHLSQVAQ | NTQISSGMSS | KIEDNANNIQ | RNYLSSIGKL | SEYRNSLESK | LDQAYTPNFL | HCKDSQQQIV | CIAEQSKHSE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| TCSPGNTASE | ESQMPNNCFV | TSLRSPIKQI | AWEQKQRGFI | LDMSNFKPER | VKPRSLSEAI | SQTKALSQCK | NRNVSTPSAF |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| GEGQSGLAVL | KELLQKRQQK | AQNANTTQDP | LSNKHQPNKN | ISGSLEHNKA | NKRTRSVTSP | RKPRTPRSTK | QKEKIPKLLK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| VDSLNLQNSS | QLDNSVSDDS | PIFFSDPGFE | SCYSLEDSLS | PEHNYNFDIN | TIGQTGFCSF | YSGSQFVPAD | QNLPQKFLSD |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| AVQDLFPGQA | IEKNEFLSHD | NQKCDEDKHH | TTDSASWIRS | GTLSPEIFEK | STIDSNENRR | HNQWKNSFHP | LTTRSNSIMD |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SFCVQQAEDC | LSEKSRLNRS | SVSKEVFLSL | PQPNNSDWIQ | GHTRKEMGQS | LDSANTSFTA | ILSSPDGELV | DVACEDLELY |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| VSRNNDMLTP | TPDSSPRSTS | SPSQSKNGSF | TPRTANILKP | LMSPPSREEI | MATLLDHDLS | ETIYQEPFCS | NPSDVPEKPR |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| EIGGRLLMVE | TRLANDLAEF | EGDFSLEGLR | LWKTAFSAMT | QNPRPGSPLR | SGQGVVNKGS | SNSPKMVEDK | KIVIMPCKCA |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| PSRQLVQVWL | QAKEEYERSK | KLPKTKPTGV | VKSAENFSSS | VNPDDKPVVP | PKMDVSPCIL | PTTAHTKEDV | DNSQIALQAP |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| TTGCSQTASE | SQMLPPVASA | SDPEKDEDDD | DNYYISYSSP | DSPVIPPWQQ | PISPDSKALN | GDDRPSSPVE | ELPSLAFENF |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 727 | 2 | 517.1500 | -168.10 | 2 | 37.5 | 14.5 | 1 | 431-438 | R.NRMPSPCR.S | Carbamidomethyl: 7;<br>Oxidation: 3 |

# Detailed Protein Report

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## Protein 585: zinc finger protein 865 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|307219238 | **Score:** | 26.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 111.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.6 |
|  |  | **Sequence Coverage [%]:** | 2.7 |
|  |  | **No. of unique Peptides:** | 2 |

## Quantitation

***QU:MU*** **Median:** 1.21 **CV:** 0.00 % **No. of Peptides:** 1

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEANPAGSGA | GGGGSSGIGG | EDGVHFQSYP | FDFLEFLNHQ | RFEPMELYGE | HAKAVAALPC | APGPPPQPPP | QPPPPQYDYP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PQSTFKPKAE | VPSSSSSSSS | SSSSSSSSSS | SSSSSSSQAK | KPDPPLPPAF | GAPPPPLFDA | AFPTPQWGIV | DLSGHQHLFG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NLKRGGPASG | PGVTPGLGAP | AGAPGPLPAP | SQTPPGPPAA | AACDPTKDDK | GYFRRLKYLM | ERRFPCGVCQ | KSFKQSSHLV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QHMLVHSGER | PYECGVCGRT | YNHVSSLIRH | RRCHKDVPPA | AGGPPQPGPH | LPPLGLPAPA | ASAATAAAPS | TVSSGPPATP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VAPAPSADGS | AAPAGVGVPP | PATGGGDGPF | ACPLCWKVFK | KPSHLHQHQI | IHTGEKPFSC | SVCSKSFNRR | ESLKRHVKTH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SADLLRLPCG | ICGKAFRDAS | YLLKHQAAHA | GAGAGGPRPV | YPCDLCGKSY | SAPQSLLRHK | AAHAPPAAAA | EAPKDGAASA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PQPPPTFPPG | PYLLPPDPPT | TDSEKAAAAA | AAVVYGAVPV | PLLGAHPLLL | GGAGTSGAGG | SGASVPGKTF | CCGICGRGFG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RRETLKRHER | IHTGEKPHQC | PVCGKRFRES | FHLSKHHVVH | TRERPYKCEL | CGKVFGYPQS | LTRHRQVHRL | QLPCALAGAA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GLPSTQGTPG | ACGPGASGTS | AGPTDGLSYA | CSDCGEHFPD | LFHVMSHKEV | HMAEKPYGCD | ACGKTFGFIE | NLMWHKLVHQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AAPERLLPPA | PGGLQPPDGS | SGTDAASVLD | NGLAGEVGAA | VAALAGVSGG | EDAGGAAVAG | AGGGASSGPE | RFSCATCGQS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FKHFLGLVTH | KYVHLVRRTL | GCGLCGQSFA | GAYDLLLHRR | SHRQKRGFRC | PVCGKRFWEA | ALLMRHQRCH | TEQRPYRCGV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| CGRGFLRSWY | LRQHRVVHTG | ERAFKCGVCA | KRFAQSSSLA | EHRRLHAVAR | PQRCSACGKT | FRYRSNLLEH | QRLHLGERAY |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RCEHCGKGFF | YLSSVLRHQR | AHEPPRPELR | CPACLKAFKD | PGYFRKHLAA | HQGGRPFRCS | SCGEGFANTY | GLKKHRLAHK |
| 1050 | 1060 |  |  |  |  |  |  |
| AENLGGPGAG | AGTLAGKDA |  |  |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 10 | 2 | 819.8432 | -130.81 | 2 | 29.6 | 16.4 | 2 | 260-272 | R.TYNHVSSLIRHRR.C |  |  |
| 2279 | 1 | 869.2738 | -114.47 | 2 | 58.9 | 10.1 | 0 | 689-704 | K.EVHMAEKPYGCDACGK.T |  | QU:MU 1.21 |

# Detailed Protein Report

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## Protein 586: zinc finger protein 20 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|322303718 | **Score:** | 26.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 61.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDSVAFEDVA | VSFTQEEWAL | LDPSQKNLYR | DVMQETFKNL | TSVGKTWKVQ | NIEDEYKNPR | RNLSLMREKL | CESKESHHCG |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| ESFNQIADDM | LNRKTLPGIT | PCESSVCGEV | GTGHSSLNTH | IRADTGHKSS | EYQEYGENPY | RNKECKKAFS | YLDSFQSHDK |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| ACTKEKPYDG | KECTETFISH | SCIQRHRVMH | SGDGPYKCKF | CGKAFYFLNL | CLIHERIHTG | VKPYKCKQCG | KAFTRSTTLP |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| VHERTHTGVN | ADECKECGNA | FSFPSEIRRH | KRSHTGEKPY | ECKQCGKVFI | SFSSIQYHKM | THTGEKPYEC | KQCGKAFRCG |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| SHLQKHGRTH | TGEKPYECRQ | CGKAFRCTSD | LQRHEKTHTE | DKPYGCKQCG | KGFRCASQLQ | IHERTHSGEK | PHECKECGKV |
| **410** | **420** | **430** | **440** | **450** | **460** | **470** | **480** |
| FKYFSSLRIH | ERTHTGEKPH | ECKQCGKAFR | YFSSLHIHER | THTGDKPYEC | KVCGKAFTCS | SSIRYHERTH | TGEKPYECKH |
| **490** | **500** | **510** | **520** | **530** | | | |
| CGKAFISNYI | RYHERTHTGE | KPYQCKQCGK | AFIRASSCRE | HERTHTINR | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2376 | 1 | 1130.4062 | -64.30 | 2 | 58.0 | 12.0 | 0 | 75-93 | K.ESHHCGESFNQIADDMLNR.K | Carbamidomethyl: 5 |

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# Detailed Protein Report

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**Protein 587:** **ral GTPase-activating protein subunit alpha-1 isoform 1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|51226124 | **Score:** | 26.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 229.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MFSKKPHGDV KKSTQKVLDT KKDALTRLKH LRIVIENAES IDLKQFFDQH FSHIYYVFFE NFVTIEASLK QKGHKSQREE
        90        100        110        120        130        140        150        160
LDAILFIFEK ILQLLPERIH QRWQFHSIGL ILKKLLHTGN SLKIRREGVR LFLLWLQALQ NNCSKEQLWM FSCLIPGFSA
       170        180        190        200        210        220        230        240
PQSEHGPRTL DNLINPPLNL QETQVTIEEI TPLVPPQSGD KGQEDLTSYF LEALLKYIVI QVKSLEWKNK ENQERGFSFL
       250        260        270        280        290        300        310        320
FSHFKKYYLP YIFPNICKEN SLYHPILDIP QMRPKPHYVV IKKDAETNEA IYCTKEPFIK ARVIVIRWLV SFWLEPKPHT
       330        340        350        360        370        380        390        400
GPHIPGMEGE VLPKNIQRAA ASLVSREESK NDNADKTDRT TEPEQSHSNT STLTEREPSS SSLCSIDEEH LTDIEIVRRV
       410        420        430        440        450        460        470        480
FSSKRSNVNF VTEIFRQAFL LPICEAAAMR KVVKVYQEWI QQEEKPLFMQ EPEEIVITSS DLPCIENVTD HDISMEEGEK
       490        500        510        520        530        540        550        560
REEENGTNTA DHVRNSSWAK NGSYQGALHN ASEEATEQNI RAGTQAVLQV FIINSSNIFL LEPANEIKNL LDEHTDMCKR
       570        580        590        600        610        620        630        640
ILNIYRYMVV QVSMDKKTWE QMLLVLLRVT ESVLKMPSQA FLQFQGKKNM TLAGRLAGPL FQTLIVAWIK ANLNVYISRE
       650        660        670        680        690        700        710        720
LWDDLLSVLS SLTYWEELAT EWSLTMETLT KVLARNLYSL DLSDLPLDKL SEQKQKKHKG KGVGHEFQKV SVDKSFSRGW
       730        740        750        760        770        780        790        800
SRDQPGQAPM RQRSATTTGS PGTEKARSIV RQKTVDIDDA QILPRSTRVR HFSQSEETGN EVFGALNEEQ PLPRSSSTSD
       810        820        830        840        850        860        870        880
ILEPFTVERA KVNKEDMSQK LPPLNSDIGG SSANVPDLMD EFIAERLRSG NASTMTRRGS SPGSLEIPKD LPDILNKQNQ
       890        900        910        920        930        940        950        960
MRPIDDPGVP SEWTSPASAG SSDLISSDSH SDSFSAFQYD GRKFDNFGFG TDTGVTSSAD VDSGSGHHQS AEEQEVASLT
       970        980        990       1000       1010       1020       1030       1040
TLHIDSETSS LNQQAFSAEV ATITGSESAS PVHSPLGSRS QTPSPSTLNI DHMEQKDLQL DEKLHHSVLQ TPDDLEISEF
      1050       1060       1070       1080       1090       1100       1110       1120
PSECCSVMAG GTLTGWHADV ATVMWRRMLG ILGDVNSIMD PEIHAQVFDY LCELWQNLAK IRDNLGISTD NLTSPSPPVL
      1130       1140       1150       1160       1170       1180       1190       1200
IPPLRILTPW LFKATMLTDK YKQGKLHAYK LICNTMKRRQ DVSPNRDFLT HFYNIMHCGL LHIDQDIVNT IIKHCSPQFF
      1210       1220       1230       1240       1250       1260       1270       1280
SLGLPGATML IMDFIVAAGR VASSAFLNAP RVEAQVLLGS LVCFPNLYCE LPSLHPNIPD VAVSQFTDVK ELIIKTVLSS
      1290       1300       1310       1320       1330       1340       1350       1360
ARDEPSGPAR CVALCSLGIW ICEELVHESH HPQIKEALNV ICVSLKFTNK TVAHVACNML HMLVHYVPRL QIYQPDSPLK
      1370       1380       1390       1400       1410       1420       1430       1440
IIQILIATIT HLLPSTEASS YEMDKRLVVS LLLCLLDWIM ALPLKTLLQP FHATGAESDK TEKSVLNCIY KVLHGCVYGA
      1450       1460       1470       1480       1490       1500       1510       1520
QCFSNPRYFP MSLSDLASVD YDPFMHLESL KEPEPLHSPD SERSSKLQPV TEVKTQMQHG LISIAARTVI THLVNHLGHY
      1530       1540       1550       1560       1570       1580       1590       1600
PMSGGPAMLT SQVCENHDNH YSESTELSPE LFESPNIQFF VLNNTTLVSC IQIRSEENMP GGGLSAGLAS ANSNVRIIVR
      1610       1620       1630       1640       1650       1660       1670       1680
DLSGKYSWDS AILYGPPPVS GLSEPTSFML SLSHQEKPEE PPTSNECLED ITVKDGLSLQ FKRFRETVPT WDTIRDEEDV
      1690       1700       1710       1720       1730       1740       1750       1760
LDELLQYLGV TSPECLQRTG ISLNIPAPQP VCISEKQEND VINAILKQHT EEKEFVEKHF NDLNMKAVEQ DEPIPQKPQS
      1770       1780       1790       1800       1810       1820       1830       1840
AFYYCRLLLS ILGMNSWDKR RSFHLLKKNE KLLRELRNLD SRQCRETHKI AVFYVAEGQE DKHSILTNTG GSQAYEDFVA
      1850       1860       1870       1880       1890       1900       1910       1920
GLGWEVNLTN HCGFMGGLQK NKSTGLTTPY FATSTVEVIF HVSTRMPSDS DDSLTKKLRH LGNDEVHIVW SEHTRDYRRG
      1930       1940       1950       1960       1970       1980       1990       2000
IIPTEFGDVL IVIYPMKNHM FSIQIMKKPE VPFFGPLFDG AIVNGKVLPI MVRATAINAS RALKSLIPLY QNFYEERARY
      2010       2020       2030       2040
LQTIVQHHLE PTTFEDFAAQ VFSPAPYHHL PSDADH
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 800 | 1 | 709.3960 | 15.98 | 2 | 39.5 | 11.8 | 2 | 1-12 | -.MFSKKPHGDVKK.S | Oxidation: 1 |

# Detailed Protein Report

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## Protein 588: PREDICTED: poly [ADP-ribose] polymerase 14 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530374806 | **Score:** | 26.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 187.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.1 |
| | | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***WUP:QUP*** **Median:** 0.04 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEDIPEECEN | ISSLVAFENL | KANVTDIMLI | LLVENISGLS | NDDFQVEIIR | DFDVAVVTFQ | KHIDTIRFVD | DCTKHHSIKQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LQLSPRLLEV | TNTIRVENLP | PGADDYSLKL | FFENPYNGGG | RVANVEYFPE | ESSALIEFFD | RKVLDTIMAT | KLDFNKMPLS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VFPYYASLGT | ALYGKEKPLI | KLPAPFEESL | DLPLWKFLQK | KNHLIEEIND | EMRRCHCELT | WSQLSGKVTI | RPAATLVNEG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RPRIKTWQAD | TSTTLSSIRS | KYKVNPIKVD | PTMWDTIKND | VKDDRILIEF | DTLKEMVILA | GKSEDVQSIE | VQVRELIEST |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TQKIKREEQS | LKEKMIISPG | RYFLLCHSSL | LDHLLTECPE | IEICYDRVTQ | HLCLKGPSAD | VYKAKCEIQE | KVYTMAQKNI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QVSPEIFQFL | QQVNWKEFSK | CLFIAQKILA | LYELEGTTVL | LTSCSSEALL | EAEKQMLSAL | NYKRIEVENK | EVLHGKKWKG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LTHNLLKKQN | SSPNTVIINE | LTSETTAEVI | ITGCVKEVNE | TYKLLFNFVE | QNMKIERLVE | VKPSLVIDYL | KTEKKLFWPK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IKKVNVQVSF | NPENKQKGIL | LTGSKTEVLK | AVDIVKQVWD | SVCVKSVHTD | KPGAKQFFQD | KARFYQSEIK | RLFGCYIELQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ENEVMKEGGS | PAGQKCFSRT | VLAPGVVLIV | QQGDLARLPV | DVVVNASNED | LKHYGGLAAA | LSKAAGPELQ | ADCDQIVKRE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GRLLPGNATI | SKAGKLPYHH | VIHAVGPRWS | GYEAPRCVYL | LRRAVQLSLC | LAEKYKYRSI | AIPAISSGVF | GFPLGRCVET |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IVSAIKENFQ | FKKDGHCLKE | IYLVDVSEKT | VEAFAEAVKT | VFKATLPDTA | APPGLPPAAA | GPGKTSWEKG | SLVSPGGLQM |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LLVKEGVQNA | KTDVVVNSVP | LDLVLSRGPL | SKSLLEKAGP | ELQEELDTVG | QGVAVSMGTV | LKTSSWNLDC | RYVLHVVAPE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| WRNGSTSSLK | IMEDIIRECM | EITESLSLKS | IAFPAIGTGN | LGFPKNIFAE | LIISEVFKFS | SKNQLKTLQE | VHFLLHPSDH |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ENIQAFSDEF | ARRANGNLVS | DKIPKAKDTQ | GFYGTVSSPD | SGVYEMKIGS | IIFQVASGDI | TKEEADVIVN | STSNSFNLKA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GVSKAILECA | GQNVERECSQ | QAQQRKNDYI | ITGGGFLRCK | NIIHVIGGND | VKSSVSSVLQ | ECEKKNYSSI | CLPAIGTGNA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KQHPDKVAEA | IIDAIEDFVQ | KGSAQSVKKV | KVVIFLPQVL | DVFYANMKKR | EGTQLSSQQS | VMSKLASFLG | FSKQSPQKKN |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| HLVLEKKTES | ATFRVCGENV | TCVEYAISWL | QDLIEKEQCP | YTSEDECIKD | FDEKEYQELN | ELQKKLNINI | SLDHKRPLIK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VLGISRDVMQ | ARDEIEAMIK | RVRLAKEQES | RADCISEFIE | WQYNDNNTSH | CFNKMTNLKL | EDARREKKKT | VDVKINHRHY |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| TVNLNTYTAT | DTKGHSLSVQ | RLTKSKVDIP | AHWSDMKQQN | FCVVELLPSD | PEYNTVASKF | NQTCSHFRIE | KIERIQNPDL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| WNSYQAKKKT | MDAKNGQTMN | EKQLFHGTDA | GSVPHVNRNG | FNRSYAGKNA | VAYGKGTYFA | VNANYSANDT | YSRPDANGRK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | |
| HVYYVRVLTG | IYTHGNHSLI | VPPSKNPQNP | TDLYDTVTDN | VHHPSLFVAF | YDYQAYPEYL | ITFRK | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 554 | 1 | 476.1400 | -265.76 | 2 | 36.9 | 12.8 | 1 | 1019- | K.FSSKNQLK.T | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | 1026 | | | |
| 2539 | 1 | 648.3564 | 69.94 | 2 | 62.4 | 13.6 | 0 | 1173-<br>1184 | K.SSVSSVLQECEK.K | | WUP:QUP 0.04 |

# Detailed Protein Report

## Protein 589: huntingtin [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|90903231 | **Score:** | 26.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 347.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| | | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MATLEKLMKA | FESLKSFQQQ | QQQQQQQQQQ | QQQQQQQQQQ | PPPPPPPPPP | PQLPQPPPQA | QPLLPQPQPP | PPPPPPPPGP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AVAEEPLHRP | KKELSATKKD | RVNHCLTICE | NIVAQSVRNS | PEFQKLLGIA | MELFLLCSDD | AESDVRMVAD | ECLNKVIKAL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MDSNLPRLQL | ELYKEIKKNG | APRSLRAALW | RFAELAHLVR | PQKCRPYLVN | LLPCLTRTSK | RPEESVQETL | AAAVPKIMAS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FGNFANDNEI | KVLLKAFIAN | LKSSSPTIRR | TAAGSAVSIC | QHSRRTQYFY | SWLLNVLLGL | LVPVEDEHST | LLILGVLLTL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RYLVPLLQQQ | VKDTSLKGSF | GVTRKEMEVS | PSAEQLVQVY | ELTLHHTQHQ | DHNVVTGALE | LLQQLFRTPP | PELLQTLTAV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GGIGQLTAAK | EESGGRSRSG | SIVELIAGGG | SSCSPVLSRK | QKGKVLLGEE | EALEDDSESR | SDVSSSALTA | SVKDEISGEL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AASSGVSTPG | SAGHDIITEQ | PRSQHTLQAD | SVDLASCDLT | SSATDGDEED | ILSHSSSQVS | AVPSDPAMDL | NDGTQASSPI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SDSSQTTTEG | PDSAVTPSDS | SEIVLDGTDN | QYLGLQIGQP | QDEDEEATGI | LPDEASEAFR | NSSMALQQAH | LLKNMSHCRQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PSDSSVDKFV | LRDEATEPGD | QENKPCRIKG | DIGQSTDDDS | APLVHCVRLL | SASFLLTGGK | NVLVPDRDVR | VSVKALALSC |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VGAAVALHPE | SFFSKLYKVP | LDTTEYPEEQ | YVSDILNYID | HGDPQVRGAT | AILCGTLICS | ILSRSRFHVG | DWMGTIRTLT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GNTFSLADCI | PLLRKTLKDE | SSVTCKLACT | AVRNCVMSLC | SSSYSELGLQ | LIIDVLTLRN | SSYWLVRTEL | LETLAEIDFR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LVSFLEAKAE | NLHRGAHHYT | GLLKLQERVL | NNVVIHLLGD | EDPRVRHVAA | ASLIRLVPKL | FYKCDQGQAD | PVVAVARDQS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SVYLKLLMHE | TQPPSHFSVS | TITRIYRGYN | LLPSITDVTM | ENNLSRVIAA | VSHELITSTT | RALTFGCCEA | LCLLSTAFPV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| CIWSLGWHCG | VPPLSASDES | RKSCTVGMAT | MILTLLSSAW | FPLDLSAHQD | ALILAGNLLA | ASAPKSLRSS | WASEEEANPA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ATKQEEVWPA | LGDRALVPMV | EQLFSHLLKV | INICAHVLDD | VAPGPAIKAA | LPSLTNPPSL | SPIRRKGKEK | EPGEQASVPL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SPKKGSEASA | ASRQSDTSGP | VTTSKSSSLG | SFYHLPSYLK | LHDVLKATHA | NYKVTLDLQN | STEKFGGFLR | SALDVLSQIL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| ELATLQDIGK | CVEEILGYLK | SCFSREPMMA | TVCVQQLLKT | LFGTNLASQF | DGLSSNPSKS | QGRAQRLGSS | SVRPGLYHYC |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| FMAPYTHFTQ | ALADASLRNM | VQAEQENDTS | GWFDVLQKVS | TQLKTNLTSV | TKNRADKNAI | HNHIRLFEPL | VIKALKQYTT |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| TTCVQLQKQV | LDLLAQLVQL | RVNYCLLDSD | QVFIGFVLKQ | FEYIEVGQFR | ESEAIIPNIF | FFLVLLSYER | YHSKQIIGIP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| KIIQLCDGIM | ASGRKAVTHA | IPALQPIVHD | LFVLRGTNKA | DAGKELETQK | EVVVSMLLRL | IQYHQVLEMF | ILVLQQCHKE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| NEDKWKRLSR | QIADIILPML | AKQQMHIDSH | EALGVLNTLF | EILAPSSLRP | VDMLLRSMFV | TPNTMASVST | VQLWISGILA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| ILRVLISQST | EDIVLSRIQE | LSFSPYLISC | TVINRLRDGD | STSTLEEHSE | GKQIKNLPEE | TFSRFLLQLV | GILLEDIVTK |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| QLKVEMSEQQ | HTFYCQELGT | LLMCLIHIFK | SGMFRRITAA | ATRLFRSDGC | GGSFYTLDSL | NLRARSMITT | HPALVLLWCQ |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| ILLLVNHTDY | RWWAEVQQTP | KRHSLSSTKL | LSPQMSGEEE | DSDLAAKLGM | CNREIVRRGA | LILFCDYVCQ | NLHDSEHLTW |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LIVNHIQDLI | SLSHEPPVQD | FISAVHRNSA | ASGLFIQAIQ | SRCENLSTPT | MLKKTLQCLE | GIHLSQSGAV | LTLYVDRLLC |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| TPFRVLARMV | DILACRRVEM | LLAANLQSSM | AQLPMEELNR | IQEYLQSSGL | AQRHQRLYSL | LDRFRLSTMQ | DSLSPSPPVS |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| SHPLDGDGHV | SLETVSPDKD | WYVHLVKSQC | WTRSDSALLE | GAELVNRIPA | EDMNAFMMNS | EFNLSLLAPC | LSLGMSEISG |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 347 | 1 | 524.3773 | 160.20 | 2 | 33.0 | 15.3 | 2 | 93-101 | K.ELSATKKDR.V | |

# Detailed Protein Report

**Protein 590:** **PREDICTED: zinc finger protein 841 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578834341 | **Score:** | 26.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 99.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.1 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MALPQGSLTF | RDVAVEFSQE | EWKCLDPVQK | ALYRDVMLEN | YRNLGFLGLC | LPDLNIISML | EQGKEPWTVV | SQVKIARNPN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CGECMKGVIT | GISPKCVIKE | LPPIQNSNTG | EKFQAVMLEG | HESYDTENFY | FREIRKNLQE | VDFQWKDGEI | NYKEGPMTHK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NNLTGQRVRH | SQGDVENKHM | ENQLILRFQS | GLGELQKFQT | AEKIYGCNQI | ERTVNNCFLA | SPLQRIFPGV | QTNISRKYGN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DFLQLSLPTQ | DEKTHIREKP | YIGNECGKAF | RVSSSLINHQ | MIHTTEKPYR | CNESGKAFHR | GSLLTVHQIV | HTRGKPYQCD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VCGRIFRQNS | DLVNHRRSHT | GDKPYICNEC | GKSFSKSSHL | AVHQRIHTGE | KPYKCNRCGK | CFSQSSSLAT | HQTVHTGDKP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YKCNECGKTF | KRNSSLTAHH | IIHAGKKPYT | CDVCGKVFYQ | NSQLVRHQII | HTGETPYKCN | ECGKVFFQRS | RLAGHRRIHT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GEKPYKCNEC | GKVFSQHSHL | AVHQRVHTGE | KPYKCNECGK | AFNWGSLLTV | HQRIHTGEKP | YKCNVCGKVF | IDSGNLSIHR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RSHTGEKPFQ | CNECGKVFSY | YSCLARHRKI | HTGEKPYKCN | DCGKAYTQRS | SLTKHLVIHT | GENPYHCNEF | GEAFIQSSKL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ARYHRNPTGE | KPHKCSECGR | TFSHKTSLVY | HQRRHTGEMP | YKCIECGKVF | NSTTTLARHR | RIHTGEKPYK | CNECGKVFRY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RSGLARHWSI | HTGEKPYKCN | ECGKAFRVRS | ILLNHQMMHT | GEKPYKCNEC | GKAFIERSNL | VYHQRNHTGE | KPYKCMECGK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | |
| AFGRRSCLTK | HQRIHSSEKP | YKCNECGKSY | ISRSGLTKHQ | IKHAGENLTT | KLNVERPLDV | VLTSGIPK | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1732 | 1 | 1061.1490 | -2.43 | 3 | 51.5 | 11.3 | 2 | 561-586 | R.RSHTGEKPFQCNECGKVFSYYSCLAR.H | Carbamidomethyl: 11, 14, 23 |
| 1286 | 1 | 738.4255 | 114.34 | 3 | 45.7 | 15.0 | 2 | 643-660 | R.YHRNPTGEKPHKCSECGR.T | Carbamidomethyl: 13, 16 |

# Detailed Protein Report

## Protein 591: integrator complex subunit 1 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|160948599 | **Score:** | 26.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 244.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.7 |
|  |  | **No. of unique Peptides:** | 2 |

# Detailed Protein Report

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNRAKPTTVR | RPSAAAKPSG | HPPPGDFIAL | GSKGQANESK | TASTLLKPAP | SGLPSERKRD | AAAALSSASA | LTGLTKRPKL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SSTPPLSALG | RLAEAAVAEK | RAISPSIKEP | SVVPIEVLPT | VLLDEIEAAE | LEGNDDRIEG | VLCGAVKQLK | VTRAKPDSTL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YLSLMYLAKI | KPNIFATEGV | IEALCSLLRR | DASINFKAKG | NSLVSVLACN | LLMAAYEEDE | NWPEIFVKVY | IEDSLGERIW |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VDSPHCKTFV | DNIQTAFNTR | MPPRSVLLQG | EAGRVAGDLG | AGSSPHPSLT | EEEDSQTELL | IAEEKLSPEQ | EGQLMPRYEE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LAESVEEYVL | DMLRDQLNRR | QPIDNVSRNL | LRLLTSTCGY | KEVRLLAVQK | LEMWLQNPKL | TRPAQDLLMS | VCMNCNTHGS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EDMDVISHLI | KIRLKPKVLL | NHFMLCIREL | LSAHKDNLGT | TIKLVIFNEL | SSARNPNNMQ | VLYTALQHSS | ELAPKFLAMV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FQDLLTNKDD | YLRASRALLR | EIIKQTKHEI | NFQAFCLGLM | QERKEPQYLE | MEFKERFVVH | ITDVLAVSMM | LGITAQVKEA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GIAWDKGEKR | NLEVLRSFQN | QIAAIQRDAV | WWLHTVVPSI | SKLAPKDYVH | CLHKVLFTEQ | PETYYKWDNW | PPESDRNFFL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RLCSEVPILE | DTLMRILVIG | LSRELPLGPA | DAMELADHLV | KRAAAVQADD | VEVLKVGRTQ | LIDAVLNLCT | YHHPENIQLP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PGYQPPNLAI | STLYWKAWPL | LLVVAAFNPE | NIGLAAWEEY | PTLKMLMEMV | MTNNYSYPPC | TLTDEETRTE | MLNRELQTAQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| REKQEILAFE | GHLAAASTKQ | TITESSSLLL | SQLTSLDPQG | PPRRPPPHIL | DQVKSLNQSL | RLGHLLCRSR | NPDFLLHIIQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RQASSQSMPW | LADLVQSSEG | SLDVLPVQCL | CEFLLHDAVD | DAASGEEDDE | GESKEQKAKK | RQRQQKQRQL | LGRLQDLLLG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PKADEQTTCE | VLDYFLRRLG | SSQVASRVLA | MKGLSLVLSE | GSLRDGEEKE | PPMEEDVGDT | DVLQGYQWLL | RDLPRLPLFD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SVRSTTALAL | QQAIHMETDP | QTISAYLIYL | SQHTPVEEQA | QHSDLALDVA | RLVVERSTIM | SHLFSKLSPS | AASDAVLSAL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LSIFSRYVRR | MRQSKEGEEV | YSWSESQDQV | FLRWSSGETA | TMHILVVHAM | VILLTLGPPR | ADDSEFQALL | DIWFPEEKPL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PTAFLVDTSE | EALLLPDWLK | LRMIRSEVLR | LVDAALQDLE | PQQLLLFVQS | FGIPVSSMSK | LLQFLDQAVA | HDPQTLEQNI |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| MDKNYMAHLV | EVQHERGASG | GQTFHSLLTA | SLPPRRDSTE | APKPKSSPEQ | PIGQGRIRVG | TQLRVLGPED | DLAGMFLQIF |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PLSPDPRWQS | SSPRPVALAL | QQALGQELAR | VVQGSPEVPG | ITVRVLQALA | TLLSSPHGGA | LVMSMHRSHF | LACPLLRQLC |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| QYQRCVPQDT | GFSSLFLKVL | LQMLQWLDSP | GVEGGPLRAQ | LRMLASQASA | GRRLSDVRGG | LLRLAEALAF | RQDLEVVSST |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| VRAVIATLRS | GEQCSVEPDL | ISKVLQGLIE | VRSPHLEELL | TAFFSATADA | ASPFPACKPV | VVVSSLLLQE | EEPLAGGKPG |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| ADGGSLEAVR | LGPSSGLLVD | WLEMLDPEVV | SSCPDLQLRL | LFSRRKGKGQ | AQVPSFRPYL | LTLFTHQSSW | PTLHQCIRVL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LGKSREQRFD | PSASLDFLWA | CIHVPRIWQG | RDQRTPQKRR | EELVLRVQGP | ELISLVELIL | AEAETRSQDG | DTAACSLIQA |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| RLPLLLSCCC | GDDESVRKVT | EHLSGCIQQW | GDSVLGRRCR | DLLLQLYLQR | PELRVPVPEV | LLHSEGAASS | SVCKLDGLIH |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| RFITLLADTS | DSRALENRGA | DASMACRKLA | VAHPLLLLRH | LPMIAALLHG | RTHLNFQEFR | QQNHLSCFLH | VLGLLELLQP |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| HVFRSEHQGA | LWDCLLSFIR | LLLNYRKSSR | HLAAFINKFV | QFIHKYITYN | APAAISFLQK | HADPLHDLSF | DNSDLVMLKS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| LLAGLSLPSR | DDRTDRGLDE | EGEEESSAGS | LPLVSVSLFT | PLTAAEMAPY | MKRLSRGQTV | EDLLEVLSDI | DEMSRRRPEI |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| LSFFSTNLQR | LMSSAEECCR | NLAFSLALRS | MQNSPSIAAA | FLPTFMYCLG | SQDFEVVQTA | LRNLPEYALL | CQEHAAVLLH |
| 2170 | 2180 | 2190 | 2200 |  |  |  |  |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1586 | 1 | 948.9589 | -43.25 | 2 | 50.1 | 10.1 | 0 | 1297-1315 | R.GASGGQTFHSLLTASLPPR.R | |
| 464 | 1 | 724.3818 | 41.56 | 3 | 35.8 | 16.2 | 1 | 2091-2109 | R.LMSSAEECCRNLAFSLALR.S | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 592: uncharacterized membrane protein C3orf80 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|270265902 | **Score:** | 26.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 25.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 13.4 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.05 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.30 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWGPGVTAEG | LSVAPAPPPL | LPLLLLLALA | LVAPSRGGGG | CAELACGERE | RCCDATNATA | VRCCKLPLHA | FLDNVGWFVR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KLSGLLILLV | LFAIGYFLQR | IICPSPRRYP | RGQARPGQRP | GPPGGAGPLG | GAGPPDDDDD | SPALLRDEAA | AGSQDSLLDS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GGGGRGRGGG | GRSDPSCASE | HEMRVVSPVF | LQLPSYEEVK | YLPTYEESMR | LQQLSPGEVV | LPVSVLGRPR | GGVAAEPDGG |
| 250 | | | | | | | |
| EGRYPLI | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 536 | 2 | 786.8751 | 66.36 | 2 | 36.7 | 12.7 | 1 | 52-65 | R.CCDATNATAVRCCK.L | Carbamidomethyl: 1, 2 | WUP:QUP 0.30<br>QU:MU 1.05 |
| 2758 | 1 | 973.5021 | 83.13 | 2 | 64.9 | 13.5 | 2 | 166-184 | R.GRGGGGRSDPSCASEHEMR.V | | |

# Detailed Protein Report

## Protein 593: PREDICTED: sarcolemmal membrane-associated protein isoform X16 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530373158 | **Score:** | 26.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 90.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| | | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 3.85 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPSALAIFTC | RPNSHPFQER | HVYLDEPIKI | GRSVARCRPA | QNNATFDCKV | LSRNHALVWF | DHKTGKFYLQ | DTKSSNGTFI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NSQRLSRGSE | ESPPCEILSG | DIIQFGVDVT | ENTRKVTHGC | IVSTIKLFLP | DGMEARLRSD | VIHAPLPSPV | DKVAANTPSM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YSQELFQLSQ | YLQEALHREQ | MLEQKLATLQ | RLLAITQEAS | DTSWQALIDE | DRLLSRLEVM | GNQLQACSKN | QTEDSLRKEL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IALQEDKHNY | ETTAKESLRR | VLQEKIEVVR | KLSEVERSLS | NTEDECTHLK | EMNERTQEEL | RELANKYNGA | VNEIKDLSDK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LKVAEGKQEE | IQQKGQAEKK | ELQHKIDEME | EKEQELQAKI | EALQADNDFT | NERLTALQEK | LIVEGHLTKA | VEETKLSKEN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QTRAKESDFS | DTLSPSKEKS | SDDTTDAQMD | EQDLNEPLAK | VSLLKDDLQG | AQSEIEAKQE | IQHLRKELIE | AQELARTSKQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KCFELQALLE | EERKAYRNQV | EESTKQIQVL | QAQLQRLHID | TENLREEKDS | EITSTRDELL | SARDEILLLH | QAAAKVASER |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DTDIASLQEE | LKKVRAELER | WRKAASEYEK | EITSLQNSFQ | LRCQQCEDQQ | REEATRLQGE | LEKLRKEWNA | LETECHSLKR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ENVLLSSELQ | RQEKELHNSQ | KQSLELTSDL | SILQMSRKEL | ENQVGSLKEQ | HLRDSADLKT | LLSKAENQAK | DVQKEYEKTQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TVLSELKLKF | EMTEQEKQSI | TDELKQCKNN | LKLLREKGNN | KPWPWMPLMA | ALVAVTAIVL | YVPGLARASP | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1042 | 1 | 586.1730 | -249.89 | 2 | 41.3 | 10.5 | 0 | 467-476 | K.ELIEAQELAR.T | | QU:MU 3.85 |

# Detailed Protein Report

## Protein 594: PREDICTED: suppressor of tumorigenicity 7 protein-like isoform X10 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530362849 | **Score:** | 26.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 35.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MADRGGVGEA | AAVGASPASV | PGLNPTLGWR | ERLRAGLAGT | GASLWFVAGL | GLLYALRIPL | RLCENLAAVT | VFLNSLTPKF |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| YVALTGTSSL | ISGLIFIFEW | WYFHKHGTSF | IEQVSVSHLQ | PLMGGTESSI | SEPGSPSRNR | ENETSRQNLS | ECKVWRNPLN |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| LFRGAEYRRY | TWVTGKEPLT | YYDMNLSAQD | HQTFFTCDTD | FLRPSDTVMQ | KAWRERNPPA | RIKAAYQALE | LNNDCATAYV |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| LLAEEEATTI | VDAERLFKQA | LKAGETIYRQ | SQQCQHQSPQ | HEAQLRRDTN | VLVYIKRRLA | MCARKLGRIR | EAVKIMRDI |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2033 | 4 | 625.2626 | -137.48 | 2 | 55.3 | 14.2 | 1 | 259-269 | K.QALKAGETIYR.Q | |
| 1102 | 2 | 836.1988 | -267.93 | 1 | 43.4 | 12.0 | 1 | 298-304 | R.RLAMCAR.K | Oxidation: 4 |

# Detailed Protein Report

## Protein 595: PREDICTED: sodium/myo-inositol cotransporter 2 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530407547 | **Score:** | 26.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.6 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.66 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.92 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MYAGAIFIQQ | SLHLDLYLAI | VGLLAITAVY | TVAGGLAAVI | YTDALQTLIM | LIGALTLMGY | SFAAVGGMEG | LKEKYFLALA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SNRSENSSCG | LPREDAFHIF | RDPLTSDLPW | PGVLFGMSIP | SLWYWCTDQV | IVQRTLAAKN | LSHAKGGALM | AAYLKVLPLF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IMVFPGMVSR | ILFPDQVACA | DPEICQKICS | NPSGCSDIAY | PKLVLELLPT | GLRGLMMAVM | VAALMSSLTS | IFNSASTIFT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MDLWNHLRPR | ASEKELMIVG | RVFVLLLVLV | SILWIPVVQA | SQGGQLFIYI | QSISSYLQPP | VAVVFIMGCF | WKRTNEKGAF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WGLISGLLLG | LVRLVLDFIY | VQPRCDQPDE | RPVLVKSIHY | LYFSMILSTV | TLITVSTVSW | FTEPPSKEMV | SHLTWFTRHD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PVVQKEQAPP | AAPLSLTLSQ | NGMPEASSSS | SVQFEMVQEN | TSKTHSCDMT | PKQSKVVKAI | LWLCGIQEKG | KEELPARAEA |
| 490 | 500 | 510 | 520 | | | | |
| IIVSLEENPL | VKTLLDVNLI | FCVSCAIFIW | GYFA | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2244 | 1 | 714.6704 | -20.12 | 3 | 58.5 | 12.0 | 1 | 75-93 | K.YFLALASNRSENSSCGLPR.E | Carbamidomethyl: 15 | |
| 816 | 1 | 812.9497 | -14.41 | 2 | 40.2 | 14.1 | 0 | 478-492 | R.AEAIIVSLEENPLVK.T | | QU:MU 0.66<br>WUP:QUP 1.92 |

# Detailed Protein Report

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## Protein 596: glutamate decarboxylase 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4503875 | **Score:** | 26.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 65.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|197276620 | refseq_human (refseq_human_20140103.fasta) | glutamate decarboxylase 2 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MASPGSGFWS | FGSEDGSGDS | ENPGTARAWC | QVAQKFTGGI | GNKLCALLYG | DAEKPAESGG | SQPPRAAARK | AACACDQKPC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SCSKVDVNYA | FLHATDLLPA | CDGERPTLAF | LQDVMNILLQ | YVVKSFDRST | KVIDFHYPNE | LLQEYNWELA | DQPQNLEEIL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MHCQTTLKYA | IKTGHPRYFN | QLSTGLDMVG | LAADWLTSTA | NTNMFTYEIA | PVFVLLEYVT | LKKMREIIGW | PGGSGDGIFS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PGGAISNMYA | MMIARFKMFP | EVKEKGMAAL | PRLIAFTSEH | SHFSLKKGAA | ALGIGTDSVI | LIKCDERGKM | IPSDLERRIL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EAKQKGFVPF | LVSATAGTTV | YGAFDPLLAV | ADICKKYKIW | MHVDAAWGGG | LLMSRKHKWK | LSGVERANSV | TWNPHKMMGV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PLQCSALLVR | EEGLMQNCNQ | MHASYLFQQD | KHYDLSYDTG | DKALQCGRHV | DVFKLWLMWR | AKGTTGFEAH | VDKCLELAEY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LYNIIKNREG | YEMVFDGKPQ | HTNVCFWYIP | PSLRTLEDNE | ERMSRLSKVA | PVIKARMMEY | GTTMVSYQPL | GDKVNFFRMV |
| 570 | 580 | 590 | | | | | |
| ISNPAATHQD | IDFLIEEIER | LGQDL | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2204 | 1 | 767.2614 | -182.11 | 2 | 57.4 | 12.9 | 0 | 397-410 | K.MMGVPLQCSALLVR.E | Oxidation: 2 |

# Detailed Protein Report

## Protein 597: PREDICTED: zinc finger protein 40 isoform X2 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|578811634 | **Score:** | 26.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 222.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.3 |
|  |  | **No. of unique Peptides:** | 2 |

## Quantitation

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.91 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.10 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPRTKQIHPR | NLRDKIEEAQ | KELNGAEVSK | KEILQAGVKG | TSESLKGVKR | KKIVAENHLK | KIPKSPLRNP | LQAKHKQNTE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ESSFAVLHSA | SESHKKQNYI | PVKNGKQFTK | QNGETPGIIA | EASKSEESVS | PKKPLFLQQP | SELRRWRSEG | ADPAKFSDLD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EQCDSSSLSS | KTRTDNSECI | SSHCGTTSPS | YTNTAFDVLL | KAMEPELSTL | SQKGSPCAIK | TEKLRPNKTA | RSPPKLKNSS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MDAPNQTSQE | LVAESQSSCT | SYTVHMSAAQ | KNEQGAMQSA | SHLYHQHEHF | VPKSNQHNQQ | LPGCSGFTGS | LTNLQNQENA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KLEQVYNIAV | TSSVGLTSPS | SRSQVTPQNQ | QMDSASPLSI | SPANSTQSPP | MPIYNSTHVA | SVVNQSVEQM | CNLLLKDQKP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KKQGKYICEY | CNRACAKPSV | LLKHIRSHTG | ERPYPCVTCG | FSFKTKSNLY | KHKKSHAHTI | KLGLVLQPDA | GGLFLSHESP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KALSIHSDVE | DSGESEEEGA | TDERQHDLGA | MELQPVHIIK | RMSNAETLLK | SSFTPSSPEN | VIGDFLLQDR | SAESQAVTEL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PKVVVHHVTV | SPLRTDSPKA | MDPKPELSSA | QKQKDLQVTN | VQPLSANMSQ | GGVSRLETNE | NSHQKGDMNP | LEGKQDSHVG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TVHAQLQRQQ | ATDYSQEQQG | KLLSPRSLGS | TDSGYFSRSE | SADQTVSPPT | PFARRLPSTE | QDSGRSNGPS | AALVTTSTPS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ALPTGEKALL | LPGQMRPPLA | TKTLEERISK | LISDNEALVD | DKQLDSVKPR | RTSLSRRGSI | DSPKSYIFKD | SFQFDLKPVG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RRTSSSSDIP | KSPFTPTEKS | KQVFLLSVPS | LDCLPITRSN | SMPTTGYSAV | PANIIPPPHP | LRGSQSFDDK | IGAFYDDVFV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SGPNAPVPQS | GHPRTLVRQA | AIEDSSANES | HVLGTGQSLD | ESHQGCHAAG | EAMSVRSKAL | AQGPHIEKKK | SHQGRGTMFE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| CETCRNRYRK | LENFENHKKF | YCSELHGPKT | KVAMREPEHS | PVPGGLPQPI | LHYRVAGSSG | IWEQTPQIRK | RRKMKSVGDD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EELQQNESGT | SPKSSEGLQF | QNALGCNPSL | PKHNVTIRSD | QQHKNIQLQN | SHIHLVARGP | EQTMDPKLST | IMEQQISSAA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QDKIELQRHG | TGISVIQHTN | SLSRPNSFDK | PEPFERASPV | SFQELNRTGK | SGSLKVIGIS | QEESHPSRDG | SHPHQLALSD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ALRGELQESS | RKSPSERHVL | GQPSRLVRQH | NIQVPEILVT | EEPDRDLEAQ | CHDQEKSEKF | SWPQRSETLS | KLPTEKLPPK |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KKRLRLAEIE | HSSTESSFDS | TLSRSLSRES | SLSHTSSFSA | SLDIEDVSKT | EASPKIDFLN | KAEFLMIPAG | LNTLNVPGCH |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| REMRRTASEQ | INCTQTSMEV | SDLRSKSFDC | GSITPPQTTP | LTELQPPSSP | SRVGVTGHVP | LLERRRGPLV | RQISLNIAPD |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SHLSPVHPTS | FQNTALPSVN | AVPYQGPQLT | STSLAEFSAN | TLHSQTQVKD | LQAETSNSSS | TNVFPVQQLC | DINLLNQIHA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PPSHQSTQLS | LQVSTQGSKP | DKNSVLSGSS | KSEDCFAPKY | QLHCQVFTSG | PSCSSNPVHS | LPNQVISDPV | GTDHCVTSAT |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LPTKLIDSMS | NSHPLLPPEL | RPLGSQVQKV | PSSFMLPIRL | QSSVPAYCFA | TLTSLPQILV | TQDLPNQPIC | QTNHSVVPIS |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| EEQNSVPTLQ | KGHQNALPNP | EKEFLCENVF | SEMSQNSSLS | ESLPITQKIS | VGRLSPQQES | SASSKRMLSP | ANSLDIAMEK |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| HQKRAKDENG | AVCATDVRPL | EALSSRVNEA | SKQKKPILVR | QVCTTEPLDG | VMLEKDVFSQ | PEISNEAVNL | TNVLPADNSS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| TGCSKFVVIE | PISELQEFEN | IKSSTSLTLT | VRSSPAPSEN | THISPLKCTD | NNQERKSPGV | KNQGDKVNIQ | EQSQQPVTSL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| SLFNIKDTQQ | LAFPSLKTTT | NFTWCYLLRQ | KSLHLPQKDQ | KTSAYTDWTV | SASNPNPLGL | PTKVALALLN | SKQNTGKSLY |
| 2010 | 2020 | 2030 | | | | | |
| CQAITTHSKS | DLLVYSSKWK | SSLSKI | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1515 | 1 | 719.8406 | -37.88 | 2 | 49.1 | 13.1 | 0 | 1176-1188 | K.VIGISQEESHPSR.D | | WUP:QUP 2.10<br>QU:MU 0.91 |
| 52 | 1 | 776.2895 | -107.95 | 2 | 30.3 | 12.9 | 0 | 1747-1760 | R.MLSPANSLDIAMEK.H | Oxidation: 1, 12 | |

# Detailed Protein Report

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**Protein 598:** **lengsin isoform a [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|221307485 | **Score:** | 26.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 4.45 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.60 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNNEEDLLQE | DSTRDEGNET | EANSMNTLRR | TRKKVTKPYV | CSTEVGETDM | SNSNDCMRDS | SQILTPPQLS | SRMKHIRQAM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AKNRLQFVRF | EATDLHGVSR | SKTIPAHFFQ | EKVSHGVCMP | RGYLEVIPNP | KDNEMNNIRA | TCFNSDIVLM | PELSTFRVLP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WADRTARVIC | DTFTVTGEPL | LTSPRYIAKR | QLSHLQASGF | SLLSAFIYDF | CIFGVPEILN | SKIISFPALT | FLNNHDQPFM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QELVDGLYHT | GANVESFSSS | TRPGQMEISF | LPEFGISSAD | NAFTLRTGVK | EVARKYNYIA | SFFIETGFCD | SGILSHSLWD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VDRKKNMFCS | TSGTEQLTIT | GKKWLAGLLK | HSAALSCLMA | PSVSCRKRYS | KDRKDLKKSV | PTTWGYNDNS | CIFNIKCHGE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KGTRIENKLG | SATANPYLVL | AATVAAGLDG | LHSSNEVLAG | PDESTDFYQV | EPSEIPLKLE | DALVALEEDQ | CLRQALGETF |
| 490 | 500 | 510 | | | | | |
| IRYFVAMKKY | ELENEEIAAE | RNKFLEYFI | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 109 | 1 | 981.4823 | 13.57 | 2 | 30.3 | 10.6 | 1 | 326-343 | K.NMFCSTSGTEQLTITGKK.W | Oxidation: 2 | QU:MU 4.45<br>WUP:QUP 0.60 |

# Detailed Protein Report

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**Protein 599:** **PREDICTED: mediator of RNA polymerase II transcription subunit 1 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530412429 | **Score:** | 26.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 149.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.02 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.04 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MYLALQSLEQ DLSKMAIMYW KATNAGPLDK ILHGSVGYLT PRSGGHLMNL KYYVSPSDLL DDKTASPIIL HENNVSRSLG
        90        100        110        120        130        140        150        160
MNASVTIEGT SAVYKLPIAP LIMGSHPVDN KWTPSFSSIT SANSVDLPAC FFLKFPQPIP VSRAFVQKLQ NCTGIPLFET
       170        180        190        200        210        220        230        240
QPTYAPLYEL ITQFELSKDP DPIPLNHNMR FYAALPGQQH CYFLNKDAPL PDGRSLQGTL VSKITFQHPG RVPLILNLIR
       250        260        270        280        290        300        310        320
HQVAYNTLIG SCVKRTILKE DSPGLLQFEV CPLSESRFSV SFQHPVNDSL VCVVMDVQDS THVSCKLYKG LSDALICTDD
       330        340        350        360        370        380        390        400
FIAKVVQRCM SIPVTMRAIR RKAETIQADT PALSLIAETV EDMVKKNLPP ASSPGYGMTT GNNPMSGTTT PTNTFPGGPI
       410        420        430        440        450        460        470        480
TTLFNMSMSI KDRHESVGHG EDFSKVSQNP ILTSLLQITG NGGSTIGSSP TPPHHTPPPV SSMAGNTKNH PMLMNLLKDN
       490        500        510        520        530        540        550        560
PAQDFSTLYG SSPLERQNSS SGSPRMEICS GSNKTKKKKS SRLPPEKPKH QTEDDFQREL FSMDVDSQNP IFDVNMTADT
       570        580        590        600        610        620        630        640
LDTPHITPAP SQCSTPPTTY PQPVPHPQPS IQRMVRLSSS DSIGPDVTDI LSDIAEEASK LPSTSDDCPA IGTPLRDSSS
       650        660        670        680        690        700        710        720
SGHSQSTLFD SDVFQTNNNE NPYTDPADLI ADAAGSPSSD SPTNHFFHDG VDFNPDLLNS QSQSGFGEEY FDESSQSGDN
       730        740        750        760        770        780        790        800
DDFKGFASQA LNTLGVPMLG GDNGETKFKG NNQADTVDFS IISVAGKALA PADLMEHHSG SQGPLLTTGD LGKEKTQKRV
       810        820        830        840        850        860        870        880
KEGNGTSNST LSGPGLDSKP GKRSRTPSND GKSKDKPPKR KKADTEGKSP SHSSSNRPFT PPTSTGGSKS PGSAGRSQTP
       890        900        910        920        930        940        950        960
PGVATPPIPK ITIQIPKGTV MVGKPSSHSQ YTSSGSVSSS GSKSHHSHSS SSSSSASTSG KMKSSKSEGS SSSKLSSSMY
       970        980        990       1000       1010       1020       1030       1040
SSQGSSGSSQ SKNSSQSGGK PGSSPITKHG LSSGSSSTKM KPQGKPSSLM NPSLSKPNIS PSHSRPPGGS DKLASPMKPV
      1050       1060       1070       1080       1090       1100       1110       1120
PGTPPSSKAK SPISSGSGGS HMSGTSSSSG MKSSSGLGSS GSLSQKTPPS SNSCTASSSS FSSSGSSMSS SQNQHGSSKG
      1130       1140       1150       1160       1170       1180       1190       1200
KSPSRNKKPS LTAVIDKLKH GVVTSGPGGE DPLDGQMGVS TNSSSHPMSS KHNMSGGEFQ GKREKSDKDK SKVSTSGSSV
      1210       1220       1230       1240       1250       1260       1270       1280
DSSKKTSESK NVGSTGVAKI IISKHDGGSP SIKAKVTLQK PGESSGEGLR PQMASSKNYG SPLISGSTPK HERGSPSHSK
      1290       1300       1310       1320       1330       1340       1350       1360
SPAYTPQNLD SESESGSSIA EKSYQNSPSS DDGIRPLPEY STEKHKKHKK EKKKVKDKDR DRDRDKDRDK KKSHSIKPES
      1370       1380       1390       1400       1410
WSKSPISSDQ SLSMTSNTIL SADRPSRLSP DFMIGEEDDD LMDVALIGN
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2702 | 1 | 842.5321 | 94.33 | 3 | 62.2 | 11.9 | 2 | 307-328 | K.LYKGLSDALICTDDFIAKVVQR.C | Carbamidomethyl: 11 | |
| 1993 | 1 | 918.3565 | -113.08 | 2 | 53.3 | 14.1 | 0 | 750-767 | K.GNNQADTVDFSIISVAGK.A | | WUP:QUP 1.04<br>QU:MU 1.02 |

# Detailed Protein Report

**Protein 600:** **PREDICTED: pulmonary surfactant-associated protein C isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530387966 | **Score:** | 26.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 28.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.8 |
| | | **Sequence Coverage [%]:** | 14.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAPRDAHRDP | EMPAVLGSPA | GQLPTWLRPS | THPGHTWERR | RGEHSTCSKM | DVGSKEVLME | SPPDYSAAPR | GRFGIPCCPV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HLKRLLIVVV | VVVLIVVVIV | GALLMGLHMS | QKHTEMVLEM | SIGAPEAQQR | LALSEHLVTT | ATFSIGSTGL | VVYDYQQLLI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AYKPAPGTCC | YIMKIAPESI | PSLEALTRKV | HNFQGQWKPQ | RERKRPGQRV | FCSFCRRARS | CFCPHRRDKP | WRNGSLGRGW |
| 250 | 260 | | | | | | |
| EWAEVAPRGP | GTPATTE | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1479 | 1 | 1006.6165 | 136.56 | 2 | 46.9 | 11.4 | 1 | 239-257 | R.GWEWAEVAPRGPGTPATTE.- | |

# Detailed Protein Report

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## Protein 601: PREDICTED: microtubule-associated protein 2 isoform X12 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530370373 | **Score:** | 25.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 192.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.8 |
| | | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530370375 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: microtubule-associated protein 2 isoform X13 [Homo sapiens] |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MEFHDQQELT PSTAEPSDQK EKESEKQSKP GEDLKHAALV SQPETTKTYP DKKDMQGTEE EKAPLALFGH TLVASLEDMK
        90        100        110        120        130        140        150        160
QKTEPSLVVP GIDLPKEPPT PKEQKDWFIE MPTEAKKDEW GLVAPISPGP LTPMREKDVF DDIPKWEGKQ FDSPMPSPFQ
       170        180        190        200        210        220        230        240
GGSFTLPLDV MKNEIVTETS PFAPAFLQPD DKKSLQQTSG PATAKDSFKI EEPHEAKPDK MAEAPPSEAM TLPKDAHIPV
       250        260        270        280        290        300        310        320
VEEHVMGKVL EEEKEAINQE TVQQRDTFTP SGQEPILTEK ETELKLEEKT TISDKEAVPK ESKPPKPADE EIGIIQTSTE
       330        340        350        360        370        380        390        400
HTFSEQKDQE PTTDMLKQDS FPVSLEQAVT DSAMTSKTLE KAMTEPSALI EKSSIQELFE MRVDDKDKIE GVGAATSAEL
       410        420        430        440        450        460        470        480
DMPFYEDKSG MSKYFETSAL KEEATKSIEP GSDYYELSDT RESVHESIDT MSPMHKNGDK EFQTGKESQP SPPAQEAGYS
       490        500        510        520        530        540        550        560
TLAQSYPSDL PEEPSSPQER MFTIDPKVYG EKRDLHSKNK DDLTLSRSLG LGGRSAIEQR SMSINLPMSC LDSIALGFNF
       570        580        590        600        610        620        630        640
GRGHDLSPLA SDILTNTSGS MDEGDDYLPA TTPALEKAPC FPVESKEEEQ IEKVKATGEE STQAEISCES PFLAKDFYKN
       650        660        670        680        690        700        710        720
GTVMAPDLPE MLDLAGTRSR LASVSADAEV ARRKSVPSET VVEDSRTGLP PVTDENHVIV KTDSQLEDLG YCVFNKYTVP
       730        740        750        760        770        780        790        800
LPSPVQDSEN LSGESGTFYE GTDDKVRRDL ATDLSLIEVK LAAAGRVKDE FSVDKEASAH ISGDKSGLSK EFDQEKKAND
       810        820        830        840        850        860        870        880
RLDTVLEKSE EHADSKEHAK KTEEAGDEIE TFGLGVTYEQ ALAKDLSIPT DASSEKAEKG LSSVPEIAEV EPSKKVEQGL
       890        900        910        920        930        940        950        960
DFAVQGQLDV KISDFGQMAS GLNIDDRRAT ELKLEATQDM TPSSKAPQEA DAFMGVESGH MKEGTKVSET EVKEKVAKPD
       970        980        990       1000       1010       1020       1030       1040
LVHQEAVDKE ESYESSGEHE SLTMESLKAD EGKKETSPES SLIQDEIAVK LSVEIPCPPA VSEADLATDE RADVQMEFIQ
      1050       1060       1070       1080       1090       1100       1110       1120
GPKEESKETP DISITPSDVA EPLHETIVSE PAEIQSEEEE IEAQGEYDKL LFRSDTLQIT DLGVSGAREE FVETCPSEHK
      1130       1140       1150       1160       1170       1180       1190       1200
GVIESVVTIE DDFITVVQTT TDEGESGSHS VRFAALEQPE VERRPSPHDE EEFEVEEAAE AQAEPKDGSP EAPASPEREE
      1210       1220       1230       1240       1250       1260       1270       1280
VALSEYKTET YDDYKDETTI DDSIMDADSL WVDTQDDDRS IMTEQLETIP KEEKAEKEAR RSSLEKHRKE KPFKTGRGRI
      1290       1300       1310       1320       1330       1340       1350       1360
STPERKVAKK EPSTVSRDEV RRKKAVYKKA ELAKKTEVQA HSPSRKFILK PAIKYTRPTH LSCVKRKTTA AGGESALAPS
      1370       1380       1390       1400       1410       1420       1430       1440
VFKQAKDKVS NSTLSKIPAL QGSTKSPRYS SACPSTTKRA TFSDSLLIQP TSAGSTDRLP YSKSGNKDGV TKSPEKRSSL
      1450       1460       1470       1480       1490       1500       1510       1520
PRPSSILPPR RGVSGDRDEN SFSLNSSISS SARRTTRSEP IRRAGKSGTS TPTTPGSTAI TPGTPPSYSS RTPGTPGTPS
      1530       1540       1550       1560       1570       1580       1590       1600
YPRTPHTPGT PKSAILVPSE KKVAIIRTPP KSPATPKQLR LINQPLPDLK NVKSKIGSTD NIKYQPKGGQ VRILNKKIDF
      1610       1620       1630       1640       1650       1660       1670       1680
SKVQSRCGSK DNIKHSAGGG NVQIVTKKID LSHVTSKCGS LKNIRHRPGG GRVKIESVKL DFKEKAQAKV GSLDNAHHVP
      1690       1700       1710       1720       1730       1740       1750       1760
GGGNVKIDSQ KLNFREHAKA RVDHGAEIIT QSPGRSSVAS PRRLSNVSSS GSINLLESPQ LATLAEDVTA ALAKQGL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2357 | 1 | 994.6851 | 123.33 | 2 | 57.7 | 11.8 | 2 | 1524-1542 | R.TPHTPGTPKSAILVPSEKK.V | |

# Detailed Protein Report

## Protein 602: collagen alpha-1(IV) chain preproprotein [Homo sapiens]

**Accession:** gi|148536825
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 25.9
**MW [kDa]:** 160.5
**pI:** 9.4
**Sequence Coverage [%]:** 2.5
**No. of unique Peptides:** 2

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGPRLSVWLL | LLPAALLLHE | EHSRAAAKGG | CAGSGCGKCD | CHGVKGQKGE | RGLPGLQGVI | GFPGMQGPEG | PQGPPGQKGD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TGEPGLPGTK | GTRGPPGASG | YPGNPGLPGI | PGQDGPPGPP | GIPGCNGTKG | ERGPLGPPGL | PGFAGNPGPP | GLPGMKGDPG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EILGHVPGML | LKGERGFPGI | PGTPGPPGLP | GLQGPVGPPG | FTGPPGPPGP | PGPPGEKGQM | GLSFQGPKGD | KGDQGVSGPP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GVPGQAQVQE | KGDFATKGEK | GQKGEPGFQG | MPGVGEKGEP | GKPGPRGKPG | KDGDKGEKGS | PGFPGEPGYP | GLIGRQGPQG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EKGEAGPPGP | PGIVIGTGPL | GEKGERGYPG | TPGPRGEPGP | KGFPGLPGQP | GPPGLPVPGQ | AGAPGFPGER | GEKGDRGFPG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TSLPGPSGRD | GLPGPPGSPG | PPGQPGYTNG | IVECQPGPPG | DQGPPGIPGQ | PGFIGEIGEK | GQKGESCLIC | DIDGYRGPPG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PQGPPGEIGF | PGQPGAKGDR | GLPGRDGVAG | VPGPQGTPGL | IGQPGAKGEP | GEFYFDLRLK | GDKGDPGFPG | QPGMTGRAGS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PGRDGHPGLP | GPKGSPGSVG | LKGERGPPGG | VGFPGSRGDT | GPPGPPGYGP | AGPIGDKGQA | GFPGGPGSPG | LPGPKGEPGK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IVPLPGPPGA | EGLPGSPGFP | GPQGDRGFPG | TPGRPGLPGE | KGAVGQPGIG | FPGPPGPKGV | DGLPGDMGPP | GTPGRPGFNG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LPGNPGVQGQ | KGEPGVGLPG | LKGLPGLPGI | PGTPGEKGSI | GVPGVPGEHG | AIGPPGLQGI | RGEPGPPGLP | GSVGSPGVPG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IGPPGARGPP | GGQGPPGLSG | PPGIKGEKGF | PGFPGLDMPG | PKGDKGAQGL | PGITGQSGLP | GLPGQQGAPG | IPGFPGSKGE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| MGVMGTPGQP | GSPGPVGAPG | LPGEKGDHGF | PGSSGPRGDP | GLKGDKGDVG | LPGKPGSMDK | VDMGSMKGQK | GDQGEKGQIG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PIGEKGSRGD | PGTPGVPGKD | GQAGQPGQPG | PKGDPGISGT | PGAPGLPGPK | GSVGGMGLPG | TPGEKGVPGI | PGPQGSPGLP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GDKGAKGEKG | QAGPPGIGIP | GLRGEKGDQG | IAGFPGSPGE | KGEKGSIGIP | GMPGSPGLKG | SPGSVGYPGS | PGLPGEKGDK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GLPGLDGIPG | VKGEAGLPGT | PGPTGPAGQK | GEPGSDGIPG | SAGEKGEPGL | PGRGFPGFPG | AKGDKGSKGE | VGFPGLAGSP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| GIPGSKGEQG | FMGPPGPQGQ | PGLPGSPGHA | TEGPKGDRGP | QGQPGLPGLP | GPMGPPGLPG | IDGVKGDKGN | PGWPGAPGVP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| GPKGDPGFQG | MPGIGGSPGI | TGSKGDMGPP | GVPGFQGPKG | LPGLQGIKGD | QGDQGVPGAK | GLPGPPGPPG | PYDIIKGEPG |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LPGPEGPPGL | KGLQGLPGPK | GQQGVTGLVG | IPGPPGIPGF | DGAPGQKGEM | GPAGPTGPRG | FPGPPGPDGL | PGSMGPPGTP |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SVDHGFLVTR | HSQTIDDPQC | PSGTKILYHG | YSLLYVQGNE | RAHGQDLGTA | GSCLRKFSTM | PFLFCNINNV | CNFASRNDYS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| YWLSTPEPMP | MSMAPITGEN | IRPFISRCAV | CEAPAMVMAV | HSQTIQIPPC | PSGWSSLWIG | YSFVMHTSAG | AEGSGQALAS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | |
| PGSCLEEFRS | APFIECHGRG | TCNYYANAYS | FWLATIERSE | MFKKPTPSTL | KAGELRTHVS | RCQVCMRRT | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 177 | 1 | 942.3962 | -112.61 | 2 | 32.2 | 12.0 | 1 | 808-828 | R.GPPGGQGPPGLSGPPGIKGEK.G | |
| 62 | 1 | 713.3305 | -7.33 | 3 | 30.5 | 13.9 | 1 | 927-947 | K.GDVGLPGKPGSMDKVDMGSMK.G | Oxidation: 12, 17 |

# Detailed Protein Report

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**Protein 603:** **endoplasmic reticulum-Golgi intermediate compartment protein 2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|50959176 | **Score:** | 25.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 42.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRRLNRKKTL | SLVKELDAFP | KVPESYVETS | ASGGTVSLIA | FTTMALLTIM | EFSVYQDTWM | KYEYEVDKDF | SSKLRINIDI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TVAMKCQYVG | ADVLDLAETM | VASADGLVYE | PTVFDLSPQQ | KEWQRMLQLI | QSRLQEEHSL | QDVIFKSAFK | STSTALPPRE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DDSSQSPNAC | RIHGHLYVNK | VAGNFHITVG | KAIPHPRGHA | HLAALVNHES | YNFSHRIDHL | SFGELVPAII | NPLDGTEKIA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IDHNQMFQYF | ITVVPTKLHT | YKISADTHQF | SVTERERIIN | HAAGSHGVSG | IFMKYDLSSL | MVTVTEEHMP | FWQFFVRLCG |
| 330 | 340 | 350 | 360 | 370 | 380 | | |
| IVGGIFSTTG | MLHGIGKFIV | EIICCRFRLG | SYKPVNSVPF | EDGHTDNHLP | LLENNTH | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1411 | 1 | 1095.6964 | 116.34 | 1 | 47.3 | 11.8 | 0 | 338-346 | K.FIVEIICCR.F | |

# Detailed Protein Report

## Protein 604: centrosomal protein of 162 kDa isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|555289992 | **Score:** | 25.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 153.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578812505 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: centrosomal protein of 162 kDa isoform X7 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEIEEESAEK | IQFLKSSGTS | LLSTDSLETN | ELVVSELNHS | SLGVGLDTLE | EQEEKEQFFA | RLEKGLTSSI | DYSRLNKELD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SNDSTHFKAL | HSNQANAELT | DDEHENESKH | EELAENYSDD | FEDEYVGAPL | TTKDEEMPSK | ENSKSEKISV | PKQEEEKTGM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LANVVLLDSL | DSVAEVNLDE | QDKITPKPRC | LPEMTENEMT | GTGVSYGQSS | SDVEALHQAY | CHIAHSLGDE | DKQKIESNTV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EDIKSSVKGH | PQENEENSKN | ISTMESDLPT | VEELMKPIRI | DSFGISGFDL | QPVSSEKVAE | RKETEFFSSL | PLKMNPNILS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QDSQHVNLFF | DKNDENVILQ | KTTNESMENS | CPQVTEVTAT | EEHVDKMYLN | ILRKKITVNS | SSLSQDDKIN | KTYRSQLSSE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EEGAVMGKQV | PYKKARSAPP | LLKRKPQSGL | YASVRSSGYG | KPSSPLKMFS | TLEKKTSEDI | IKSKNLRSIS | TSNQPRKKEI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LSGTKLIKPA | ALDKPAHKTE | SCLSTRKKSE | NPTETDSCIQ | FQTDSLGYCG | ENKEKKLLMF | KRVQEAEDKW | RGAQALIEQI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KATFSEKEKE | LENKLEELKK | QQEKELFKLN | QDNYILQAKL | SSFEETNKKQ | RWLHFGEAAD | PVTGEKLKQI | QKEIQEQETL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LQGYQQENER | LYNQVKDLQE | QNKKNEERMF | KENQSLFSEV | ASLKEQMHKS | RFLSQVVEDS | EPTRNQNFTD | LLAELRMAQK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EKDSLLEDIK | RLKQDKQALE | VDFEKMKKER | DQAKDQIAYV | TGEKLYEIKI | LEETHKQEIS | RLQKRLQWYA | ENQELLDKDA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LRLREANEEI | EKLKLEIEKL | KAESGNPSIR | QKIRLKDKAA | DAKKIQDLER | QVKEMEGILK | RRYPNSLPAL | ILAASAAGDT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VDKNTVEFME | KRIKKLEADL | EGKDEDAKKS | LRTMEQQFQK | MKIQYEQRLE | QQEQLLACKL | NQHDSPRIKA | LEKELDDIKE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| AHQITVRNLE | AEIDVLKHQN | AELDVKKNDK | DDEDFQSIEF | QVEQAHAKAK | LVRLNEELAA | KKREIQDLSK | TVERLQKDRR |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| MMLSNQNSKG | REEMSAKRAK | KDVLHSSKGN | ANSFPGTLDS | KLYQPHTFTD | SHVSEVLQEN | YRLKNELEGL | ISEKNELKMK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SEAVMNQFEN | SMRRVKEDTA | AHIASLKASH | QREIEKLLCQ | NAVENSSSKV | AELNRKIATQ | EVLIRHFQSQ | VNELQSKQES |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LVVSEVREEI | LQKEITKLLE | ELREAKENHT | PEMKHFVGLE | KKIKQMEMRH | AQREQELQQI | IQQTHQVVET | EQNKEVEKWK |
| 1290 | 1300 | 1310 | 1320 | 1330 | | | |
| RLAQLKNREL | EKFRTELDSI | LDVLRELHRQ | GVVVPVAFAD | EMNAPEY | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 377 | 1 | 657.6657 | -223.40 | 2 | 34.7 | 10.5 | 1 | 913-922 | R.TMEQQFQKMK.I | Oxidation: 2 |

# Detailed Protein Report

**Protein 605:** **PREDICTED: tolloid-like protein 1 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530378097 | **Score:** | 25.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 82.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MISTVSCTMP GTPSQGWSLR GMFLDTILPS RDDNGIRPAI GQRTRLSKGD IAQARKLYRC PACGETLQES NGNLSSPGFP
        90        100        110        120        130        140        150        160
NGYPSYTHCI WRVSVTPGEK IVLNFTTMDL YKSSLCWYDY IEVRDGYWRK SPLLGRFCGD KLPEVLTSTD SRMWIEFRSS
       170        180        190        200        210        220        230        240
SNWVGKGFAA VYEAICGGEI RKNEGQIQSP NYPDDYRPMK ECVWKITVSE SYHVGLTFQS FEIERHDNCA YDYLEVRDGT
       250        260        270        280        290        300        310        320
SENSPLIGRF CGYDKPEDIR STSNTLWMKF VSDGTVNKAG FAANFFKEED ECAKPDRGGC EQRCLNTLGS YQCACEPGYE
       330        340        350        360        370        380        390        400
LGPDRRSCEA ACGGLLTKLN GTITTPGWPK EYPPNKNCVW QVVAPTQYRI SVKFEFFELE GNEVCKYDYV EIWSGLSSES
       410        420        430        440        450        460        470        480
KLHGKFCGAE VPEVITSQFN NMRIEFKSDN TVSKKGFKAH FFSDKDECSK DNGGCQHECV NTMGSYMCQC RNGFVLHDNK
       490        500        510        520        530        540        550        560
HDCKEAECEQ KIHSPSGLIT SPNWPDKYPS RKECTWEISA TPGHRIKLAF SEFEIEQHQE CAYDHLEVFD GETEKSPILG
       570        580        590        600        610        620        630        640
RLCGNKIPDP LVATGNKMFV RFVSDASVQR KGFQATHSTE CGGRLKAESK PRDLYSHAQF GDNNYPGQVD CEWLLVSERG
       650        660        670        680        690        700        710        720
SRLELSFQTF EVEEEADCGY DYVELFDGLD STAVGLGRFC GSGPPEEIYS IGDSVLIHFH TDDTINKKGF HIRYKSIRYP
       730
DTTHTKK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2771 | 1 | 848.8935 | -73.79 | 2 | 65.0 | 12.1 | 1 | 562-577 | R.LCGNKIPDPLVATGNK.M | Carbamidomethyl: 2 |

# Detailed Protein Report

## Protein 606: PREDICTED: chondroadherin-like protein isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530419599 | **Score:** | 25.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 81.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.4 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

*QU:MU* **Median:** 1.45 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEGPRSSTHV | PLVLPLLVLL | LLAPARQAAA | QRCPQACICD | NSRRHVACRY | QNLTEVPDAI | PELTQRLDLQ | GNLLKVIPAA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AFQGVPHLTH | LDLRHCEVEL | VAEGAFRGLG | RLLLLNLASN | HLRELPQEAL | DGLGSLRRLE | LEGNALEELR | PGTFGALGAL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ATLNLAHNAL | VYLPAMAFQG | LLRVRWLRLS | HNALSVLAPE | ALAGLPALRR | LSLHHNELQA | LPGPVLSQAR | GLARLELGHN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PLTYAGEEDG | LALPGLRELL | LDGGALQALG | PRAFAHCPRL | HTLDLRGNQL | DTLPPLQGPG | QLRRLRLQGN | PLWCGCQARP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LLEWLARARV | RSDGACQGPR | RLRGEALDAL | RPWDLRCPGD | AAQEEEELEE | RAVAGPRAPP | RGPPRGPGEE | RAVAPCPRAC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VCVPESRHSS | CEGCGLQAVP | RGFPSDTQLL | DLRRNHFPSV | PRAAFPGLGH | LVSLHLQHCG | IAELEAGALA | GLGRLIYLYL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SDNQLAGLSA | AALEGAPRLG | YLYLERNRFL | QVPGAALRAL | PSLFSLHLQD | NAVDRLAPGD | LGRTRALRWV | YLSGNRITEV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SLGALGPARE | LEKLHLDRNQ | LREVPTGALE | GLPALLELQL | SGNPLRALRD | GAFQPVGRSL | QHLFLNSSGL | EQICPGAFSG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LGPGLQSLHL | QKNQLRALPA | LPSLSQLELI | DLSSNPFHCD | CQLLPLHRWL | TGLNLRVGAT | CATPPNARGQ | RVKAAAAVFE |
| 730 | 740 | 750 | 760 | | | | |
| DCPGWAARKA | KRTPASRPSA | RRTPIKGRQC | GADKGTL | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 173 | 1 | 679.8611 | 32.65 | 2 | 32.1 | 14.2 | 2 | 330-341 | R.VRSDGACQGPRR.L | Carbamidomethyl: 7 | QU:MU 1.45 |
| 2204 | 1 | 1130.1280 | 10.71 | 2 | 58.0 | 11.7 | 1 | 549-569 | R.WVYLSGNRITEVSLGALGPAR.E | | |

# Detailed Protein Report

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## Protein 607: E3 SUMO-protein ligase PIAS3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|115298686 | **Score:** | 25.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 68.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.9 |
| | | **Sequence Coverage [%]:** | 5.4 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAELGELKHM | VMSFRVSELQ | VLLGFAGRNK | SGRKHELLAK | ALHLLKSSCA | PSVQMKIKEL | YRRRFPRKTL | GPSDLSLLSL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PPGTSPVGSP | GPLAPIPPTL | LAPGTLLGPK | REVDMHPPLP | QPVHPDVTMK | PLPFYEVYGE | LIRPTTLAST | SSQRFEEAHF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TFALTPQQVQ | QILTSREVLP | GAKCDYTIQV | QLRFCLCETS | CPQEDYFPPN | LFVKVNGKLC | PLPGYLPPTK | NGAEPKRPSR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PINITPLARL | SATVPNTIVV | NWSSEFGRNY | SLSVYLVRQL | TAGTLLQKLR | AKGIRNPDHS | RALIKEKLTA | DPDSEVATTS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LRVSLMCPLG | KMRLTVPCRA | LTCAHLQSFD | AALYLQMNEK | KPTWTCPVCD | KKAPYESLII | DGLFMEILSS | CSDCDEIQFM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EDGSWCPMKP | KKEASEVCPP | PGYGLDGLQY | SPVQGGDPSE | NKKKVEVIDL | TIESSSDEED | LPPTKKHCSV | TSAAIPALPG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SKGVLTSGHQ | PSSVLRSPAM | GTLGGDFLSS | LPLHEYPPAF | PLGADIQGLD | LFSFLQTESQ | HYGPSVITSL | DEQDALGHFF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| QYRGTPSHFL | GPLAPTLGSS | HCSATPAPPP | GRVSSIVAPG | GALREGHGGP | LPSGPSLTGC | RSDIISLD | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2323 | 1 | 965.9652 | -82.27 | 2 | 57.3 | 14.9 | 2 | 16-33 | R.VSELQVLLGFAGRNKSGR.K | |
| 2512 | 1 | 856.9301 | -38.31 | 2 | 62.0 | 11.0 | 1 | 41-56 | K.ALHLLKSSCAPSVQMK.I | |

# Detailed Protein Report

**Protein 608:** **PREDICTED: LIM/homeobox protein Lhx3 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530426634 | **Score:** | 25.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 42.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 8.5 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTLNMKETRW | GAPAPEIPLC | AGCDQHILDR | FILKALDRHW | HSKCLKCSDC | HTPLAERCFS | RGESVYCKDD | FFKRFGTKCA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ACQLGIPPTQ | VVRRAQDFVY | HLHCFACVVC | KRQLATGDEF | YLMEDSRLVC | KADYETAKQR | EAEATAKRPR | TTITAKQLET |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LKSAYNTSPK | PARHVREQLS | SETGLDMRVV | QVWFQNRRAK | EKRLKKDAGR | QRWGQYFRNM | KRSRGGSKSD | KDSVQEGQDS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DAEVSFPDEP | SLAEMGPANG | LYGSLGEPTQ | ALGRPSGALG | NFSLEHGGLA | GPEQYRELRP | GSPYGVPPSP | AAPQSLPGPQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| PLLSSLVYPD | TSLGLVPSGA | PGGPPPMRVL | AGNGPSSDLS | TGSSGGYPDF | PASPASWLDE | VDHAQF | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2005 | 1 | 788.2933 | -81.32 | 2 | 55.0 | 10.3 | 1 | 44-57 | K.CLKCSDCHTPLAER.C | |
| 2172 | 1 | 1051.9909 | -51.91 | 2 | 57.0 | 15.5 | 1 | 75-93 | R.FGTKCAACQLGIPPTQVVR.R | Carbamidomethyl: 5, 8 |

# Detailed Protein Report

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**Protein 609:** **rap guanine nucleotide exchange factor 1 isoform a [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|38373675 | **Score:** | 25.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 120.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDTDSQRSHL | SSFTMKLMDK | FHSPKIKRTP | SKKGKPAEVS | VKIPEKPVNK | EATDRFLPEG | YPLPLDLEQQ | AVEFMSTSAV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ASRSQRQKNL | SWLEEKEKEV | VSALRYFKTI | VDKMAIDKKV | LEMLPGSASK | VLEAILPLVQ | NDPRIQHSSA | LSSCYSRVYQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SLANLIRWSD | QVMLEGVNSE | DKEMVTTVKG | VIKAVLDGVK | ELVRLTIEKQ | GRPSPTSPVK | PSSPASKPDG | PAELPLTDRE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VEILNKTTGM | SQSTELLPDA | TDEEVAPPKP | PLPGIRVVDN | SPPPALPPKK | RQSAPSPTRV | AVVAPMSRAT | SGSSLPVGIN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RQDFDVDCYA | QRRLSGGSHS | YGGESPRLSP | CSSIGKLSKS | DEQLSSLDRD | SGQCSRNTSC | ETLDHYDPDY | EFLQQDLSNA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DQIPQQTAWN | LSPLPESLGE | SGSPFLGPPF | QLPLGGHPQP | DGPLAPGQQT | DTPPALPEKK | RRSAASQTAD | GSGCRVSYER |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HPSQYDNISG | EDLQSTAPIP | SVPYAPFAAI | LPFQHGGSSA | PVEFVGDFTA | PESTGDPEKP | PPLPEKKNKH | MLAYMQLLED |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YSEPQPSMFY | QTPQNEHIYQ | QKNKLLMEVY | GFSDSFSGVD | SVQELAPPPA | LPPKQRQLEP | PAGKDGHPRD | PSAVSGVPGK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DSRDGSERAP | KSPDALESAQ | SEEEVDELSL | IDHNEIMSRL | TLKQEGDDGP | DVRGGSGDIL | LVHATETDRK | DLVLYCEAFL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TTYRTFISPE | ELIKKLQYRY | EKFSPFADTF | KKRVSKNTFF | VLVRVVDELC | LVELTEEILK | LLMELVFRLV | CNGELSLARV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LRKNILDKVD | QKKLLRCATS | SQPLAARGVA | ARPGTLHDFH | SHEIAEQLTL | LDAELFYKIE | IPEVLLWAKE | QNEEKSPNLT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QFTEHFNNMS | YWVRSIIMLQ | EKAQDRERLL | LKFIKIMKHL | RKLNNFNSYL | AILSALDSAP | IRRLEWQKQT | SEGLAEYCTL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| IDSSSSFRAY | RAALSEVEPP | CIPYLGLILQ | DLTFVHLGNP | DYIDGKVNFS | KRWQQFNILD | SMRCFQQAHY | DMRRNDDIIN |
| 1050 | 1060 | 1070 | 1080 | | | | |
| FFNDFSDHLA | EEALWELSLK | IKPRNITRRK | TDREEKT | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2613 | 3 | 885.4451 | -28.15 | 2 | 62.7 | 13.1 | 1 | 292-308 | R.QSAPSPTRVAVVAPMSR.A | Oxidation: 15 |
| 1627 | 1 | 686.4490 | 148.95 | 2 | 48.7 | 12.7 | 1 | 630-643 | R.DPSAVSGVPGKDSR.D | |

# Detailed Protein Report

## Protein 610: protein kinase C theta type isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|544063437 | **Score:** | 25.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 77.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.68 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.98 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSNQNGQMYI QKKPTMYPPW DSTFDAHINK GRVMQIIVKG KNVDLISETT VELYSLAERC RKNNGKTEIW LELKPQGRML
        90        100        110        120        130        140        150        160
MNARYFLEMS DTKDMNEFET EGFFALHQRR GAIKQAKVHH VKCHEFTATF FPQPTFCSVC HEFVWGLNKQ GYQCRQCNAA
       170        180        190        200        210        220        230        240
IHKKCIDKVI AKCTGSAINS RETMFHKERF KIDMPHRFKV YNYKSPTFCE HCGTLLWGLA RQGLKCDACG MNVHHRCQTK
       250        260        270        280        290        300        310        320
VANLCGINQK LMAEALAMIE STQQARCLRD TEQIFREGPV EIGLPCSIKN EARPPCLPTP GKREPQGISW ESPLDEVDKM
       330        340        350        360        370        380        390        400
CHLPEPELNK ERPSLQIKLK IEDFILHKML GKGSFGKVFL AEFKKTNQFF AIKALKKDVV LMDDDVECTM VEKRVLSLAW
       410        420        430        440        450        460        470        480
EHPFLTHMFC TFQTKENLFF VMEYLNGGDL MYHIQSCHKF DLSRATFYAA EIILGLQFLH SKGIVYRDLK LDNILLDKDG
       490        500        510        520        530        540        550        560
HIKIADFGMC KENMLGDAKT NTFCGTPDYI APEILLGQKY NHSVDWWSFG VLLYEMLIGQ SPFHGQDEEE LFHSIRMDNP
       570        580        590        600        610        620        630        640
FYPRWLEKEA KDLLVKLFVR EPEKRLGVRG DIRQHPLFRE INWEELERKE IDPPFRPKVK SPFDCSNFDK EFLNEKPRLS
       650        660        670        680
FADRALINSM DQNMFRNFSF MNPGMERLIS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1283 | 1 | 729.3578 | 39.18 | 2 | 46.2 | 11.3 | 0 | 1-12 | -.MSNQNGQMYIQK.K | Oxidation: 1 | WUP:QUP 0.98<br>QU:MU 0.68 |

# Detailed Protein Report

## Protein 611: PREDICTED: histone deacetylase 11 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578806599 | **Score:** | 25.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 30.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.9 |
| | | **Sequence Coverage [%]:** | 9.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.26 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLHTTQLYQH | VPETRWPIVY | SPRYNITFMG | LEKLHPFDAG | KWGKVINFLK | EEKLLSDSML | VEAREASEED | LLVVHTRRYL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NELKWSFAVA | TITEIPPVIF | LPNFLVQRKV | LRPLRTQTGG | TIMAGKLAVE | RGWAINVEAI | RRKVELEWGT | EDDEYLDKVE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RNIKKSLQEH | LPDVVVYNAG | TDILEGDRLG | GLSISPAGIV | KRDELVFRMV | RGRRVPILMV | TSGGYQKRTA | RIIADSILNL |
| 250 | 260 | 270 | | | | | |
| FGLGLIGPES | PSVSAQNSDT | PLLPPAVP | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 653 | 1 | 564.6821 | -229.40 | 2 | 38.2 | 10.2 | 0 | 132-141 | R.GWAINVEAIR.R | | WUP:QUP 0.26 |

# Detailed Protein Report

## Protein 612: E3 ubiquitin-protein ligase BRE1A [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|34878777 | **Score:** | 25.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 113.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSGIGNKRAA | GEPGTSMPPE | KKAAVEDSGT | TVETIKLGGV | SSTEELDIRT | LQTKNRKLAE | MLDQRQAIED | ELREHIEKLE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RRQATDDASL | LIVNRYWSQF | DENIRIILKR | YDLEQGLGDL | LTERKALVVP | EPEPDSDSNQ | ERKDDRERGE | GQEPAFSFLA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TLASSSSEEM | ESQLQERVES | SRRAVSQIVT | VYDKLQEKVE | LLSRKLNSGD | NLIVEEAVQE | LNSFLAQENM | RLQELTDLLQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EKHRTMSQEF | SKLQSKVETA | ESRVSVLESM | IDDLQWDIDK | IRKREQRLNR | HLAEVLERVN | SKGYKVYGAG | SSLYGGTITI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NARKFEEMNA | ELEENKELAQ | NRLCELEKLR | QDFEEVTTQN | EKLKVELRSA | VEQVVKETPE | YRCMQSQFSV | LYNESLQLKA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HLDEARTLLH | GTRGTHQHQV | ELIERDEVSL | HKKLRTEVIQ | LEDTLAQVRK | EYEMLRIEFE | QTLAANEQAG | PINREMRHLI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SSLQNHNHQL | KGEVLRYKRK | LREAQSDLNK | TRLRSGSALL | QSQSSTEDPK | DEPAELKPDS | EDLSSQSSAS | KASQEDANEI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KSKRDEEERE | RERREKERER | EREREKEKER | EREKQKLKES | EKERDSAKDK | EKGKHDDGRK | KEAEIIKQLK | IELKKAQESQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KEMKLLLDMY | RSAPKEQRDK | VQLMAAEKKS | KAELEDLRQR | LKDLEDKEKK | ENKKMADEDA | LRKIRAVEEQ | IEYLQKKLAM |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AKQEEEALLS | EMDVTGQAFE | DMQEQNIRLM | QQLREKDDAN | FKLMSERIKS | NQIHKLLKEE | KEELADQVLT | LKTQVDAQLQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VVRKLEEKEH | LLQSNIGTGE | KELGLRTQAL | EMNKRKAMEA | AQLADDLKAQ | LELAQKKLHD | FQDEIVENSV | TKEKDMFNFK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RAQEDISRLR | RKLETTKKPD | NVPKCDEILM | EEIKDYKARL | TCPCCNMRKK | DAVLTKCFHV | FCFECVKTRY | DTRQRKCPKC |
| 970 | 980 | | | | | | |
| NAAFGANDFH | RIYIG | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1957 | 1 | 918.3405 | -92.02 | 2 | 52.8 | 13.9 | 2 | 956-971 | R.KCPKCNAAFGANDFHR.I | Carbamidomethyl: 5 |

# Detailed Protein Report

## Protein 613: PREDICTED: rho guanine nucleotide exchange factor 18 isoform X6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578833130 | **Score:** | 25.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 149.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEDLSLDLGA | LQGSEYLQDL | GLGAPSHSQP | GETPDSRPTG | EEPGRDSLFS | SLAGSQDLSR | RRSWERSRSC | SESWRRLSLD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ASAVDEEPCL | PRTLASLALN | LPGGGLKTWT | QGCLSGGGTP | AESPGKECDS | PKKRGRSRSV | PVSFYEIRSP | EISPGLEVPT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PPVQGLEPPV | LECMEKDHVE | PDHVLIVQQV | LQELRQYHGA | RQRACMSASP | GGAHSNLTWF | EFLSESEDGA | GKNEKSDKST |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SVKRRLSCLR | SRVTRQKEKG | KSPAHLKDKG | QDARERRECV | NGHQLLQGTF | SGPSSCPLCG | KPFLSSASLK | EHPRGTLLSD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GSPALSRNVG | MTVSQKGGPQ | PTPSPAGPGT | QLGPITGEMD | EADSAFLKFK | QTADDSLSLT | SPNTESIFVE | DPYTASLRSE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IESDGHEFEA | ESWSLAVDAA | YAKKQKREVV | KRQDVLYELM | QTEVHHVRTL | KIMLKVYSRA | LQEELQFSSK | AIGRLFPCAD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DLLETHSHFL | ARLKERRQES | LEEGSDRNYV | IQKIGDLLVQ | QFSGENGERM | KEKYGVFCSG | HNEAVSHYKL | LLQQNKKFQN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LIKKIGNFSI | VRRLGVQECI | LLVTQRITKY | PVLVERIIQN | TEAGTEDYED | LTQALNLIKD | IISQVDAKVS | ECEKGQRLRE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IAGKMDLKSS | SKLKNGLTFR | KEDMLQRQLH | LEGMLCWKTT | SGRLKDILAI | LLTDVLLLLQ | EKDQKYVFAS | VDSKPPVISL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QKLIVREVAN | EEKAMFLISA | SLQGPEMYEI | YTSSKEDRNA | WMAHIQRAVE | SCPDEEEGPF | SLPEEERKVV | EARATRLRDF |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QERLSMKDQL | IAQSLLEKQQ | IYLEMAEMGG | LEDLPQPRGL | FRGGDPSETL | QGELILKSAM | SEIEGIQSLI | CRQLGSANGQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| AEDGGSSTGP | PRRAETFAGY | DCTNSPTKNG | SFKKKVSSTD | PRPRDWRGPP | NSPDLKLSDS | DIPGSSEESP | QVVEAPGTES |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DPRLPTVLES | ELVQRIQTLS | QLLLNLQAVI | AHQDSYVETQ | RAAIQEREKQ | FRLQSTRGNL | LLEQERQRNF | EKQREERAAL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EKLQSQLRHE | QQRWERERQW | QHQELERAGA | RLQEREGEAR | QLRERLEQER | AELERQRQAY | QHDLERLREA | QRAVERERER |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LELLRRLKKQ | NTAPGALPPD | TLAEAQPPSH | PPSFNGEGLE | GPRVSMLPSG | VGPEYAERPE | VARRDSAPTE | NRLAKSDVPI |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| QLLSATNQFQ | RQAAVQQQIP | TKLAASTKGG | KDKGGKSRGS | QRWESSASFD | LKQQLLLNKL | MGKDESTSRN | RRSLSPILPG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | |
| RHSPAPPPDP | GFPAPSPPPA | DSPSEGFSLK | AGGTALLPGP | PAPSPLPATP | LSAKEDASKE | DVIFF | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1663 | 1 | 720.3283 | -79.69 | 2 | 51.1 | 10.6 | 1 | 137-148 | R.SRSVPVSFYEIR.S | |
| 2777 | 1 | 899.4794 | 83.49 | 2 | 65.9 | 15.1 | 0 | 534-549 | K.YGVFCSGHNEAVSHYK.L | |

# Detailed Protein Report

## Protein 614: complement component C7 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|45580688 | **Score:** | 25.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 93.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 4.4 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***QU:MU*** **Median:** 1.04 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKVISLFILV | GFIGEFQSFS | SASSPVNCQW | DFYAPWSECN | GCTKTQTRRR | SVAVYGQYGG | QPCVGNAFET | QSCEPTRGCP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TEEGCGERFR | CFSGQCISKS | LVCNGDSDCD | EDSADEDRCE | DSERRPSCDI | DKPPPNIELT | GNGYNELTGQ | FRNRVINTKS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FGGQCRKVFS | GDGKDFYRLS | GNVLSYTFQV | KINNDFNYEF | YNSTWSYVKH | TSTEHTSSSR | KRSFFRSSSS | SSRSYTSHTN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EIHKGKSYQL | LVVENTVEVA | QFINNNPEFL | QLAEPFWKEL | SHLPSLYDYS | AYRRLIDQYG | THYLQSGSLG | GEYRVLFYVD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SEKLKQNDFN | SVEEKKCKSS | GWHFVVKFSS | HGCKELENAL | KAASGTQNNV | LRGEPFIRGG | GAGFISGLSY | LELDNPAGNK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RRYSAWAESV | TNLPQVIKQK | LTPLYELVKE | VPCASVKKLY | LKWALEEYLD | EFDPCHCRPC | QNGGLATVEG | THCLCHCKPY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TFGAACEQGV | LVGNQAGGVD | GGWSCWSSWS | PCVQGKKTRS | RECNNPPPSG | GGRSCVGETT | ESTQCEDEEL | EHLRLLEPHC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FPLSLVPTEF | CPSPPALKDG | FVQDEGTMFP | VGKNVVYTCN | EGYSLIGNPV | ARCGEDLRWL | VGEMHCQKIA | CVLPVLMDGI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QSHPQKPFYT | VGEKVTVSCS | GGMSLEGPSA | FLCGSSLKWS | PEMKNARCVQ | KENPLTQAVP | KCQRWEKLQN | SRCVCKMPYE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CGPSLDVCAQ | DERSKRILPL | TVCKMHVLHC | QGRNYTLTGR | DSCTLPASAE | KACGACPLWG | KCDAESSKCV | CREASECEEE |
| 810 | 820 | 830 | 840 | 850 | | | |
| GFSICVEVNG | KEQTMSECEA | GALRCRGQSI | SVTSIRPCAA | ETQ | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1397 | 1 | 786.4380 | 113.40 | 3 | 47.6 | 11.7 | 2 | 717-736 | K.MPYECGPSLDVCAQDERSKR.I | Carbamidomethyl: 5; Oxidation: 1 | |
| 2693 | 1 | 559.3108 | 17.19 | 4 | 64.8 | 14.1 | 2 | 736-753 | K.RILPLTVCKMHVLHCQGR.N | Carbamidomethyl: 8, 15; Oxidation: 10 | QU:MU 1.04 |

# Detailed Protein Report

**Protein 615:** **latent-transforming growth factor beta-binding protein 4 isoform c precursor [Homo sapiens]**

**Accession:** gi|110347437
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 25.8
**MW [kDa]:** 165.6
**pI:** 4.8
**Sequence Coverage [%]:** 1.9
**No. of unique Peptides:** 2

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.68 | **CV:** | 40.93 % | **No. of Peptides:** | 2 |
| ***WUP:QUP*** | **Median:** | 1.94 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAGGVRLLWV | SLLVLLAQLG | PQPGLGRLGE | RLRVRFTPVV | CGLRCVHGPT | GSRCTPTCAP | RNATSVDSGA | PGGAAPGGPG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FRAFLCPLIC | HNGGVCVKPD | RCLCPPDFAG | KFCQLHSSGA | RPPAPAVPGL | TRSVYTMPLA | NHRDDEHGVA | SMVSVHVEHP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QEASVVVHQV | ERVSGPWEEA | DAEAVARAEA | AARAEAAAPY | TVLAQSAPRE | DGYSDASGFG | YCFRELRGGE | CASPLPGLRT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QEVCCRGAGL | AWGVHDCQLC | SERLGNSERV | SAPDGPCPTG | FERVNGSCED | VDECATGGRC | QHGECANTRG | GYTCVCPDGF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LLDSSRSSCI | SQHVISEAKG | PCFRVLRDGG | CSLPILRNIT | KQICCCSRVG | KAWGRGCQLC | PPFGSEGFRE | ICPAGPGYHY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SASDLRYNTR | PLGQEPPRVS | LSQPRTLPAT | SRPSAGFLPT | HRLEPRPEPR | PDPRPGPELP | LPSIPAWTGP | EIPESGPSSG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| MCQRNPQVCG | PGRCISRPSG | YTCACDSGFR | LSPQGTRCID | VDECRRVPPP | CAPGRCENSP | GSFRCVCGPG | FRAGPRAAEC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LDVDECHRVP | PPCDLGRCEN | TPGSFLCVCP | AGYQAAPHGA | SCQDVDECTQ | SPGLCGRGAC | KNLPGSFRCV | CPAGFRGSAC |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EEDVDECAQE | PPPCGPGRCD | NTAGSFHCAC | PAGFRSRGPG | APCQDVDECA | RSPPPCTYGR | CENTEGSFQC | VCPMGFQPNT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AGSECEDVDE | CENHLACPGQ | ECVNSPGSFQ | CRTCPSGHHL | HRGRCTDVDE | CSSGAPPCGP | HGHCTNTEGS | FRCSCAPGYR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| APSGRPGPCA | DVNECLEGDF | CFPHGECLNT | DGSFACTCAP | GYRPGPRGAS | CLDVDECSEE | DLCQSGICTN | TDGSFECICP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PGHRAGPDLA | SCLDVDECRE | RGPALCGSQR | CENSPGSYRC | VRDCDPGYHA | GPEGTCDDVD | ECQEYGPEIC | GAQRCENTPG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SYRCTPACDP | GYQPTPGGGC | QDVDECRNRS | FCGAHAVCQN | LPGSFQCLCD | QGYEGARDGR | HCVDVNECET | LQGVCGAALC |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ENVEGSFLCV | CPNSPEEFDP | MTGRCVPPRT | SAGTFPGSQP | QAPASPVLPA | RPPPPPLPRR | PSTPRQGPVG | SGRRECYFDT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| AAPDACDNIL | ARNVTWQECC | CTVGEGWGSG | CRIQQCPGTE | TAEYQSLCPH | GRGYLAPSGD | LSLRRDVDEC | QLFRDQVCKS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| GVCVNTAPGY | SCYCSNGYYY | HTQRLECIDN | DECADEEPAC | EGGRCVNTVG | SYHCTCEPPL | VLDGSQRRCV | SNESQSLDDN |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LGVCWQEVGA | DLVCSHPRLD | RQATYTECCC | LYGEAWGMDC | ALCPAQDSDD | FEALCNVLRP | PAYSPPRPGG | FGLPYEYGPD |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LGPPYQGLPY | GPELYPPPAL | PYDPYPPPPG | PFARREAPYG | APRFDMPDFE | DDGGPYGESE | APAPPGPGTR | WPYRSRDTRR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SFPEPEEPPE | GGSYAGSLAE | PYEELEAEEC | GILDGCTNGR | CVRVPEGFTC | RCFDGYRLDM | TRMACVDINE | CDEAEAASPL |
| 1530 | 1540 | 1550 | 1560 | | | | |
| CVNARCLNTD | GSFRCICRPG | FAPTHQPHHC | APARPRA | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 407 | 1 | 846.5265 | 154.58 | 2 | 33.7 | 10.2 | 1 | 511-525 | R.LSPQGTRCIDVDECR.R | | WUP:QUP 1.94 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | QU:MU 1.00 |
| 1279 | 1 | 955.9599 | 14.50 | 2 | 46.1 | 15.5 | 2 | 1185-1199 | R.RDVDECQLFRDQVCK.S | Carbamidomethyl: 6 | QU:MU 0.46 |

# Detailed Protein Report

**Protein 616:** **NF-kappa-B inhibitor zeta isoform a [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|13899229 | **Score:** | 25.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 78.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 4.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MIVDKLLDDS | RGGEGLRDAA | GGCGLMTSPL | NLSYFYGASP | PAAAPGACDA | SCSVLGPSAP | GSPGSDSSDF | SSASSVSSCG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AVESRSRGGA | RAERQPVEPH | MGVGRQQRGP | FQGVRVKNSV | KELLLHIRSH | KQKASGQAVD | DFKTQGVNIE | QFRELKNTVS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YSGKRKGPDS | LSDGPACKRP | ALLHSQFLTP | PQTPTPGESM | EDVHLNEPKQ | ESSADLLQNI | INIKNECSPV | SLNTVQVSWL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NPVVVPQSSP | AEQCQDFHGG | QVFSPPQKCQ | PFQVRGSQQM | IDQASLYQYS | PQNQHVEQQP | HYTHKPTLEY | SPFPIPPQSP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AYEPNLFDGP | ESQFCPNQSL | VSLLGDQRES | ENIANPMQTS | SSVQQQNDAH | LHSFSMMPSS | ACEAMVGHEM | ASDSSNTSLP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FSNMGNPMNT | TQLGKSLFQW | QVEQEESKLA | NISQDQFLSK | DADGDTFLHI | AVAQGRRALS | YVLARKMNAL | HMLDIKEHNG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QSAFQVAVAA | NQHLIVQDLV | NIGAQVNTTD | CWGRTPLHVC | AEKGHSQVLQ | AIQKGAVGSN | QFVDLEATNY | DGLTPLHCAV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IAHNAVVHEL | QRNQQPHSPE | VQELLLKNKS | LVDTIKCLIQ | MGAAVEAKDR | KSGRTALHLA | AEEANLELIR | LFLELPSCLS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FVNAKAYNGN | TALHVAASLQ | YRLTQLDAVR | LLMRKGADPS | TRNLENEQPV | HLVPDGPVGE | QIRRILKGKS | IQQRAPPY |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1761 | 1 | 823.3000 | -143.58 | 2 | 52.3 | 10.0 | 2 | 129-143 | R.SHKQKASGQAVDDFK.T | |

# Detailed Protein Report

## Protein 617: zinc finger protein 471 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|150170667 | **Score:** | 25.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 73.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| | | **Sequence Coverage [%]:** | 4.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNVEVVKVMP | QDLVTFKDVA | IDFSQEEWQW | MNPAQKRLYR | SMMLENYQSL | VSLGLCISKP | YVISLLEQGR | EPWEMTSEMT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RSPFSDWESI | YVTQELPLKQ | FMYDDACMEG | ITSYGLECST | FEENWKWEDL | FEKQMGSHEM | FSKKEIITHK | ETITKETEFK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YTKFGKCIHL | ENIEESIYNH | TSDKKSFSKN | SMVIKHKKVY | VGKKLFKCNE | CDKTFTHSSS | LTVHFRIHTG | EKPYACEECG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KAFKQRQHLA | QHHRTHTGEK | LFECKECRKA | FKQSEHLIQH | QRIHTGEKPY | KCKECRKAFR | QPAHLAQHQR | IHTGEKPYEC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KECGKAFSDG | SSFARHQRCH | TGKRPYECIE | CGKAFRYNTS | FIRHWRSYHT | GEKPFNCIDC | GKAFSVHIGL | ILHRRIHTGE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KPYKCGVCGK | TFSSGSSRTV | HQRIHTGEKP | YECDICGKDF | SHHASLTQHQ | RVHSGEKPYE | CKECGKAFRQ | NVHLVSHLRI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HTGEKPYECK | ECGKAFRISS | QLATHQRIHT | GEKPYECIEC | GNAFKQRSHL | AQHQKTHTGE | KPYECNECGK | AFSQTSNLTQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| HQRIHTGEKP | YKCTECGKAF | SDSSSCAQHQ | RLHTGQRPYQ | CFECGKAFRR | KLSLICHQRS | HTGEEP | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 442 | 3 | 690.4633 | 161.23 | 2 | 34.0 | 15.1 | 1 | 357-366 | R.YNTSFIRHWR.S | |

# Detailed Protein Report

**Protein 618:** **PREDICTED: glycylpeptide N-tetradecanoyltransferase 2 isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578818655 | **Score:** | 25.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 50.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAEDSESAAS | QQSLELDDQD | TCGIDGDNEE | ETEHAKGSPG | GYLGAKKKKK | KQKRKKEKPN | SGGTKSDSAS | DSQEIKIQQP |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| SKNPSVPMQK | LQDIQRAMEL | LSACQGPARN | IDEAAKHRYQ | FWDTQPVPKL | DEVITSHGAI | EPDKDNVRQE | PYSLPQGFMW |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| DTLDLSDAEV | LKELYTLLNE | NYVEDDDNMF | RFDYSPEFLL | WALRPPGWLL | QWHCGVRVSS | NKKLVGFISA | IPANIRIYDR |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| YWHRSLNPRK | LVEVKFSHLS | RNMTLQRTMK | LYRLPDVTKT | SGLRPMEPKD | IKSVRELINT | YLKQFHLAPV | MDEEEVAHWF |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| LPREHIIDTF | VVESPNGKLT | DFLSFYTLPS | TVMHHPAHKS | LKAAYSFYNI | HTETPLLDLM | SDALILAKSK | GFDVFNALDL |
| **410** | **420** | **430** | **440** | **450** | | | |
| MENKTFLEKL | KFGIGDGNLQ | YYLYNWRCPG | TDSEKVGLVL | Q | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1331 | 1 | 721.8048 | -169.98 | 2 | 46.2 | 14.7 | 2 | 250-261 | R.KLVEVKFSHLSR.N | |

# Detailed Protein Report

## Protein 619: PREDICTED: ALS2 C-terminal-like protein isoform X7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578805946 | **Score:** | 25.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 58.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 5.2 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MCNPEEAALL | RLEEVFSATL | AHVNSLVLQP | LLPAAPDPSD | PWGRECLRLL | QQLHKSSQQL | WEVTEESLHS | LQERLRYPDS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TGLESLLLLR | GADRVLQAHI | EYIESYTSCM | VVQAFQKAAK | RRSEYWRGQR | KALRQLLSGV | SSEGSVGASL | GQALHQPLAH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HVQQYVLLLL | SLGDTIGEHH | PTRELVVNAV | TLFGNLQSFM | KQELDQAVAT | QALWHTLRGR | LRDVLCTPAH | RLLQDSQDVP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VTVAPLRAER | VLLFDDALVL | LQGHNVHTFD | LKLVWVDPGQ | DGCTFHLLTP | EEEFSFCAKD | SQGQAVWQWK | VTWAVHQALH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GKKDFPVLGA | GLEPSQPPDC | RCAEYTFQAE | GRLCQATYEG | EWCRGRPHGK | GTLKWPDGRN | HVGNFCQGLE | HGFGIRLLPQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ASEDKFDCYK | CHWREGSMCG | YGICTAPTRC | TRATSRRACG | TDLGSLRVVR | RPPSPSGTRA | TGRGARGAAM | ALRRMVTEVS |
| 490 | 500 | 510 | 520 | 530 | | | |
| ATLACGRLVS | ATAQGSWSPR | QVSATRAPSR | RTRRCVSLVN | DK | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1521 | 1 | 828.8811 | -23.41 | 2 | 49.2 | 13.7 | 1 | 397-410 | R.LLPQASEDKFDCYK.C | |

# Detailed Protein Report

## Protein 620: spectrin alpha chain, non-erythrocytic 1 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|306966132 | **Score:** | 25.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 282.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| | | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.28 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.55 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDPSGVKVLE | TAEDIQERRQ | QVLDRYHRFK | ELSTLRRQKL | EDSYRFQFFQ | RDAEELEKWI | QEKLQIASDE | NYKDPTNLQG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KLQKHQAFEA | EVQANSGAIV | KLDETGNLMI | SEGHFASETI | RTRLMELHRQ | WELLLEKMRE | KGIKLLQAQK | LVQYLRECED |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VMDWINDKEA | IVTSEELGQD | LEHVEVLQKK | FEEFQTDMAA | HEERVNEVNQ | FAAKLIQEQH | PEEELIKTKQ | DEVNAAWQRL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KGLALQRQGK | LFGAAEVQRF | NRDVDETISW | IKEKEQLMAS | DDFGRDLASV | QALLRKHEGL | ERDLAALEDK | VKALCAEADR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LQQSHPLSAT | QIQVKREELI | TNWEQIRTLA | AERHARLNDS | YRLQRFLADF | RDLTSWVTEM | KALINADELA | SDVAGAEALL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DRHQEHKGEI | DAHEDSFKSA | DESGQALLAA | GHYASDEVRE | KLTVLSEERA | ALLELWELRR | QQYEQCMDLQ | LFYRDTEQVD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NWMSKQEAFL | LNEDLGDSLD | SVEALLKKHE | DFEKSLSAQE | EKITALDEFA | TKLIQNNHYA | MEDVATRRDA | LLSRRNALHE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RAMRRRAQLA | DSFHLQQFFR | DSDELKSWVN | EKMKTATDEA | YKDPSNLQGK | VQKHQAFEAE | LSANQSRIDA | LEKAGQKLID |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VNHYAKDEVA | ARMNEVISLW | KKLLEATELK | GIKLREANQQ | QQFNRNVEDI | ELWLYEVEGH | LASDDYGKDL | TNVQNLQKKH |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ALLEADVAAH | QDRIDGITIQ | ARQFQDAGHF | DAENIKKKQE | ALVARYEALK | EPMVARKQKL | ADSLRLQQLF | RDVEDEETWI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| REKEPIAAST | NRGKDLIGVQ | NLLKKHQALQ | AEIAGHEPRI | KAVTQKGNAM | VEEGHFAAED | VKAKLHELNQ | KWEALKAKAS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QRRQDLEDSL | QAQQYFADAN | EAESWMREKE | PIVGSTDYGK | DEDSAEALLK | KHEALMSDLS | AYGSSIQALR | EQAQSCRQQV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| APTDDETGKE | LVLALYDYQE | KSPREVTMKK | GDILTLLNST | NKDWWKVEVN | DRQGFVPAAY | VKKLDPAQSA | SRENLLEEQG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SIALRQEQID | NQYHSLLELG | EKRKGMLEKS | CKKFMLFREA | NELQQWINEK | EAALTSEEVG | ADLEQVEVLQ | KKFDDFQKDL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KANESRLKDI | NKVAEDLESE | GLMAEEVQAV | QQQEVYGMMP | RDETDSKTAS | PWKSARLMVH | TVATFNSIKE | LNERWRSLQQ |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LAEERSQLLG | SAHEVQRFHR | DADETKEWIE | EKNQALNTDN | YGHDLASVQA | LQRKHEGFER | DLAALGDKVN | SLGETAERLI |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| QSHPESAEDL | QEKCTELNQA | WSSLGKRADQ | RKAKLGDSHD | LQRFLSDFRD | LMSWINGIRG | LVSSDELAKD | VTGAEALLER |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| HQEHRTEIDA | RAGTFQAFEQ | FGQQLLAHGH | YASPEIKQKL | DILDQERADL | EKAWVQRRMM | LDQCLELQLF | HRDCEQAENW |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| MAAREAFLNT | EDKGDSLDSV | EALIKKHEDF | DKAINVQEEK | IAALQAFADQ | LIAAGHYAKG | DISSRRNEVL | DRWRRLKAQM |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| IEKRSKLGES | QTLQQFSRDV | DEIEAWISEK | LQTASDESYK | DPTNIQSKHQ | KHQAFEAELH | ANADRIRGVI | DMGNSLIERG |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| ACAGSEDAVK | ARLAALADQW | QFLVQKSAEK | SQKLKEANKQ | QNFNTGIKDF | DFWLSEVEAL | LASEDYGKDL | ASVNNLLKKH |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| QLLEADISAH | EDRLKDLNSQ | ADSLMTSSAF | DTSQVKDKRD | TINGRFQKIK | SMAASRRAKL | NESHRLHQFF | RDMDDEESWI |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| KEKKLLVGSE | DYGRDLTGVQ | NLRKKHKRLE | AELAAHEPAI | QGVLDTGKKL | SDDNTIGKEE | IQQRLAQFVE | HWKELKQLAA |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| ARGQRLEESL | EYQQFVANVE | EEEAWINEKM | TLVASEDYGD | TLAAIQGLLK | KHEAFETDFT | VHKDRVNDVC | TNGQDLIKKN |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| NHHEENISSK | MKGLNGKVSD | LEKAAAQRKA | KLDENSAFLQ | FNWKADVVES | WIGEKENSLK | TDDYGRDLSS | VQTLLTKQET |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| FDAGLQAFQQ | EGIANITALK | DQLLAAKHVQ | SKAIEARHAS | LMKRWSQLLA | NSAARKKKLL | EAQSHFRKVE | DLFLTFAKKA |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| SAFNSWFENA | EEDLTDPVRC | NSLEEIKALR | EAHDAFRSSL | SSAQADFNQL | AELDRQIKSF | RVASNPYTWF | TMEALEETWR |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2184 | 3 | 873.3319 | -120.21 | 2 | 57.2 | 11.5 | 1 | 1810-1824 | K.LSDDNTIGKEEIQQR.L |  | QU:MU 1.28<br>WUP:QUP 1.55 |

# Detailed Protein Report

## Protein 621: mucin-17 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|91982772 | **Score:** | 25.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 451.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 3.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.6 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPRPGTMALC | LLTLVLSLLP | PQAAAEQDLS | VNRAVWDGGG | CISQGDVLNR | QCQQLSQHVR | TGSAANTATG | TTSTNVVEPR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MYLSCSTNPE | MTSIESSVTS | DTPGVSSTRM | TPTESRTTSE | STSDSTTLFP | SSTEDTSSPT | TPEGTDVPMS | TPSEESISST |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MAFVSTAPLP | SFEAYTSLTY | KVDMSTPLTT | STQASSSPTT | PESTTIPKST | NSEGSTPLTS | MPASTMKVAS | SEAITLLTTP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VEISTPVTIS | AQASSSPTTA | EGPSLSNSAP | SGGSTPLTRM | PLSVMLVVSS | EASTLSTTPA | ATNIPVITST | EASSSPTTAE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GTSIPTSTYT | EGSTPLTSTP | ASTMPVATSE | MSTLSITPVD | TSTLVTTSTE | PSSLPTTAEA | TSMLTSTLSE | GSTPLTNMPV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| STILVASSEA | STTSTIPVDS | KTFVTTASEA | SSSPTTAEDT | SIATSTPSEG | STPLTSMPVS | TTPVASSEAS | NLSTTPVDSK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TQVTTSTEAS | SSPPTAEVNS | MPTSTPSEGS | TPLTSMSVST | MPVASSEAST | LSTTPVDTST | PVTTSSEASS | SSTTPEGTSI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PTSTPSEGST | PLTNMPVSTR | LVVSSEASTT | STTPADSNTF | VTTSSEASSS | STTAEGTSMP | TSTYSERGTT | ITSMSVSTTL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VASSEASTLS | TTPVDSNTPV | TTSTEATSSS | TTAEGTSMPT | STYTEGSTPL | TSMPVNTTLV | ASSEASTLST | TPVDTSTPVT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TSTEASSSPT | TADGASMPTS | TPSEGSTPLT | SMPVSKTLLT | SSEASTLSTT | PLDTSTHITT | STEASCSPTT | TEGTSMPIST |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PSEGSPLLTS | IPVSITPVTS | PEASTLSTTP | VDSNSPVTTS | TEVSSSPTPA | EGTSMPTSTY | SEGRTPLTSM | PVSTTLVATS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| AISTLSTTPV | DTSTPVTNST | EARSSPTTSE | GTSMPTSTPG | EGSTPLTSMP | DSTTPVVSSE | ARTLSATPVD | TSTPVTTSTE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ATSSPTTAEG | TSIPTSTPSE | GTTPLTSTPV | SHTLVANSEA | STLSTTPVDS | NTPLTTSTEA | SSPPPTAEGT | SMPTSTPSEG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| STPLTRMPVS | TTMVASSETS | TLSTTPADTS | TPVTTYSQAS | SSSTTADGTS | MPTSTYSEGS | TPLTSVPVST | RLVVSSEAST |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LSTTPVDTSI | PVTTSTEASS | SPTTAEGTSI | PTSPPSEGTT | PLASMPVSTT | LVVSSEANTL | STTPVDSKTQ | VATSTEASSP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PPTAEVTSMP | TSTPGERSTP | LTSMPVRHTP | VASSEASTLS | TSPVDTSTPV | TTSAETSSSP | TTAEGTSLPT | STTSEGSTLL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TSIPVSTTLV | TSPEASTLLT | TPVDTKGPVV | TSNEVSSSPT | PAEGTSMPTS | TYSEGRTPLT | SIPVNTTLVA | SSAISILSTT |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PVDNSTPVTT | STEACSSPTT | SEGTSMPNSN | PSEGTTPLTS | IPVSTTPVVS | SEASTLSATP | VDTSTPGTTS | AEATSSPTTA |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EGISIPTSTP | SEGKTPLKSI | PVSNTPVANS | EASTLSTTPV | DSNSPVVTST | AVSSSPTPAE | GTSIAISTPS | EGSTALTSIP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| VSTTTVASSE | INSLSTTPAV | TSTPVTTYSQ | ASSSPTTADG | TSMQTSTYSE | GSTPLTSLPV | STMLVVSSEA | NTLSTTPIDS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KTQVTASTEA | SSSTTAEGSS | MTISTPSEGS | PLLTSIPVST | TPVASPEAST | LSTTPVDSNS | PVITSTEVSS | SPTPAEGTSM |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| PTSTYTEGRT | PLTSITVRTT | PVASSAISTL | STTPVDNSTP | VTTSTEARSS | PTTSEGTSMP | NSTPSEGTTP | LTSIPVSTTP |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| VLSSEASTLS | ATPIDTSTPV | TTSTEATSSP | TTAEGTSIPT | STLSEGMTPL | TSTPVSHTLV | ANSEASTLST | TPVDSNSPVV |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| TSTAVSSSPT | PAEGTSIATS | TPSEGSTALT | SIPVSTTTVA | SSETNTLSTT | PAVTSTPVTT | YAQVSSSPTT | ADGSSMPTST |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| PREGRPPLTS | IPVSTTTVAS | SEINTLSTTL | ADTRTPVTTY | SQASSSPTTA | DGTSMPTPAY | SEGSTPLTSM | PLSTTLVVSS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| EASTLSTTPV | DTSTPATTST | EGSSSPTTAG | GTSIQTSTPS | ERTTPLAGMP | VSTTLVVSSE | GNTLSTTPVD | SKTQVTNSTE |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| ASSSATAEGS | SMTISAPSEG | SPLLTSIPLS | TTPVASPEAS | TLSTTPVDSN | SPVITSTEVS | SSPIPTEGTS | MQTSTYSDRR |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 193 | 2 | 613.7845 | -35.89 | 2 | 32.4 | 14.1 | 0 | 51-60 | R.QCQQLSQHVR.T | |
| 490 | 1 | 636.2255 | -63.89 | 3 | 36.1 | 11.6 | 1 | 4132-4148 | R.TTTCFGDGCQNTASRCK.N | Carbamidomethyl: 9, 16 |

# Detailed Protein Report

**Protein 622:** **PREDICTED: receptor-type tyrosine-protein phosphatase F isoform X12 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578799535 | **Score:** | 25.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 192.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAPEPAPGRT | MVPLVPALVM | LGLVAGAHGD | SKPVFIKVPE | DQTGLSGGVA | SFVCQATGEP | KPRITWMKKG | KKVSSQRFEV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IEFDDGAGSV | LRIQPLRVQR | DEAIYECTAT | NSLGEINTSA | KLSVLEEEQL | PPGFPSIDMG | PQLKVVEKAR | TATMLCAAGG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NPDPEISWFK | DFLPVDPATS | NGRIKQLRSG | ALQIESSEES | DQGKYECVAT | NSAGTRYSAP | ANLYVRDQRE | VRRVAPRFSI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PPSSQEVMPG | GSVNLTCVAV | GAPMPYVKWM | MGAEELTKED | EMPVGRNVLE | LSNVVRSANY | TCVAISSLGM | IEATAQVTVK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ALPKPPIDLV | VTETTATSVT | LTWDSGNSEP | VTYYGIQYRA | AGTEGPFQEV | DGVATTRYSI | GGLSPFSEYA | FRVLAVNSIG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RGPPSEAVRA | RTGEQAPSSP | PRRVQARMLS | ASTMLVQWEP | PEEPNGLVRG | YRVYYTPDSR | RPPNAWHKHN | TDAGLLTTVG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SLLPGITYSL | RVLAFTAVGD | GPPSPTIQVK | TQQGVPAQPA | DFQAEVESDT | RIQLSWLLPP | QERIIMYELV | YWAAEDEDQQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HKVTFDPTSS | YTLEDLKPDT | LYRFQLAARS | DMGVGVFTPT | IEARTAQSTP | SAPPQKVMCV | SMGSTTVRVS | WVPPPADSRN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GVITQYSVAY | EAVDGEDRGR | HVVDGISREH | SSWDLVGLEK | WTEYRVWVRA | HTDVGPGPES | SPVLVRTDED | VPSGPPRKVE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VEPLNSTAVH | VYWKLPVPSK | QHGQIRGYQV | TYVRLENGEP | RGLPIIQDVM | LAEAQWRPEE | SEDYETTISG | LTPETTYSVT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VAAYTTKGDG | ARSKPKIVTT | TGAVFAKNFR | VAAAMKTSVL | LSWEVPDSYK | SAVPFKILYN | GQSVEVDGHS | MRKLIADLQP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| NTEYSFVLMN | RGSSAGGLQH | LVSIRTAPDL | LPHKPLPASA | YIEDGRFDLS | MPHVQDPSLV | RWFYIVVVPI | DRVGGSMLTP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RWSTPEELEL | DELLEAIEQG | GEEQRRRRRQ | AERLKPYVAA | QLDVLPETFT | LGDKKNYRGF | YNRPLSPDLS | YQCFVLASLK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EPMDQKRYAS | SPYSDEIVVQ | VTPAQQQEEP | EMLWVTGPVL | AVILIILIVI | AILLFKRKRT | HSPSSKDEQS | IGLKDSLLAH |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SSDPVEMRRL | NYQTPGSSVP | SCPNTSSMRD | HPPIPITDLA | DNIERLKAND | GLKFSQEYES | IDPGQQFTWE | NSNLEVNKPK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| NRYANVIAYD | HSRVILTSID | GVPGSDYINA | NYIDGYRKQN | AYIATQGPLP | ETMGDFWRMV | WEQRTATVVM | MTRLEEKSRV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KCDQYWPARG | TETCGLIQVT | LLDTVELATY | TVRTFALHKS | GSSEKRELRQ | FQFMAWPDHG | VPEYPTPILA | FLRRVKACNP |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LDAGPMVVHC | SAGVGRTGCF | IVIDAMLERM | KHEKTVDIYG | HVTCMRSQRN | YMVQTEDQYV | FIHEALLEAA | TCGHTEVPAR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| NLYAHIQKLG | QVPPGESVTA | MELEFKLLAS | SKAHTSRFIS | ANLPCNKFKN | RLVNIMPYEL | TRVCLQPIRG | VEGSDYINAS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| FLDGYRQQKA | YIATQGPLAE | STEDFWRMLW | EHNSTIIVML | TKLREMGREK | CHQYWPAERS | ARYQYFVVDP | MAEYNMPQYI |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LREFKVTDAR | DGQSRTIRQF | QFTDWPEQGV | PKTGEGFIDF | IGQVHKTKEQ | FGQDGPITVH | CSAGVGRTGV | FITLSIVLER |
| 1690 | 1700 | 1710 | 1720 | 1730 | | | |
| MRYEGVVDMF | QTVKTLRTQR | PAMVQTEDQY | QLCYRAALEY | LGSFDHYAT | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2797 | 1 | 1024.5150 | 17.18 | 2 | 65.4 | 15.2 | 2 | 1390-1406 | R.MKHEKTVDIYGHVTCMR.S | |

# Detailed Protein Report

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**Protein 623:** **PREDICTED: cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578812355 | **Score:** | 25.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 87.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 3.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MATLYGLTDE | KVKAYLSLHP | QVLDEFVSES | VSAETVEKWL | KRKNNKSEDE | SAPKEVSRYQ | DTNMQGVVYE | LNSYIEQRLD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TGGDNQLLLY | ELSSIIKIAT | KADGFALYFL | GECNNSLCIF | TPPGIKEGKP | RLIPAGPITQ | GTTVSAYVAK | SRKTLLVEDI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LGDERFPRGT | GLESGTRIQS | VLCLPIVTAI | GDLIGILELY | RHWGKEAFCL | SHQEVATANL | AWASVAIHQV | QVCRGLAKQT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ELNDFLLDVS | KTYFDNIVAI | DSLLEHIMIY | AKNLVNADRC | ALFQVDHKNK | ELYSDLFDIG | EEKEGKPVFK | KTKEIRFSIE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KGIAGQVART | GEVLNIPDAY | ADPRFNREVD | LYTGYTTRNI | LCMPIVSRGS | VIGVVQMVNK | ISGSAFSKTD | ENNFKMFAVF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CALALHCANM | YHRIRHSECI | YRVTMEKLSY | HSICTSEEWQ | GLMQFTLPVR | LCKEIELFHF | DIGPFENMWP | GIFVYMVHRS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CGTSCFELEK | LCRFIMSVKK | NYRRVPYHNW | KHAVTVAHCM | YAILQNNHTL | FTDLERKGLL | IACLCHDLDH | RGFSNSYLQK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FDHPLAALYS | TSTMEQHHFS | QTVSILQLEG | HNIFSTLSSS | EYEQVLEIIR | KAIIATDLAL | YFGNRKQLEE | MYQTGSLNLN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NQSHRDRVIG | LMMTACDLCS | VTKLWPVTKL | TANDIYAEFW | AEGDEMKKLG | IQPIPMMDRD | KKDEVPQGQL | GFYNAVAIPC |
| 730 | 740 | 750 | 760 | 770 | 780 | | |
| YTTLTQILPP | TEPLLKACRD | NLSQWEKVIR | GEETATWISS | PSVAQKAAAS | ED | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2459 | 1 | 1014.8801 | -101.31 | 2 | 60.6 | 12.6 | 1 | 646-663 | R.DRVIGLMMTACDLCSVTK.L | Carbamidomethyl: 11;<br>Oxidation: 7 |

# Detailed Protein Report

**Protein 624:** **tubulin beta-4B chain [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5174735 | **Score:** | 25.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 9.2 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MREIVHLQAG | QCGNQIGAKF | WEVISDEHGI | DPTGTYHGDS | DLQLERINVY | YNEATGGKYV | PRAVLVDLEP | GTMDSVRSGP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FGQIFRPDNF | VFGQSGAGNN | WAKGHYTEGA | ELVDSVLDVV | RKEAESCDCL | QGFQLTHSLG | GGTGSGMGTL | LISKIREEYP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DRIMNTFSVV | PSPKVSDTVV | EPYNATLSVH | QLVENTDETY | CIDNEALYDI | CFRTLKLTTP | TYGDLNHLVS | ATMSGVTTCL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RFPGQLNADL | RKLAVNMVPF | PRLHFFMPGF | APLTSRGSQQ | YRALTVPELT | QQMFDAKNMM | AACDPRHGRY | LTVAAVFRGR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MSMKEVDEQM | LNVQNKNSSY | FVEWIPNNVK | TAVCDIPPRG | LKMSATFIGN | STAIQELFKR | ISEQFTAMFR | RKAFLHWYTG |
| 410 | 420 | 430 | 440 | 450 | | | |
| EGMDEMEFTE | AESNMNDLVS | EYQQYQDATA | EEEGEFEEEA | EEEVA | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1621 | 1 | 1061.1775 | -37.83 | 3 | 50.0 | 12.9 | 2 | 351-379 | K.TAVCDIPPRGLKMSATFIGNSTAIQELFK.R | Carbamidomethyl: 4;<br>Oxidation: 13 |

# Detailed Protein Report

## Protein 625: double-stranded RNA-specific adenosine deaminase isoform d [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|70167113 | **Score:** | 25.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 103.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578800414 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: double-stranded RNA-specific adenosine deaminase isoform X5 [Homo sapiens] |
| gi\|578800412 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: double-stranded RNA-specific adenosine deaminase isoform X4 [Homo sapiens] |
| gi\|578800410 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: double-stranded RNA-specific adenosine deaminase isoform X3 [Homo sapiens] |
| gi\|301601658 | refseq_human (refseq_human_20140103.fasta) | double-stranded RNA-specific adenosine deaminase isoform d [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAEIKEKICD | YLFNVSDSSA | LNLAKNIGLT | KARDINAVLI | DMERQGDVYR | QGTTPPIWHL | TDKKRERMQI | KRNTNSVPET |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| APAAIPETKR | NAEFLTCNIP | TSNASNNMVT | TEKVENGQEP | VIKLENRQEA | RPEPARLKPP | VHYNGPSKAG | YVDFENGQWA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TDDIPDDLNS | IRAAPGEFRA | IMEMPSFYSH | GLPRCSPYKK | LTECQLKNPI | SGLLEYAQFA | SQTCEFNMIE | QSGPPHEPRF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KFQVVINGRE | FPPAEAGSKK | VAKQDAAMKA | MTILLEEAKA | KDSGKSEESS | HYSTEKESEK | TAESQTPTPS | ATSFFSGKSP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VTTLLECMHK | LGNSCEFRLL | SKEGPAHEPK | FQYCVAVGAQ | TFPSVSAPSK | KVAKQMAAEE | AMKALHGEAT | NSMASDNQPE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GMISESLDNL | ESMMPNKVRK | IGELVRYLNT | NPVGGLLEYA | RSHGFAAEFK | LVDQSGPPHE | PKFVYQAKVG | GRWFPAVCAH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SKKQGKQEAA | DAALRVLIGE | NEKAERMGFT | EVTPVTGASL | RRTMLLLSRS | PEAQPKTLPL | TGSTFHDQIA | MLSHRCFNTL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TNSFQPSLLG | RKILAAIIMK | KDSEDMGVVV | SLGTGNRCVK | GDSLSLKGET | VNDCHAEIIS | RRGFIRFLYS | ELMKYNSQTA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KDSIFEPAKG | GEKLQIKKTV | SFHLYISTAP | CGDGALFDKS | CSDRAMESTE | SRHYPVFENP | KQGKLRTKVE | NGEGTIPVES |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SDIVPTWDGI | RLGERLRTMS | CSDKILRWNV | LGLQGALLTH | FLQPIYLKSV | TLGYLFSQGH | LTRAICCRVT | RDGSAFEDGL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RHPFIVNHPK | VGRVSIYDSK | RQSGKTKETS | VNWCLADGYD | LEILDGTRGT | VDGPRNELSR | VSKKNIFLLF | KKLCSFRYRR |
| 890 | 900 | 910 | 920 | 930 | 940 | | |
| DLLRLSYGEA | KKAARDYETA | KNYFKKGLKD | MGYGNWISKP | QEEKNFYLCP | V | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 5 | 1 | 1205.0611 | -63.23 | 2 | 29.5 | 11.4 | 2 | 451-472 | K.LVDQSGPPHEPKFVYQAKVGGR.W | |
| 500 | 1 | 642.6194 | -75.95 | 3 | 35.9 | 14.3 | 1 | 556-572 | R.CFNTLTNSFQPSLLGRK.I | |

# Detailed Protein Report

## Protein 626: PREDICTED: uncharacterized protein C7orf63 isoform X7 [Homo sapiens]

**Accession:** gi|578814624
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 25.6
**MW [kDa]:** 89.5
**pI:** 8.9
**Sequence Coverage [%]:** 3.5
**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MKIPSSELRI QICKCIVDFY HAEPPKKHIP GYQQASSSYK IQMAEVGGLA KTMVQSMTLL ENQLVEKLWV LKVLQHLSTS
        90        100        110        120        130        140        150        160
EVNCTIMMKA QAASGICTHL NDPDPSGQLL FRSSEILWNL LEKSSKEEVI QQLSNLECLL ALKEVFKNLF MRGFSHYDRQ
       170        180        190        200        210        220        230        240
LRNDILVITT IIAQNPEAPM IECGFTKDLI LFATFNEVKS QNLLVKGLKL SNSYEDFELK KLLFNVIVIL CKDLPTVQLL
       250        260        270        280        290        300        310        320
IDGKVILALF TYVKKPEKQK IIDWSAAQHE ELQLHAIATL SSVAPLLIEE YMSCQGNARV LAFLEWCESE DPFFSHGNSF
       330        340        350        360        370        380        390        400
HGTGGRGNKF AQMRYSLRLL RAVVYLEDET VNKDLCEKGT IQQMIGIFKN IISKPNEKEE AIVLEIQSDI LLILSGLCEN
       410        420        430        440        450        460        470        480
HIQRKEIFGT EGVDIVLHVM KTDPRKLQSG LGYNVLLFST LDSIWCCILG CYPSEDYFLE KEGIFLLLDL LALNQKKFCN
       490        500        510        520        530        540        550        560
LILGIMVEFC DNPKTAAHVN AWQGKKDQTA ASLLIKLWRK EEKELGVKRD KNGKIIDTKK PLFTSFQEEQ KIIPLPANCP
       570        580        590        600        610        620        630        640
SIAVMDVSEN IRAKIYAILG KLDFENLPGL SAEDFVTLCI IHRYLDFKIG EIWNEIYEEI KLEKLRPVTT DKKALEAITT
       650        660        670        680        690        700        710        720
ASENIGKMVA SLQSDIIESQ ACQDMQNEQK VYAKIQATHK QRELANKSWE DFLARTSNAK TLKKAKSLQE KAIEASRYHK
       730        740        750        760        770        780        790        800
RPQNAIFHQT HIKGLNTTVP SGGVVTVEST PARLVGGPLV DTDIALKKLP IRGGALQRVK AVKIVDAPKK SIPT
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2785 | 1 | 711.3716 | -1.34 | 3 | 66.0 | 10.9 | 2 | 10-27 | R.IQICKCIVDFYHAEPPKK.H | |

# Detailed Protein Report

**Protein 627:** **ERC protein 2 [Homo sapiens]**

**Accession:** gi|34577114
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 25.6
**MW [kDa]:** 110.5
**pI:** 6.5
**Sequence Coverage [%]:** 2.9
**No. of unique Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MYGSARTITN | LEGSPSRSPR | LPRSPRLGHR | RTSSGGGGGT | GKTLSMENIQ | SLNAAYATSG | PMYLSDHEGV | ASTTYPKGTM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TLGRATNRAV | YGGRVTAMGS | SPNIASAGLS | HTDVLSYTDQ | HGGLTGSSHH | HHHQVPSMLR | QVRDSTMLDL | QAQLKELQRE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NDLLRKELDI | KDSKLGSSMN | SIKTFWSPEL | KKERVLRKEE | AARMSVLKEQ | MRVSHEENQH | LQLTIQALQD | ELRTQRDLNH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LLQQESGNRG | AEHFTIELTE | ENFRRLQAEH | DRQAKELFLL | RKTLEEMELR | IETQKQTLNA | RDESIKKLLE | MLQSKGLPSK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SLEDDNERTR | RMAEAESQVS | HLEVILDQKE | KENIHLREEL | HRRSQLQPEP | AKTKALQTVI | EMKDTKIASL | ERNIRDLEDE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IQMLKANGVL | NTEDREEEIK | QIEVYKSHSK | FMKTKIDQLK | QELSKKESEL | LALQTKLETL | SNQNSDCKQH | IEVLKESLTA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KEQRAAILQT | EVDALRLRLE | EKESFLNKKT | KQLQDLTEEK | GTLAGEIRDM | KDMLEVKERK | INVLQKKIEN | LQEQLRDKDK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QLTNLKDRVK | SLQTDSSNTD | TALATLEEAL | SEKERIIERL | KEQRERDDRE | RLEEIESFRK | ENKDLKEKVN | ALQAELTEKE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SSLIDLKEHA | SSLASAGLKR | DSKLKSLEIA | IEQKKEECSK | LEAQLKKAHN | IEDDSRMNPE | FADQIKQLDK | EASYYRDECG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KAQAEVDRLL | EILKEVENEK | NDKDKKIAEL | ESLTLRHMKD | QNKKVANLKH | NQQLEKKKNA | QLLEEVRRRE | DSMADNSQHL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QIEELMNALE | KTRQELDATK | ARLASTQQSL | AEKEAHLANL | RIERRKQLEE | ILEMKQEALL | AAISEKDANI | ALLELSASKK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KKTQEEVMAL | KREKDRLVHQ | LKQQTQNRMK | LMADNYDDDH | HHYHHHHHHH | HHRSPGRSQH | SNHRPSPDQD | DEEGIWA |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2013 | 1 | 703.2744 | -137.93 | 2 | 53.5 | 13.3 | 2 | 676-687 | K.EECSKLEAQLKK.A | |

# Detailed Protein Report

## Protein 628: PREDICTED: retinoblastoma-like protein 2 isoform X1 [Homo sapiens]

**Accession:** gi|530424182
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 25.6
**MW [kDa]:** 120.4
**pI:** 9.7
**Sequence Coverage [%]:** 1.9
**No. of unique Peptides:** 1

## Quantitation

***WUP:QUP*** **Median:** 1.08 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MQSLTKGNDL HWLACALYVA CRKSVPTVSK GTVEGNYVSL TRILKCSEQS LIEFFNKMKK WEDMANLPPH FRERTERLER
        90        100        110        120        130        140        150        160
NFTVSAVIFK KYEPIFQDIF KYPQEEQPRQ QRGRKQRRQP CTVSEIFHFC WVLFIYAKGN FPMISDDLVN SYHLLLCALD
       170        180        190        200        210        220        230        240
LVYGNALQCS NRKELVNPNF KGLSEDFHAK DSKPSSDPPC IIEKLCSLHD GLVLEAKGIK EHFWKPYIRK LYEKKLLKGK
       250        260        270        280        290        300        310        320
EENLTGFLEP GNFGESFKAI NKAYEEYVLS VGNLDERIFL GEDAEEEIGT LSRCLNAGSG TETAERVQMK NILQQHFDKS
       330        340        350        360        370        380        390        400
KALRISTPLT GVRYIKENSP CVTPVSTATH SLSRLHTMLT GLRNAPSEKL EQILRTCSRD PTQAIANRLK EMFEIYSQHF
       410        420        430        440        450        460        470        480
QPDEDFSNCA KEIASKHFRF AEMLYYKVLE SVIEQEQKRL GDMDLSGILE QDAFHRSLLA CCLEVVTFSY KPPGNFPFIT
       490        500        510        520        530        540        550        560
EIFDVPLYHF YKVIEVFIRA EDGLCREVVK HLNQIEEQIL DHLAWKPESP LWEKIRDNEN RVPTCEEVMP PQNLERADEI
       570        580        590        600        610        620        630        640
CIAGSPLTPR RVTEVRADTG GLGRSITSPT TLYDRYSSPP ASTTRRRLFV ENDSPSDGGT PGRMPPQPLV NAVPVQNVSG
       650        660        670        680        690        700        710        720
ETVSVTPVPG QTLVTMATAT VTANNGQTVT IPVQGIANEN GGITFFPVQV NVGGQAQAVT GSIQPLSAQA LAGSLSSQQV
       730        740        750        760        770        780        790        800
TGTTLQVPGQ VAIQQISPGG QQQKQGQSVT SSSNRPRKTS SLSLFFRKVY HLAAVRLRDL CAKLDISDEL RKKIWTCFEF
       810        820        830        840        850        860        870        880
SIIQCPELMM DRHLDQLLMC AIYVMAKVTK EDKSFQNIMR CYRTQPQARS QVYRSVLIKG KRKRRNSGSS DSRSHQNSPT
       890        900        910        920        930        940        950        960
ELNKDRTSRD SSPVMRSSST LPVPQPSSAP PTPTRLTGAN SDMEEEERGD LIQFYNNIYI KQIKTFAMKY SQANMDAPPL
       970        980        990       1000       1010       1020       1030       1040
SPYPFVRTGS PRRIQLSQNH PVYISPHKNE TMLSPREKIF YYFSNSPSKR LREINSMIRT GETPTKKRGI LLEDGSESPA
      1050       1060       1070
KRICPENHSA LLRRLQDVAN DRGSH
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 701 | 2 | 606.1713 | -198.83 | 2 | 37.2 | 13.4 | 1 | 1055-1065 | R.LQDVANDRGSH.- |  | WUP:QUP 1.08 |

# Detailed Protein Report

## Protein 629: PREDICTED: serine/arginine repetitive matrix protein 1-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578794871 | **Score:** | 25.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.4 |
| | | **Sequence Coverage [%]:** | 7.5 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.66 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.78 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MTVATKSQRS LSARCGTELA QQGKPGPRAL SFSLAQPQCS AGYGLRKPQL PYVKNGGQEI HGLLRARVHP CMAVNAPPQV
        90        100        110        120        130        140        150        160
MTKSTTSFPF LAMENKSALL QGSFWGAPPK PREEAGEPSL QPRAAQRRHR TCESLCAPLR APATRRRDSE PAPAATPHPP
       170        180        190        200        210        220        230        240
ARQPARPVRP PAQASQPRVA RSLVGPRPLV LPLAYSPPAR EKPGRSEARR PGPGCYIGRR PNPAWTRQRP PAPPLGSPPP
       250        260        270        280        290        300        310        320
RAAQHPGGPP NCRRGSASFF RVGKAVPRSW EINHLQKAEG ARPARTRVET TEDQKGSRKD GCSGSRCHQY RPPPQNQKKN
       330        340        350        360        370        380        390        400
LKGCPPHRKR MATLARGYKG SRAICRDVSL NLWQSRRSTE SCIGHRINYR NPLQWSHAEG VRRSSGPGVI SKAVGAEMWR
       410        420
TGAHHFLGSS AVL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2683 | 1 | 913.4777 | 3.59 | 2 | 63.7 | 10.3 | 2 | 146-162 | R.RRDSEPAPAATPHPPAR.Q | | WUP:QUP 0.78<br>QU:MU 1.66 |

# Detailed Protein Report

## Protein 630: PREDICTED: phosphatidylinositol 4-phosphate 5-kinase type-1 alpha isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530365472 | **Score:** | 25.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 60.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGGRARPKRV | PVAGNVLRVT | AASGIKRPMA | SEVPYASGMP | IKKIGHRSVD | SSGETTYKKT | TSSALKGAIQ | LGITHTVGSL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| STKPERDVLM | QDFYVVESIF | FPSEGSNLTP | AHHYNDFRFK | TYAPVAFRYF | RELFGIRPDD | YLYSLCSEPL | IELCSSGASG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SLFYVSSDDE | FIIKTVQHKE | AEFLQKLLPG | YYMNLNQNPR | TLLPKFYGLY | CVQAGGKNIR | IVVMNNLLPR | SVKMHIKYDL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KGSTYKRRAS | QKEREKPLPT | FKDLDFLQDI | PDGLFLDADM | YNALCKTLQR | DCLVLQSFKI | MDYSLLMSIH | NIDHAQREPL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SSETQYSVDT | RRPAPQKALY | STAMESIQGE | ARRGGTMETD | DHMGGIPARN | SKGERLLLYI | GIIDILQSYR | FVKKLEHSWK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ALVHDGDTVS | VHRPGFYAER | FQRFMCNTVF | KKIPLKPSPS | KKFRSGSSFS | RRAGSSGNSC | ITYQPSVSGE | HKAQVTTKAE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | |
| VEPGVHLGRP | DVLPQTPPLE | EISEGSPIPD | PSFSPLVGET | LQMLTTSTTL | EKLEVAESEF | TH | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 989 | 3 | 581.1819 | -159.70 | 2 | 42.5 | 14.9 | 0 | 533-542 | K.LEVAESEFTH.- | |

# Detailed Protein Report

**Protein 631:** **pro-MCH preproprotein [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|71361684 | **Score:** | 25.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 18.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 15.8 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MAKMNLSSYI LILTFSLFSQ GILLSASKSI RNLDDDMVFN TFRLGKGFQK EDTAEKSVIA PSLEQYKNDE SSFMNEEENK
        90        100        110        120        130        140        150        160
VSKNTGSKHN FLNHGLPLNL AIKPYLALKG SVAFPAENGV QNTESTQEKR EIGDEENSAK FPIGRRDFDM LRCMLGRVYR
       170
PCWQV
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 118 | 1 | 929.9543 | 13.99 | 2 | 31.2 | 15.3 | 1 | 29-43 | K.SIRNLDDDMVFNTFR.L | Oxidation: 9 |

# Detailed Protein Report

## Protein 632: PREDICTED: sperm-associated antigen 17 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578798575 | **Score:** | 25.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 149.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAPKKEKGGT | VNTSSKIWEP | SLIAAQFNQN | DWQASIAFVV | GNQIEDDLLI | QALTVAVQVP | QRKLFSMVSW | QDILQQINEI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NTLVGSASSK | KAKKPVGGNA | PLYYEVLTAA | KAIMDSGEKL | TLPLIGKLLK | FQLLQIKFKD | QQRRENEKKV | IEDKPKLEKD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KGKAKSPKEK | KAPSAKPAKG | KGKDQPEANA | PVKKTTQLKR | RGEDDHTNRY | IDDEPDDGAQ | HYIIVVGFNN | PQLLAIMAEL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GIPITSVIKI | SSENYEPLQT | HLAAVNQQQE | VLLQSEDLEA | EKLKKENAIK | ELKTFWKYLE | PVLNNEKPET | NLFDVARLEY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MVKAADFPSD | WSDGEMMLKL | GTDIFENIAC | LMYDILDWKR | QHQHYLESMQ | LINVPQVVNE | KPVLEAMPTS | EAPQPAVPAP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GKKKAQYEEP | QAPPPVTSVI | TTEVDMRYYN | YLLNPIREEF | ISVPLILHCM | LEQVVATEED | LVPPSLREPS | PRADGLDHRI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AAHIVSLLPS | LCLSEREKKN | LHDIFLSEEE | NESKAVPKGP | LLLNYHDAHA | HKKYALQDQK | NFDPVQIEQE | MQSKLPLWEF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LQFPLPPPWN | NTKRLATIHE | LMHFCTSDVL | SWNEVERAFK | VFTFESLKLS | EVDEKGKLKP | SGMMCGSDSE | MFNIPWDNPA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RFAKQIRQQY | VMKMNTQEAK | QKADIKIKDR | TLFVDQNLSM | SVQDNESNRE | PSDPSQCDAN | NMKHSDLNNL | KLSVPDNRQL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LEQESIMKAQ | PQHESLEQTT | NNEIKDDAVT | KADSHEKKPK | KMMVEADLED | IKKTQQRSLM | DWSFTEHFKP | KVLLQVLQEA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| HKQYRCVDSY | YHTQDNSLLL | VFHNPMNRQR | LHCEYWNIAL | HSNVGFRNYL | ELVAKSIQDW | ITKEEAIYQE | SKMNEKIIRT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RAELELKSSA | NAKLTSASKI | FSIKESKSNK | GISKTEISDQ | EKEKEKEKIP | FILEGSLKAW | KEEQHRLAEE | ERLREEKKAE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KKGKEAGKKK | GKDNAEKEDS | RSLKKKSPYK | EKSKEEQVKI | QEVTEESPHQ | PEPKITYPFH | GYNMGNIPTQ | ISGSNYYLYP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SDGGQIEVEK | TMFEKGPTFI | KVRVVKDNHN | FMIHLNDPKE | IVKKEEKGDY | YLEEEEEGDE | EQSLETEVSD | AKNKAFSKFG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SFSATLENGI | CLSISYYGSN | GMAPEDKDPD | LETILNIPSA | LTPTVVPVIV | TVPQSKAKGK | IKGKEKPKES | LKEEEHPKEE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EKKEEEVEPE | PVLQETLDVP | TFQSLNVSCP | SGLLLTFIGQ | ESTGQYVIDE | EPTWDIMVRQ | SYPQRVKHYE | FYKTVMPPAE |
| 1290 | 1300 | 1310 | | | | | |
| QEASRVITSQ | GTVVKYMLDG | STQIR | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2219 | 1 | 900.3315 | -71.18 | 3 | 57.6 | 13.7 | 0 | 618-641 | K.LKPSGMMCGSDSEMFNIPWDNPAR.F | Oxidation: 6 |

# Detailed Protein Report

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## Protein 633: PREDICTED: adenylate kinase 8 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578817081 | **Score:** | 25.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 8.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDATIAPHRI | PPEMPQYGEE | NHIFELMQAM | WLCKHLNSSL | LTLENLILNE | FSYTATEARR | LYLQRKTVPS | ALLVQLIQER |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LAEEDCIKQG | WILDGIPETR | EQALRIQTLG | ITPRHVIVLS | APDTVLIERN | LGKRIDPQTG | EIYHTTFDWP | PESEIQNRLM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VPEDISELET | AQKLLEYHRN | IVRVIPSYPK | ILKVISADQP | CVDVFYQALT | YVQSNHRTNA | PFTPRVLLLG | PVGSGKSLQA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ALLAQKYRLV | NVCCGQLLKE | AVADRTTFGE | LIQPFFEKEM | AVPDSLLMKV | LSQRLDQQDC | IQKGWVLHGV | PRDLDQAHLL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NRLGYNPNRV | FFLNVPFDSI | MERLTLRRID | PVTGERYHLM | YKPPPTMEIQ | ARLLQNPKDA | EEQVKLKMDL | FYRNSADLEQ |
| 410 | 420 | 430 | 440 | | | | |
| LYGSAITLNG | DQDPYTVFEY | IESGIINPLP | KKIP | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1430 | 1 | 1022.7032 | -95.12 | 3 | 46.3 | 10.1 | 0 | 10-34 | R.IPPEMPQYGEENHIFELMQAMWLCK.H | Oxidation: 18, 21 |

# Detailed Protein Report

**Protein 634:** **PREDICTED: tudor domain-containing protein 7 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578817240 | **Score:** | 25.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 74.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAFGYLSFHI | FTKSYIKKTL | IKEFYNSLNT | GLIFARYVGK | DYSAAQELME | DEMKEYYSKN | PKITPVQAVN | VGQLLAVNAE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EDAWLRAQVI | STEENKIKVC | YVDYGFSENV | EKSKAYKLNP | KFCSLSFQAT | KCKLAGLEVL | SDDPDLVKVV | ESLTCGKIFA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VEILDKADIP | LVVLYDTSGE | DDININATCL | KAICDKSLEV | HLQVDAMYTN | VKVTNICSDG | TLYCQVPCKG | LNKLSDLLRK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IEDYFHCKHM | TSECFVSLPF | CGKICLFHCK | GKWLRVEITN | VHSSRALDVQ | FLDSGTVTSV | KVSELREIPP | RFLQEMIAIP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PQAIKCCLAD | LPQSIGMWTP | DAVLWLRDSV | LNCSDCSIKV | TKVDETRGIA | HVYLFTPKNF | PDPHRSINRQ | ITNADLWKHQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KDVFLSAISS | GADSPNSKNG | NMPMSGNTGE | NFRKNLTDVI | KKSMVDHTSA | FSTEELPPPV | HLSKPGEHMD | VYVPVACHPG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YFVIQPWQEI | HKLEVLMEEM | ILYYSVSEER | HIAVEKDQVY | AAKVENKWHR | VLLKGILTNG | LVSVYELDYG | KHELVNIRKV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QPLVDMFRKL | PFQAVTAQLA | GVKCNQWSEE | ASMVFRNHVE | KKPLVALVQT | VIENANPWDR | KVVVYLVDTS | LPDTDTWIHD |
| 650 | 660 | | | | | | |
| FMSEYLIELS | KVN | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1797 | 1 | 851.2615 | -133.71 | 2 | 52.3 | 11.4 | 0 | 249-263 | K.HMTSECFVSLPFCGK.I | Oxidation: 2 |

# Detailed Protein Report

## Protein 635: transcriptional protein SWT1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|157502207 | **Score:** | 25.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 103.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|157502209 | refseq_huma<br>(refseq_human_20140103.fasta) | transcriptional protein SWT1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSKESCGKK | ETSQRKDTTT | SSPNFGEKDK | KERKTPASST | SSSSIRSVSS | EKRKLKSDHT | DVLYYNIKRR | QGLKRLSVEI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DTLRRRPKIG | SSSQRPIKLK | EASYSNDNQI | ILQSPSSNGT | KKDIHKCVDF | KPKDIKLTNA | GSKLDHGIKS | LSSPKIASDV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KPKAEGQASE | NKWSHLLVQR | EKMKELKKGR | NSKFRDNSEK | CVLEKWKRNQ | FSQDYNSNKI | IKEPLGSRRQ | KISFKIPIKS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RDTLQKLVEE | NVFNIDSNNS | KTKQEEREYL | ESSQVSLNVT | RQKTEHLLSD | FTYKRTVHEW | KRKHHYDHQE | SNDSHSRENL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TQSFEAPCCS | VSSESIQDAD | QEMQIVEELH | AARVGKSVDL | PGELMSMEID | LEDDVHSSSA | NNTSDRKLLI | VIDTNILMNH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LKFVRILKTT | EVPGFDKLVL | IIPWVVMQEL | DRMKEGKLLK | RAQHKAIPAV | HFINDSLKNQ | DRKLWGQSIQ | LASQKHYGLS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DENNDDRVLK | CCLQHQELFP | CSFVILCTDD | RNLRNKGLIS | GVKSLSKEEL | SAELLHLSLN | TDVCHQPCIP | KQQLKAETTP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LKESYKEEST | NSGLSILLES | IVSDLEKSLG | TGLSSILETE | MKIAFGNLWM | EILYLKPPWT | LLHLLQCFKK | HWLAVFGLVM |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EKNLLLTIES | LYKNLRKANK | AVDFTTVKFL | LQDSRSLLHA | FSTRSNYDGI | LPQTFAQVNN | LLQTFAEVKT | KLKPNSSENT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VTKKQEGTSL | KNSHNQEITV | FSSSHLPQPS | RHQEIWSILE | SVWITIYQNS | TDVFQRLGSN | SALTTSNIAS | FEEAFICLQK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LMAAVRDILE | GIQRILAPNS | NYQDVETLYN | FLIKYEVNKN | VKFTAQEIYD | CVSQTEYREK | LTIGCRQLVE | MEYTMQQCNA |
| 890 | 900 | 910 | | | | | |
| SVYMEAKNRG | WCEDMLNYRI | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1636 | 1 | 682.3058 | -115.98 | 3 | 50.7 | 10.7 | 2 | 441-458 | K.RAQHKAIPAVHFINDSLK.N | |

# Detailed Protein Report

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## Protein 636: PREDICTED: B-cell CLL/lymphoma 9 protein isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530432132 | **Score:** | 25.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 141.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MHSSNPKVRS | SPSGNTQSSP | KSKQEVMVRP | PTVMSPSGNP | QLDSKFSNQE | CNSADHIKSQ | DSQHTPHSMT | PSNATAPRSS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TPSHGQTTAT | EPTPAQKTPA | KVVYVFSTEM | ANKAAEAVLK | GQVETIVSFH | IQNISNNKTE | RSTAPLNTQI | SALRNDPKPL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PQQPPAPANQ | DQNSSQNTRL | QPTPPIPAPA | PKPAAPPRPL | DRESPGVENK | LIPSVGSPAS | STPLPPDGTG | PNSTPNNRAV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TPVSQGSNSS | SADPKAPPPP | PVSSGEPPTL | GENPDGLSQE | QLEHRERSLQ | TLRDIQRMLF | PDEKEFTGAQ | SGGPQQNPGV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LDGPQKKPEG | PIQAMMAQSQ | SLGKGPGPRT | DVGAPFGPQG | HRDVPFSPDE | MVPPSMNSQS | GTIGPDHLDH | MTPEQIAWLK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LQQEFYEEKR | RKQEQVVVQQ | CSLQDMMVHQ | HGPRGVVRGP | PPPYQMTPSE | GWAPGGTEPF | SDGINMPHSL | PPRGMAPHPN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| MPGSQMRLPG | FAGMINSEME | GPNVPNPASR | PGLSGVSWPD | DVPKIPDGRN | FPPGQGIFSG | PGRGERFPNP | QGLSEEMFQQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QLAEKQLGLP | PGMAMEGIRP | SMEMNRMIPG | SQRHMEPGNN | PIFPRIPVEG | PLSPSRGDFP | KGIPPQMGPG | RELEFGMVPS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GMKGDVNLNV | NMGSNSQMIP | QKMREAGAGP | EEMLKLRPGG | SDMLPAQQKM | VPLPFGEHPQ | QEYGMGPRPF | LPMSQGPGSN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SGLRNLREPI | GPDQRTNSRL | SHMPPLPLNP | SSNPTSLNTA | PPVQRGLGRK | PLDISVAGSQ | VHSPGINPLK | SPTMHQVQSP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| MLGSPSGNLK | SPQTPSQLAG | MLAGPAAAAS | IKSPPVLGSA | AASPVHLKSP | SLPAPSPGWT | SSPKPPLQSP | GIPPNHKAPL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TMASPAMLGN | VESGGPPPPT | ASQPASVNIP | GSLPSSTPYT | MPPEPTLSQN | PLSIMMSRMS | KFAMPSSTPL | YHDAIKTVAS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SDDDSPPARS | PNLPSMNNMP | GMGINTQNPR | ISGPNPVVPM | PTLSPMGMTQ | PLSHSNQMPS | PNAVGPNIPP | HGVPMGPGLM |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SHNPIMGHGS | QEPPMVPQGR | MGFPQGFPPV | QSPPQQVPFP | HNGPSGGQGS | FPGGMGFPGE | GPLGRPSNLP | QSSADAALCK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PGGPGGPDSF | TVLGNSMPSV | FTDPDLQEVI | RPGATGIPEF | DLSRIIPSEK | PSQTLQYFPR | GEVPGRKQPQ | GPGPGFSHMQ |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| GMMGEQAPRM | GLALPGMGGP | GPVGTPDIPL | GTAPSMPGHN | PMRPPAFLQQ | GMMGPHHRMM | SPAQSTMPGQ | PTLMSNPAAA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VGMIPGKDRG | PAGLYTHPGP | VGSPGMMMSM | QGMMGPQQNI | MIPPQMRPRG | MAADVGMGGF | SQGPGNPGNM | MF |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1573 | 1 | 1023.5251 | 33.57 | 2 | 49.9 | 10.0 | 0 | 644-662 | K.GDVNLNVNMGSNSQMIPQK.M | |

# Detailed Protein Report

## Protein 637: potassium voltage-gated channel subfamily KQT member 2 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|26051260 | **Score:** | 25.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 93.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***WUP:QUP*** **Median:** 0.35 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVQKSRNGGV | YPGPSGEKKL | KVGFVGLDPG | APDSTRDGAL | LIAGSEAPKR | GSILSKPRAG | GAGAGKPPKR | NAFYRKLQNF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LYNVLERPRG | WAFIYHAYVF | LLVFSCLVLS | VFSTIKEYEK | SSEGALYILE | IVTIVVFGVE | YFVRIWAAGC | CCRYRGWRGR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LKFARKPFCV | IDIMVLIASI | AVLAAGSQGN | VFATSALRSL | RFLQILRMIR | MDRRGGTWKL | LGSVVYAHSK | ELVTAWYIGF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LCLILASFLV | YLAEKGENDH | FDTYADALWW | GLITLTTIGY | GDKYPQTWNG | RLLAATFTLI | GVSFFALPAG | ILGSGFALKV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QEQHRQKHFE | KRRNPAAGLI | QSAWRFYATN | LSRTDLHSTW | QYYERTVTVP | MYRLIPPLNQ | LELLRNLKSK | SGLAFRKDPP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PEPSPSQKVS | LKDRVFSSPR | GVAAKGKGSP | QAQTVRRSPS | ADQSLEDSPS | KVPKSWSFGD | RSRARQAFRI | KGAASRQNSE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EASLPGEDIV | DDKSCPCEFV | TEDLTPGLKV | SIRAVCVMRF | LVSKRKFKES | LRPYDVMDVI | EQYSAGHLDM | LSRIKSLQSR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VDQIVGRGPA | ITDKDRTKGP | AEAELPEDPS | MMGRLGKVEK | QVLSMEKKLD | FLVNIYMQRM | GIPPTETEAY | FGAKEPEPAP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PYHSPEDSRE | HVDRHGCIVK | IVRSSSSTGQ | KNFSAPPAAP | PVQCPPSTSW | QPQSHPRQGH | GTSPVGDHGS | LVRIPPPPAH |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ERSLSAYGGG | NRASMEFLRQ | EDTPGCRPPE | GNLRDSDTSI | SIPSVDHEEL | ERSFSGFSIS | QSKENLDALN | SCYAAVAPCA |
| 810 | 820 | 830 | 840 | 850 | | | |
| KVRPYIAEGE | SDTDSDLCTP | CGPPPRSATG | EGPFGDVGWA | GPRK | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1607 | 1 | 720.3800 | -23.52 | 2 | 48.4 | 13.2 | 1 | 333-345 | R.RNPAAGLIQSAWR.F | | WUP:QUP 0.35 |
| 1678 | 1 | 938.9348 | -60.69 | 2 | 50.7 | 12.2 | 2 | 398-414 | K.DPPPEPSPSQKVSLKDR.V | | |

# Detailed Protein Report

## Protein 638: zinc finger protein 670 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|323635444 | **Score:** | 25.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 44.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 5.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDSVSFEDVA | VAFTQEEWAL | LDPSQKNLYR | DVMQEIFRNL | ASVGNKSEDQ | NIQDDFKNPG | RNLSHVVERL | FEIKEGSQYG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ETFSQDSNLN | LNKKVSTGVK | PCECSVCGKV | FICHSALHRH | ILSHIGNKLF | ECEECPEKLY | HCKQCGKAFI | SLTSVDRHMV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| THTSNGPYKG | PVYEKPFDFP | SVFQMPQSTY | TGEKTYKCKH | CDKAFNYSSY | LREHERTHTG | EKPYACKKCG | KSFTFSSSLR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QHERSHTGEK | PYECKECGKA | FSRSTYLGIH | ERTHTGEKPY | ECIKCGKAFR | CSRVLRVHER | THSGEKPYEC | KQCGKAFKYS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| SNLCEHERTH | TGVKPYGCKE | CGKSFTSSSA | LRSHERTHTG | EKPYECKKCG | KAFSCSSSLR | KHERAYMW | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1723 | 2 | 1108.8589 | 233.76 | 1 | 51.9 | 12.9 | 0 | 148-157 | K.AFISLTSVDR.H | |

# Detailed Protein Report

## Protein 639: protein PRRC2B [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|149192855 | **Score:** | 25.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 242.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSDRLGQITK | GKDGKSKYST | LSLFDKYKGK | SVDAIRSSVI | PRHGLQSLGK | VAAARRMPPP | ANLPSLKSEN | KGNDPNIVIV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PKDGTGWANK | QDQQDPKSSS | ATASQPPESL | PQPGLQKSVS | NLQKPTQSIS | QENTNSVPGG | PKSWAQLNGK | PVGHEGGLRG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SSRLLSFSPE | EFPTLKAAGG | QDKAGKEKGV | LDLSYGPGPS | LRPQNVTSWR | EGGGRHIISA | TSLSTSPTEL | GSRNSSTGDG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| APSSACTSDS | KDPSLRPAQP | VRKGASQFMG | NVYHPPTYHD | MLPAFMCSPK | SSENQGTVER | GSFPLPQLRL | EPRVPFRQFQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MNDQDGKENR | LGLSRPLRPL | RQLVERAPRP | TIINAENLKG | LDDLDADADD | GWAGLHEEVD | YSEKLKFSDD | EEEEEVVKDG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RPKWNSWDPR | RQRQLSMSSA | DSADAKRTRE | EGKDWAEAVG | ASRVVRKAPD | PQPPPRKLHG | WAPGPDYQKS | SMGSMFRQQS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IEDKEDKPPP | RQKFIQSEMS | EAVERARKRR | EEEERRAREE | RLAACAAKLK | QLDQKCKQAR | KAGEARKQAE | KEVPWSPSAE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KASPQENGPA | VHKGSPEFPA | QETPTTFPEE | APTVSPAVAQ | SNSSEEEARE | AGSPAQEFKY | QKSLPPRFQR | QQQQQQQEQL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| YKMQHWQPVY | PPPSHPQRTF | YPHHPQMLGF | DPRWMMMPSY | MDPRITPTRT | PVDFYPSALH | PSGLMKPMMP | QESLNGTGCR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SEDQNCVPPL | QERKVTPIDS | PPVWSPEGYM | ALQSKGYPLP | HPKSSDTLAM | DMRVRNESSF | SASLGRAGGV | SAQRDLFEER |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GEEYLSAFDK | KAQADFDSCI | SSQRIGQELL | FPPQENVQDA | GAPGGHTQNL | RCSPLEPDFV | PDEKKPECGS | WDVSHQPETA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DTAHGVERET | PREGTAFNIS | SWDKNGSPNK | QPSSEPEWTP | EPRSSSSQHP | EQTGRTRRSG | PIKKPVLKAL | KVEDKEKELE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KIKQELGEES | TRLAKEKEQS | PTAEKDEDEE | NDASLANSST | TTLEDKGPGH | ATFGREATKF | EEEEKPDKAW | EARPPRESSD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VPPMKRNNWI | FIDEEQAFGV | RGQARGRGRG | FREFTFRGRP | AGGNGSGLCG | GGVLGARSIY | CSSQRSGRGR | GLREFARPED |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| CPRAKPRRRV | ASETHSEGSE | YEELPKRRRQ | RGSENGNEGS | LLEREESTLK | KGDCRDSWRS | NKGCSEDHSG | LDAKSRGPRA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| FGRALPPRLS | NCGYGRRTFV | SKESPHWQSK | SPGSSWQEYG | PSDTCGSRRP | TDRDYVPDSY | RHPDAFGGRG | FEDSRAEDKR |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SFFQDEHVAD | SENAENRPFR | RRRPPRQDKP | PRFRRLRQER | ESLGLWGPEE | EPHLLAGQWP | GRPKLCSGDK | SGTVGRRSPE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LSYQNSSDHA | NEEWETASES | SDFSERRERR | EGPGSEPDSQ | VDGGLSGASL | GEKKELAKRS | FSSQRPVVDR | QSRKLEPGGF |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GEKPVRPGGG | DTSPRYESQQ | NGTPLKVKRS | PDEALPGGLS | GCSSGSGHSP | YALERAAHAS | ADLPEASSKK | AEKEAKLAAP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| RAGEQGEAMK | QFDLNYGSAI | IENCGSSPGE | ESEVGSMVGE | GFIEVLTKKQ | RRLLEEERRK | KEQAVQVPVK | GRGLSSRIPP |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| RFAKKQNNLC | LEQGDVTVPG | SSLGTEIWES | SSQALPVQAP | ANDSWRKAVT | AFSSTETGSA | EQGFKSSQGD | SGVDLSAESR |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| ESSATSSQRS | SPYGTLKPEE | MSGPGLAEPK | ADSHKEQAPK | PSEQKDSEQG | SGQSKEHRPG | PIGNERSLKN | RKGSEGAERL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| QGAVVPPVNG | VEIHVDSVLP | VPPIEFGVSP | KDSDFSLPPG | SASGPTGSPV | VKLQDALASN | AGLTQSIPIL | RRDHHIQRAI |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| GLSPMSFPTA | DLTLKMESAR | KAWENSPSLP | EQSSPGGAGS | GIQPPSSVGA | SSGVNYSSFG | GVSMPPMPVA | SVAPSASMPG |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| SHLPPLYLDG | HVFASQPRLV | PQTIPQQQSY | QQAAAAQQIP | ISLHTSLQAQ | AQLGLRGGLP | VSQSQEIFSS | LQPFRSQVYM |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| HPSLSPPSTM | ILSGGTALKP | PYSAFPGMQP | LEMVKPQSGS | PYQPMSGNQA | LVYEGQLSQA | AGLGASQMLD | SQLPQLTMPL |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| PRYGSGQQPL | ILPQSIQLPP | GQSLSVGAPR | RIPPPGSQPP | VLNTSREPSQ | MEMKGFHFAD | SKQNVPSGGP | VPSPQTYRPS |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1757 | 1 | 897.9578 | -24.93 | 2 | 51.8 | 13.3 | 2 | 56-71 | R.RMPPPANLPSLKSENK.G | Oxidation: 2 |

# Detailed Protein Report

**Protein 640:** **PREDICTED: focal adhesion kinase 1 isoform X12 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530389222 | **Score:** | 25.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 108.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEMLLMSGYE | LRIRYLPKGF | LNQFTEDKPT | LNFFYQQVKS | DYMLEIADQV | DQEIALKLGC | LEIRRSYWEM | RGNALEKKSN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YEVLEKDVGL | KRFFPKSLLD | SVKAKTLRKL | IQQTFRQFAN | LNREESILKF | FEILSPVYRF | DKECFKCALG | SSWIISVELA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IGPEEGISYL | TDKGCNPTHL | ADFTQVQTIQ | YSNSEDKDRK | GMLQLKIAGA | PEPLTVTAPS | LTIAENMADL | IDGYCRLVNG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TSQSFIIRPQ | KEGERALPSI | PKLANSEKQG | MRTHAVSVSD | EISGDETDDY | AEIIDEEDTY | TMPSKSYGID | EARDYEIQRE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RIELGRCIGE | GQFGDVHQGI | YMSPENPALA | VAIKTCKNCT | SDSVREKFLQ | EALTMRQFDH | PHIVKLIGVI | TENPVWIIME |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LCTLGELRSF | LQVRKYSLDL | ASLILYAYQL | STALAYLESK | RFVHRDIAAR | NVLVSSNDCV | KLGDFGLSRY | MEDSTYYKAS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KGKLPIKWMA | PESINFRRFT | SASDVWMFGV | CMWEILMHGV | KPFQGVKNND | VIGRIENGER | LPMPPNCPPT | LYSLMTKCWA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YDPSRRPRFT | ELKAQLSTIL | EEEKAQQEER | MRMESRRQAT | VSWDSGGSDE | APPKPSRPGY | PSPRSSEGFY | PSPQHMVQTN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HYQVSGYPGS | HGITAMAGSI | YPGQASLLDQ | TDSWNHRPQE | IAMWQPNVED | STVLDLRGIG | QVLPTHLMEE | RLIRQQQEME |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EDQRWLEKEE | RFLKPDVRLS | RGSIDREDGS | LQGPIGNQHI | YQPVGKPDPA | APPKKPPRPG | APGHLGSLAS | LSSPADSYNE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GVKPWRLQPQ | EISPPPTANL | DRSNDKVYEN | VTGLVKAVIE | MSSKIQPAPP | EEYVPMVKEV | GLALRTLLAT | VDETIPLLPA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| STHREIEMAQ | KLLNSDLGEL | INKMKLAQQY | VMTSLQQEYK | KQMLTAAHAL | AVDAKNLLDV | IDQARLKMLG | QTRPH |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2292 | 1 | 920.6271 | 128.21 | 2 | 59.1 | 13.3 | 2 | 256-272 | R.ALPSIPKLANSEKQGMR.T | |

# Detailed Protein Report

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## Protein 641: transcriptional repressor p66-alpha [Homo sapiens]

**Accession:** gi|164519146
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 25.2
**MW [kDa]:** 68.0
**pI:** 10.6
**Sequence Coverage [%]:** 4.4
**No. of unique Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTEEACRTRS | QKRALERDPT | EDDVESKKIK | MERGLLASDL | NTDGDMRVTP | EPGAGPTQGL | LRATEATAMA | MGRGEGLVGD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GPVDMRTSHS | DMKSERRPPS | PDVIVLSDNE | QPSSPRVNGL | TTVALKETST | EALMKSSPEE | RERMIKQLKE | ELRLEEAKLV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLKKLRQSQI | QKEATAQKPT | GSVGSTVTTP | PPLVRGTQNI | PAGKPSLQTS | SARMPGSVIP | PPLVRGGQQA | SSKLGPQASS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QVVMPPLVRG | AQQIHSIRQH | SSTGPPPLLL | APRASVPSVQ | IQGQRIIQQG | LIRVANVPNT | SLLVNIPQPT | PASLKGTTAT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SAQANSTPTS | VASVVTSAES | PASRQAAAKL | ALRKQLEKTL | LEIPPPKPPA | PEMNFLPSAA | NNEFIYLVGL | EEVVQNLLET |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QGRMSAATVL | SREPYMCAQC | KTDFTCRWRE | EKSGAIMCEN | CMTTNQKKAL | KVEHTSRLKA | AFVKALQQEQ | EIEQRLLQQG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TAPAQAKAEP | TAAPHPVLKQ | VIKPRRKLAF | RSGEARDWSN | GAVLQASSQL | SRGSATTPRG | VLHTFSPSPK | LQNSASATAL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VSRTGRHSER | TVSAGKGSAT | SNWKKTPLST | GGTLAFVSPS | LAVHKSSSAV | DRQREYLLDM | IPPRSIPQSA | TWK |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2479 | 1 | 1044.5214 | 41.67 | 2 | 61.5 | 10.6 | 1 | 74-93 | R.GEGLVGDGPVDMRTSHSDMK.S | |

# Detailed Protein Report

## Protein 642: PREDICTED: nuclear receptor coactivator 5 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530418236 | **Score:** | 25.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 48.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 6.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNTAPSRPSP | TRRDPYGFGD | SRDSRRDRSP | IRGSPRREPR | DGRNGRDARD | SRDIRDPRDL | RDHRHSRDLR | DHRDSRSVRD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VRDVRDLRDF | RDLRDSRDFR | DQRDPMYDRY | RDMRDSRDPM | YRREGSYDRY | LRMDDYCRRK | DDSYFDRYRD | SFDGRGPPGP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ESQSRAKERL | KREERRREEL | YRQYFEEIQR | RFDAERPVDC | SVIVVNKQTK | DYAESVGRKV | RDLGMVVDLI | FLNTEVSLSQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ALEDVSRGGS | PFAIVITQQH | QIHRSCTVNI | MFGTPQEHRN | MPQADAMVLV | ARNYERYKNE | CREKEREEIA | RQAAKMADEA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ILQERERGGP | EEGVRGGHPP | AIQSLINLLA | DNRYLTAEET | DKIINYLRER | KERLMRSSTD | SLPGELRGRA | EARFPANHSG |
| 410 | | | | | | | |
| RPRVPR | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 163 | 1 | 896.0924 | 148.95 | 2 | 31.8 | 10.4 | 0 | 192-207 | R.FDAERPVDCSVIVVNK.Q | |

# Detailed Protein Report

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**Protein 643:** **PREDICTED: thyroid hormone receptor-associated protein 3 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530363679 | **Score:** | 25.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 65.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MKSDSFAPKT DSEKPFRGSQ SPKRYKLRDD FEKKMADFHK EEMDDQDKDK AKGRKESEFD DEPKFMSKVI GANKNQEEEK
        90        100        110        120        130        140        150        160
SGKWEGLVYA PPGKEKQRKT EELEEESFPE RSKKEDRGKR SEGGHRGFVP EKNFRVTAYK AVQEKSSSPP PRKTSESRDK
       170        180        190        200        210        220        230        240
LGAKGDFPTG KSSFSITREA QVNVRMDSFD EDLARPSGLL AQERKLCRDL VHSNKKEQEF RSIFQHIQSA QSQRSPSELF
       250        260        270        280        290        300        310        320
AQHIVTIVHH VKEHHFGSSG MTLHERFTKY LKRGTEQEAA KNKKSPEIHR RIDISPSTFR KHGLAHDEMK SPREPGYKAE
       330        340        350        360        370        380        390        400
GKYKDDPVDL RLDIERRKKH KERDLKRGKS RESVDSRDSS HSRERSAEKT EKTHKGSKKQ KKHRRARDRS RSSSSSSQSS
       410        420        430        440        450        460        470        480
HSYKAEEYTE ETEEREESTT GFDKSRLGTK DFVGPSERGG GRARGTFQFR ARGRGWGRGN YSGNNNNNSN NDFQKRNREE
       490        500        510        520        530        540        550        560
EWDPEYTPKS KKYYLHDDRE GEGSDKWVSR GRGRGAFPRG RGRFMFRKSS TSPKWAHDKF SGEEGEIEDD ESGTENREEK
       570
DNIQPTTE
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2487 | 1 | 856.3995 | -21.47 | 2 | 61.6 | 13.8 | 1 | 3-17 | K.SDSFAPKTDSEKPFR.G | |
| 374 | 1 | 734.1603 | -332.18 | 1 | 33.3 | 11.4 | 1 | 528-534 | R.KSSTSPK.W | |

# Detailed Protein Report

## Protein 644: ran GTPase-activating protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4506411 | **Score:** | 25.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 63.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.3 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578837322 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: ran GTPase-activating protein 1 isoform X3 [Homo sapiens] |
| gi\|520975387 | refseq_human (refseq_human_20140103.fasta) | ran GTPase-activating protein 1 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MASEDIAKLA ETLAKTQVAG GQLSFKGKSL KLNTAEDAKD VIKEIEDFDS LEALRLEGNT VGVEAARVIA KALEKKSELK
        90        100        110        120        130        140        150        160
RCHWSDMFTG RLRTEIPPAL ISLGEGLITA GAQLVELDLS DNAFGPDGVQ GFEALLKSSA CFTLQELKLN NCGMGIGGGK
       170        180        190        200        210        220        230        240
ILAAALTECH RKSSAQGKPL ALKVFVAGRN RLENDGATAL AEAFRVIGTL EEVHMPQNGI NHPGITALAQ AFAVNPLLRV
       250        260        270        280        290        300        310        320
INLNDNTFTE KGAVAMAETL KTLRQVEVIN FGDCLVRSKG AVAIADAIRG GLPKLKELNL SFCEIKRDAA LAVAEAMADK
       330        340        350        360        370        380        390        400
AELEKLDLNG NTLGEEGCEQ LQEVLEGFNM AKVLASLSDD EDEEEEEEGE EEEEEAEEEE EEDEEEEEEE EEEEEEEPQQ
       410        420        430        440        450        460        470        480
RGQGEKSATP SRKILDPNTG EPAPVLSSPP PADVSTFLAF PSPEKLLRLG PKSSVLIAQQ TDTSDPEKVV SAFLKVSSVF
       490        500        510        520        530        540        550        560
KDEATVRMAV QDAVDALMQK AFNSSSFNSN TFLTRLLVHM GLLKSEDKVK AIANLYGPLM ALNHMVQQDY FPKALAPLLL
       570        580        590
AFVTKPNSAL ESCSFARHSL LQTLYKV
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2615 | 1 | 589.1847 | -155.39 | 2 | 61.0 | 13.1 | 0 | 149-160 | K.LNNCGMGIGGGK.I | Carbamidomethyl: 4 |

# Detailed Protein Report

## Protein 645: protein SON isoform F [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|520261969 | **Score:** | 25.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 263.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MATNIEQIFR | SFVVSKFREI | QQELSSGRNE | GQLNGETNTP | IEGNQAGDAA | ASARSLPNEE | IVQKIEEVLS | GVLDTELRYK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PDLKEGSRKS | RCVSVQTDPT | DEIPTKKSKK | HKKHKNKKKK | KKKEKEKKYK | RQPEESESKT | KSHDDGNIDL | ESDSFLKFDS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EPSAVALELP | TRAFGPSETN | ESPAVVLEPP | VVSMEVSEPH | ILETLKPATK | TAELSVVSTS | VISEQSEQSV | AVMPEPSMTK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ILDSFAAAPV | PTTTLVLKSS | EPVVTMSVEY | QMKSVLKSVE | STSPEPSKIM | LVEPPVAKVL | EPSETLVVSS | ETPTEVYPEP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| STSTTMDFPE | SSAIEALRLP | EQPVDVPSEI | ADSSMTRPQE | LPELPKTTAL | ELQESSVASA | MELPGPPATS | MPELQGPPVT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PVLELPGPSA | TPVPELPGPL | STPVPELPGP | PATAVPELPG | PSVTPVPQLS | QELPGLPAPS | MGLEPPQEVP | EPPVMAQELP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GLPLVTAAVE | LPEQPAVTVA | MELTEQPVTT | TELEQPVGMT | TVEHPGHPEV | TTATGLLGQP | EATMVLELPG | QPVATTALEL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PGQPSVTGVP | ELPGLPSATR | ALELSGQPVA | TGALELPGPL | MAAGALEFSG | QSGAAGALEL | LGQPLATGVL | ELPGQPGAPE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LPGQPVATVA | LEISVQSVVT | TSELSTMTVS | QSLEVPSTTA | LESYNTVAQE | LPTTLVGETS | VTVGVDPLMA | PESHILASNT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| METHILASNT | MDSQMLASNT | MDSQMLASNT | MDSQMLASST | MDSQMLATSS | MDSQMLATSS | MDSQMLATST | MDSQMLATSS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| MDSQMLATSS | MDSQMLATSS | MDSQMLATSS | MDSQMLATST | MDSQMLATST | MDSQMLATSS | MDSQMLASGT | MDSQMLASGT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| MDAQMLASGT | MDAQMLASST | QDSAMLGSKS | PDPYRLAQDP | YRLAQDPYRL | GHDPYRLGHD | AYRLGQDPYR | LGHDPYRLTP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DPYRMSPRPY | RIAPRSYRIA | PRPYRLAPRP | LMLASRRSMM | MSYAAERSMM | SSYERSMMSY | ERSMMSPMAE | RSMMSAYERS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| MMSAYERSMM | SPMAERSMMS | AYERSMMSAY | ERSMMSPMAD | RSMMSMGADR | SMMSSYSAAD | RSMMSSYSAA | DRSMMSSYTA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DRSMMSMAAD | SYTDSYTDTY | TEAYMVPPLP | PEEPPTMPPL | PPEEPPMTPP | LPPEEPPEGP | ALPTEQSALT | AENTWPTEVP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SLPSEESVSQ | PEPPVSQSEI | SEPSAVPTDY | SVSASDPSVL | VSEAAVTVPE | PPPEPESSIT | LTPVESAVVA | EEHEVVPERP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VTCMVSETPA | MSAEPTVLAS | EPPVMSETAE | TFDSMRASGH | VASEVSTSLL | VPAVTTPVLA | ESILEPPAMA | APESSAMAVL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ESSAVTVLES | STVTVLESST | VTVLEPSVVT | VPEPPVVAEP | DYVTIPVPVV | SALEPSVPVL | EPAVSVLQPS | MIVSEPSVSV |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| QESTVTVSEP | AVTVSEQTQV | IPTEVAIEST | PMILESSIMS | SHVMKGINLS | SGDQNLAPEI | GMQEIALHSG | EEPHAEEHLK |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| GDFYESEHGI | NIDLNINNHL | IAKEMEHNTV | CAAGTSPVGE | IGEEKILPTS | ETKQRTVLDT | YPGVSEADAG | ETLSSTGPFA |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LEPDATGTSK | GIEFTTASTL | SLVNKYDVDL | SLTTQDTEHD | MVISTSPSGG | SEADIEGPLP | AKDIHLDLPS | NNNLVSKDTE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| EPLPVKESDQ | TLAALLSPKE | SSGGEKEVPP | PPKETLPDSG | FSANIEDINE | ADLVRPLLPK | DMERLTSLRA | GIEGPLLASD |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| VGRDRSAASP | VVSSMPERAS | ESSSEEKDDY | EIFVKVKDTH | EKSKKNKNRD | KGEKEKKRDS | SLRSRSKRSK | SSEHKSRKRT |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| SESRSRARKR | SSKSKSHRSQ | TRSRSRSRRR | RRSSRSRSKS | RGRRSVSKEK | RKRSPKHRSK | SRERKRKRSS | SRDNRKTVRA |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| RSRTPSRRSR | SHTPSRRRRS | RSVGRRRSFS | ISPSRRSRTP | SRRSRTPSRR | SRTPSRRSRT | PSRRSRTPSR | RSRTPSRRRR |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| SRSVVRRRSF | SISPVRLRRS | RTPLRRRFSR | SPIRRKRSRS | SERGRSPKRL | TDLDKAQLLE | IAKANAAAMC | AKAGVPLPPN |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| LKPAPPPTIE | EKVAKKSGGA | TIEELTEKCK | QIAQSKEDDD | VIVNKPHVSD | EEEEEPPFYH | HPFKLSEPKP | IFFNLNIAAA |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1493 | 2 | 513.1115 | -200.27 | 2 | 48.3 | 12.8 | 0 | 1073-1081 | R.SMMSPMADR.S | |

# Detailed Protein Report

## Protein 646: non-receptor tyrosine-protein kinase TYK2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|187608615 | **Score:** | 25.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 133.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPLRHWGMAR | GSKPVGDGAQ | PMAAMGGLKV | LLHWAGPGGG | EPWVTFSESS | LTAEEVCIHI | AHKVGITPPC | FNLFALFDAQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AQVWLPPNHI | LEIPRDASLM | LYFRIRFYFR | NWHGMNPREP | AVYRCGPPGT | EASSDQTAQG | MQLLDPASFE | YLFEQGKHEF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VNDVASLWEL | STEEEIHHFK | NESLGMAFLH | LCHLALRHGI | PLEEVAKKTS | FKDCIPRSFR | RHIRQHSALT | RLRLRNVFRR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FLRDFQPGRL | SQQMVMVKYL | ATLERLAPRF | GTERVPVCHL | RLLAQAEGEP | CYIRDSGVAP | TDPGPESAAG | PPTHEVLVTG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TGGIQWWPVE | EEVNKEEGSS | GSSGRNPQAS | LFGKKAKAHK | AVGQPADRPR | EPLWAYFCDF | RDITHVVLKE | HCVSIHRQDN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KCLELSLPSR | AAALSFVSLV | DGYFRLTADS | SHYLCHEVAP | PRLVMSIRDG | IHGPLLEPFV | QAKLRPEDGL | YLIHWSTSHP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YRLILTVAQR | SQAPDGMQSL | RLRKFPIEQQ | DGAFVLEGWG | RSFPSVRELG | AALQGCLLRA | GDDCFSLRRC | CLPQPGETSN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LIIMRGARAS | PRTLNLSQLS | FHRVDQKEIT | QLSHLGQGTR | TNVYEGRLRV | EGSGDPEEGK | MDDEDPLVPG | RDRGQELRVV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LKVLDPSHHD | IALAFYETAS | LMSQVSHTHL | AFVHGVCVRG | PENIMVTEYV | EHGPLDVWLR | RERGHVPMAW | KMVVAQQLAS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ALSYLENKNL | VHGNVCGRNI | LLARLGLAEG | TSPFIKLSDP | GVGLGALSRE | ERVERIPWLA | PECLPGGANS | LSTAMDKWGF |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GATLLEICFD | GEAPLQSRSP | SEKEHFYQRQ | HRLPEPSCPQ | LATLTSQCLT | YEPTQRPSFR | TILRDLTRLQ | PHNLADVLTV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| NPDSPASDPT | VFHKRYLKKI | RDLGEGHFGK | VSLYCYDPTN | DGTGEMVAVK | ALKADCGPQH | RSGWKQEIDI | LRTLYHEHII |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KYKGCCEDQG | EKSLQLVMEY | VPLGSLRDYL | PRHSIGLAQL | LLFAQQICEG | MAYLHAQHYI | HRDLAARNVL | LDNDRLVKIG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| DFGLAKAVPE | GHEYYRVRED | GDSPVFWYAP | ECLKEYKFYY | ASDVWSFGVT | LYELLTHCDS | SQSPPTKFLE | LIGIAQGQMT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | |
| VLRLTELLER | GERLPRPDKC | PCEVYHLMKN | CWETEASFRP | TFENLIPILK | TVHEKYQGQA | PSVFSVC | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2015 | 1 | 731.8181 | -73.05 | 2 | 55.1 | 13.5 | 0 | 282-294 | R.LLAQAEGEPCYIR.D | |

# Detailed Protein Report

## Protein 647: PREDICTED: phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530418228 | **Score:** | 25.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 106.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGLEQIIKIP | DQPDTLCFQI | RGAAPPYVYA | VGRGSEAMAA | GLCAGQCILK | VNGSNVMNDG | APEVLEHFQA | FRSRREEALG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LYQWIYHTHE | DAQEARASQE | ASTEDPSGEQ | AQEEDQADSA | FPLLSLGPRL | SLCEDSPMVT | LTVDNVHLEH | GVVYEYVSTA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GVRCHVLEKI | VEPRGCFGLT | AKILEAFAAN | DSVFVENCRR | LMALSSAIVT | MPHFEFRNIC | DTKLESIGQR | IACYQEFAAQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LKSRVSPPFK | QAPLEPHPLC | GLDFCPTNCH | INLMEVSYPK | TTPSVGRSFS | IRFGRKPSLI | GLDPEQGHLN | PMSYTQHCIT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TMAAPSWKCL | PAAEGDPQGQ | GLHDGSFGPA | SGTLGQEDRG | LSFLLKQEDR | EIQDAYLQLF | TKLDVALKEM | KQYVTQINRL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LSTITEPTSG | GSCDASLAEE | ASSLPLVSEE | SEMDRSDHGG | IKKVCFKVAE | EDQEDSGHDT | MSYRDSYSEC | NSNRDSVLSY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TSVRSNSSYL | GSDEMGSGDE | LPCDMRIPSD | KQDKLHGCLE | HLFNQVDSIN | ALLKGPVMSR | AFEETKHFPM | NHSLQEFKQK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EECTIRGRSL | IQISIQEDPW | NLPNSIKTLV | DNIQRYVEDG | KNQLLLALLK | CTDTELQLRR | DAIFCQALVA | AVCTFSKQLL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AALGYRYNNN | GEYEESSRDA | SRKWLEQVAA | TGVLLHCQSL | LSPATVKEER | TMLEDIWVTL | SELDNVTFSF | KQLDENYVAN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TNVFYHIEGS | RQALKVIFYL | DSYHFSKLPS | RLEGGASLRL | HTALFTKVLE | NVEGLPSPGS | QAAEDLQQDI | NAQSLEKVQQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| YYRKLRAFYL | ERSNLPTDAS | TTAVKIDQLI | RPINALDELC | RLMKSFVHPK | PGAAGSVGAG | LIPISSELCY | RLGACQMVMC |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GTGMQRSTLS | VSLEQAAILA | RSHGLLPKCI | MQATDIMRKQ | GPRVEILAKN | LRVKDQMPQG | APRLYRLCQP | PVDGDL |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2660 | 2 | 734.8652 | -30.72 | 2 | 63.3 | 12.9 | 0 | 371-382 | R.EIQDAYLQLFTK.L | |
| 946 | 1 | 628.3451 | -22.84 | 2 | 41.9 | 12.2 | 1 | 748-759 | K.LPSRLEGGASLR.L | |

# Detailed Protein Report

## Protein 648: growth/differentiation factor 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|7705308 | **Score:** | 25.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 47.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MCPGALWVAL | PLLSLLAGSL | QGKPLQSWGR | GSAGGNAHSP | LGVPGGGLPE | HTFNLKMFLE | NVKVDFLRSL | NLSGVPSQDK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TRVEPPQYMI | DLYNRYTSDK | STTPASNIVR | SFSMEDAISI | TATEDFPFQK | HILLFNISIP | RHEQITRAEL | RLYVSCQNHV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DPSHDLKGSV | VIYDVLDGTD | AWDSATETKT | FLVSQDIQDE | GWETLEVSSA | VKRWVRSDST | KSKNKLEVTV | ESHRKGCDTL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DISVPPGSRN | LPFFVVFSND | HSSGTKETRL | ELREMISHEQ | ESVLKKLSKD | GSTEAGESSH | EEDTDGHVAA | GSTLARRKRS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AGAGSHCQKT | SLRVNFEDIG | WDSWIIAPKE | YEAYECKGGC | FFPLADDVTP | TKHAIVQTLV | HLKFPTKVGK | ACCVPTKLSP |
| 410 | 420 | 430 | | | | | |
| ISVLYKDDMG | VPTLKYHYEG | MSVAECGCR | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1810 | 1 | 599.2960 | -61.59 | 2 | 53.0 | 13.6 | 1 | 226-235 | K.LEVTVESHRK.G | |

# Detailed Protein Report

**Protein 649:** **PREDICTED: coiled-coil domain-containing protein 150 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578804109 | **Score:** | 25.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 126.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| | | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDCKVHMETT | VSRPVLSPTH | INATASETFT | VLQQRMRIVE | EQTSSLRDDL | IMLDFGEKRG | YLEAPDCLED | LDSQKVISPI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QNEAICAGKT | DILWKNCEFL | VNRMCRLESL | MQSLKMNIFR | LQTEKDLNPQ | KTAFLKDRLN | AIQEEHSKDL | KLLHLEVMNL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RQQLRAVKEE | EDKAQDEVQR | LTATLKIASQ | TKKNAAIIEE | ELKTTKRKMN | LKIQELRRQL | AQEKYLRESL | EKSASAMLLK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IQEMGSTVEV | ERKQVHILQQ | NCIALRDSIQ | SAQELLAQEQ | KKKEELEIAT | SQLKSDLTSR | DDLISKLVEE | NKNLQISFNK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EHEENAYLRS | EIMSLHEASE | KAQVLNDQLT | KKCSELSCML | QTVTMEKARI | IADHQAILQV | EQKMMTQTFQ | EQNLLLDAAH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ASITNELQTV | QNEKTQLQAH | LDHLILEHNQ | CIQKAQDAEK | RTAVQKELLE | STIARLRGEL | EASMQEKKSL | LEEKERFQRE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VNKTEKEIVQ | ERCNLEKELA | KNKVDINTLT | HNLQTLEEEN | KHLADQMASL | ELQQVTSDYH | GLAQQKVEKI | TESKNKLAYE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NGKLQIKVKQ | LEEQVQSFTD | TSLQNDHLRK | MNKYLQTKYA | QVKSILERSK | EELSRTVKCR | NAALKESQKL | KEDLEAVEDR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ENKKVGNFQR | QLAEAKEDNC | KVTIMLENVL | ASHSKMQGAL | EKVQIELGRR | DSEIAGLKKE | RDLNQQRVQK | LEAEVDQWQA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RMLVMEDQHN | SEIESLQKAL | GVAREDNRKL | AMSLEQALQT | NNHLQTKLDH | IQEQLESKEL | ERQNLETFKD | RMTEESKVEA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ELHAERIEAL | RKQFQTERET | TKKVAQREVA | ELKKALDEAN | FRSVEVSRTN | RELRQKLAEL | EKILESNKEK | IKNQKTQIKL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| HLSAKANNAQ | NIERMKQIEK | ELKQMELIKD | QYQKKNYEQS | LSIQRFVCEM | TNLQKEMQML | AKSQYDASVR | NKQQELHLEA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ERKIRQELEN | RCQELEETVR | HLKKCKEATE | NTLKEASVES | EQITANLEEA | HRWFKHRFDG | LQLELTKNRL | QRPSGEDRWQ |
| 1050 | 1060 | 1070 | 1080 | 1090 | | | |
| EKDQDVKHDV | MSNQSVLHRW | ERKQNLRPMP | KKYHSEVQRK | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 533 | 2 | 524.1612 | -224.39 | 2 | 36.3 | 13.0 | 1 | 493-501 | R.CNLEKELAK.N | |

# Detailed Protein Report

**Protein 650:** **PREDICTED: mitogen-activated protein kinase-binding protein 1 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578826739 | **Score:** | 25.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 99.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MISCGADKSI | YFRTAQKSGD | GVQFTRTHHV | VRKTTLYDMD | VEPSWKYTAI | GCQDRNIRIF | NISSGKQKKL | FKGSQGEDGT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LIKVQTDPSG | IYIATSCSDK | NLSIFDFSSG | ECVATMFGHS | EIVTGMKFSN | DCKHLISVSG | DSCIFVWRLS | SEMTISMRQR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LAELRQRQRG | GKQQGPSSPQ | RASGPNRHQA | PSMLSPGPAL | SSDSDKEGED | EGTEEELPAL | PVLAKSTKKA | LASVPSPALP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RSLSHWEMSR | AQESVGFLDP | APAANPGPRR | RGRWVQPGVE | LSVRSMLDLR | QLETLAPSLQ | DPSQDSLAII | PSGPRKHGQE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ALETSLTSQN | EKPPRPQASQ | PCSYPHIIRL | LSQEEGVFAQ | DLEPAPIEDG | IVYPEPSDNP | TMDTSEFQVQ | APARGTLGRV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YPGSRSSEKH | SPDSACSVDY | SSSCLSSPEH | PTEDSESTEP | LSVDGISSDL | EEPAEGDEEE | EEEEGGMGPY | GLQEGSPQTP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DQEQFLKQHF | ETLASGAAPG | APVQVPERSE | SRSISSRFLL | QVQTRPLREP | SPSSSSLALM | SRPAQVPQAS | GEQPRGNGAN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PPGAPPEVEP | SSGNPSPQQA | ASVLLPRCRL | NPDSSWAPKR | VATASPFSGL | QKAQSVHSLV | PQERHEASLQ | APSPGALLSR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EIEAQDGLGS | LPPADGRPSR | PHSYQNPTTS | SMAKISRSIS | VGENLGLVAE | PQAHAPIRVS | PLSKLALPSR | AHLVLDIPKP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LPDRPTLAAF | SPVTKGRAPG | EAEKPGFPVG | LGKAHSTTER | WACLGEGTTP | KPRTECQAHP | GPSSPCAQQL | PVSSLFQGPE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NLQPPPPEKT | PNPMECTKPG | AALSQDSEPA | VSLEQCEQLV | AELRGSVRQA | VRLYHSVAGC | KMPSAEQSRI | AQLLRDTFSS |
| 890 | 900 | 910 | 920 | 930 | 940 | | |
| VRQELEAVAG | AVLSSPGSSP | GAVGAEQTQA | LLEQYSELLL | RAVERRMERK | L | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 827 | 1 | 697.8253 | -42.16 | 2 | 38.7 | 11.7 | 1 | 14-26 | R.TAQKSGDGVQFTR.T | |

# Detailed Protein Report

## Protein 651: uncharacterized protein C5orf42 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|242332527 | **Score:** | 25.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 361.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| | | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEIRLEILTS | TGIKQKKPWP | RVSWLGKEKE | AVFLLDDKFI | NEINLLSGKI | KKKIPSLQPF | LKDVIVLTTS | SNDAWLAGVL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TTGELFLWNK | DQDCLKTIPI | TEKPKEMIKA | TVASSLRLYL | YVSGNGKRIV | LITPSGCIFL | WEYLELKNIL | SSKSLSLAGR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WSQVIPEEAV | LLPSTEDKEA | VVNAVFIKNE | LFGDCCLCSF | TFYSGECLKL | TFLAIRWHEN | VFTSVRSLPY | HVHWAQQDCH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LCSLIPKCES | VKSRGALISA | FSRDGLTLAV | TLNQKDPKAT | QVLFINTLNF | VTLCGSLKGC | SNKSPVVPAT | LIRSYWVGDI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SWTHDSLFLA | CMLKRGSLVL | LTCQGELLTL | ITFGCSIEFG | PAEFIPLHPL | ITYRPQQFTF | QDSNNSVDSS | ASDSDPMRQR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FSIKAHSRLP | YLVISDGYMV | TTLRFLDSLS | PSVHMRSLLL | DSTQRLEKIY | QSVILSKPKG | KGLNLRSLNS | LRSSLLEHQG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NESSADFTVP | KFLQAEETIN | ENAADFQDFE | AEETNEGRHF | PDNLCPFWNK | RDDVLCSSMK | EGRLEFASMF | DTIHAKDDSE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ETDRTITELH | SIQKSLLAAW | TIGISKTVTE | KNLMLNYIVV | CITHFFYILQ | FIKCPFPKLD | LVLSKSSRHN | AWILCIFQLF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HQCLSIHYWD | IRYKQDVGHL | IKLTSNTVKL | LLTQQQKGQL | FSEKLLACFY | LLKMVADNLN | GVYILQPEVI | SASADGSKIT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AQDSLVVPIF | QMFQDSGFQK | NWSWNSFFKI | HPQVVNPVQQ | PGHRLLILWR | ILYKKTLWYQ | AQLNRRVPEA | DSQLTEKMTH |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EASTVKSLLC | HLQANLQSTG | DCLNQTLELK | SINGEECFLL | GSYEKSVQLW | KKALQEIEEK | GGRRTYFLQI | RYYLSLLYCH |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LYSYNLNDAQ | GLCDQLAREI | LRWSQLPVKE | NKDFSGAAKS | HFECGMVGGV | HPEAAVRVVQ | SMARFMAAYF | TNQQLCILPP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| HHVNVLPPLH | IKTEQSFRLI | PLQHSKVASV | VRDQNLSNVW | TVEYALELLF | IGGLVPEAVW | LAYKLGDWKT | SVSIGVAFQL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| FCKRDSNFMR | SKKKSLNLPL | RMTPAQIFQE | KLQCVLGQPA | SLEAKNEMGS | KYKQFTDPIE | EEDANLLFGS | VQEVLKASVM |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ADADILSETF | QLLIDSAKDF | SKRLWGLVPF | GLYLPAPPLY | CPQPAILSEE | DGDDLLLKAE | KNNRQKVSGI | LQRVLLLFRA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| AQCSFPVAQW | YILQLRWARK | VMQKIRMKGS | LPSLSPFPQS | LLNYCKGGIA | FFRPGAAGDH | KLDEVSIRAI | GCFRELCALC |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| WMLHVRDKLS | YSCRQYQKAR | ENVKGEKDLE | VEFDSCMIEH | CLSAVEWAYR | MLPFSRFFNM | EELIQDIILS | LIGELPPIRK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VAEIFVKAFP | YPEDVRVPLR | DKYHSLHQRL | RHCVVKGPQT | EEMMSVVMHS | IQKVRVKALK | RVQRNIGSFE | VNIWEPIEEE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KPDEAPGVDR | YSLGTSLSRS | TLTELGDSVV | HSDADTFSEA | LSVEEKSRIN | IYQRNAPNHM | ELTSIHKPTD | KRKMCNQKEN |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PTKKEDHEKL | SQNTLPVIGV | WEFERDDDEY | IKFLDLFLSY | ILERDLPYSR | DADIPFLTSF | SGKLREHELN | SLLFDVHTTL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KRHQSKTKSQ | NVFRAGSCFV | VAPESYESEK | SSSLNDEYGM | HLENQKLSSS | VLVNQGIKPF | LQYPSNEVNK | NEGMSGLFGL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| KQRSIYKIQD | DTREKCLIQR | SSNHIFWTPK | SIKTRRCIFK | AIQCNDINPQ | EDLPLALNTF | GSIGRLLEWM | IRWSNRRLLC |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| DSGITESSSE | YSPVIRVKTS | TAAILTSLWL | LEQPYFATYK | AKNAIIKMVE | NRDTGCQIGP | NIERESKSDA | GGSVAVATPG |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| GTEERNGQNK | SCQNILNRMP | TEAKNPDIKE | INDDIISITH | NTKKEFIDID | ENLLEVEAFT | EEEMDMHISD | YEEDIEESVG |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| GFRSPSLAIC | MMTLPQQLEE | EFTEEVQCQR | EEPLETIMEE | KSTEQKGMIE | AFSHPGHTTP | QSMQVDTSSE | ISSAQISTYK |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| EKSSSVPLLI | SNGVNVASQP | PAPTPQKTQR | NEFTAQLPDC | SESVRQMLQD | EMFKLVQLQQ | INFMSLMQIV | GSSFANLPDT |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| QQLVQQSQSV | HLGESQESNL | RGCGDVEDSN | KNLKERFFIK | PQSMGENARE | PRKNSPHCHE | GTIPSGQNST | GNVQNVPHGS |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1525 | 1 | 1052.1493 | 111.26 | 2 | 48.7 | 10.2 | 1 | 1072-1091 | K.LQCVLGQPASLEAKNEMGSK.Y | |

# Detailed Protein Report

## Protein 652: protein CASP isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|148277064 | **Score:** | 25.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 164.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 5.17 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.04 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLCVAGARLK | RELDATATVL | ANRQDESEQS | RKRLIEQSRE | FKKNTPEDLR | KQVAPLLKSF | QGEIDALSKR | SKEAEAAFLN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VYKRLIDVPD | PVPALDLGQQ | LQLKVQRLHD | IETENQKLRE | TLEEYNKEFA | EVKNQEVTIK | ALKEKIREYE | QTLKNQAETI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ALEKEQKLQN | DFAEKERKLQ | ETQMSTTSKL | EEAEHKVQSL | QTALEKTRTE | LFDLKTKYDE | ETTAKADEIE | MIMTDLERAN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QRAEVAQREA | ETLREQLSSA | NHSLQLASQI | QKAPDVEQAI | EVLTRSSLEV | ELAAKEREIA | QLVEDVQRLQ | ASLTKLRENS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ASQISQLEQQ | LSAKNSTLKQ | LEEKLKGQAD | YEEVKKELNI | LKSMEFAPSE | GAGTQDAAKP | LEVLLLEKNR | SLQSENAALR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ISNSDLSGSA | RRKGKDQPES | RRPGSLPAPP | PSQLPRNPGE | QASNTNGTHQ | FSPAGLSQDF | FSSSLASPSL | PLASTGKFAL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NSLLQRQLMQ | SFYSKAMQEA | GSTSMIFSTG | PYSTNSISSQ | SPLQQSPDVN | GMAPSPSQSE | SAGSVSEGEE | MDTAEIARQV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KEQLIKHNIG | QRIFGHYVLG | LSQGSVSEIL | ARPKPWNKLT | VRGKEPFHKM | KQFLSDEQNI | LALRSIQGRQ | RENPGQSLNR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LFQEVPKRRN | GSEGNITTRI | RASETGSDEA | IKSILEQAKR | ELQVQKTAEP | AQPSSASGSG | NSDDAIRSIL | QQARREMEAQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QAALDPALKQ | APLSQSDITI | LTPKLLSTSP | MPTVSSYPPL | AISLKKPSAA | PEAGASALPN | PPALKKEAQD | APGLDPQGAA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DCAQGVLRQV | KNEVGRSGAW | KDHWWSAVQP | ERRNAASSEE | AKAEETGGGK | EKGSGGSGGG | SQPRAERSQL | QGPSSSEYWK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EWPSAESPYS | QSSELSLTGA | SRSETPQNSP | LPSSPIVPMS | KPTKPSVPPL | TPEQYEVYMY | QEVDTIELTR | QVKEKLAKNG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ICQRIFGEKV | LGLSQGSVSD | MLSRPKPWSK | LTQKGREPFI | RMQLWLNGEL | GQGVLPVQGQ | QQGPVLHSVT | SLQDPLQQGC |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VSSESTPKTS | ASCSPAPESP | MSSSESVKSL | TELVQQPCPP | IEASKDSKPP | EPSDPPASDS | QPTTPLPLSG | HSALSIQELV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| AMSPELDTYG | ITKRVKEVLT | DNNLGQRLFG | ETILGLTQGS | VSDLLARPKP | WHKLSLKGRE | PFVRMQLWLN | DPNNVEKLMD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| MKRMEKKAYM | KRRHSSVSDS | QPCEPPSVGT | EYSQGASPQP | QHQLKKPRVV | LAPEEKEALK | RAYQQKPYPS | PKTIEDLATQ |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LNLKTSTVIN | WFHNYRSRIR | RELFIEEIQA | GSQGQAGASD | SPSARSGRAA | PSSEGDSCDG | VEATEGPGSA | DTEEPKSQGE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| AEREEVPRPA | EQTEPPPSGT | PGPDDARDDD | HEGGPVEGPG | PLPSPASATA | TAAPAAPEDA | ATSAAAAPGE | GPAAPSSAPP |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | |
| PSNSSSSSAP | RRPSSLQSLF | GLPEAAGARD | SRDNPLRKKK | AANLNSIIHR | LEKAASREEP | IEWEF | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 597 | 3 | 661.1918 | -220.59 | 2 | 37.0 | 14.5 | 1 | 959-969 | K.NGICQRIFGEK.V | Carbamidomethyl: 4 | WUP:QUP 1.04<br>QU:MU 5.17 |

# Detailed Protein Report

**Protein 653:** **transport and Golgi organization protein 6 homolog [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|153791502 | **Score:** | 25.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 120.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAARQAVGSG | AQETCGLDRI | LEALKLLLSP | GGSGSSSLQV | TKHDVLLATL | KSNLSALEDK | FLKDPQWKNL | KLLRDEIADK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AEWPQNSVDV | TWSFTSQTLL | LLLCLKETMI | RLAANFNPGK | PNPRTPEVAP | ALSPDALSIS | QQKTVQFVLQ | FVVTLGICPY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LMPGVGVPLR | YRTEFGAVVQ | DVVCFDAAPD | ATRRLYTSCK | ALLNVAQHTS | LGSLIFCHHF | GDIAAGLCQL | GFCPTKRKLL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TPAEEVLTEE | ERTLSRGALR | DMLDQVYQPL | AVRELLILQG | GPPQSCTDVK | TQMRCRAPAW | LRRLCGQLLS | ERLMRPNGVQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AVVRGILEGA | GAGAAGGSDA | EVTAADWKKC | DLIAKILASC | PQQSLSPENY | YRDICPQVLD | LFHFQDKLTA | RQFQRVATTT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FITLSRERPH | LAAKYLLQPV | LAPLHRCLNT | AELSESDMVP | GTILVTEEEL | SRCIEDVFKV | YVVGNEPLTV | LMDSLLPVLG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VLFLLYCFTK | QSVSHIRSLC | QEILLWILGK | LERKKAIASL | KGFAGLDKAV | PSLHSLCQFR | VATQGGIMIT | IKEAISDEDE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DEALYQKVSS | EQGRVEHLGD | LLSHCQECGL | AGDFFIFCLK | ELTHVASENE | TELKTEPFSS | KSLLELEQHQ | TLLVEGQERK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LLVLQLMAVL | CERMSEQIFT | NVTQVVDFVA | ATLQRACASL | AHQAESTVES | QTLSMSMGLV | AVMLGGAVQL | KSSDFAVLKQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LLPLLEKVSN | TYPDPVIQEL | AVDLRITIST | HGAFATEAVS | MAAQSTLNRK | DLEGKIEEQQ | QTSHERPTDV | AHSHLEQQQS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| HETAPQTGLQ | SNAPIIPQGV | NEPSTTTSQK | SGSVTTEQLQ | EVLLSAYDPQ | IPTRAAALRT | LSHWIEQREA | KALEMQEKLL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KIFLENLEHE | DTFVYLSAIQ | GVALLSDVYP | EKILPDLLAQ | YDSSKDKHTP | ETRMKVGEVL | MRIVRALGDM | VSKYREPLIH |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TFLRGVRDPD | GAHRASSLAN | LGELCQRLDF | LLGSVVHEVT | ACLIAVAKTD | GEVQVRRAAI | HVVVLLLRGL | SQKATEVLSA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | | |
| VLKDLYHLLK | HVVCLEPDDV | AKLHAQLALE | ELDDIMKNFL | FPPQKLEKKI | MVLP | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2043 | 2 | 698.2867 | -131.01 | 2 | 55.4 | 13.1 | 0 | 112-124 | R.LAANFNPGKPNPR.T | |
| 1030 | 1 | 809.4708 | -1.60 | 3 | 43.0 | 11.9 | 2 | 1029-1050 | R.GLSQKATEVLSAVLKDLYHLLK.H | |

# Detailed Protein Report

**Protein 654:** **G patch domain-containing protein 3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|205277458 | **Score:** | 25.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 7.0 |
| | | **No. of unique Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MAVPGEAEEE ATVYLVVSGI PSVLRSAHLR SYFSQFREER GGGFLCFHYR HRPERAPPQA APNSALIPTD PAAEGQLLSQ
        90        100        110        120        130        140        150        160
TSATDVRPLS TRDSTPIQTR TCCCVISVRG LAQAQRLIRM YSGRRWLDSH GTWLPGRCLI RRLRLPTEAS GLGSFPFKTR
       170        180        190        200        210        220        230        240
KELQSWKAEN EAFTLADLKQ LPELNPPVLM PRGNVGTPLR VFLELIRACR LPPRIITQLQ LQFPKTGSSR RYGNVPFEYE
       250        260        270        280        290        300        310        320
DSETVEQEEL VYTAEGEEIP QGTYLADIPA SPCGEPEEEV GKEEEEESHS DEDDDRGEEW ERHEALHEDV TGQERTTEQL
       330        340        350        360        370        380        390        400
FEEEIELKWE KGGSGLVFYT DAQFWQEEEG DFDEQTADDW DVDMSVYYDR DGGDKDARDS VQMRLEQRLR DGQEDGSVIE
       410        420        430        440        450        460        470        480
RQVGTFERHT KGIGRKVMER QGWAEGQGLG CRCSGVPEAL DSDGQHPRCK RGLGYHGEKL QPFGQLKRPR RNGLGLISTI
       490        500        510        520        530
YDEPLPQDQT ESLLRRQPPT SMKFRTDMAF VRGSSCASDS PSLPD
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2000 | 1 | 918.3556 | -161.95 | 2 | 55.4 | 14.2 | 2 | 145-161 | R.LPTEASGLGSFPFKTRK.E | |
| 1493 | 1 | 705.9667 | -4.88 | 3 | 47.0 | 10.8 | 1 | 506-525 | R.TDMAFVRGSSCASDSPSLPD.- | Carbamidomethyl: 11;<br>Oxidation: 3 |

# Detailed Protein Report

## Protein 655: nucleosome-remodeling factor subunit BPTF isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|38788260 | **Score:** | 25.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 322.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRGRRGRPPK | QPAAPAAERC | APAPPPPPPP | PTSGPIGGLR | SRHRGSSRGR | WAAAQAEVAP | KTRLSSPRGG | SSSRRKPPPP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PPAPPSTSAP | GRGGRGGGGG | RTGGGGGGGH | LARTTAARRA | VNKVVYDDHE | SEEEEEEEDM | VSEEEEEEDG | DAEETQDSED |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DEEDEMEEDD | DDSDYPEEME | DDDDDASYCT | ESSFRSHSTY | SSTPGRRKPR | VHRPRSPILE | EKDIPPLEFP | KSSEDLMVPN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EHIMNVIAIY | EVLRNFGTVL | RLSPFRFEDF | CAALVSQEQC | TLMAEMHVVL | LKAVLREEDT | SNTTFGPADL | KDSVNSTLYF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IDGMTWPEVL | RVYCESDKEY | HHVLPYQEAE | DYPYGPVENK | IKVLQFLVDQ | FLTTNIAREE | LMSEGVIQYD | DHCRVCHKLG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DLLCCETCSA | VYHLECVKPP | LEEVPEDEWQ | CEVCVAHKVP | GVTDCVAEIQ | KNKPYIRHEP | IGYDRSRRKY | WFLNRRLIIE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EDTENENEKK | IWYYSTKVQL | AELIDCLDKD | YWEAELCKIL | EEMREEIHRH | MDITEDLTNK | ARGSNKSFLA | AANEEILESI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RAKKGDIDNV | KSPEETEKDK | NETENDSKDA | EKNREEFEDQ | SLEKDSDDKT | PDDDPEQGKS | EEPTEVGDKG | NSVSANLGDN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TTNATSEETS | PSEGRSPVGC | LSETPDSSNM | AEKKVASELP | QDVPEEPNKT | CESSNTSATT | TSIQPNLENS | NSSSELNSSQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SESAKAADDP | ENGERESHTP | VSIQEEIVGD | FKSEKSNGEL | SESPGAGKGA | SGSTRIITRL | RNPDSKLSQL | KSQQVAAAAH |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EANKLFKEGK | EVLVVNSQGE | ISRLSTKKEV | IMKGNINNYF | KLGQEGKYRV | YHNQYSTNSF | ALNKHQHRED | HDKRRHLAHK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| FCLTPAGEFK | WNGSVHGSKV | LTISTLRLTI | TQLENNIPSS | FLHPNWASHR | ANWIKAVQMC | SKPREFALAL | AILECAVKPV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VMLPIWRESL | GHTRLHRMTS | IEREEKEKVK | KKEKKQEEEE | TMQQATWVKY | TFPVKHQVWK | QKGEEYRVTG | YGGWSWISKT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| HVYRFVPKLP | GNTNVNYRKS | LEGTKNNMDE | NMDESDKRKC | SRSPKKIKIE | PDSEKDEVKG | SDAAKGADQN | EMDISKITEK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KDQDVKELLD | SDSDKPCKEE | PMEVDDDMKT | ESHVNCQESS | QVDVVNVSEG | FHLRTSYKKK | TKSSKLDGLL | ERRIKQFTLE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EKQRLEKIKL | EGGIKGIGKT | STNSSKNLSE | SPVITKAKEG | CQSDSMRQEQ | SPNANNDQPE | DLIQGCSESD | SSVLRMSDPS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| HTTNKLYPKD | RVLDDVSIRS | PETKCPKQNS | IENDIEEKVS | DLASRGQEPS | KSKTKGNDFF | IDDSKLASAD | DIGTLICKNK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KPLIQEESDT | IVSSSKSALH | SSVPKSTNDR | DATPLSRAMD | FEGKLGCDSE | SNSTLENSSD | TVSIQDSSEE | DMIVQNSNES |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ISEQFRTREQ | DVEVLEPLKC | ELVSGESTGN | CEDRLPVKGT | EANGKKPSQQ | KKLEERPVNK | CSDQIKLKNT | TDKKNNENRE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| SEKKGQRTST | FQINGKDNKP | KIYLKGECLK | EISESRVVSG | NVEPKVNNIN | KIIPENDIKS | LTVKESAIRP | FINGDVIMED |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| FNERNSSETK | SHLLSSSDAE | GNYRDSLETL | PSTKESDSTQ | TTTPSASCPE | SNSVNQVEDM | EIETSEVKKV | TSSPITSEEE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| SNLSNDFIDE | NGLPINKNEN | VNGESKRKTV | ITEVTTMTST | VATESKTVIK | VEKGDKQTVV | SSTENCAKST | VTTTTTTVTK |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| LSTPSTGGSV | DIISVKEQSK | TVVTTTVTDS | LTTTGGTLVT | SMTVSKEYST | RDKVKLMKFS | RPKKTRSGTA | LPSYRKFVTK |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| SSKKSIFVLP | NDDLKKLARK | GGIREVPYFN | YNAKPALDIW | PYPSPRPTFG | ITWRYRLQTV | KSLAGVSLML | RLLWASLRWD |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| DMAAKAPPGG | GTTRTETSET | EITTTEIIKR | RDVGPYGIRS | EYCIRKIICP | IGVPETPKET | PTPQRKGLRS | SALRPKRPET |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| PKQTGPVIIE | TWVAEEELEL | WEIRAFAERV | EKEKAQAVEQ | QAKKRLEQQK | PTVIATSTTS | PTSSTTSTIS | PAQKVMVAPI |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| SGSVTTGTKM | VLTTKVGSPA | TVTFQQNKNF | HQTFATWVKQ | GQSNSGVVQV | QQKVLGIIPS | STGTSQQTFT | SFQPRTATVT |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| IRPNTSGSGG | TTSNSQVITG | PQIRPGMTVI | RTPLQQSTLG | KAIIRTPVMV | QPGAPQQVMT | QIIRGQPVST | AVSAPNTVSS |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| TPGQKSLTSA | TSTSNIQSSA | SQPPRPQQGQ | VKLTMAQLTQ | LTQGHGGNQG | LTVVIQGQGQ | TTGQLQLIPQ | GVTVLPGPGQ |
| 2330 | 2340 | 2350 | 2360 | 2370 | 2380 | 2390 | 2400 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2124 | 1 | 732.2973 | -129.78 | 2 | 56.9 | 12.0 | 0 | 2075-2089 | K.VMVAPISGSVTTGTK.M | Oxidation: 2 |

# Detailed Protein Report

## Protein 656: PREDICTED: macrophage mannose receptor 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578844889 | **Score:** | 25.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 88.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGLELISEYT | RQFLIYNEDH | KRCVDAVSPS | AVQTAACNQD | AESQKFRWVS | ESQIMSVAFK | LCLGVPSKTD | WVAIPLYACD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SKSEFQKWEC | KNDTLLGIKG | EDLFFNYGNR | QEKNIMLYKG | SGLWSRWKIY | GTTDNLCSRG | YEAMYTLLGN | ANGATCAFPF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KFENKWYADC | TSAGRSDGWL | WCGTTTDYDT | DKLFGYCPLK | FEGSESLWNK | DPLTSVSYQI | NSKSALTWHQ | ARKSCQQQNA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ELLSITEIHE | QTYLTGKDMK | SRNVLGHENN | PAAAYEQFLG | YSVSTYPGKF | TVEDNNGIRT | EPNDELWIGL | NDIKIQMYFE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WSDGTPVTFT | KWLRGEPSHE | NNRQEDCVVM | KGKDGYWADR | GCEWPLGYIC | KMKSRSQGPE | IVEVEKGCRK | DKHQNLSQHQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LLKTWKYVNR | NDAQSAYFIG | LLISLDKKFA | WMDGSKVDYV | SWATGEPNFA | NEDENCVTMY | SNSGFWNDIN | CGYPNAFICQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RHNSSINATT | VMPTMPSVPS | GCKEGWNFYS | NKADCVVIIG | GASNEAGKWM | DDTCDSKRGY | ICQTRSEIPA | TEPPQLPGRC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PESDHTAWIP | FHGHCYYIES | SYTRNWGQAS | LECLRMGSSL | VSIESAAESS | FLSYRVEPLK | SKTNFWIGLF | RNVEGTWLWI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NNSPVSFVNW | NTGDPSGERN | DCVALHASSG | FWSNIHCSSY | KGYICKRPKI | IDAKPTHELL | TTKADTRKMD | PSKPSSNVAG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | |
| VVIIVILLIL | TGAGLAAYFF | YKKRRVHLPQ | EGAFENTLYF | NSQSSPGTSD | MKDLVGNIEQ | NEHSVI | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2567 | 1 | 673.3649 | -8.13 | 2 | 62.8 | 10.6 | 0 | 393-403 | K.HQNLSQHQLLK.T | |

# Detailed Protein Report

**Protein 657:** **TRIO and F-actin-binding protein isoform 2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|88501741 | **Score:** | 24.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 47.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 8.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 3.22 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MGGWKGPGQR RGKEGPEARR RAAERGGGGG GGGVPAPRSP AREPRPRSCL LLPPPWGAAM TPDLLNFKKG WMSILDEPGE
        90        100        110        120        130        140        150        160
PPSPSLTTTS TSQWKKHWFV LTDSSLKYYR DSTAEEADEL DGEIDLRSCT DVTEYAVQRN YGFQIHTKDA VYTLSAMTSG
       170        180        190        200        210        220        230        240
IRRNWIEALR KTVRPTSAPD VTKLSDSNKE NALHSYSTQK GPLKAGEQRA GSEVISRGGP RKADGQRQAL DYVELSPLTQ
       250        260        270        280        290        300        310        320
ASPQRARTPA RTPDRLAKQE ELERDLAQRS EERRKWFEAT DSRTPEVPAG EGPRRGLGAP LTEDQQNRLS EEIEKKWQEL
       330        340        350        360        370        380        390        400
EKLPLRENKR VPLTALLNQS RGERRGPPSD GHEALEKEVQ ALRAQLEAWR LQGEAPQSAL RSQEDGHIPP GYISQLVGVI
       410        420        430        440
TVPVLQTRPL SSERLCDLPK VTPPAGLKGG I
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1361 | 1 | 711.8629 | -0.75 | 2 | 45.3 | 11.9 | 1 | 22-38 | R.AAERGGGGGGGGVPAPR.S | | QU:MU 3.22 |

# Detailed Protein Report

## Protein 658: PREDICTED: rootletin isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578800146 | **Score:** | 24.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 196.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVFLPSLLGG | GCPTGPRSQP | CAHCPLPVLL | PATEMASLLS | LQEENQLLQQ | ELSRVEDLLA | QSRAERDELA | IKYNAVSERL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EQALRLEPGE | LETQEPRGLV | RQSVELRRQL | QEEQASYRRK | LQAYQEGQQR | QAQLVQRLQG | KILQYKKRCS | ELEQQLLERS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GELEQQRLRD | TEHSQDLESA | LIRLEEEQQR | SASLAQVNAM | LREQLDQAGS | ANQALSEDIR | KVTNDWTRCR | KELEHREAAW |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RREEESFNAY | FSNEHSRLLL | LWRQVVGFRR | LVSEVKMFTE | RDLLQLGGEL | ARTSRAVQEA | GLGLSTGLRL | AESRAEAALE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KQALLQAQLE | EQLRDKVLRE | KDLAQQQMQS | DLDKADLSAR | VTELGLAVKR | LEKQNLEKDQ | VNKDLTEKLE | ALESLRLQEQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AALETEDGEG | LQQTLRDLAQ | AVLSDSESGV | QLSGSERTAD | ASNGSLRGLS | GQRTPSPPRR | SSPGRGRSPR | RGPSPACSDS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| STLALIHSAL | HKRQLQVQDM | RGRYEASQDL | LGTLRKQLSD | SESERRALEE | QLQRLRDKTD | GAMQAHEDAQ | REVQRLRSAN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ELLSREKSNL | AHSLQVAQQQ | AEELRQEREK | LQAAQEELRR | QRDRLEEEQE | DAVQDGARVR | RELERSHRQL | EQLEGKRSVL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AKELVEVREA | LSRATLQRDM | LQAEKAEVAE | ALTKAEAGRV | ELELSMTKLR | AEEASLQDSL | SKLSALNESL | AQDKLDLNRL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VAQLEEEKSA | LQGRQRQAEQ | EATVAREEQE | RLEELRLEQE | VARQGLEGSL | RVAEQAQEAL | EQQLPTLRHE | RSQLQEQLAQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LSRQLSGREQ | ELEQARREAQ | RQVEALERAA | REKEALAKEH | AGLAVQLVAA | EREGRTLSEE | ATRLRLEKEA | LEGSLFEVQR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QLAQLEARRE | QLEAEGQALL | LAKETLTGEL | AGLRQQIIAT | QEKASLDKEL | MAQKLVQAER | EAQASLREQR | AAHEEDLQRL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QREKEAAWRE | LEAERAQLQS | QLQREQEELL | ARLEAEKEEL | SEEIAALQQE | RDEGLLLAES | EKQQALSLKE | SEKTALSEKL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| MGTRHSLATI | SLEMERQKRD | AQSRQEQDRS | TVNALTSELR | DLRAQREEAA | AAHAQEVRRL | QEQARDLGKQ | RDSCLREAEE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LRTQLRLLED | ARDGLRRELL | EAQRKLRESQ | EGREVQRQEA | GELRRSLGEG | AKEREALRRS | NEELRSAVKK | AESERISLKL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ANEDKEQKLA | LLEEARTAVG | KEAGELRTGL | QEVERSRLEA | RRELQELRRQ | MKMLDSENTR | LGRELAELQG | RLALGERAEK |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| ESRRETLGLR | QRLLKGEASL | EVMRQELQVA | QRKLQEQEGE | FRTRERRLLG | SLEEARGTEK | QQLDHARGLE | LKLEAARAEA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| AELGLRLSAA | EGRAQGLEAE | LARVEVQRRA | AEAQLGGLRS | ALRRGLGLGR | APSPAPRPVP | GSPARDAPAE | GSGEGLNSPS |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| TLECSPGSQP | PSPGPATSPA | SPDLDPEAVR | GALREFLQEL | RSAQRERDEL | RTQTSALNRQ | LAEMEAERDS | ATSRARQLQK |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| AVAESEEARR | SVDGRLSGVQ | AELALQEESV | RRSERERRAT | LDQVATLERS | LQATESELRA | SQEKISKMKA | NETKLEGDKR |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| RLKEVLDASE | SRTVKLELQR | RSLEGELQRS | RLGLSDREAQ | AQALQDRVDS | LQRQVADSEV | KAGTLQLTVE | RLNGALAKVE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | | |
| ESEGALRDKV | RGLTEALAQS | SASLNSTRDK | NLHLQKALTA | CEHDRQVLQR | YRIERTP | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2749 | 1 | 863.9191 | -72.24 | 2 | 64.7 | 13.7 | 2 | 1616-1629 | K.LELQRRSLEGELQR.S | |

# Detailed Protein Report

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## Protein 659: PREDICTED: kinesin-like protein KIF24 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530389882 | **Score:** | 24.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 110.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRRKKQLTSL | NIFCRLFARE | DSKHMVQIVG | LQELQVDSVE | LLLEVILKGS | KERSTGATGV | NADSSRSHAV | IQIQIKDSAK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RTFGRISFID | LAGSERAADA | RDSDRQTKME | GAEINQSLLA | LKECIRALDQ | EHTHTPFRQS | KLTQVLKDSF | IGNAKTCMIA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NISPSHVATE | HTLNTLRYAD | RVKELKKGIK | CCTSVTSRNR | TSGNSSPKRI | QSSPGALSED | KCSPKKVKLG | FQQSLTVAAP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GSTRGKVHPL | TSHPPNIPFT | SAPKVSGKRG | GSRGSPSQEW | VIHASPVKGT | VRSGHVAKKK | PEESAPLCSE | KNRMGNKTVL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GWESRASGPG | EGLVRGKLST | KCKKVQTVQP | VQKQLVSRVE | LSFGNAHHRA | EYSQDSQRGT | PARPASEAWT | NIPPHQKERE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EHLRFYHQQF | QQPPLLQQKL | KYQPLKRSLR | QYRPPEGQLT | NETPPLFHSY | SENHDGAQVE | ELDDSDFSED | SFSHISSQRA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TKQRNTLENS | EDSFFLHQTW | GQGPEKQVAE | RQQSLFSSPR | TGDKKDLTKS | WVDSRDPINH | RRAALDHSCS | PSKGPVDWSR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ENSTSSGPSP | RDSLAEKPYC | SQVDFIYRQE | RGGGSSFDLR | KDASQSEVSG | ENEGNLPSPE | EDGFTISLSH | VAVPGSPDQR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DTVTTPLREV | SADGPIQVTS | TVKNGHAVPG | EDPRGQLGTH | AEYASGLMSP | LTMSLLENPD | NEGSPPSEQL | VQDGATHSLV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AESTGGPVVS | HTVPSGDQEA | ALPVSSATRH | LWLSSSPPDN | KPGGDLPALS | PSPIRQHPAD | KLPSREADLG | EACQSRETVL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FSHEHMGSEQ | YDADAEETGL | DGSWGFPGKP | FTTIHMGVPH | SGPTLTPRTG | SSDVADQLWA | QERKHPTRLG | WQEFGLSTDP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| IKLPCNSENV | TWLKPRPISR | CLARPSSPLV | PSCSPKTAGT | LRQPTLEQAQ | QVVIRAHQEQ | LDEMAELGFK | EETLMSQLAS |
| 970 | 980 | 990 | 1000 | 1010 | | | |
| NDFEDFVTQL | DEIMVLKSKC | IQSLRSQLQL | YLTCHGPTAA | PEGTVPS | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1869 | 2 | 604.2765 | -71.18 | 2 | 53.7 | 12.8 | 0 | 86-96 | R.ISFIDLAGSER.A | |
| 2259 | 1 | 1023.8759 | 66.82 | 3 | 58.1 | 12.0 | 2 | 543-571 | R.AALDHSCSPSKGPVDWSRENSTSSGPSPR.D | Carbamidomethyl: 7 |

# Detailed Protein Report

---

**Protein 660:** **low molecular weight phosphotyrosine protein phosphatase isoform d [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|96304457 | **Score:** | 24.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 12.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 25.0 |
| | | **No. of unique Peptides:** | 2 |

```
         10          20          30          40          50          60          70          80
MAEQATKSVL  FVCLGNICRS  PIAEAVFRKL  VTDQNISENW  RVDSAATSGY  EIGNPPDYRG  QSCMKRHGIP  MSHVARQVPS
         90         100         110         120
LDLKLCVLCF  SGSLTAVLFL  TGTWAGPQTQ  EL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1657 | 1 | 1061.8014 | -69.49 | 3 | 50.5 | 13.5 | 2 | 1-28 | -.MAEQATKSVLFVCLGNICRSPIAEAVFR.K | Carbamidomethyl: 13, 18;<br>Oxidation: 1 |
| 2031 | 1 | 719.2691 | -141.18 | 2 | 55.8 | 11.3 | 0 | 8-19 | K.SVLFVCLGNICR.S | Carbamidomethyl: 6, 11 |

# Detailed Protein Report

**Protein 661:** **PREDICTED: dehydrogenase/reductase SDR family member 7B isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578829832 | **Score:** | 24.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 8.9 |
| | | **No. of unique Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MVSPATRQRP GPRMDPIHPA PCLPQAKWSP GPGDQGWPVM LCQVLKESQK CTRRKSLPKV KAMDFITSTA ILPLLFGCLG
        90        100        110        120        130        140        150        160
VFGLFRLLQW VRGKAYLRNA VVVITGATSG LGKECAKVFY AAGAKLVLCG RNGGALEELI RELTASHATK VQTHKPYLVT
       170        180        190        200        210        220        230        240
FDLTDSGAIV AAAAEILQCF GYVDILVNNA GISYRGTIMD TTVDVDKRVM ETNYFGPVAL TKALLPSMIK RRQGHIVAIS
       250        260        270        280        290        300        310        320
SIQGKMSIPF RSAYAASKHA TQAFFDCLRA EMEQYEIEVT VISPGYIHTN LSVNAITADG SRYGVMDTTT AQGRSPVEVA
       330        340        350        360        370        380
QDVLAAVGKK KKDVILADLL PSLAVYLRTL APGLFFSLMA SRARKERKSK NS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2770 | 1 | 1086.0137 | -9.69 | 2 | 65.8 | 12.0 | 0 | 28-46 | K.WSPGPGDQGWPVMLCQVLK.E | Carbamidomethyl: 15;<br>Oxidation: 13 |
| 2279 | 4 | 734.2810 | -176.54 | 2 | 56.8 | 12.8 | 1 | 118-131 | K.VFYAAGAKLVLCGR.N | |

# Detailed Protein Report

**Protein 662:** **PREDICTED: leucine-rich repeat and IQ domain-containing protein 3 isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530361769 | **Score:** | 24.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 9.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFHGTVTEEL | TSHEEWSHYN | ENIREGQKDF | VFVKFNGLHL | KSMENLQSCI | SLRVCIFSNN | FITDIHPLQS | CIKLIKLDLH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GNQIKSLPNT | KFWNGLKNLK | LLYLHDNGFA | KLKNICVLSA | CPTLIALTMF | DCPVSLKKGY | RHVLVNSIWP | LKALDHHVIS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DEEIIQNWHL | PERFKACNHR | LFFNFCPALR | KGTTYEEEIN | NIKHITSKIN | AILAHNSPVL | IVQRWIRGFL | VRKNLSPVFF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HKKKQQEKII | RGYEAKWIYI | TKGYEDKLLK | DLFFKPETNI | KGKLAYWKHN | IYYPVDLKNS | SEHRKHVSSI | LCELKPKDLG |
| 330 | 340 | | | | | | |
| MKSKTSRHLI | QKDGS | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1395 | 1 | 727.3741 | 43.73 | 2 | 47.1 | 12.0 | 0 | 42-53 | K.SMENLQSCISLR.V | Carbamidomethyl: 8;<br>Oxidation: 2 |

# Detailed Protein Report

## Protein 663: trophoblast glycoprotein-like precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|306922420 | **Score:** | 24.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 6.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | |
|---|---|---|---|
| ***WUP:QUP*** | **Median:** 1.33 | **CV:** 0.00 % | **No. of Peptides:** 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAPRAGQPGL | QGLLLVAAAL | SQPAAPCPFQ | CYCFGGPKLL | LRCASGAELR | QPPRDVPPDA | RNLTIVGANL | TVLRAAAFAG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GDGDGDQAAG | VRLPLLSALR | LTHNHIEVVE | DGAFDGLPSL | AALDLSHNPL | RALGGGAFRG | LPALRSLQLN | HALVRGGPAL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LAALDAALAP | LAELRLLGLA | GNALSRLPPA | ALRLARLEQL | DVRLNALAGL | DPDELRALER | DGGLPGPRLL | LADNPLRCGC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AARPLLAWLR | NATERVPDSR | RLRCAAPRAL | LDRPLLDLDG | ARLRCADSGA | DARGEEAEAA | GPELEASYVF | FGLVLALIGL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| IFLMVLYLNR | RGIQRWMRNL | REACRDQMEG | YHYRYEQDAD | PRRAPAPAAP | AGSRATSPGS | GL | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2021 | 1 | 890.3901 | -128.12 | 2 | 55.7 | 10.1 | 2 | 39-54 | K.LLLRCASGAELRQPPR.D | | WUP:QUP 1.33 |

# Detailed Protein Report

## Protein 664: PREDICTED: ceramide-1-phosphate transfer protein isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530360429 | **Score:** | 24.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 17.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.0 |
| | | **Sequence Coverage [%]:** | 21.2 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MERLRGGPQS EHYRSLQAMV AHELSNRLVD LERRSHHPES GCRTVLRLHR ALHWLQLFLE GLRTSPEDAR TSALCADSYN
        90        100        110        120        130        140        150        160
ASLAAYHPWV VRRAVTVAFC TLPTREVFLE AMNVGPPEQA VQMLGEALPF IQRVYNVSQK LYAEHSLLDL P
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2006 | 1 | 1044.9286 | -117.90 | 2 | 55.5 | 11.6 | 1 | 134-151 | R.VYNVSQKLYAEHSLLDLP.- | |

# Detailed Protein Report

## Protein 665: DIS3-like exonuclease 1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|19115966 | **Score:** | 24.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 111.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530405359 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: DIS3-like exonuclease 1 isoform X4 [Homo sapiens] |
| gi\|530405355 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: DIS3-like exonuclease 1 isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQTACQAVQH | QRGRRQYNKL | RNLLKDARHD | CILFANEFQQ | CCYLPRERGE | SMEKWQTRSI | YNAAVWYYHH | CQDRMPIVMV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TEDEEAIQQY | GSETEGVFVI | TFKNYLDNFW | PDLKAAHELC | DSILQSRRER | ENESQESHGK | EYPEHLPLEV | LEAGIKSGRY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IQGILNVNKH | RAQIEAFVRL | QGASSKDSDL | VSDILIHGMK | ARNRSIHGDV | VVVELLPKNE | WKGRTVALCE | NDCDDKASGE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SPSEPMPTGR | VVGILQKNWR | DYVVTFPSKE | EVQSQGKNAQ | KILVTPWDYR | IPKIRISTQQ | AETLQDFRVV | VRIDSWESTS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VYPNGHFVRV | LGRIGDLEGE | IATILVENSI | SVIPFSEAQM | CEMPVNTPES | PWKVSPEEEQ | KRKDLRKSHL | VFSIDPKGCE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DVDDTLSVRT | LNNGNLELGV | HIADVTHFVA | PNSYIDIEAR | TRATTYYLAD | RRYDMLPSVL | SADLCSLLGG | VDRYAVSIMW |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ELDKASYEIK | KVWYGRTIIR | SAYKLFYEAA | QELLDGNLSV | VDDIPEFKDL | DEKSRQAKLE | ELVWAIGKLT | DIARHVRAKR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DGCGALELEG | VEVCVQLDDK | KNIHDLIPKQ | PLEVHETVAE | CMILANHWVA | KKIWESFPHQ | ALLRQHPPPH | QEFFSELREC |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AKAKGFFIDT | RSNKTLADSL | DNANDPHDPI | VNRLLRSMAT | QAMSNALYFS | TGSCAEEEFH | HYGLALDKYT | HFTSPIRRYS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DIVVHRLLMA | AISKDKKMEI | KGNLFSNKDL | EELCRHINNR | NQAAQHSQKQ | STELFQCMYF | KDKDPATEER | CISDGVIYSI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RTNGVLLFIP | RFGIKGAAYL | KNKDGLVISC | GPDSCSEWKP | GSLQRFQNKI | TSTTTDGESV | TFHLFDHVTV | RISIQASRCH |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SDTIRLEIIS | NKPYKIPNTE | LIHQSSPLLK | SELVKEVTKS | VEEAQLAQEV | KVNIIQEEYQ | EYRQTKGRSL | YTLLEEIRDL |
| 970 | 980 | | | | | | |
| ALLDVSNNYG | I | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1921 | 2 | 655.2832 | -155.36 | 2 | 52.4 | 10.4 | 2 | 812-823 | R.FGIKGAAYLKNK.D | |

# Detailed Protein Report

## Protein 666: tropomyosin alpha-3 chain isoform 6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|499137516 | **Score:** | 24.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 11.5 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MMQRSELSAS SEKLREKGGP GNRGMKVIEN RALKDEEKME LQEIQLKEAK HIAEEADRKY EEVARKLVII EGDLERTEER
        90        100        110        120        130        140        150        160
AELAESRCRE MDEQIRLMDQ NLKCLSAAEE KYSQKEDKYE EEIKILTDKL KEAETRAEFA ERSVAKLEKT IDDLEDKLKC
       170        180        190
TKEEHLCTQR MLDQTLLDLN EM
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2779 | 2 | 626.8528 | 125.66 | 2 | 63.3 | 11.5 | 1 | 88-96 | R.CREMDEQIR.L | Carbamidomethyl: 1;<br>Oxidation: 4 |

# Detailed Protein Report

## Protein 667: PREDICTED: WD repeat-containing protein 59 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530424315 | **Score:** | 24.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 76.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMMWSWSSSG | GSRRKLCAND | ILDGVDEFIE | SISLLPEPEK | TLHTEDTDHQ | HTASHGEEEA | LKEDPPRNLL | EERKSDQLGL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PQTLQQEFSL | INVQIRNVNV | EMDAADRSCT | VSVHCSNHRV | KMLVKFPAQY | PNNAAPSFQF | INPTTITSTM | KAKLLKILKD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TALQKVKRGQ | SCLEPCLRQL | VSCLESFVNQ | EDSASSNPFA | LPNSVTPPLP | TFARVTTAYG | SYQDANIPFP | RTSGARFCGA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GYLVYFTRPM | TMHRAVSPTE | PTPRSLSALS | AYHTGLIAPM | KIRTEAPGNL | RLYSGSPTRS | EKEQVSISSF | YYKERMSPRS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ARRRWSIQAI | NDFPKSRRWK | SKREGSDSGN | RQIKAAGKVI | IQDIACLLPV | HKSLGELYIL | NVNDIQETCQ | KNAASALLVG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RKDLVQVWSL | ATVATDLCLG | PKSDPDLETP | WARHPFGRQL | LESLLAHYCR | LRDVQTLAML | CSVFEAQSRP | QGLPNPFGPF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PNRSSNLVVS | HSRYPSFTSS | GSCSSMSDPG | LNTGGWNIAG | REAEHLSSPW | GESSPEELRF | GSLTYSDPRE | RERDQHDKNK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RLLDPANTQQ | FDDFKKCYGE | ILYRWGLREK | RAEVLKFVSC | PPDPHKGIEF | GVYCSHCRSE | VRGTQCAICK | GFTFQCAICH |
| 650 | 660 | 670 | 680 | 690 | | | |
| VAVRGSSNFC | LTCGHGGHTS | HMMEWFRTQE | VCPTGCGCHC | LLESTF | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1549 | 1 | 1023.0071 | -55.90 | 2 | 49.6 | 10.6 | 1 | 265-283 | R.SLSALSAYHTGLIAPMKIR.T | Oxidation: 16 |

# Detailed Protein Report

## Protein 668: PREDICTED: adenomatous polyposis coli protein 2 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578832904 | **Score:** | 24.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 243.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.29 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 3.48 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASSVAPYEQ | LVRQVEALKA | ENSHLRQELR | DNSSHLSKLE | TETSGMKEVL | KHLQGKLEQE | ARVLVSSGQT | EVLEQLKALQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MDITSLYNLK | FQPPTLGPEP | AARTPEGSPV | HGSGPSKDSF | GELSRATIRL | LEELDRERCF | LLNEIEKEEK | EKLWYYSQLQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GLSKRLDELP | HVETFSMQMD | LIRQQLEFEA | QHIRSLMEER | FGTSDEMVQR | AQIRASRLEQ | IDKELLEAQD | RVQQTEPQAL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LAVKSVPVDE | DPETEVPTHP | EDGTPQPGNS | KVEVVFWLLS | MLATRDQEDT | ARTLLAMSSS | PESCVAMRRS | GCLPLLLQIL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HGTEAAAGGR | AGAPGAPGAK | DARMRANAAL | HNIVFSQPDQ | GLARKEMRVL | HVLEQIRAYC | ETCWDWLQAR | DGGPEGGGAG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SAPIPIEPQI | CQATCAVMKL | SFDEEYRRAM | NELGGLQAVA | ELLQVDYEMH | KMTRDPLNLA | LRRYAGMTLT | NLTFGDVANK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ATLCARRGCM | EAIVAQLASD | SEELHQVVSS | ILRNLSWRAD | INSKKVLREA | GSVTALVQCV | LRATKESTLK | SVLSALWNLS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AHSTENKAAI | CQVDGALGFL | VSTLTYKCQS | NSLAIIESGG | GILRNVSSLV | ATREDYRQVL | RDHNCLQTLL | QHLTSHSLTI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VSNACGTLWN | LSARSARDQE | LLWDLGAVGM | LRNLVHSKHK | MIAMGSAAAL | RNLLAHRPAK | HQAAATAVSP | GSCVPSLYVR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KQRALEAELD | ARHLAQALEH | LEKQGPPAAE | AATKKPLPPL | RHLDGLAQDY | ASDSGCFDDD | DAPSSLAAAA | ATGEPASPAA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LSLFLGSPFL | QGQALARTPP | TRRGGKEAEK | DTSGEAAVAA | KAKAKLALAV | ARIDQLVEDI | SALHTSSDDS | FSLSSGDPGQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EAPREGRAQS | CSPCRGPEGG | RREAGSRAHP | LLRLKAAHAS | LSNDSLNSGS | ASDGYCPREH | MLPCPLAALA | SRREDPRCGQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PRPSRLDLDL | PGCQAEPPAR | EATSADARVR | TIKLSPTYQH | VPLLEGASRA | GAEPLAGPGI | SPGARKQAWL | PADHLSKVPE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KLAAAPLSVA | SKALQKLAAQ | EGPLSLSRCS | SLSSLSSAGR | PGPSEGGDLD | DSDSSLEGLE | EAGPSEAELD | STWRAPGATS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LPVAIPAPRR | NRGRGLGVED | ATPSSSSENY | VQETPLVLSR | CSSVSSLGSF | ESPSIASSIP | SEPCSGQGSG | TISPSELPDS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PGQTMPPSRS | KTPPLAPAPQ | GPPEATQFSL | QWESYVKRFL | DIADCRERCR | LPSELDAGSV | RFTVEKPDEN | FSCASSLSAL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| ALHEHYVQQD | VELRLLPSAC | PERGGGAGGA | GLHFAGHRRR | EEGPAPTGSR | PRGAADQELE | LLRECLGAAV | PARLRKVASA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LVPGRRALPV | PVYMLVPAPA | PAQEDDSCTD | SAEGTPVNFS | SAASLSDETL | QGPPRDQPGG | PAGRQRPTGR | PTSARQAMGH |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| RHKAGGAGRS | AEQSRGAGKN | RAGLELPLGR | PPSAPADKDG | SKPGRTRGDG | ALQSLCLTTP | TEEAVYCFYG | NDSDEEPPAA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| APTPTHRRTS | AIPRAFTRER | PQGRKEAPAP | SKAAPAAPPP | ARTQPSLIAD | ETPPCYSLSS | SASSLSEPEP | SEPPAVHPRG |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| REPAVTKDPG | PGGGRDSSPS | PRAAEELLQR | CISSALPRRR | PPVSGLRRRK | PRATRLDERP | AEGSRERGEE | AAGSDRASDL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| DSVEWRAIQE | GANSIVTWLH | QAAAATREAS | SESDSILSFV | SGLSVGSTLQ | PPKHRKGRQA | EGEMGSARRP | EKRGAASVKT |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SGSPRSPAGP | EKPRGTQKTT | PGVPAVLRGR | TVIYVPSPAP | RAQPKGTPGP | RATPRKVAPP | CLAQPAAPAK | VPSPGQQRSR |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| SLHRPAKTSE | LATLSQPPRS | ATPPARLAKT | PSSSSSQTSP | ASQPLPRKRP | PVTQAAGALP | GPGASPVPKT | PARTLLAKQH |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| KTQRSPVRIP | FMQRPARRGP | PPLARAVPEP | GPRGRAGTEA | GPGARGGRLG | LVRVASALSS | GSESSDRSGF | RRQLTFIKES |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| PGLRRRRSEL | SSAESAASAP | QGASPRRGRP | ALPAVFLCSS | RCEELRAAPR | QGPAPARQRP | PAARPSPGER | PARRTTSESP |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| SRLPVRAPAA | RPETVKRYAS | LPHISVARRP | DGAVPAAPAS | ADAARRSSDG | EPRPLPRVAA | PGTTWRRIRD | EDVPHILRST |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1997 | 1 | 731.3112 | -143.18 | 2 | 54.9 | 10.6 | 1 | 1816-1830 | R.KVAPPCLAQPAAPAK.V |  | WUP:QUP 3.48<br>QU:MU 0.29 |

# Detailed Protein Report

## Protein 669: retinoic acid receptor responder protein 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4506427 | **Score:** | 24.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 18.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 12.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.87 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MRRLLIPLAL WLGAVGVGVA ELTEAQRRGL QVALEEFHKH PPVQWAFQET SVESAVDTPF PAGIFVRLEF KLQQTSCRKR
        90        100        110        120        130        140        150        160
DWKKPECKVR PNGRKRKCLA CIKLGSEDKV LGRLVHCPIE TQVLREAEEH QETQCLRVQR AGEDPHSFYF PGQFAFSKAL
       170
PRS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2028 | 1 | 909.8408 | -155.00 | 2 | 53.7 | 13.3 | 2 | 98-113 | K.CLACIKLGSEDKVLGR.L | Carbamidomethyl: 1, 4 | WUP:QUP 0.87 |

# Detailed Protein Report

**Protein 670:** **PREDICTED: nck-associated protein 5 isoform X4 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578804243 | **Score:** | 24.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 205.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.8 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 3.14 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.05 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MHEKLIHELE | EERHLRLQSE | KRLQEVTLES | ERNRIQMRSL | QQQFSRMEET | VRNLLQSQGS | PEQKKEETVN | IMVYQEKLSE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EERKHKEALE | DLHMVVDEDS | RSESSSTDEG | KEKTKLLLER | LKALEAENSA | LALENENQRE | QYERCLDEVA | NQVVQALLTQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KDLREECVKL | KTRVFDLEQQ | NRTLSILFQQ | RVRPTSDLLL | QKLHSRLLDL | SSGDLLSEVE | RNRSLTQSRT | DAEVHEHQLN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TKSALKCPGL | GAVIPGHLCP | RNSYSSSSEL | SLSSTCSEYS | SGSSYTWHDG | KNLRKRQSSQ | NWDKRLSIDS | SLPSGFASPT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NELPPTRIKE | SHILEGLRKL | QKRKVLLEPP | SVITKWGYKD | CMNSNEGIYS | PGIKSSSLKE | YPPCKTADLG | SPCKEPHKTF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VYDLDSHVDA | DDDPSTLALL | QAVPNQSCRP | HGSKLTHSVS | DSLFGWETNR | KHFLEGTSSV | YPKERPEKLT | SCASSCPLEM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KLCPSVQTPQ | VQRERGPQGQ | GHGRMALNLQ | LSDTDDNETF | DELHIESSDE | KSPSDVSLAA | DTDKSVENLD | VLVGFGKSLC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GSPEEEEKQV | PIPSETRPKT | FSFIKQQRVV | KRTSSEECVT | VIFDAEDGEP | IEFSSHQTGV | VTVTRNEISI | NSTPAGPKAE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HTELLPQGIA | CLQPRAAARD | YTFFKRSEED | TEKNIPKDNV | DNVPRVSTES | FSSRTVTQNP | QQQKLVKPTH | NISCQSNSRS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SAPMGIYQKQ | NLTKIPPRGK | SSPQKSKLME | PEATTLLPSS | GLVTLEKSPA | LAPGKLSRFM | KTESSGPLFE | LRSDPHIPKH |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SAQLPHSSRM | PSRRDWVQCP | KSQTPGSRSR | PAIESSDSGE | PPTRDEHCGS | GPEAGVKSPS | PPPPPGRSVS | LLARPSYDYS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PAPSSTKSET | RVPSETARTP | FKSPLLKGIS | APVISSNPAT | TEVQRKKPSV | AFKKPIFTHP | MPSPEAVIQT | RCPAHAPSSS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FTVMALGPPK | VSPKRGVPKT | SPRQTLGTPQ | RDIGLQTPRI | SPSTHEPLEM | TSSKSVSPGR | KGQLNDSAST | PPKPSFLGVN |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ESPSSQVSSS | SSSSSPAKSH | NSPHGCQSAH | EKGLKTRLPV | GLKVLMKSPQ | LLRKSSTVPG | KHEKDSLNEA | SKSSVAVNKS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KPEDSKNPAS | MEITAGERNV | TLPDSQAQGS | LADGLPLETA | LQEPLESSIP | GSDGRDGVDN | RSMRRSLSSS | KPHLKPALGM |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| NGAKARSHSF | STHSGDKPST | PPIEGSGKVR | TQIITNTAER | GNSLTRQNSS | TESSPNKAPS | APMLESLPSV | GRPSGHPSSG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KGSLGSSGSF | SSQHGSPSKL | PLRIPPKSEG | LLIPPGKEDQ | QAFTQGECPS | ANVAVLGEPG | SDRRSCPPTP | TDCPEALQSP |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| GRTQHPSTFE | TSSTSKLETS | GRHPDASATA | TDAVSSEAPL | SPTIEEKVML | CIQENVEKGQ | VQTKPTSVEA | KQKPGPSFAS |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| WFGFRKSRLP | ALSSRKMDIS | KTKVEKKDAK | VLGFGNRQLK | SERKKEKKKP | ELQCETENEL | IKDTKSADNP | DGGLQSKNNR |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| RTPQDIYNQL | KIEPRNRHSP | VACSTKDTFM | TELLNRVDKK | AAPQTESGSS | NASCRNVLKG | SSQGSCLIGS | SISTQGNHKK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| NMKIKADMEV | PKDSLVKEAN | ENLQEDEDDA | VADSVFQSHI | IESNCQMRTL | DSGIGTFPLP | DSGNRSTGRY | LCQPDSPEDA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| EPLLPLQSAL | SAVSSMRAQT | LEREVPSSTD | GQRPADSAIV | HSTSDPIMTA | RGMRPLQSRL | PKPASSGKVS | SQKQNEAEPR |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| PQTCSSFGYA | EDPMASQPLP | DWGSEVAATG | TQKLRQLEET | KDDPENRLSK | ISLESFNKFN | SNTVILLEKE | KNSLNKVEGQ |
| 1850 | 1860 | 1870 | 1880 | 1890 | | | |
| KEEKEKNEET | SLSSSDRPGV | DNLESLSDSL | YDSFSSCASQ | GSNDV | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1394 | 1 | 533.7488 | -137.10 | 2 | 45.8 | 10.2 | 1 | 730-738 | K.QNLTKIPPR.G | | WUP:QUP 0.05<br>QU:MU 3.14 |

# Detailed Protein Report

## Protein 671: kinesin-like protein KIF1C [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|40254834 | **Score:** | 24.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 122.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530409731 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: kinesin-like protein KIF1C isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAGASVKVAV | RVRPFNARET | SQDAKCVVSM | QGNTTSIINP | KQSKDAPKSF | TFDYSYWSHT | STEDPQFASQ | QQVYRDIGEE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MLLHAFEGYN | VCIFAYGQTG | AGKSYTMMGR | QEPGQQGIVP | QLCEDLFSRV | SENQSAQLSY | SVEVSYMEIY | CERVRDLLNP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KSRGSLRVRE | HPILGPYVQD | LSKLAVTSYA | DIADLMDCGN | KARTVAATNM | NETSSRSHAV | FTIVFTQRCH | DQLTGLDSEK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VSKISLVDLA | GSERADSSGA | RGMRLKEGAN | INKSLTTLGK | VISALADMQS | KKRKSDFIPY | RDSVLTWLLK | ENLGGNSRTA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MIAALSPADI | NYEETLSTLR | YADRTKQIRC | NAIINEDPNA | RLIRELQEEV | ARLRELLMAQ | GLSASALEGL | KTEEGSVRGA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LPAVSSPPAP | VSPSSPTTHN | GELEPSFSPN | TESQIGPEEA | MERLQETEKI | IAELNETWEE | KLRKTEALRM | EREALLAEMG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VAVREDGGTV | GVFSPKKTPH | LVNLNEDPLM | SECLLYHIKD | GVTRVGQVDM | DIKLTGQFIR | EQHCLFRSIP | QPDGEVVVTL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EPCEGAETYV | NGKLVTEPLV | LKSGNRIVMG | KNHVFRFNHP | EQARLERERG | VPPPPGPPSE | PVDWNFAQKE | LLEQQGIDIK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LEMEKRLQDL | ENQYRKEKEE | ADLLLEQQRL | YADSDSGDDS | DKRSCEESWR | LISSLREQLP | PTTVQTIVKR | CGLPSSGKRR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| APRRVYQIPQ | RRRLQGKDPR | WATMADLKMQ | AVKEICYEVA | LADFRHGRAE | IEALAALKMR | ELCRTYGKPD | GPGDAWRAVA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RDVWDTVGEE | EGGGAGSGGG | SEEGARGAEV | EDLRAHIDKL | TGILQEVKLQ | NSSKDRELQA | LRDRMLRMER | VIPLAQDHED |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ENEEGGEVPW | APPEGSEAAE | EAAPSDRMPS | ARPPSPPLSS | WERVSRLMEE | DPAFRRGRLR | WLKQEQLRLQ | GLQGSGGRGG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GLRRPPARFV | PPHDCKLRFP | FKSNPQHRES | WPGMGSGEAP | TPLQPPEEVT | PHPATPARRP | PSPRRSHHPR | RNSLDGGGRS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | |
| RGAGSAQPEP | QHFQPKKHNS | YPQPPQPYPA | QRPPGPRYPP | YTTPPRMRRQ | RSAPDLKESG | AAV | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 911 | 1 | 512.1169 | -231.37 | 2 | 41.5 | 10.9 | 1 | 255-264 | R.ADSSGARGMR.L | Oxidation: 9 |
| 1261 | 1 | 1044.6916 | 131.82 | 2 | 44.1 | 13.7 | 2 | 630-646 | K.ELLEQQGIDIKLEMEKR.L | Oxidation: 14 |

# Detailed Protein Report

## Protein 672: cullin-4A isoform 3 [Homo sapiens]

**Accession:** gi|511772963
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 24.6
**MW [kDa]:** 77.7
**pI:** 7.0
**Sequence Coverage [%]:** 4.6
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLYKQLRQAC | EDHVQAQILP | FREDSLDSVL | FLKKINTCWQ | DHCRQMIMIR | SIFLFLDRTY | VLQNSTLPSI | CPVSYCLYRD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MGLELFRTHI | ISDKMVQSKT | IDGILLLIER | ERSGEAVDRS | LLRSLLGMLS | DLQVYKDSFE | LKFLEETNCL | YAAEGQRLMQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EREVPEYLNH | VSKRLEEEGD | RVITYLDHST | QKPLIACVEK | QLLGEHLTAI | LQKGLDHLLD | ENRVPDLAQM | YQLFSRVRGG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QQALLQHWSE | YIKTFGTAIV | INPEKDKDMV | QDLLDFKDKV | DHVIEVCFQK | NERFVNLMKE | SFETFINKRP | NKPAELIAKH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VDSKLRAGNK | EATDEELERT | LDKIMILFRF | IHGKDVFEAF | YKKDLAKRLL | VGKSASVDAE | KSMLSKLKHE | CGAAFTSKLE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GMFKDMELSK | DIMVHFKQHM | QNQSDSGPID | LTVNILTMGY | WPTYTPMEVH | LTPEMIKLQE | VFKAFYLGKH | SGRKLQWQTT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LGHAVLKAEF | KEGKKEFQVS | LFQTLVLLMF | NEGDGFSFEE | IKMATGIEDS | ELRRTLQSLA | CGKARVLIKS | PKGKEVEDGD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KFIFNGEFKH | KLFRIKINQI | QMKETVEEQV | STTERVFQDR | QYQIDAAIVR | IMKMRKTLGH | NLLVSELYNQ | LKFPVKPGDL |
| 650 | 660 | 670 | | | | | |
| KKRIESLIDR | DYMERDKDNP | NQYHYVA | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2598 | 1 | 625.3169 | -85.65 | 2 | 63.1 | 10.6 | 1 | 340-349 | R.TLDKIMILFR.F | |

# Detailed Protein Report

## Protein 673: ras-related protein Rab-44 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|390635651 | **Score:** | 24.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 110.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| METGQRTSRK | VRKLGSNRRR | QTREPADGEG | AAVAPEPESW | SSQAAAELQA | FFQDCGAKER | GFVTREDLAV | AKFSFLGSKE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ESEMIFDWVD | VERKGHLSLE | EFSSGLKNIF | GSSQSPHRLR | RRKPLPSKRV | SATTSFPALE | EADAEEKEAF | LAFMEQLGTG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HLLPKQMEIW | QLWGQLRQEE | PQLAGNLAGF | LAKMTSRLQE | AQADKEALEL | TLRKRDSDHH | REVQQLYEEM | EQQIRQEKQQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LQAESDSRGL | ALTSQMQDVL | EAKEREVQRL | AEGQRELEAQ | LSHLRSTHQE | AASENQQLQE | AKRDLAGRLE | EVRGQLQVTR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GRLDAARGRV | SWQVEEKLSF | PGAGEKTPDP | QAASPEEAPL | PGLFGDNDDW | DQLLSNFGSP | PHGALQLCWS | PPPTPRATSG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PQTPRVVRQI | SISEPQAFLF | GQEPSSDPDG | APRTPPGVTF | SAKDNKGVDP | HEQDIRAEQP | VEPHDPDPNQ | EPGSTPEGRL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LWGLSGSLVA | PAFKVLIPLE | DGPPPPANSP | PPQAPAGSSK | QIQASDPDDK | GPGSWAPPSG | AQPGAGAGPQ | EPTQTPPTMT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ERETQPGPSP | TTALTGVGPA | KPPRQRDALQ | QDLHATGSEP | RLGTQRARAL | TLGPAEPFQG | LEFVGPVPTE | RLEQGQAGPA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VQEGLPEGLR | EAHGQVLGLG | ELSAFPHQEL | EEEPRSEEGK | QEGRGGQDLS | SEQSEQSVEA | HGLETAHSEL | PQQDSLLVSL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PSATPQAQVE | AEGPTPGKSA | PPRGSPPRGA | QPGAGAGPQE | PTQTPPTMAE | QEAQPRPSLT | TAHAEEQGPP | HSREPRAESR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LEDPGMDSRE | AGLTPSPGDP | MAGGGPQANP | DYLFHVIFLG | DSNVGKTSFL | HLLHQNSFAT | GLTATVGVDF | RVKTLLVDNK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| CFVLQLWDTA | GQERYHSMTR | QLLRKADGVV | LMYDITSQES | FAHVRYWLDC | LQDAGSDGVV | ILLLGNKMDC | EEERQVSVEA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | |
| GQQLAQELGV | YFGECSAALG | HNILEPVVNL | ARSLRMQEEG | LKDSLVKVAP | KRPPKRFGCC | S | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1160 | 1 | 1207.8157 | -48.25 | 3 | 44.6 | 14.3 | 0 | 24-58 | R.EPADGEGAAVAPEPESWSSQAAAELQAFFQDCGAK.E | Carbamidomethyl: 32 |

BRUKER

# Detailed Protein Report

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**Protein 674:** **sodium/hydrogen exchanger 11 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|224465231 | **Score:** | 24.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 129.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSYFWAQNE | SNRPDLLCGQ | PADYLVEEKH | FTTLVCFIVV | LGGLLKMCLK | NCEVIVLTIL | SLSGFVIGHM | AYNSVEVHQI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VYPLLRTSSF | SLYSYFSPLI | IFMVALDVEF | YTLKKMFWQV | LLTGLISFST | ASIIIGYVVI | KFNKDSWDLQ | SCLLFSITLG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IIDPLRSVNS | LKTIGISKIY | IDLIRGESLI | ICSIASIFFG | NFRGNRIHFS | IFRDLHVGIE | LSYDILGSII | FGYWCAKIIQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CILADVFSNM | LTNIILCFSM | VYMTFYIVEF | LGMSGTLALA | AVGLNLDSLT | FKPKIELVIT | KFLRIFSSVY | EHLIYAFFGI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VIGCGELSHY | EFHTIPFIFI | LFTTVNLVRL | LTILLVSPIL | MHSNYEYNWR | WGVVITWSGI | KGVFNLLWAP | DVYNLAERKV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EVPQMFILYV | QVISLLTMGI | NSYVMTQSAR | KLDLCVLSLP | RQMILQNATQ | HIQEIVQNTI | TLFKTEKILT | NVNWTLVEDK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TRIEYIPFSH | VSHNDMKTES | TTDEALMEEA | RLHVAAIQMS | SFEKQRNNGI | LEIEAARILI | GAAKCYYSIQ | GKFMSIYDVS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TYMRTRSWLI | KFKNVLTFLE | YCIEKIHFIP | PESNTFLTFI | FHIVFSEEFE | YTGQIINLIY | IYPMIIHLWP | MARGLNVSAL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ISINYYFMFL | YVLESTLKII | ILKRKYFQQC | WNTLEFFILV | IGIIDIFCVY | FVKLRPDNLA | LIQLTVIMGY | LRIIRFLPLF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KIIVPILIRI | ADVQIKKRLS | LMYSITKGYI | KSQEDAKLLI | KQIAVCESIY | QKLCEILETN | KQDAVKELVL | MEHEGRDVVI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ALKTKQAIRN | VIAKALKNLT | FLCSRGIIDK | HEVIEINKVL | LKKLKALNNF | PKAIPPPTPD | IYLHNIIWLE | GKDVLIDFFK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ERAKLACFDS | GDTICKGGEM | PQGIYLIISG | MAILHSLSPT | FGIESNQRCD | RGSRDMFTEF | CTTGDIIGEL | SCLLKREIEY |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TVICETSLQA | CFISLEDLYE | GFDAFWPSLE | YKIWLKLALS | TAYQYFESSL | IDEDLRFQNC | VMFNQAYVET | LSSYSDMIID |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| NMTMKFVIIV | YGSVIDTKTE | EPYFAPCIIP | TTCEQVQGTS | DLSKLLIIQA | SELTQRNSNT | NVMASVNTVF | EQPGKNINGR |
| 1130 | | | | | | | |
| QKMS | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2425 | 1 | 893.4053 | -14.86 | 2 | 58.6 | 13.4 | 1 | 553-566 | K.FMSIYDVSTYMRTR.S | Oxidation: 2 |

# Detailed Protein Report

**Protein 675:** **carboxyl-terminal PDZ ligand of neuronal nitric oxide synthase protein isoform 3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|258613965 | **Score:** | 24.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 55.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.2 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.28 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.55 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPSKTKYNLV | DDGHDLRIPL | HNEDAFQHGI | CFEAKYVGSL | DVPRPNSRVE | IVAAMRRIRY | EFKAKNIKKK | KVSIMVSVDG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VKVILKKKKK | KKEWTWDESK | MLVMQDPIYR | IFYVSHDSQD | LKIFSYIARD | GASNIFRCNV | FKSKKKSQAM | RIVRTVGQAF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EVCHKLSLQH | TQQNADGQED | GESERNSNSS | GDPGRQLTGA | ERASTATAEE | TDIDAVEVPL | PGNDVLEFSR | GVTDLDAVGK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EGGSHTGSKV | SHPQEPMLTA | SPRMLLPSSS | SKPPGLGTET | PLSTHHQMQL | LQQLLQQQQQ | QTQVAVAQVH | LLKDQLAAEA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AARLEAQARV | HQLLLQNKDM | LQHISLLVKQ | VQELELKLSG | QNAMGSQDSL | LEITFRSGAL | PVLCDPTTPK | PEDLHSPPLG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AGLADFAHPA | GSPLGRRDCL | VKLECFRFLP | PEDTPPPAQG | EALLGGLELI | KFRESGIASE | YESNTDESEE | RDSWSQEELP |
| 490 | 500 | 510 | | | | | |
| RLLNVLQRQE | LGDGLDDEIA | V | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2276 | 1 | 873.4565 | 51.32 | 2 | 58.9 | 11.6 | 1 | 186-202 | R.NSNSSGDPGRQLTGAER.A | | QU:MU 1.28<br>WUP:QUP 1.55 |
| 1604 | 1 | 783.2767 | -145.45 | 2 | 50.3 | 12.9 | 0 | 250-263 | K.VSHPQEPMLTASPR.M | Oxidation: 8 | |

# Detailed Protein Report

## Protein 676: sterile alpha motif domain-containing protein 9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|38201706 | **Score:** | 24.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 184.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|300863105 | refseq_human (refseq_human_20140103.fasta) | sterile alpha motif domain-containing protein 9 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAKQLNLPEN | TDDWTKEDVN | QWLESHKIDQ | KHREILTEQD | VNGAVLKWLK | KEHLVDMGIT | HGPAIQIEEL | FKELRKTAIE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DSIQTSKMGK | PSKNAPKDQT | VSQKERRETS | KQKQKGKENP | DMANPSAMST | TAKGSKSLKV | ELIEDKIDYT | KERQPSIDLT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CVSYPFDEFS | NPYRYKLDFS | LQPETGPGNL | IDPIHEFKAF | TNTATATEED | VKMKFSNEVF | RFASACMNSR | TNGTIHFGVK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DKPHGKIVGI | KVTNDTKEAL | INHFNLMINK | YFEDHQVQQA | KKCIREPRFV | EVLLPNSTLS | DRFVIEVDII | PQFSECQYDY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FQIKMQNYNN | KIWEQSKKFS | LFVRDGTSSK | DITKNKVDFR | AFKADFKTLA | ESRKAAEEKF | RAKTNKKERE | GPKLVKLLTG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NQDLLDNSYY | EQYILVTNKC | HPDQTKHLDF | LKEIKWFAVL | EFDPESNING | VVKAYKESRV | ANLHFPSVYV | EQKTTPNETI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| STLNLYHQPS | WIFCNGRLDL | DSEKYKPFDP | SSWQRERASD | VRKLISFLTH | EDIMPRGKFL | VVFLLLSSVD | DPRDPLIETF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| CAFYQDLKGM | ENILCICVHP | HIFQGWKDLL | EARLIKHQDE | ISSQCISALS | LEEINGTILK | LKSVTQSSKR | LLPSIGLSTV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LLKKEEDIMT | ALEIICENEC | EGTLLEKDKN | KFLEFKASKE | EDFYRGGKVS | WWNFYFSSES | YSSPFVKRDK | YERLEAMIQN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CADSSKPTST | KIIHLYHHPG | CGGTTLAMHI | LWELRKKFRC | AVLKNKTVDF | SEIGEQVTSL | ITYGAMNRQE | YVPVLLLVDD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FEEQDNVYLL | QYSIQTAIAK | KYIRYEKPLV | IILNCMRSQN | PEKSARIPDS | IAVIQQLSPK | EQRAFELKLK | EIKEQHKNFE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DFYSFMIMKT | NFNKEYIENV | VRNILKGQNI | FTKEAKLFSF | LALLNSYVPD | TTISLSQCEK | FLGIGNKKAF | WGTEKFEDKM |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GTYSTILIKT | EVIECGNYCG | VRIIHSLIAE | FSLEELKKSY | HLNKSQIMLD | MLTENLFFDT | GMGKSKFLQD | MHTLLLTRHR |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| DEHEGETGNW | FSPFIEALHK | DEGNEAVEAV | LLESIHRFNP | NAFICQALAR | HFYIKKKDFG | NALNWAKQAK | IIEPDNSYIS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DTLGQVYKSK | IRWWIEENGG | NGNISVDDLI | ALLDLAEHAS | SAFKESQQQS | EDREYEVKER | LYPKSKRRYD | TYNIAGYQGE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| IEVGLYTIQI | LQLIPFFDNK | NELSKRYMVN | FVSGSSDIPG | DPNNEYKLAL | KNYIPYLTKL | KFSLKKSFDF | FDEYFVLLKP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| RNNIKQNEEA | KTRRKVAGYF | KKYVDIFCLL | EESQNNTGLG | SKFSEPLQVE | RCRRNLVALK | ADKFSGLLEY | LIKSQEDAIS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| TMKCIVNEYT | FLLEQCTVKI | QSKEKLNFIL | ANIILSCIQP | TSRLVKPVEK | LKDQLREVLQ | PIGLTYQFSE | PYFLASLLFW |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| PENQQLDQHS | EQMKEYAQAL | KNSFKGQYKH | MHRTKQPIAY | FFLGKGKRLE | RLVHKGKIDQ | CFKKTPDINS | LWQSGDVWKE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | |
| EKVQELLLRL | QGRAENNCLY | IEYGINEKIT | IPITPAFLGQ | LRSGRSIEKV | SFYLGFSIGG | PLAYDIEIV | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1963 | 1 | 840.7936 | -83.45 | 2 | 54.4 | 11.1 | 0 | 118-133 | K.ENPDMANPSAMSTTAK.G | Oxidation: 5 |
| 382 | 1 | 591.8148 | -46.01 | 2 | 34.8 | 13.4 | 0 | 1344- | K.FSGLLEYLIK.S | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | 1353 | | |

# Detailed Protein Report

## Protein 677: inner centromere protein isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|102467242 | **Score:** | 24.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 104.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 4.18 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.13 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGTTAPGPIH | LLELCDQKLM | EFLCNMDNKD | LVWLEEIQEE | AERMFTREFS | KEPELMPKTP | SQKNRRKKRR | ISYVQDENRD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PIRRRLSRRK | SRSSQLSSRR | LRSKDSVEKL | ATVVGENGSV | LRRVTRAAAA | AAAATMALAA | PSSPTPESPT | MLTKKPEDNH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TQCQLVPVVE | IGISERQNAE | QHVTQLMSTE | PLPRTLSPTP | ASATAPTSQG | IPTSDEESTP | KKSKARILES | ITVSSLMATP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QDPKGQGVGT | GRSASKLRIA | QVSPGPRDSP | AFPDSPWRER | VLAPILPDNF | STPTGSRTDS | QSVRHSPIAP | SSPSPQVLAQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KYSLVAKQES | VVRRASRRLA | KKTAEEPAAS | GRIICHSYLE | RLLNVEVPQK | VGSEQKEPPE | EAEPVAAAEP | EVPENNGNNS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| WPHNDTEIAN | STPNPKPAAS | SPETPSAGQQ | EAKTDQADGP | REPPQSARRK | RSYKQAVSEL | DEEQHLEDEE | LQPPRSKTPS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SPCPASKVVR | PLRTFLHTVQ | RNQMLMTPTS | APRSVMKSFI | KRNTPLRMDP | KEKERQRLEN | LRRKEEAEQL | RRQKVEEDKR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RRLEEVKLKR | EERLRKVLQA | RERVEQMKEE | KKKQIEQKFA | QIDEKTEKAK | EERLAEEKAK | KKAAAKKMEE | VEARRKQEEE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ARRLRWLQQE | EEERRHQELL | QKKKEEEQER | LRKAAEAKRL | AEQREQERRE | QERREQERRE | QERREQERRE | QERQLAEQER |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RREQERLQAE | RELQEREKAL | RLQKEQLQRE | LEEKKKKEEQ | QRLAERQLQE | EQEKKAKEAA | GASKALNVTV | DVQSPACTSY |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QMTPQGHRAP | PKINPDNYGM | DLNSDDSTDD | EAHPRKPIPT | WARGTPLSQA | IIHQYYHPPN | LLELFGTILP | LDLEDIFKKS |
| 890 | 900 | 910 | 920 | | | | |
| KPRYHKRTSS | AVWNSPPLQG | ARVPSSLAYS | LKKH | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1737 | 3 | 502.2720 | 31.12 | 2 | 50.1 | 13.7 | 1 | 611-618 | K.EERLAEEK.A | | WUP:QUP 0.13<br>QU:MU 4.18 |

# Detailed Protein Report

## Protein 678: solute carrier family 12 member 6 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|110224452 | **Score:** | 24.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 121.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|110224454 | refseq_human (refseq_human_20140103.fasta) | solute carrier family 12 member 6 isoform c [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSEMSGATTS | LATVALDPPS | DRTSHPQDVI | EDLSQNSITG | EHSQLLDDGH | KKARNAYLNN | SNYEEGDEYF | DKNLALFEEE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MDTRPKVSSL | LNRMANYTNL | TQGAKEHEEA | ENITEGKKKP | TKTPQMGTFM | GVYLPCLQNI | FGVILFLRLT | WVVGTAGVLQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AFAIVLICCC | CTMLTAISMS | AIATNGVVPA | GGSYFMISRA | LGPEFGGAVG | LCFYLGTTFA | AAMYILGAIE | IFLVYIVPRA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AIFHSDDALK | ESAAMLNNMR | VYGTAFLVLM | VLVVFIGVRY | VNKFASLFLA | CVIVSILAIY | AGAIKSSFAP | PHFPVCMLGN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RTLSSRHIDV | CSKTKEINNM | TVPSKLWGFF | CNSSQFFNAT | CDEYFVHNNV | TSIQGIPGLA | SGIITENLWS | NYLPKGEIIE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KPSAKSSDVL | GSLNHEYVLV | DITTSFTLLV | GIFFPSVTGI | MAGSNRSGDL | KDAQKSIPIG | TILAILTTSF | VYLSNVVLFG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ACIEGVVLRD | KFGDAVKGNL | VVGTLSWPSP | WVIVIGSFFS | TCGAGLQSLT | GAPRLLQAIA | KDNIIPFLRV | FGHSKANGEP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TWALLLTAAI | AELGILIASL | DLVAPILSMF | FLMCYLFVNL | ACALQTLLRT | PNWRPRFRYY | HWALSFMGMS | ICLALMFISS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| WYYAIVAMVI | AGMIYKYIEY | QGAEKEWGDG | IRGLSLSAAR | FALLRLEEGP | PHTKNWRPQL | LVLLKLDEDL | HVKHPRLLTF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ASQLKAGKGL | TIVGSVIVGN | FLENYGEALA | AEQTIKHLME | AEKVKGFCQL | VVAAKLREGI | SHLIQSCGLG | GMKHNTVVMG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| WPNGWRQSED | ARAWKTFIGT | VRVTTAAHLA | LLVAKNISFF | PSNVEQFSEG | NIDVWWIVHD | GGMLMLLPFL | LKQHKVWRKC |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SIRIFTVAQL | EDNSIQMKKD | LATFLYHLRI | EAEVEVVEMH | DSDISAYTYE | RTLMMEQRSQ | MLRHMRLSKT | ERDREAQLVK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DRNSMLRLTS | IGSDEDEETE | TYQEKVHMTW | TKDKYMASRG | QKAKSMEGFQ | DLLNMRPDQS | NVRRMHTAVK | LNEVIVNKSH |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | | |
| EAKLVLLNMP | GPPRNPEGDE | NYMEFLEVLT | EGLERVLLVR | GGGSEVITIY | S | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2796 | 1 | 974.5012 | 23.40 | 2 | 65.4 | 11.9 | 2 | 932-946 | R.TLMMEQRSQMLRHMR.L | |

# Detailed Protein Report

## Protein 679: fibrous sheath-interacting protein 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|297206791 | **Score:** | 24.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 789.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 0.5 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKFQLWSSQI | RPLGPIFPAL | RALYALARAA | PQEATALLGP | LPLEAWNAGG | GAEVVGLWPF | LVRSGQRDNG | VLEKESGAGE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EGAEGAVPAM | ELYLGACSKP | AKVAVTKTVA | SVLAADTQQC | RDGVHKTHFA | GVGPAQLLDL | PLGVKLPVIP | GSNAVFYTTN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FGEKLFRPSY | GFNLTDPYCR | LLENQYKSLH | DPHLKAYYKR | KDILKRLKKG | GYITSNNKVV | CTLRELNKYR | QYLTSLKLDF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ERNYIKEQRI | LAKQLHNIPE | NNQIPQHCDV | AQVQNWLLKE | GTESIKDQER | LMRHRYLDMI | SRKLEQLERT | AEEQRLFLMD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| REERRQREHT | RRKLTLRRKI | EEEWKTKEML | LLTRMAEDVK | REERIEEQQH | RNREESDRKK | QDLLEKKMAY | HLQKMQDTGF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NGEDIGKNTF | KYRGQDGTHA | SPKNKKKTSE | DIMLVYPAGD | QNTYKETHGH | TANAAHQRQN | SSNNFTKKNS | ASVVYQADVQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DNGINQKRDG | MVSKNSSIFD | DRGGINISGQ | GSIISAQVSP | TRNFSRVSQA | FLDPSKEEKE | TNADWDGRPT | KRSSYLCESG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PQAHATDPGI | FSSPVYTNMQ | QNLLQNCLQE | KVTSEELNII | IQNVMTWVVA | TVTSILYPAI | TKYEKRLQNN | TYPVSDDSIL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SSDSSSFCST | CSEDFTYRSY | TSATTKTFQA | EPCAFVVDTS | VRRPTTPIKP | PPAHVEKTVV | GKTCHIKGQS | IISKHKYNKT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NLLYSYPKLR | SCKSDSHLLA | SFETGTKKSK | DATTETDSLG | SSLHCDKTAK | AMDEMKNLKN | VFVNFKCYLK | GETEVILESI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LREIMSDLTQ | AIPSLSSVTA | EVFVEQCERE | KEILLSNAHI | PSVASEIVEN | MLEKLESAVE | KKCVEMFSQD | LSVDIKPSLA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ASDELLTSSN | GKPLKNSMPH | TLDPMCDIAE | DMVHAILEKL | MTLVSFKQNE | FLHLKDTNKL | SCQQHKTDPI | CMFLQRAGKN |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KSSLESDEAS | LIVNEEVQNL | ISNIFSQSSL | VAYIEEAINA | ILGYIQTELN | NERIIASEET | VVLLQLLEDI | LFQLHQEPVN |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ESFQKSRQPR | ISSPSDTKEK | YRLTGTRLSN | SPRSGRPFPP | INVPGMVLYS | DDENEEIDNI | VKNVLDSTFK | DEKVKSQEQI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PNHWFTKGNT | CFECKRNIKP | PTKPGSRSKA | AFHDWELKTE | PPSTNHEDIL | KKKLSSNKDI | STFSQDQKHQ | IEKASENIVT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SILKEMLKDI | SSVPFGHLDS | KTGSEASVLV | SEKPQGLSHQ | EWIDQMFSVS | EISTVAQEIT | DSVLNILHKA | SNYISNTTKS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SISSSVHQIS | LHNSDTEHIV | KEAPNKYPLK | TWFDSEKKMK | YLSLFDVDPE | KPPWLKSGKS | EPKPVDDIND | KIIRTIFKRL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KSFICPKLHM | GFKSSLRSQL | SKYTAKIVNI | VLCAIQNELE | LHKENLNLRE | IDHTKSLTDK | GFFANTDKKL | ESLVTSIDDD |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ILASPLLTCI | YDMLLSSENA | HQRSISLSSR | KPKSATDSVD | VQSILPNRQD | KKSFHKYLAT | PCTHHSVNGG | NHIKENAKLQ |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| VLERIGETLH | EMLSKLLGTH | LHSQLSCSQQ | SREMTNKNQK | MAAALQSNIQ | LISKAILDYI | LAKLCGVDMD | TSFASCGLKA |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| ISESLDIDNP | SFASIIEKMA | KSTKIISSIV | SRRVQEDNKE | ETKSKAKPVA | PVSSKTPSTK | EMHPNKLKAV | ASDILNMVFA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| KLEGFANGHL | EILGAINDGN | KKSNKIGWEY | ESTNISRDTH | EASFLSALYM | HAKKVSSAIL | KVIQTELNVT | SSDLKTSVEN |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| PPPETQILKY | VVKLILDAVS | SDMFNEMESE | GGGIETYRYR | PTYGSLPGGA | ESDSFLEDDA | YTAKKIIDER | SPQREEVKTR |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| SLKQWALEKT | LNKIEVKLKE | PHISPIAPII | RNILNEIFQS | TLINQLNVLS | LSHSNFNGMP | HNVDEPTPQT | SVQFMDKMMD |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| PLLSEADITI | VTDNIVRTVF | HKLYSAAMTE | RNVRENRYKT | ITFSANVSSH | EHTYKGKSSV | TALDENPCTF | QSRFSVADKE |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| TKVNLAEDIV | QAILTNLETF | ATSKVKSLFY | SQVNFTVPVA | LPIQQDHSTL | SKALSAKDSY | SDEQFSCCSV | DHTKSGKTNL |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| CQLSLSKLNT | YALQVARRNL | QGIKQELDKE | RENPFLTHDI | GISESIASQI | VNALLDIISR | KGKCDKNSSD | KEIDLDQQKG |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| VIEKLLNETK | YRKVLQLQIQ | DTIEGILCDI | YEKTLFQNNL | SFATPTLKCS | IADKHSEENS | EMFMEGANKI | IPKLSVPKSD |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| VILISNDIVN | IVLHNLSSAA | TLVINAKNPT | SARLPLTFCD | TFPKIDCQQP | LKGSKTERKT | ERFSYSRNQK | SAYADDNQIT |
| 2330 | 2340 | 2350 | 2360 | 2370 | 2380 | 2390 | 2400 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 59 | 1 | 841.4513 | 24.83 | 3 | 30.6 | 11.0 | 2 | 5590-5613 | K.SGMINLTSGLATGVTNKKEVDENK.V | Oxidation: 3 |

# Detailed Protein Report

## Protein 680: lysozyme C precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4557894 | **Score:** | 24.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 16.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 37.2 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKALIVLGLV | LLSVTVQGKV | FERCELARTL | KRLGMDGYRG | ISLANWMCLA | KWESGYNTRA | TNYNAGDRST | DYGIFQINSR |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | |
| YWCNDGKTPG | AVNACHLSCS | ALLQDNIADA | VACAKRVVRD | PQGIRAWVAW | RNRCQNRDVR | QYVQGCGV | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2481 | 1 | 938.4534 | 2.74 | 3 | 59.3 | 13.5 | 0 | 88-115 | K.TPGAVNACHLSCSALLQDNIADAVACAK.R | Carbamidomethyl: 26 |

# Detailed Protein Report

## Protein 681: uncharacterized protein KIAA0513 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|557440789 | **Score:** | 24.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| | | **Sequence Coverage [%]:** | 7.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| METPEVPVGS | LIDFGPEAPT | SSPLEAPPPV | LQDGDGSLGD | GASESETTES | ADSENDMGES | PSHPSWDQDR | RSSSNESFSS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NQSTESTQDE | ETLALRDFMR | GYVEKIFSGG | EDLDQEEKAK | FGEYCSSENG | KGREWFARYV | SAQRCNSKCV | SEATFYRLVQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SFAVVLFECH | QMDDFGPAKN | LMTMCFTYYH | IGKPQLLPPE | SREKPAGSID | SYLKSANSWL | AEKKDIAERL | LKNTSARTEN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VKGFFGGLET | KLKGPLARRN | EEDENKPQEK | RPRAVTAYSP | EDEKKGEKIY | LYTHLKQQPI | WHTLRFWNAA | FFDAVHCERT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KRSPTTREKW | CHMTQEERDD | SLRFNENITF | GQLGTFTHNM | LAFGLNKKLC | NDFLKKQAVI | GNLDEEQYKL | LSDHIEQMAT |
| 410 | | | | | | | |
| E | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 470 | 1 | 564.2533 | -129.11 | 3 | 35.5 | 14.4 | 2 | 243-258 | K.GFFGGLETKLKGPLAR.R | |

# Detailed Protein Report

## Protein 682: probable ATP-dependent RNA helicase DHX37 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|29029601 | **Score:** | 24.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 129.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGKLRRRYNI | KGRQQAGPGP | SKGPPEPPPV | QLELEDKDTL | KGVDASNALV | LPGKKKKKTK | APPLSKKEKK | PLTKKEKKVL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QKILEQKEKK | SQRAEMLQKL | SEVQASEAEM | RLFYTTSKLG | TGNRMYHTKE | KADEVVAPGQ | EKISSLSGAH | RKRRRWPSAE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EEEEEEEESE | SELEEESELD | EDPAAEPAEA | GVGTTVAPLP | PAPAPSSQPV | PAGMTVPPPP | AAAPPLPRAL | AKPAVFIPVN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RSPEMQEERL | KLPILSEEQV | IMEAVAEHPI | VIVCGETGSG | KTTQVPQFLY | EAGFSSEDSI | IGVTEPRRVA | AVAMSQRVAK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EMNLSQRVVS | YQIRYEGNVT | EETRIKFMTD | GVLLKEIQKD | FLLLRYKVVI | IDEAHERSVY | TDILIGLLSR | IVTLRAKRNL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PLKLLIMSAT | LRVEDFTQNP | RLFAKPPPVI | KVESRQFPVT | VHFNKRTPLE | DYSGECFRKV | CKIHRMLPAG | GILVFLTGQA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EVHALCRRLR | KAFPPSRARP | QEKDDDQKDS | VEEMRKFKKS | RARAKKARAE | VLPQINLDHY | SVLPAGEGDE | DREAEVDEEE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GALDSDLDLD | LGDGGQDGGE | QPDASLPLHV | LPLYSLLAPE | KQAQVFKPPP | EGTRLCVVAT | NVAETSLTIP | GIKYVVDCGK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VKKRYYDRVT | GVSSFRVTWV | SQASADQRAG | RAGRTEPGHC | YRLYSSAVFG | DFEQFPPPEI | TRRPVEDLIL | QMKALNVEKV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| INFPFPTPPS | VEALLAAEEL | LIALGALQPP | QKAERVKQLQ | ENRLSCPITA | LGRTMATFPV | APRYAKMLAL | SRQHGCLPYA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ITIVASMTVR | ELFEELDRPA | ASDEELTRLK | SKRARVAQMK | RTWAGQGASL | KLGDLMVLLG | AVGACEYASC | TPQFCEANGL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RYKAMMEIRR | LRGQLTTAVN | AVCPEAELFV | DPKMQPPTES | QVTYLRQIVT | AGLGDHLARR | VQSEEMLEDK | WRNAYKTPLL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DDPVFIHPSS | VLFKELPEFV | VYQEIVETTK | MYMKGVSSVE | VQWIPALLPS | YCQFDKPLEE | PAPTYCPERG | RVLCHRASVF |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| YRVGWPLPAI | EVDFPEGIDR | YKHFARFLLE | GQVFRKLASY | RSCLLSSPGT | MLKTWARLQP | RTESLLRALV | AEKADCHEAL |
| 1130 | 1140 | 1150 | 1160 | | | | |
| LAAWKKNPKY | LLAEYCEWLP | QAMHPDIEKA | WPPTTVH | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1513 | 1 | 671.4128 | 46.52 | 2 | 48.6 | 10.1 | 0 | 703-713 | R.RPVEDLILQMK.A | |

# Detailed Protein Report

## Protein 683: serine/threonine-protein kinase PINK1, mitochondrial precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|14165272 | **Score:** | 24.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 62.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.6 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.73 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.55 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MAVRQALGRG LQLGRALLLR FTGKPGRAYG LGRPGPAAGC VRGERPGWAA GPGAEPRRVG LGLPNRLRFF RQSVAGLAAR
        90        100        110        120        130        140        150        160
LQRQFVVRAW GCAGPCGRAV FLAFGLGLGL IEEKQAESRR AVSACQEIQA IFTQKSKPGP DPLDTRRLQG FRLEEYLIGQ
       170        180        190        200        210        220        230        240
SIGKGCSAAV YEATMPTLPQ NLEVTKSTGL LPGRGPGTSA PGEGQERAPG APAFPLAIKM MWNISAGSSS EAILNTMSQE
       250        260        270        280        290        300        310        320
LVPASRVALA GEYGAVTYRK SKRGPKQLAP HPNIIRVLRA FTSSVPLLPG ALVDYPDVLP SRLHPEGLGH GRTLFLVMKN
       330        340        350        360        370        380        390        400
YPCTLRQYLC VNTPSPRLAA MMLLQLLEGV DHLVQQGIAH RDLKSDNILV ELDPDGCPWL VIADFGCCLA DESIGLQLPF
       410        420        430        440        450        460        470        480
SSWYVDRGGN GCLMAPEVST ARPGPRAVID YSKADAWAVG AIAYEIFGLV NPFYGQGKAH LESRSYQEAQ LPALPESVPP
       490        500        510        520        530        540        550        560
DVRQLVRALL QREASKRPSA RVAANVLHLS LWGEHILALK NLKLDKMVGW LLQQSAATLL ANRLTEKCCV ETKMKMLFLA
       570        580        590
NLECETLCQA ALLLCSWRAA L
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2329 | 1 | 1002.8159 | -41.27 | 3 | 59.0 | 13.9 | 2 | 527-553 | K.<br>MVGWLLQQSAATLLANRLTEKCC<br>M | | |
| 274 | 1 | 605.6515 | -235.18 | 2 | 33.1 | 10.5 | 1 | 544-553 | R.LTEKCCVETK.M | Carbamidomethyl: 6 | WUP:QUP 0.55<br>QU:MU 2.73 |

# Detailed Protein Report

## Protein 684: uncharacterized protein C1orf87 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|22748811 | **Score:** | 24.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 62.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.03 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.72 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSAWKTPRG | SDAMPEIMVK | IIGSKHFQYL | VEKPKIKEND | SLKTETQTMH | QKPMTDNARQ | MSRDTPVPIN | FTDQQTTDNP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DDVKEKKHPE | NNQKSENNQK | LLTGANSSRF | LDGNIPSQAN | VHCSSVPTGD | QSLSYVHGIP | RRKLRDWSLE | QMVRGSSDQP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EDIGQSPSGT | TNEDAFLLAL | VRRELKSRPL | SSNLLEKLQK | ELKILDPISS | GFLLQSQLSR | LFLKHEVPLQ | LPTVKILCQR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FSKRGSPEMV | NYEKLLWFLN | SAASDYPQQN | KAAADLRKTE | SHGTHSQSTP | PQHSSSQPEV | NRSLLEILKM | ALRTTNGRLN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IDNLNLSFRK | EDRSFSGCLP | LPKVRAICGK | HGLYLTLSLL | ETLLNHQDLG | YQNEIKWQNF | VEMLTRASSD | LLSDLPTGKN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EKKAPAPPME | PEVPEMSQSK | TEHMKTPEEE | LQPESSPAET | SACKDPLKPL | KIRPVSQPFV | NPAVKNKAEE | CETWIDRFRK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | |
| LENALYLCDL | SNTGVLEKER | ARRLIHNYNL | IYNLSLSPQK | IDQALRRFRS | GENMLLEPAL | RYLKEL | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 660 | 1 | 459.6081 | -316.84 | 2 | 37.8 | 10.5 | 0 | 101-109 | K.LLTGANSSR.F | | WUP:QUP 0.72<br>QU:MU 2.03 |

# Detailed Protein Report

**Protein 685:** **phenylalanine--tRNA ligase alpha subunit [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4758340 | **Score:** | 24.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 7.96 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MADGQVAELL | LRRLEASDGG | LDSAELAAEL | GMEHQAVVGA | VKSLQALGEV | IEAELRSTKH | WELTAEGEEI | AREGSHEARV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FRSIPPEGLA | QSELMRLPSG | KVGFSKAMSN | KWIRVDKSAA | DGPRVFRVVD | SMEDEVQRRL | QLVRGGQAEK | LGEKERSELR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KRKLLAEVTL | KTYWVSKGSA | FSTSISKQET | ELSPEMISSG | SWRDRPFKPY | NFLAHGVLPD | SGHLHPLLKV | RSQFRQIFLE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MGFTEMPTDN | FIESSFWNFD | ALFQPQQHPA | RDQHDTFFLR | DPAEALQLPM | DYVQRVKRTH | SQGGYGSQGY | KYNWKLDEAR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KNLLRTHTTS | ASARALYRLA | QKKPFTPVKY | FSIDRVFRNE | TLDATHLAEF | HQIEGVVADH | GLTLGHLMGV | LREFFTKLGI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TQLRFKPAYN | PYTEPSMEVF | SYHQGLKKWV | EVGNSGVFRP | EMLLPMGLPE | NVSVIAWGLS | LERPTMIKYG | INNIRELVGH |
| 490 | 500 | 510 | | | | | |
| KVNLQMVYDS | PLCRLDAEPR | PPPTQEAA | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2536 | 1 | 1044.5961 | 47.08 | 2 | 62.3 | 24.4 | 2 | 128-144 | R.VVDSMEDEVQRRLQLVR.G | Oxidation: 5 | WUP:QUP | 7.96 |

# Detailed Protein Report

## Protein 686: autophagy-related protein 13 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|41281462 | **Score:** | 24.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 52.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.8 |
| | | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|326806956 | refseq_human(refseq_human_20140103.fasta) | autophagy-related protein 13 isoform 2 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| METDLNSQDR | KDLDKFIKFF | ALKTVQVIVQ | ARLGEKICTR | SSSSPTGSDW | FNLAIKDIPE | VTHEAKKALA | GQLPAVGRSM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CVEISLKTSE | GDSMELEIWC | LEMNEKCDKE | IKVSYTVYNR | LSLLLKSLLA | ITRVTPAYRL | SRKQGHEYVI | LYRIYFGEVQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LSGLGEGFQT | VRVGTVGTPV | GTITLSCAYR | INLAFMSTRQ | FERTPPIMGI | IIDHFVDRPY | PSSSPMHPCN | YRTAGEDTGV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IYPSVEDSQE | VCTTSFSTSP | PSQLMVPGKE | GGVPLAPNQP | VHGTQADQER | LATCTPSDRT | HCAATPSSSE | DTETVSNSSE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GRASPHDVLE | TIFVRKVGAF | VNKPINQVTL | TSLDIPFAMF | APKNLELEDT | DPMVNPPDSP | ETESPLQGSL | HSDGSSGGSS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GNTHDDFVMI | DFKPAFSKDD | ILPMDLGTFY | REFQNPPQLS | SLSIDIGAQS | MAEDLDSLPE | KLAVHEKNVR | EFDAFVETLQ |
| 490 | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 515 | 1 | 686.3549 | -17.68 | 2 | 36.4 | 11.0 | 1 | 110-120 | K.EIKVSYTVYNR.L | |

# Detailed Protein Report

## Protein 687: Krueppel-like factor 10 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|73760403 | **Score:** | 24.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 51.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| | | **Sequence Coverage [%]:** | 6.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.33 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 4.55 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEERMEMISE | RPKESMYSWN | KTAEKSDFEA | VEALMSMSCS | WKSDFKKYVE | NRPVTPVSDL | SEEENLLPGT | PDFHTIPAFC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LTPPYSPSDF | EPSQVSNLMA | PAPSTVHFKS | LSDTAKPHIA | APFKEEEKSP | VSAPKLPKAQ | ATSVIRHTAD | AQLCNHQTCP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MKAASILNYQ | NNSFRRRTHL | NVEAARKNIP | CAAVSPNRSK | CERNTVADVD | EKASAALYDF | SVPSSETVIC | RSQPAPVSPQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QKSVLVSPPA | VSAGGVPPMP | VICQMVPLPA | NNPVVTTVVP | STPPSQPPAV | CPPVVFMGTQ | VPKGAVMFVV | PQPVVQSSKP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PVVSPNGTRL | SPIAPAPGFS | PSAAKVTPQI | DSSRIRSHIC | SHPGCGKTYF | KSSHLKAHTR | THTGEKPFSC | SWKGCERRFA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | |
| RSDELSRHRR | THTGEKKFAC | PMCDRRFMRS | DHLTKHARRH | LSAKKLPNWQ | MEVSKLNDIA | LPPTPAPTQ | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 19 | 1 | 797.4613 | 101.35 | 2 | 29.2 | 11.8 | 2 | 199-212 | R.SKCERNTVADVDEK.A | | WUP:QUP 4.55<br>QU:MU 0.33 |

BRUKER

# Detailed Protein Report

## Protein 688: hemopexin precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|11321561 | **Score:** | 24.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 51.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| | | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530395269 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: hemopexin isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MARVLGAPVA | LGLWSLCWSL | AIATPLPPTS | AHGNVAEGET | KPDPDVTERC | SDGWSFDATT | LDDNGTMLFF | KGEFVWKSHK |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| WDRELISERW | KNFPSPVDAA | FRQGHNSVFL | IKGDKVWVYP | PEKKEKGYPK | LLQDEFPGIP | SPLDAAVECH | RGECQAEGVL |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| FFQGDREWFW | DLATGTMKER | SWPAVGNCSS | ALRWLGRYYC | FQGNQFLRFD | PVRGEVPPRY | PRDVRDYFMP | CPGRGHGHRN |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| GTGHGNSTHH | GPEYMRCSPH | LVLSALTSDN | HGATYAFSGT | HYWRLDTSRD | GWHSWPIAHQ | WPQGPSAVDA | AFSWEEKLYL |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| VQGTQVYVFL | TKGGYTLVSG | YPKRLEKEVG | TPHGIILDSV | DAAFICPGSS | RLHIMAGRRL | WWLDLKSGAQ | ATWTELPWPH |
| **410** | **420** | **430** | **440** | **450** | **460** | **470** | |
| EKVDGALCME | KSLGPNSCSA | NGPGLYLIHG | PNLYCYSDVE | KLNAAKALPQ | PQNVTSLLGC | TH | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1637 | 2 | 919.3696 | -84.22 | 2 | 50.2 | 24.4 | 0 | 387-402 | K.SGAQATWTELPWPHEK.V | |

# Detailed Protein Report

## Protein 689: ankyrin repeat domain-containing protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|38327522 | **Score:** | 24.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 36.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 14.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMVLKVEELV | TGKKNGNGEA | GEFLPEDFRD | GEYEAAVTLE | KQEDLKTLLA | HPVTLGEQQW | KSEKQREAEL | KKKKLEQRSK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LENLEDLEII | IQLKKRKKYR | KTKVPVVKEP | EPEIITEPVD | VPTFLKAALE | NKLPVVEKFL | SDKNNPDVCD | EYKRTALHRA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CLEGHLAIVE | KLMEAGAQIE | FRDMLESTAI | HWASRGGNLD | VLKLLLNKGA | KISARDKLLS | TALHVAVRTG | HYECAEHLIA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CEADLNAKDR | EGDTPLHDAV | RLNRYKMIRL | LIMYGADLNI | KNCAGKTPMD | LVLHWQNGTK | AIFDSLRENS | YKTSRIATF |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1699 | 1 | 1135.8408 | -57.62 | 3 | 51.5 | 12.3 | 1 | 218-248 | K.LLSTALHVAVRTGHYECAEHLIACEADLNAK.D | Carbamidomethyl: 24 |

# Detailed Protein Report

## Protein 690: PREDICTED: putative GTP-binding protein 6 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578837777 | **Score:** | 24.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 42.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 7.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.66 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.78 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578838996 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: putative GTP-binding protein 6 isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVVSTKTPDR | KLIFGKGNFE | HLTEKIRGSP | DITCVFLNVE | RMAAPTKKEL | EAAWGVEVFD | RFTVVLHIFR | CNARTKEARL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QVALAEMPLH | RSNLKRDVAH | LYRGVGSRYI | MGSGESFMQL | QQRLLREKEA | KIRKALDRLR | KKRHLLRRQR | TRREFPVISV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VGYTNCGKTT | LIKALTGDAA | IQPRDQLFAT | LDVTAHAGTL | PSRMTVLYVD | TIGFLSQLPH | GLIESFSATL | EDVAHSDLIL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HVRDVSHPEA | ELQKCSVLST | LRGLQLPAPL | LDSMVEVHNK | VDLVPGYSPT | EPNVVPVSAL | RGHGLQELKA | ELDAAVLKAT |
| 330 | 340 | 350 | 360 | 370 | 380 | | |
| GRQILTLRVR | LAGAQLSWLY | KEATVQEVDV | IPEDGAADVR | VIISNSAYGK | FRKLFPG | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2802 | 1 | 913.4638 | -3.45 | 2 | 63.6 | 10.3 | 1 | 153-168 | R.REFPVISVVGYTNCGK.T | Carbamidomethyl: 14 | WUP:QUP 0.78<br>QU:MU 1.66 |

# Detailed Protein Report

## Protein 691: PREDICTED: zinc finger protein 320 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578834064 | **Score:** | 24.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 9.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MALSQGLLTF | RDVAIEFSQE | EWKCLDPAQR | TLYRDVMLEN | YRNLVSLDIS | SKCMMNTLSS | TGQGNTEVIH | TGTLQRQASY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HIGAFCSQEI | EKDIHDFVFQ | WQEDETNDHE | APMTEIKKLT | SSTDRYDQRH | AGNKPIKGQL | ESRFHLHLRR | HRRIHTGEKP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YKCEECEKVF | SCKSHLEIHR | IIHTGEKPYK | CKVCDKAFRS | DSRLAEHQRV | HTGERPYTCN | ECGKVFSTKA | YLACHQKLHT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GEKLYECEEC | DKVYIRKSHL | ERHRRIHTGE | KPHKCGDCGK | AFNSPSHLIR | HQRIHTGQKS | YKCHQCGKVF | SLRSLLAEHQ |
| 330 | 340 | 350 | | | | | |
| KIPFGDNCFK | CNEYSKPSSI | N | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 25 | 1 | 1132.0072 | -3.81 | 2 | 30.0 | 12.0 | 1 | 322-341 | K.IPFGDNCFKCNEYSKPSSIN.- | |

# Detailed Protein Report

**Protein 692:** **histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific isoform b [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|19923586 | **Score:** | 24.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 296.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.55 **CV:** 0.00 % **No. of Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578811198 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific isoform X5 [Homo sapiens] |
| gi\|530381144 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific isoform X1 [Homo sapiens] |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDQTCELPRR | NCLLPFSNPV | NLDAPEDKDS | PFGNGQSNFS | EPLNGCTMQL | STVSGTSQNA | YGQDSPSCYI | PLRRLQDLAS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MINVEYLNGS | ADGSESFQDP | EKSDSRAQTP | IVCTSLSPGG | PTALAMKQEP | SCNNSPELQV | KVTKTIKNGF | LHFENFTCVD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DADVDSEMDP | EQPVTEDESI | EEIFEETQTN | ATCNYETKSE | NGVKVAMGSE | QDSTPESRHG | AVKSPFLPLA | PQTETQKNKQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RNEVDGSNEK | AALLPAPFSL | GDTNITIEEQ | LNSINLSFQD | DPDSSTSTLG | NMLELPGTSS | SSTSQELPFC | QPKKKSTPLK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YEVGDLIWAK | FKRRPWWPCR | ICSDPLINTH | SKMKVSNRRP | YRQYYVEAFG | DPSERAWVAG | KAIVMFEGRH | QFEELPVLRR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RGKQKEKGYR | HKVPQKILSK | WEASVGLAEQ | YDVPKGSKNR | KCIPGSIKLD | SEEDMPFEDC | TNDPESEHDL | LLNGCLKSLA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FDSEHSADEK | EKPCAKSRAR | KSSDNPKRTS | VKKGHIQFEA | HKDERRGKIP | ENLGLNFISG | DISDTQASNE | LSRIANSLTG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SNTAPGSFLF | SSCGKNTAKK | EFETSNGDSL | LGLPEGALIS | KCSREKNKPQ | RSLVCGSKVK | LCYIGAGDEE | KRSDSISICT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TSDDGSSDLD | PIEHSSESDN | SVLEIPDAFD | RTENMLSMQK | NEKIKYSRFA | ATNTRVKAKQ | KPLISNSHTD | HLMGCTKSAE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PGTETSQVNL | SDLKASTLVH | KPQSDFTNDA | LSPKFNLSSS | ISSENSLIKG | GAANQALLHS | KSKQPKFRSI | KCKHKENPVM |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AEPPVINEEC | SLKCCSSDTK | GSPLASISKS | GKVDGLKLLN | NMHEKTRDSS | DIETAVVKHV | LSELKELSYR | SLGEDVSDSG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TSKPSKPLLF | SSASSQNHIP | IEPDYKFSTL | LMMLKDMHDS | KTKEQRLMTA | QNLVSYRSPG | RGDCSTNSPV | GVSKVLVSGG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| STHNSEKKGD | GTQNSANPSP | SGGDSALSGE | LSASLPGLLS | DKRDLPASGK | SRSDCVTRRN | CGRSKPSSKL | RDAFSAQMVK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| NTVNRKALKT | ERKRKLNQLP | SVTLDAVLQG | DRERGGSLRG | GAEDPSKEDP | LQIMGHLTSE | DGDHFSDVHF | DSKVKQSDPG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KISEKGLSFE | NGKGPELDSV | MNSENDELNG | VNQVVPKKRW | QRLNQRRTKP | RKRMNRFKEK | ENSECAFRVL | LPSDPVQEGR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DEFPEHRTPS | ASILEEPLTE | QNHADCLDSA | GPRLNVCDKS | SASIGDMEKE | PGIPSLTPQA | ELPEPAVRSE | KKRLRKPSKW |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LLEYTEEYDQ | IFAPKKKQKK | VQEQVHKVSS | RCEEESLLAR | GRSSAQNKQV | DENSLISTKE | EPPVLEREAP | FLEGPLAQSE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LGGGHAELPQ | LTLSVPVAPE | VSPRPALESE | ELLVKTPGNY | ESKRQRKPTK | KLLESNDLDP | GFMPKKGDLG | LSKKCYEAGH |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LENGITESCA | TSYSKDFGGG | TTKIFDKPRK | RKRQRHAAAK | MQCKKVKNDD | SSKEIPGSEG | ELMPHRTATS | PKETVEEGVE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| HDPGMPASKK | MQGERGGGAA | LKENVCQNCE | KLGELLLCEA | QCCGAFHLEC | LGLTEMPRGK | FICNECRTGI | HTCFVCKQSG |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| EDVKRCLLPL | CGKFYHEECV | QKYPPTVMQN | KGFRCSLHIC | ITCHAANPAN | VSASKGRLMR | CVRCPVAYHA | NDFCLAAGSK |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| ILASNSIICP | NHFTPRRGCR | NHEHVNVSWC | FVCSEGGSLL | CCDSCPAAFH | RECLNIDIPE | GNWYCNDCKA | GKKPHYREIV |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| WVKVGRYRWW | PAEICHPRAV | PSNIDKMRHD | VGEFPVLFFG | SNDYLWTHQA | RVFPYMEGDV | SSKDKMGKGV | DGTYKKALQE |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| AAARFEELKA | QKELRQLQED | RKNDKKPPPY | KHIKVNRPIG | RVQIFTADLS | EIPRCNCKAT | DENPCGIDSE | CINRMLLYEC |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| HPTVCPAGGR | CQNQCFSKRQ | YPEVEIFRTL | QRGWGLRTKT | DIKKGEFVNE | YVGELIDEEE | CRARIRYAQE | HDITNFYMLT |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| LDKDRIIDAG | PKGNYARFMN | HCCQPNCETQ | KWSVNGDTRV | GLFALSDIKA | GTELTFNYNL | ECLGNGKTVC | KCGAPNCSGF |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| LGVRPKNQPI | ATEEKSKKFK | KKQQGKRRTQ | GEITKEREDE | CFSCGDAGQL | VSCKKPGCPK | VYHADCLNLT | KRPAGKWECP |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1121 | 1 | 509.6492 | -167.81 | 2 | 42.3 | 11.4 | 0 | 2-9 | M.DQTCELPR.R | Carbamidomethyl: 4 | WUP:QUP 0.55 |

# Detailed Protein Report

## Protein 693: DNA replication ATP-dependent helicase/nuclease DNA2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|320461728 | **Score:** | 24.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 120.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.9 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.99 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.46 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEQLNELELL | MEKSFWEEAE | LPAELFQKKV | VASFPRTVLS | TGMDNRYLVL | AVNTVQNKEG | NCEKRLVITA | SQSLENKELC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ILRNDWCSVP | VEPGDIIHLE | GDCTSDTWII | DKDFGYLILY | PDMLISGTSI | ASSIRCMRRA | VLSETFRSSD | PATRQMLIGT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VLHEVFQKAI | NNSFAPEKLQ | ELAFQTIQEI | RHLKEMYRLN | LSQDEIKQEV | EDYLPSFCKW | AGDFMHKNTS | TDFPQMQLSL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PSDNSKDNST | CNIEVVKPMD | IEESIWSPRF | GLKGKIDVTV | GVKIHRGYKT | KYKIMPLELK | TGKESNSIEH | RSQVVLYTLL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SQERRADPEA | GLLLYLKTGQ | MYPVPANHLD | KRELLKLRNQ | MAFSLFHRIS | KSATRQKTQL | ASLPQIIEEE | KTCKYCSQIG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NCALYSRAVE | QQMDCSSVPI | VMLPKIEEET | QHLKQTHLEY | FSLWCLMLTL | ESQSKDNKKN | HQNIWLMPAS | EMEKSGSCIG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NLIRMEHVKI | VCDGQYLHNF | QCKHGAIPVT | NLMAGDRVIV | SGEERSLFAL | SRGYVKEINM | TTVTCLLDRN | LSVLPESTLF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RLDQEEKNCD | IDTPLGNLSK | LMENTFVSKK | LRDLIIDFRE | PQFISYLSSV | LPHDAKDTVA | CILKGLNKPQ | RQAMKKVLLS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KDYTLIVGMP | GTGKTTTICT | LVRILYACGF | SVLLTSYTHS | AVDNILLKLA | KFKIGFLRLG | QIQKVHPAIQ | QFTEQEICRS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KSIKSLALLE | ELYNSQLIVA | TTCMGINHPI | FSRKIFDFCI | VDEASQISQP | ICLGPLFFSR | RFVLVGDHQQ | LPPLVLNREA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RALGMSESLF | KRLEQNKSAV | VQLTVQYRMN | SKIMSLSNKL | TYEGKLECGS | DKVANAVINL | RHFKDVKLEL | EFYADYSDNP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| WLMGVFEPNN | PVCFLNTDKV | PAPEQVEKGG | VSNVTEAKLI | VFLTSIFVKA | GCSPSDIGII | APYRQQLKII | NDLLARSIGM |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VEVNTVDKYQ | GRDKSIVLVS | FVRSNKDGTV | GELLKDWRRL | NVAITRAKHK | LILLGCVPSL | NCYPPLEKLL | NHLNSEKLII |
| 1050 | 1060 | 1070 | | | | | |
| DLPSREHESL | CHILGDFQRE | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 236 | 1 | 862.4518 | -58.13 | 2 | 32.9 | 10.3 | 2 | 853-867 | K.VANAVINLRHFKDVK.L | | QU:MU 0.99<br>WUP:QUP 1.46 |

# Detailed Protein Report

## Protein 694: epididymis-specific alpha-mannosidase precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|50659093 | **Score:** | 24.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 113.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.35 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.58 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGQLCWLPLL | APLLLLRPPG | VQSAGPIRAF | VVPHSHMDVG | WVYTVQESMR | AYAANVYTSV | VEELARGQQR | RFIAVEQEFF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RLWWDGVASD | QQKYQVRQLL | EEGRLEFVIG | GQVMHDEAVT | HLDDQILQLT | EGHGFLYETF | GIRPQFSWHV | DPFGASATTP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TLFALAGFNA | HLGSRIDYDL | KAAMQEARGL | QFVWRGSPSL | SERQEIFTHI | MDQYSYCTPS | HIPFSNRSGF | YWNGVAVFPK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PPQDGVYPNM | SEPVTPANIN | LYAEALVANV | KQRAAWFRTP | HVLWPWGCDK | QFFNASVQFA | NMDPLLDHIN | SHAAELGVSV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QYATLGDYFR | ALHALNVTWR | VRDHHDFLPY | STEPFQAWTG | FYTSRSSLKG | LARRASALLY | AGESMFTRYL | WPAPRGHLDP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TWALQQLQQL | RWAVSEVQHH | DAITGTESPK | VRDMYATHLA | SGMLGMRKLM | ASIVLDELQP | QAPMAASSDA | GPAGHFASVY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NPLAWTVTTI | VTLTVGFPGV | RVTDEAGHPV | PSQIQNSTET | PSAYDLLILT | TIPGLSYRHY | NIRPTAGAQE | GTQEPAATVA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| STLQFGRRLR | RRTSHAGRYL | VPVANDCYIV | LLDQDTNLMH | SIWERQSNRT | VRVTQEFLEY | HVNGDVKQGP | ISDNYLFTPG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KAAVPAWEAV | EMEIVAGQLV | TEIRQYFYRN | MTAQNYTYAI | RSRLTHVPQG | HDGELLCHRI | EQEYQAGPLE | LNREAVLRTS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TNLNSQQVIY | SDNNGYQMQR | RPYVSYVNNS | IARNYYPMVQ | SAFMEDGKSR | LVLLSERAHG | ISSQGNGQVE | VMLHRRLWNN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FDWDLGYNLT | LNDTSVVHPV | LWLLLGSWSL | TTALRQRSAL | ALQHRPVVLF | GDLAGTAPKL | PGPQQQEAVT | LPPNLHLQIL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SIPGWRYSSN | HTEHSQNLRK | GHRGEAQADL | RRVLLRLYHL | YEVGEDPVLS | QPVTVNLEAV | LQALGSVVAV | EERSLTGTWD |
| 970 | 980 | 990 | 1000 | 1010 | | | |
| LSMLHRWSWR | TGPGRHRGDT | TSPSRPPGGP | IITVHPKEIR | TFFIHFQQQ | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1786 | 1 | 851.2906 | -97.10 | 2 | 52.2 | 13.1 | 0 | 433-447 | R.DMYATHLASGMLGMR.K | Oxidation: 2, 11, 14 | WUP:QUP 1.58<br>QU:MU 0.35 |

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# Detailed Protein Report

## Protein 695: mastermind-like protein 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|33286444 | **Score:** | 24.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 125.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGDTAPPQAP | AGGLGGASGA | GLLGGGSVTP | RVHSAIVERL | RARIAVCRQH | HLSCEGRYER | GRAESSDRER | ESTLQLLSLV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QHGQGARKAG | KHTKATATAA | TTTAPPPPPA | APPAASQAAA | TAAPPPPPDY | HHHHQQHLLN | SSNNGGSGGI | NGEQQPPAST |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PGDQRNSALI | ALQGSLKRKQ | VVNLSPANSK | RPNGFVDNSF | LDIKRIRVGE | NLSAGQGGLQ | INNGQSQIMS | GTLPMSQAPL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RKTNTLPSHT | HSPGNGLFNM | GLKEVKKEPG | ETLSCSKHMD | GQMTQENIFP | NRYGDDPGEQ | LMDPELQELF | NELTNISVPP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MSDLELENMI | NATIKQDDPF | NIDLGQQSQR | STPRPSLPME | KIVIKSEYSP | GLTQGPSGSP | QLRPPSAGPA | FSMANSALST |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SSPIPSVPQS | QAQPQTGSGA | SRALPSWQEV | SHAQQLKQIA | ANRQQHARMQ | QHQQQHQPTN | WSALPSSAGP | SPGPFGQEKI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PSPSFGQQTF | SPQSSPMPGV | AGGSGQSKVM | ANYMYKAGPS | AQGGHLDVLM | QQKPQDLSRS | FINNPHPAME | PRQGNTKPLF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HFNSDQANQQ | MPSVLPSQNK | PSLLHYTQQQ | QQQQQQQQQQ | QQQQQQQQQQ | QQQQQQQQQQ | QSSISAQQQQ | QQQSSISAQQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QQQQQQQQQQ | QQQQQQQQQQ | QQQQQPSSQP | AQSLPSQPLL | RSPLPLQQKL | LLQQMQNQPI | AGMGYQVSQQ | QRQDQHSVVG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QNTGPSPSPN | PCSNPNTGSG | YMNSQQSLLN | QQLMGKKQTL | QRQIMEQKQQ | LLLQQQMLAD | AEKIAPQDQI | NRHLSRPPPD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| YKDQRRNVGN | MQPTAQYSGG | SSTISLNSNQ | ALANPVSTHT | ILTPNSSLLS | TSHGTRMPSL | STAVQNMGMY | GNLPCNQPNT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| YSVTSGMNQL | TQQRNPKQLL | ANQNNPMMPR | PPTLGPSNNN | NVATFGAGSV | GNSQQLRPNL | THSMASMPPQ | RTSNVMITSN |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TTAPNWASQE | GTSKQQEALT | SAGVRFPTGT | PAAYTPNQSL | QQAVGSQQFS | QRAVAPPNQL | TPAVQMRPMN | QMSQTLNGQT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| MGPLRGLNLR | PNQLSTQILP | NLNQSGTGLN | QSRTGINQPP | SLTPSNFPSP | NQSSRAFQGT | DHSSDLAFDF | LSQQNDNMGP |
| 1130 | 1140 | 1150 | 1160 | | | | |
| ALNSDADFID | SLLKTEPGND | DWMKDINLDE | ILGNNS | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1771 | 1 | 1057.5151 | 4.71 | 2 | 52.0 | 24.2 | 2 | 44-60 | R.IAVCRQHHLSCEGRYER.G | Carbamidomethyl: 11 |

# Detailed Protein Report

## Protein 696: secreted frizzled-related protein 4 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|170784838 | **Score:** | 24.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 11.3 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MFLSILVALC LWLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHHST QENAILAIEQ YEELVDVNCS AVLRFFLCAM
        90        100        110        120        130        140        150        160
YAPICTLEFL HDPIKPCKSV CQRARDDCEP LMKMYNHSWP ESLACDELPV YDRGVCISPE AIVTDLPEDV KWIDITPDMM
       170        180        190        200        210        220        230        240
VQERPLDVDC KRLSPDRCKC KKVKPTLATY LSKNYSYVIH AKIKAVQRSG CNEVTTVVDV KEIFKSSSPI PRTQVPLITN
       250        260        270        280        290        300        310        320
SSCQCPHILP HQDVLIMCYE WRSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRTVQD KKKTAGRTSR SNPPKPKGKP
       330        340        350
PAPKPASPKK NIKTRSAQKR TNPKRV
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 768 | 1 | 698.4267 | 127.49 | 2 | 39.2 | 13.0 | 0 | 265-275 | R.MMLLENCLVEK.W | Carbamidomethyl: 7;<br>Oxidation: 1 |

# Detailed Protein Report

**Protein 697:** **PREDICTED: RAF proto-oncogene serine/threonine-protein kinase isoform X5 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530372930 | **Score:** | 24.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 60.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 6.4 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMANSQILLR | QATLSVFSCR | TSKEQCKKAR | LDWNTDAASL | IGEELQVDFL | DHVPLTTHNF | ARKTFLKLAF | CDICQKFLLN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GFRCQTCGYK | FHEHCSTKVP | TMCVDWSNIR | QLFSQHRYST | PHAFTFNTSS | PSSEGSLSQR | QRSTSTPNVH | MVSTTLPVDS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RMIEDAIRSH | SESASPSALS | SSPNNLSPTG | WSQPKTPVPA | QRERAPVSGT | QEKNKIRPRG | QRDSSYYWEI | EASEVMLSTR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IGSGSFGTVY | KGKWHGDVAV | KILKVVDPTP | EQFQAFRNEV | AVLRKTRHVN | ILLFMGYMTK | DNLAIVTQWC | EGSSLYKHLH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VQETKFQMFQ | LIDIARQTAQ | GMDYLHAKNI | IHRDMKSNNI | FLHEGLTVKI | GDFGLATVKS | RWSGSQQVEQ | PTGSVLWMAP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EVIRMQDNNP | FSFQSDVYSY | GIVLYELMTG | ELPYSHINNR | DQIIFMVGRG | YASPDLSKLY | KNCPKAMKRL | VADCVKKVKE |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| ERPLFPQILS | SIELLQHSLP | KINRSASEPS | LHRAAHTEDI | NACTLTTSPR | LPVF | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2671 | 1 | 822.4677 | 60.63 | 2 | 64.5 | 10.7 | 1 | 64-76 | K.TFLKLAFCDICQK.F | Carbamidomethyl: 8, 11 |
| 2739 | 1 | 806.4174 | -6.55 | 3 | 65.4 | 13.5 | 2 | 441-461 | R.DQIIFMVGRGYASPDLSKLYK.N | Oxidation: 6 |

# Detailed Protein Report

## Protein 698: PREDICTED: centrosomal protein of 290 kDa isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530400856 | **Score:** | 24.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 234.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 2 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.53 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.87 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQKLSLRQKS | AIFCQQIHEN | RADMDKSQVA | TLEEEQVHSQ | VKYADINLKE | DIIKSEVPLQ | TEILKNKLKV | NLPDPVSITA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QSKLSQINSL | ENLIEQLRRE | LVFLRSQNEI | IAQEFLIKEA | ECRNADIELE | HHRSQAEQNE | FLSRELIEKE | RDLERSRTVI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AKFQNKLKEL | VEENKQLEEG | MKEILQAIKE | MQKDPDVKGG | ETSLIIPSLE | RLVNAIESKN | AEGIFDASLH | LKAQVDQLTG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RNEELRQELR | ESRKEAINYS | QQLAKANLKI | DHLEKETSLL | RQSEGSNVVF | KGIDLPDGIA | PSSASIINSQ | NEYLIHLLQE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LENKEKKLKN | LEDSLEDYNR | KFAVIRHQQS | LLYKEYLSEK | ETWKTESKTI | KEEKRKLEDQ | VQQDAIKVKE | YNNLLNALQM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DSDEMKKILA | ENSRKITVLQ | VNEKSLIRQY | TTLVELERQL | RKENEKQKNE | LLSMEAEVCE | KIGCLQRFKE | MAIFKIAALQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KVVDNSVSLS | ELELANKQYN | ELTAKYRDIL | QKDNMLVQRT | SNLEHLECEN | ISLKEQVESI | NKELEITKEK | LHTIEQAWEQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ETKLGNESSM | DKAKKSITNS | DIVSISKKIT | MLEMKELNER | QRAEHCQKMY | EHLRTSLKQM | EERNFELETK | FAELTKINLD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AQKVEQMLRD | ELADSVSKAV | SDADRQRILE | LEKNEMELKV | EVSKLREISD | IARRQVEILN | AQQQSRDKEV | ESLRMQLLDY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QAQSDEKSLI | AKLHQHNVSL | QLSEATALGK | LESITSKLQK | MEAYNLRLEQ | KLDEKEQALY | YARLEGRNRA | KHLRQTIQSL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RRQFSGALPL | AQQEKFSKTM | IQLQNDKLKI | MQEMKNSQQE | HRNMENKTLE | MELKLKGLEE | LISTLKDTKG | AQKVINWHMK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| IEELRLQELK | LNRELVKDKE | EIKYLNNIIS | EYERTISSLE | EEIVQQNKFH | EERQMAWDQR | EVDLERQLDI | FDRQQNEILN |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| AAQKFEEATG | SIPDPSLPLP | NQLEIALRKI | KENIRIILET | RATCKSLEEK | LKEKESALRL | AEQNILSRDK | VINELRLRLP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ATAEREKLIA | ELGRKEMEPK | SHHTLKIAHQ | TIANMQARLN | QKEEVLKKYQ | RLLEKAREEQ | REIVKKHEED | LHILHHRLEL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QADSSLNKFK | QTAWDLMKQS | PTPVPTNKHF | IRLAEMEQTV | AEQDDSLSSL | LVKLKKVSQD | LERQREITEL | KVKEFENIKL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| QLQENHEDEV | KKVKAEVEDL | KYLLDQSQKE | SQCLKSELQA | QKEANSRAPT | TTMRNLVERL | KSQLALKEKQ | QKALSRALLE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LRAEMTAAAE | ERIISATSQK | EAHLNVQQIV | DRHTRELKTQ | VEDLNENLLK | LKEALKTSKN | RENSLTDNLN | DLNNELQKKQ |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KAYNKILREK | EEIDQENDEL | KRQIKRLTSG | LQGKPLTDNK | QSLIEELQRK | VKKLENQLEG | KVEEVDLKPM | KEKNAKEELI |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| RWEEGKKWQA | KIEGIRNKLK | EKEGEVFTLT | KQLNTLKDLF | AKADKEKLTL | QRKLKTTGMT | VDQVLGIRAL | ESEKELEELK |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| KRNLDLENDI | LYMRAHQALP | RDSVVEDLHL | QNRYLQEKLH | ALEKQFSKDT | YSKPSISGIE | SDDHCQREQE | LQKENLKLSS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| ENIELKFQLE | QANKDLPRLK | NQVRDLKEMC | EFLKKEKAEV | QRKLGHVRGS | GRSGKTIPEL | EKTIGLMKKV | VEKVQRENEQ |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LKKASGILTS | EKMANIEQEN | EKLKAELEKL | KAHLGHQLSM | HYESKTKGTE | KIIAENERLR | KELKKETDAA | EKLRIAKNNL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| EILNEKMTVQ | LEETGKRLQF | AESRGPQLEG | ADSKSWKSIV | VTRMYETKLK | ELETDIAKKN | QSITDLKQLV | KEATEREQKV |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| NKYNEDLEQQ | IKILKHVPEG | AETEQGLKRE | LQVLRLANHQ | LDKEKAELIH | QIEANKDQSG | AESTIPDADQ | LKEKIKDLET |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| QLKMSDLEKQ | HLKEEIKKLK | KELENFDPSF | FEEIEDLKYN | YKEEVKKNIL | LEEKVKKLSE | QLGVELTSPV | AASEEFEDEE |
| 2010 | | | | | | | |
| ESPVNFPIY | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1093 | 2 | 500.8014 | -30.66 | 2 | 41.9 | 12.3 | 2 | 2-9 | M.QKLSLRQK.S |  | WUP:QUP 1.87<br>QU:MU 0.53 |
| 1675 | 1 | 745.8585 | -74.75 | 2 | 50.7 | 11.8 | 1 | 631-643 | K.FAELTKINLDAQK.V |  |  |

# Detailed Protein Report

---

## Protein 699: uncharacterized protein C3orf67 [Homo sapiens]

**Accession:** gi|38348244

**Database:** refseq_human(refseq_human_20140103.fasta)

**Database Date:** 2015-11-30

**Modification(s):** Oxidation

**Score:** 24.1

**MW [kDa]:** 62.8

**pI:** 4.8

**Sequence Coverage [%]:** 5.0

**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MIKRKIWCNL CIDLVAFTSE IFKGAVFQSL DGIVVSANCK LRKIFTLKSK PQDTADKDAV YGVPFSTDEP TDIIPRSCQL
        90        100        110        120        130        140        150        160
MTDVPHVTQL LNMTKLRQTE IKFGGHPLRS AESDQFINRG TSITRNSKNQ DVCHIAFGSK VLGPPPLSGR RNNMKISSET
       170        180        190        200        210        220        230        240
VRSVGSKNNR SCQPSTVEKC VNGTEMSALL IPESEEQGNK ENIHQIKQTV PIHAANLHIM HPHPPQEPSA DKNNNRRRLR
       250        260        270        280        290        300        310        320
LKSTSRERTE TPSGSSSGNN RIEDKASTIL TTVSQQGAEL LNSGTLGPQS PDQSDEWIFP ENADHISYLA SSRQSLLLGD
       330        340        350        360        370        380        390        400
DSCNPSHLWL EASKESEHDQ QAEESQSVPK DIFTFSSRPR SAPHGKTQTM SPEELSFILD LKEDNSVTSR DTQSEDDFYG
       410        420        430        440        450        460        470        480
GDSSEEEYDW RNYQPSQMSE SELQMLASLR WQQNEELEDA GTSHGLSASQ VDNCNVSIST SSDDTTTWNS CLPPPVNQGR
       490        500        510        520        530        540        550        560
HYQKEMNPPS PSNPRDWLNM LSPPIVPPSQ QPAEQRPDSC ESLSVQGEED LSVEEDEEVL TLLYDPCLNC YFDPQTGKYY
       570
ELV
```

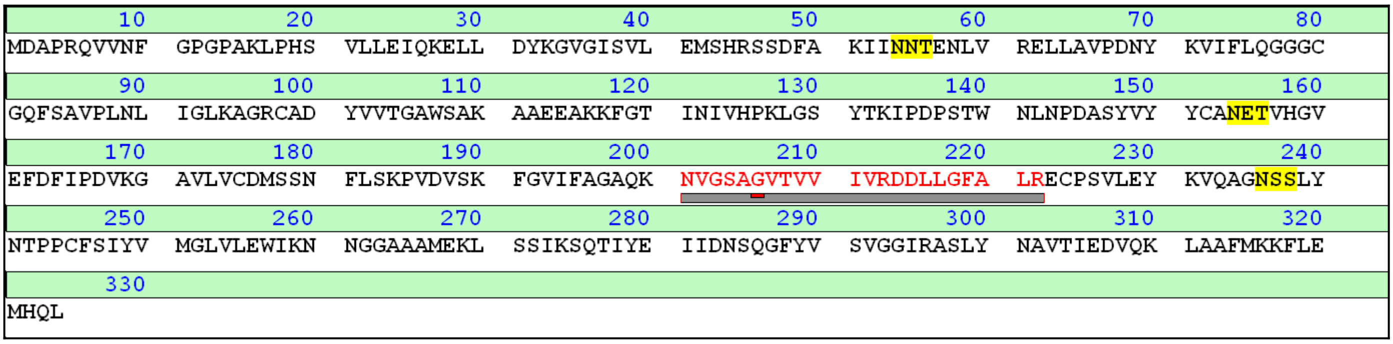
| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2960 | 1 | 826.4281 | -34.60 | 2 | 65.8 | 13.5 | 2 | 141-155 | K.VLGPPPLSGRRNNMK.I | Oxidation: 14 |

# Detailed Protein Report

## Protein 700: phosphoserine aminotransferase isoform 2 [Homo sapiens]

**Accession:** gi|10863955
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 24.1
**MW [kDa]:** 35.2
**pI:** 6.3
**Sequence Coverage [%]:** 11.4
**No. of unique Peptides:** 1



| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDAPRQVVNF | GPGPAKLPHS | VLLEIQKELL | DYKGVGISVL | EMSHRSSDFA | KIINNTENLV | RELLAVPDNY | KVIFLQGGGC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GQFSAVPLNL | IGLKAGRCAD | YVVTGAWSAK | AAEEAKKFGT | INIVHPKLGS | YTKIPDPSTW | NLNPDASYVY | YCANETVHGV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EFDFIPDVKG | AVLVCDMSSN | FLSKPVDVSK | FGVIFAGAQK | NVGSAGVTVV | IVRDDLLGFA | LRECPSVLEY | KVQAGNSSLY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NTPPCFSIYV | MGLVLEWIKN | NGGAAAMEKL | SSIKSQTIYE | IIDNSQGFYV | SVGGIRASLY | NAVTIEDVQK | LAAFMKKFLE |
| 330 | | | | | | | |
| MHQL | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1320 | 1 | 1136.1196 | -22.05 | 2 | 46.6 | 12.1 | 1 | 201-222 | K.NVGSAGVTVVIVRDDLLGFALR.E | |

# Detailed Protein Report

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## Protein 701: zinc finger protein 493 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|115511042 | **Score:** | 24.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 75.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 4.8 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578833199 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 493 isoform X3 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MNECNVHKEG | YNELNQYLTT | TQSKIFQCDK | YVKVFHKLLN | SNRHNTKHTG | KKPFKCKKCG | KSFCMLLHLC | QHKRIHIREN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SYRCEECGKA | FIWFSTLTRH | RRVHTGEKSY | KYECGKSFNQ | DSNLTTHKRI | HTGQKPYKCE | ECGTSFYQFS | YLTRHKLIHT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| REKPYKCEQY | GKTFNQSSTL | TGHKIIHNGE | KPYKCEECGK | AFSIFSTPTK | HKIIHTEEKS | HRCEEYCKAY | KESSHLTTHK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RIHTGEKPYK | CEECGKAFSI | FSTLTKHKII | HTEEKSHRCE | ECGKAYKESS | HLTTHKRIHT | GEKPYKCEEC | GKTFSVFSIL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TKHKIIHTEE | KPYKCEECGK | AFKRSSTLTK | HRIIHTEEKP | YKCEECGKAF | NQSSTLSIHK | IIHTGEKPYK | CEECGKAFKR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SSTLTIHKMI | HTGEKPYKCE | ECGKAFNRSS | HLTTHKRIHT | GHKPYKCKEC | GKSFSVFSTL | TKHKIIHTDK | KPYKCEECGK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AFNRSSILSI | HKKIHTGEKP | YKCEECGKAF | KRSSHLAGHK | QIHSVQKPYK | CEECGKAFSI | FSTLTKHKII | HTEEKPYKCE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KCGKTFYRFS | NLNTHKIIHT | GEKPCKCEEC | GKAFNHSSNL | IKHKLIHTGD | KPYKCEACGK | AFRRSSHLSR | HKIIHIGIHT |
| 650 | | | | | | | |
| EETVQK | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2085 | 1 | 939.2954 | -149.37 | 2 | 56.4 | 12.7 | 1 | 59-73 | K.CGKSFCMLLHLCQHK.R | Carbamidomethyl: 1, 6;<br>Oxidation: 7 |
| 1854 | 1 | 938.8329 | -130.94 | 2 | 53.5 | 11.5 | 1 | 521-536 | K.QIHSVQKPYKCEECGK.A | |

# Detailed Protein Report

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## Protein 702: up-regulator of cell proliferation isoform 2 [Homo sapiens]

**Accession:** gi|117968345
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 24.1
**MW [kDa]:** 100.3
**pI:** 6.2
**Sequence Coverage [%]:** 3.3
**No. of unique Peptides:** 2

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEGDDCEFRY | GDGTNEAQDN | DFPTVERSRL | QEMLSLLGLE | TYQVQKLSLQ | DSLQISFDSM | KNWAPQVPKD | LPWNFLRKLQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ALNADARNTT | MVLDVLPDAR | PVEKESQMEE | EIIYWDPADD | LAADIYSFSE | LPTPDTPVNP | LDLLCALLLS | SDSFLQQEIA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LKMALCQFAL | PLVLPDSENH | YHTFLLWAMR | GIVRTWWSQP | PRGMGSFRED | SVVLSRAPAF | AFVRMDVSSN | SKSQLLNAVL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SPGHRQWDCF | WHRDLNLGTN | AREISDGLVE | ISWFFPSGRE | DLDIFPEPVA | FLNLRGDIGS | HWLQFKLLTE | ISSAVFILTD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NISKKEYKLL | YSMKESTTKY | YFILSPYRGK | RNTNLRFLNK | LIPVLKIDHS | HVLVKVSSTD | SDSFVKRIRA | IVGNVLRAPC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RRVSVEDMAH | AARKLGLKVD | EDCEECQKAK | DRMERITRKI | KDSDAYRRDE | LRLQGDPWRK | AAQVEKEFCQ | LQWAVDPPEK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HRAELRRRLL | ELRMQQNGHD | PSSGVQEFIS | GISSPSLSEK | QYFLRWMEWG | LARVAQPRLR | QPPETLLTLR | PKHGGTTDVG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EPLWPEPLGV | EHFLREMGQF | YEAESCLVEA | GRLPAGQRRF | AHFPGLASEL | LLTGLPLELI | DGSTLSMPVR | WVTGLLKELH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VRLERRSRLV | VLSTVGVPGT | GKSTLLNTMF | GLRFATGKSC | GPRGAFMQLI | TVAEGFSQDL | GCDHILVIDS | GGLIGGALTS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AGDRFELEAS | LATLLMGLSN | VTVISLAETK | DIPAAILHAF | LRLEKTGHMP | NYQFVYQNLH | DVSVPGPRPR | DKRQLLDPPG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DLSRAAAQME | KQGDGFRALA | GLAFCDPEKQ | HIWHIPGLWH | GAPPMAAVSL | AYSEAIFELK | RCLLENIRNG | LSNQNKNIQQ |
| 890 | | | | | | | |
| LIELVRRL | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1302 | 9 | 698.6540 | -193.97 | 2 | 45.9 | 13.9 | 1 | 419-430 | K.VDEDCEECQKAK.D | |
| 2800 | 1 | 863.4092 | -128.64 | 2 | 66.2 | 10.1 | 2 | 646-662 | R.RSRLVVLSTVGVPGTGK.S | |

# Detailed Protein Report

## Protein 703: ATP-binding cassette sub-family B member 5 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|148612844 | **Score:** | 24.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 89.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| | | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MVDENDIRAL NVRHYRDHIG VVSQEPVLFG TTISNNIKYG RDDVTDEEME RAAREANAYD FIMEFPNKFN TLVGEKGAQM
        90        100        110        120        130        140        150        160
SGGQKQRIAI ARALVRNPKI LILDEATSAL DSESKSAVQA ALEKASKGRT TIVVAHRLST IRSADLIVTL KDGMLAEKGA
       170        180        190        200        210        220        230        240
HAELMAKRGL YYSLVMSQDI KKADEQMESM TYSTERKTNS LPLHSVKSIK SDFIDKAEES TQSKEISLPE VSLLKILKLN
       250        260        270        280        290        300        310        320
KPEWPFVVLG TLASVLNGTV HPVFSIIFAK IITMFGNNDK TTLKHDAEIY SMIFVILGVI CFVSYFMQGL FYGRAGEILT
       330        340        350        360        370        380        390        400
MRLRHLAFKA MLYQDIAWFD EKENSTGGLT TILAIDIAQI QGATGSRIGV LTQNATNMGL SVIISFIYGW EMTFLILSIA
       410        420        430        440        450        460        470        480
PVLAVTGMIE TAAMTGFANK DKQELKHAGK IATEALENIR TIVSLTREKA FEQMYEEMLQ TQHRNTSKKA QIIGSCYAFS
       490        500        510        520        530        540        550        560
HAFIYFAYAA GFRFGAYLIQ AGRMTPEGMF IVFTAIAYGA MAIGETLVLA PEYSKAKSGA AHLFALLEKK PNIDSRSQEG
       570        580        590        600        610        620        630        640
KKPDTCEGNL EFREVSFFYP CRPDVFILRG LSLSIERGKT VAFVGSSGCG KSTSVQLLQR LYDPVQGQVL FDGVDAKELN
       650        660        670        680        690        700        710        720
VQWLRSQIAI VPQEPVLFNC SIAENIAYGD NSRVVPLDEI KEAANAANIH SFIEGLPEKY NTQVGLKGAQ LSGGQKQRLA
       730        740        750        760        770        780        790        800
IARALLQKPK ILLLDEATSA LDNDSEKVVQ HALDKARTGR TCLVVTHRLS AIQNADLIVV LHNGKIKEQG THQELLRNRD
       810        820
IYFKLVNAQS VQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1505 | 1 | 1022.6536 | 107.11 | 2 | 48.5 | 10.6 | 1 | 97-115 | R.NPKILILDEATSALDSESK.S | |

# Detailed Protein Report

## Protein 704: uncharacterized protein LOC100144595 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|373838702 | **Score:** | 24.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 11.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.4 |
| | | **Sequence Coverage [%]:** | 13.7 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MATYILKLRA CPWETLNGVL LCRQAGVHWR NLGLLQPPPP GFKRFSCLSL PSGWDYRHAP PCRPNVLYFS RDGVSLCWPG
        90        100        110
WSQSPDLMIH LPRPPKVLGL QV
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2266 | 1 | 787.7912 | -131.21 | 2 | 58.2 | 24.1 | 0 | 10-23 | R.ACPWETLNGVLLCR.Q | |

# Detailed Protein Report

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## Protein 705: peptidyl-prolyl cis-trans isomerase A [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|10863927 | **Score:** | 24.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 18.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 18.8 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

***WUP:QUP*** **Median:** 1.47 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MVNPTVFFDI AVDGEPLGRV SFELFADKVP KTAENFRALS TGEKGFGYKG SCFHRIIPGF MCQGGDFTRH NGTGGKSIYG
         90        100        110        120        130        140        150        160
EKFEDENFIL KHTGPGILSM ANAGPNTNGS QFFICTAKTE WLDGKHVVFG KVKEGMNIVE AMERFGSRNG KTSKKITIAD
        170
CGQLE
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2768 | 1 | 973.5119 | 7.60 | 2 | 65.0 | 13.8 | 0 | 2-19 | M.VNPTVFFDIAVDGEPLGR.V | | WUP:QUP 1.47 |

# Detailed Protein Report

## Protein 706: potassium channel subfamily K member 2 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|14589851 | **Score:** | 24.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.8 |
| | | **Sequence Coverage [%]:** | 8.3 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAPDLLDPK | SAAQNSKPRL | SFSTKPTVLA | SRVESDTTIN | VMKWKTVSTI | FLVVVLYLII | GATVFKALEQ | PHEISQRTTI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VIQKQTFISQ | HSCVNSTELD | ELIQQIVAAI | NAGIIPLGNT | SNQISHWDLG | SSFFFAGTVI | TTIGFGNISP | RTEGGKIFCI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IYALLGIPLF | GFLLAGVGDQ | LGTIFGKGIA | KVEDTFIKWN | VSQTKIRIIS | TIIFILFGCV | LFVALPAIIF | KHIEGWSALD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AIYFVVITLT | TIGFGDYVAG | GSDIEYLDFY | KPVVWFWILV | GLAYFAAVLS | MIGDWLRVIS | KKTKEEVGEF | RAHAAEWTAN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VTAEFKETRR | RLSVEIYDKF | QRATSIKRKL | SAELAGNHNQ | ELTPCRRTLS | VNHLTSERDV | LPPLLKTESI | YLNGLTPHCA |
| 410 | 420 | | | | | | |
| GEEIAVIENI | K | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1783 | 1 | 823.3074 | -115.03 | 2 | 52.6 | 10.7 | 0 | 312-326 | R.AHAAEWTANVTAEFK.E | |
| 33 | 1 | 1069.0298 | -19.07 | 2 | 30.2 | 13.3 | 2 | 349-367 | R.KLSAELAGNHNQELTPCRR.T | |

# Detailed Protein Report

## Protein 707: PREDICTED: probable phospholipid-transporting ATPase IIB isoform X6 [Homo sapiens]

**Accession:** gi|530414190
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 24.0
**MW [kDa]:** 114.6
**pI:** 7.3
**Sequence Coverage [%]:** 2.7
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MADQIPLYPV | RSAAAAAANR | KRAAYYSAAG | PRPGADRHSR | YQLEDESAHL | DEMPLMMSEE | GFENEESDYH | TLPRARIMQR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KRGLEWFVCD | GWKFLCTSCC | GWLINICRRK | KELKARTVWL | GCPEKCEEKH | PRNSIKNQKY | NVFTFIPGVL | YEQFKFFLNL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YFLVISCSQF | VPALKIGYLY | TYWAPLGFVL | AVTMTREAID | EFRRFQRDKE | VNSQLYSKLT | VRGKVQVKSS | DIQVGDLIIV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EKNQRIPSDM | VFLRTSEKAG | SCFIRTDQLD | GETDWKLKVA | VSCTQQLPAL | GDLFSISAYV | YAQKPQMDIH | SFEGTFTRED |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SDPPIHESLS | IENTLWASTI | VASGTVIGVV | IYTGKETRSV | MNTSNPKNKV | GLLDLELNRL | TKALFLALVA | LSIVMVTLQG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FVGPWYRNLF | RFLLLFSYII | PISLRVNLDM | GKAVYGWMMM | KDENIPGTVV | RTSTIPEELG | RLVYLLTDKT | GTLTQNEMIF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KRLHLGTVSY | GADTMDEIQS | HVRDSYSQMQ | SQAGGNNTGS | TPLRKAQSSA | PKVRKSVSSR | IHEAVKAIVL | CHNVTPVYES |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RAGVTEETEF | AEADQDFSDE | NRTYQASSPD | EVALVQWTES | VGLTLVSRDL | TSMQLKTPSG | QVLSFCILQL | FPFTSESKRM |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GVIVRDESTA | EITFYMKGAD | VAMSPIVQYN | DWLEEECGNM | AREGLRTLVV | AKKALTEEQY | QDFESRYTQA | KLSMHDRSLK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VAAVVESLER | EMELLCLTGV | EDQLQADVRP | TLEMLRNAGI | KIWMLTGDKL | ETATCIAKSS | HLVSRTQDIH | IFRQVTSRGE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AHLELNAFRR | KHDCALVISG | DSLEVCLKYY | EHEFVELACQ | CPAVVCCRCS | PTQKARIVTL | LQQHTGRRTC | AIGDGGNDVS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| MIQAADCGIG | IEGKEGKQAS | LAADFSITQF | RHIGRLLMVH | GRNSYKRSAA | LGQFVMHRGL | IISTMQAVFS | SVFYFASVPL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | | |
| YQGFLMVGYA | TIYTMFPVFS | LVLDQDVKPE | MAMLYPELYK | DLTKFAKVAQ | TAALCVVV | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2606 | 1 | 973.0002 | 44.61 | 2 | 63.3 | 10.2 | 1 | 94-109 | K.FLCTSCCGWLINICRR.K | Carbamidomethyl: 6 |

# Detailed Protein Report

## Protein 708: PREDICTED: coiled-coil domain-containing protein 129 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530384574 | **Score:** | 24.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 104.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 1.78 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MVQMTVKDYM RSLHQFSETP ILSRGTSFNS CYSTASVPQS IPEWLEFWEI DPVEILLDLG FGADEPDICM QIPARFLGCG
        90        100        110        120        130        140        150        160
SAARGINIRV FLEAQKQRMD IENPNLYGRF RQLEILDHVT NAFSSLLSDV SILPNRAEEK AGGESVQRTS VSAAKEHRRR
       170        180        190        200        210        220        230        240
MGKLLRRASK QNIRRDCNPE VSESFKVKDE VFVPFTKPWD CGAELAATSI NHKQNHLSLS VEHQSLQACD DLLPYPPHGL
       250        260        270        280        290        300        310        320
LSKQWPCSSM PAKQAPPSCV SEGSVKGRTQ KENLFQTNKL KSLSHLAGKG PDSFEMEEVQ SFEEETGNPL DMTSGTVGAR
       330        340        350        360        370        380        390        400
VDRANSCQSD SSGFLEEPLE PLPLQMPSLP NSQSPAENGG RKPRDQSHSL VSSQDCQLES DGPDSKSRAS MSFSSQEANA
       410        420        430        440        450        460        470        480
LEQRASVSVM EEEFLLEAME GPPELYIPDM ACAKTTTRGE CPRKDSHLWQ LLPMPHAEYE VTRPTATSKY DHPLGFMVTH
       490        500        510        520        530        540        550        560
VTEMQDSFVR PEGAGKVQSH HNESQRSPGN DHTQDKFLHV DSEAPREEES SGFCPHTNHS LLVPESSSQC IPKHSEITPY
       570        580        590        600        610        620        630        640
ATDLAQTSEK LIPHLHKLPG DPAQVKSRSG TLGQILPGTE AEMENLPLNT GSSRSVMTQM SSSLVSAAQR AVALGTGPRG
       650        660        670        680        690        700        710        720
TSLECTVCDP VTATETRLGT KARQLNDASI QTSALSNKTL THGPQPLTKS VSLDSGFSSI CPMGTCHAIP AHCCICCHHH
       730        740        750        760        770        780        790        800
PHCHGERQSP GPEPSVCRHC LCSLTGHQEA QFMTTLKALQ DTTVRELCSC TVHEMEAMKT ICQSFREYLE EIEQHLMGQQ
       810        820        830        840        850        860        870        880
ALFSRDMSEE EREEAEQLQT LREALRQQVA ELEFQLGDRA QQIREGILLQ LEVLTAEPPE HYSNLHQYNW IEESNGQTSC
       890        900        910        920        930        940        950        960
SKIHPGMAPR TVFPPDDGQE APCSGGTQLA AFTPPTLENS TRMSPSSSAW AKLGPTPLSN CPVGEKDADV FL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2294 | 1 | 841.8204 | -110.73 | 2 | 59.1 | 12.2 | 0 | 615-630 | R.SVMTQMSSSLVSAAQR.A | | QU:MU 1.78 |

# Detailed Protein Report

---

## Protein 709: vinexin isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|65301112 | **Score:** | 24.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 36.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 9.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578815148 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: vinexin isoform X8 [Homo sapiens] |
| gi\|578815146 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: vinexin isoform X7 [Homo sapiens] |
| gi\|578815144 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: vinexin isoform X6 [Homo sapiens] |
| gi\|530387505 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: vinexin isoform X2 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MADGGSPFLG RRDFVYPSST RDPSASNGGG SPARREEKKR KAARLKFDFQ AQSPKELTLQ KGDIVYIHKE VDKNWLEGEH

        90        100        110        120        130        140        150        160
HGRLGIFPAN YVEVLPADEI PKPIKPPTYQ VLEYGEAVAQ YTFKGDLEVE LSFRKGEHIC LIRKVNENWY EGRITGTGRQ

       170        180        190        200        210        220        230        240
GIFPASYVQV SREPRLRLCD DGPQLPTSPR LTAAARSARH PSSPSALRSP ADPIDLGGQT SPRRTGFSFP TQEPRPQTQN

       250        260        270        280        290        300        310        320
LGTPGPALSH SRGPSHPLDL GTSSPNTSQI HWTPYRAMYQ YRPQNEDELE LREGDRVDVM QQCDDGWFVG VSRRTQKFGT

       330
FPGNYVAPV
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1731 | 1 | 803.8844 | -67.43 | 2 | 50.0 | 12.1 | 2 | 42-55 | K.AARLKFDFQAQSPK.E | |

# Detailed Protein Report

## Protein 710: PREDICTED: targeting protein for Xklp2 isoform X2 [Homo sapiens]

**Accession:** gi|530417959
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 24.0
**MW [kDa]:** 85.0
**pI:** 10.0
**Sequence Coverage [%]:** 3.6
**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MSQVKSSYSY DAPSDFINFS SLDDEGDTQN IDSWFEEKAN LENKLLGKNG TGGLFQGKTP LRKANLQQAI VTPLKPVDNT
        90        100        110        120        130        140        150        160
YYKEAEKENL VEQSIPSNAC SSLEVEAAIS RKTPAQPQRR SLRLSAQKDL EQKEKHHVKM KAKRCATPVI IDEILPSKKM
       170        180        190        200        210        220        230        240
KVSNNKKKPE EEGSAHQDTA EKNASSPEKA KGRHTVPCMP PAKQKFLKST EEQELEKSMK MQQEVVEMRK KNEEFKKLAL
       250        260        270        280        290        300        310        320
AGIGQPVKKS VSQVTKSVDF HFRTDERIKQ HPKNQEEYKE VNFTSELRKH PSSPARVTKG CTIVKPFNLS QGKKRTFDET
       330        340        350        360        370        380        390        400
VSTYVPLAQQ VEDFHKRTPN RYHLRSKKDD INLLPSKSSV TKICRDPQTP VLQTKHRARA VTCKSTAELE AEELEKLQQY
       410        420        430        440        450        460        470        480
KFKARELDPR ILEGGPILPK KPPVKPPTEP IGFDLEIEKR IQERESKKKT EDEHFEFHSR PCPTKILEDV VGVPEKKVLP
       490        500        510        520        530        540        550        560
ITVPKSPAFA LKNRIRMPTK EDEEEDEPVV IKAQPVPHYG VPFKPQIPEA RTVEICPFSF DSRDKERQLQ KEKKIKELQK
       570        580        590        600        610        620        630        640
GEVPKFKALP LPHFDTINLP EKKVKNVTQI EPFCLETDRR GALKAQTWKH QLEEELRQQK EAACFKARPN TVISQEPFVP
       650        660        670        680        690        700        710        720
KKEKKSVAVQ EPFQLATEKR AKERQELEKR MAEVEAQKAQ QLEEARLQEE EQKKEELARL RRELVHKANP IRKYQGLEIK
       730        740        750
SSDQPLTVPV SPKFSTRFHC
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1899 | 1 | 973.3824 | -143.79 | 2 | 52.1 | 12.0 | 2 | 349-365 | K.DDINLLPSKSSVTKICR.D | Carbamidomethyl: 16 |

# Detailed Protein Report

## Protein 711: neuropeptides B/W receptor type 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|53828924 | **Score:** | 24.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 36.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 8.2 |
| | | **No. of unique Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MDNASFSEPW PANASGPDPA LSCSNASTLA PLPAPLAVAV PVVYAVICAV GLAGNSAVLY VLLRAPRMKT VTNLFILNLA
        90        100        110        120        130        140        150        160
IADELFTLVL PINIADFLLR QWPFGELMCK LIVAIDQYNT FSSLYFLTVM SADRYLVVLA TAESRRVAGR TYSAARAVSL
       170        180        190        200        210        220        230        240
AVWGIVTLVV LPFAVFARLD DEQGRRQCVL VFPQPEAFWW RASRLYTLVL GFAIPVSTIC VLYTTLLCRL HAMRLDSHAK
       250        260        270        280        290        300        310        320
ALERAKKRVT FLVVAILAVC LLCWTPYHLS TVVALTTDLP QTPLVIAISY FITSLSYANS CLNPFLYAFL DASFRRNLRQ
       330
LITCRAAA
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 329 | 1 | 604.3649 | 47.17 | 2 | 32.8 | 13.6 | 2 | 146-156 | R.RVAGRTYSAAR.A | |
| 42 | 1 | 706.9621 | -93.24 | 3 | 30.4 | 10.4 | 1 | 186-201 | R.RQCVLVFPQPEAFWWR.A | Carbamidomethyl: 3 |

# Detailed Protein Report

## Protein 712: zinc finger protein 282 [Homo sapiens]

**Accession:** gi|31657109
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 23.9
**MW [kDa]:** 74.2
**pI:** 5.5
**Sequence Coverage [%]:** 4.8
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQFVSTRPQP | QQLGIQGLGL | DSGSWSWAQA | LPPEEVCHQE | PALRGEMAEG | MPPMQAQEWD | MDARRPMPFQ | FPPFPDRAPV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FPDRMMREPQ | LPTAEISLWT | VVAAIQAVER | KVDAQASQLL | NLEGRTGTAE | KKLADCEKTA | VEFGNHMESK | WAVLGTLLQE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YGLLQRRLEN | LENLLRNRNF | WVLRLPPGSK | GEAPKVPVTF | VDIAVYFSED | EWKNLDEWQK | ELYNNLVKEN | YKTLMSLDAE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GSVPKPDAPV | QAEPREEPCV | WEQRHPEERE | IPMDPEAGAE | PLVPAQDASS | QVKREDTLCV | RGQRGLEERA | IPTESITDSP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ISAQDLLSRI | KQEEHQCVWD | QQDLADRDIP | TDPNSESLIS | AHDILSWIKQ | EEQPYPWGPR | DSMDGELGLD | SGPSDSLLMV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KNPPPAPPQP | QPQPQPPQPQ | LQSQPQPQSL | PPIAVAENPG | GPPSRGLLDD | GFQVLPGERG | SGEAPPGGDR | STGGGGGDGG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GGGGGAEAGT | GAGGGCGSCC | PGGLRRSLLL | HGARSKPYSC | PECGKSFGVR | KSLIIHHRSH | TKERPYECAE | CEKSFNCHSG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LIRHQMTHRG | ERPYKCSECE | KTYSRKEHLQ | NHQRLHTGER | PFQCALCGKS | FIRKQNLLKH | QRIHTGERPY | TCGECGKSFR |
| 650 | 660 | 670 | 680 | | | | |
| YKESLKDHLR | VHSGGPGPGA | PRQLPPPPER | D | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2100 | 1 | 757.3120 | -118.88 | 2 | 54.6 | 10.8 | 0 | 112-125 | K.VDAQASQLLNLEGR.T | |

# Detailed Protein Report

---

**Protein 713:** **regulator of G-protein signaling 22 isoform 2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|557878614 | **Score:** | 23.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 145.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPEKRLTAEP | PTITEEEFED | SLATDDFLVD | YFNEFLSLPT | FSEAIRFNAD | YGVFEVANDA | PQFLEKQLKK | ILQNQQPRNP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IYDVVRKGKN | EVKPVQMNAP | DEDETINVNY | NIMCLSREEG | IKWIKKERLP | AFLESDCYFE | YRLAKLVSQV | RWSKSGMNFT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VGSNFSPWIV | KKPPSLPPPA | TEEDNLASYT | QTKDWFALAK | QSQQTVSTFS | LPCCVPYNKL | KSPAISSVSE | NFIFDDGVHP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RTKKDPSKTN | KLISEFEEEE | GEEEEVSVSL | QDTPSQALLR | VYLEKKQDVD | ESLTMHFSTC | EEFLSSYIYF | ILRGAIQQIV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GKPVGETPDY | INFNNITKVS | FDDCFESIHG | KNFLSELVQT | TKERSEEIEQ | TSLSSKNESA | GPESRADWCI | SHRTYDIGNR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KEFERFKKFI | KGTLGERYWW | LWMDIERLKV | LKDPGRHQRH | LEKMKKCYLV | SNGDYYLSAE | ILSKFKLLDG | SQWNEEHLRN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IQSEVLKPLL | LYWAPRFCVT | HSASTKYASA | ELKFWHLRQA | KPRKDIDPFP | QMATLLPLRP | KSCIPQIPEI | QKEEFSLSQP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PKSPNKSPEV | KTATQKPWKR | ELLYPGSSKD | DVIEKGSKYM | SESSKVIHLT | SFTDISECLK | PQLDRRYAYT | EEPRVKTVSD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VGALGGSDME | NLLQSLYVEN | RAGFFFTKFC | EHSGNKLWKN | SVYFWFDLQA | YHQLFYQETL | QPFKVCKQAQ | YLFATYVAPS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ATLDIGLQQE | KKKEIYMKIQ | PPFEDLFDTA | EEYILLLLLE | PWTKMVKSDQ | IAYKKVELVE | ETRQLDSTYF | RKLQALHKET |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FSKKAEDTTC | EIGTGILSLS | NVSKRTEYWD | NVPAEYKHFK | FSDLLNNKLE | FEHFRQFLET | HSSSMDLMCW | TDIEQFRRIT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| YRDRNQRKAK | SIYIKNKYLN | KKYFFGPNSP | ASLYQQNQVM | HLSGGWGKIL | HEQLDAPVLV | EIQKHVQNRL | ENVWLPLFLA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SEQFAARQKI | KVQMKDIAEE | LLLQKAEKKI | GVWKPVESKW | ISSSCKIIAF | RKALLNPVTS | RQFQRFVALK | GDLLENGLLF |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| WQEVQKYKDL | CHSHCDESVI | QKKITTIINC | FINSSIPPAL | QIDIPVEQAQ | KIIEHRKELG | PYVFREAQMT | IFGVLFKFWP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QFCEFRKNLT | DENIMSVLER | RQEYNKQKKK | LAVLEDEKSG | KDGIKQYANT | SVPAIKTALL | SDSFLGLQPY | GRQPTWCYSK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | | |
| YIEALEQERI | LLKIQEELEK | KLFAGLQPLT | NFKASSSTMS | LKKNMSAHSS | QK | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2902 | 1 | 1192.7378 | 113.29 | 2 | 65.0 | 10.5 | 0 | 172-193 | K.KPPSLPPPATEEDNLASYTQTK.D | |

# Detailed Protein Report

## Protein 714: zinc finger protein 396 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21955239 | **Score:** | 23.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.1 |
| | | **Sequence Coverage [%]:** | 6.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.46 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 5.06 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSAKLGKSSS | LLTQTSEECN | GILTEKMEEE | EQTCDPDSSL | HWSSSYSPET | FRQQFRQFGY | QDSPGPHEAL | SRLWELCHLW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LRPEVHTKEQ | ILELLVLEQF | LAILPKELQA | WVQKHHPENG | EETVTMLEDV | ERELDGPKQI | FFGRRKDMIA | EKLAPSEITE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ELPSSQLMPV | KKQLQGASWE | LQSLRPHDED | IKTTNVKSAS | RQKTSLGIEL | HCNVSNILHM | NGSQSSTYRG | TYEQDGRFEK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RQGNPSWKKQ | QKCDECGKIF | SQSSALILHQ | RIHSGKKPYA | CDECAKAFSR | SAILIQHRRT | HTDSKYEHAI | AEAQKNMYFK |
| 330 | 340 | | | | | | |
| TRLKCPRSLS | GGR | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1165 | 1 | 583.7409 | -46.79 | 2 | 44.7 | 11.0 | 2 | 249-258 | K.KQQKCDECGK.I | | QU:MU 0.46<br>WUP:QUP 5.06 |

# Detailed Protein Report

## Protein 715: PREDICTED: uncharacterized protein C3orf17 isoform X4 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|530374250 | **Score:** | 23.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.6 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKVLGACKLL | LRLLDCCCKT | FLLTVKHLGL | QEFIILNLVM | VGLVSRLWVL | YKGVLKRLIL | LYEPLFGLLQ | EVARIQPMPY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FKDFTFPSDI | TEFLGQPYFE | AFKKKMPIAF | AAKGINKLLN | KLFLINEQSP | RASEETLLGI | SKKAKQMKIN | VQNNVDLGQP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VKNKRVFKEE | SSEFDVRAFC | NQLKHKATQE | TSFDFKCSQS | RLKTTKYSSQ | KVIGTPHAKS | FVQRFREAES | FTQLSEEIQM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AVVWCRSKKL | KAQAIFLGNK | LLKSNRLKHL | EAQGTSLPKK | LECIKTSICN | HLLRGSGIKT | SKHHLRQRRS | QNKFLRRQRK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PQRKLQSTLL | REIQQFSQGT | RKSATDTSAK | WRLSHCTVHR | TDLYPNSKQL | LNSGVSMPVI | QTKEKMIHEN | LRGIHENETD |
| 410 | 420 | 430 | 440 |  |  |  |  |
| SWTVMQINKN | STSGTIKETD | DIDDIFALMG | V |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2818 | 1 | 732.4805 | 137.02 | 2 | 65.7 | 10.2 | 1 | 9-19 | K.LLLRLLDCCCK.T | Carbamidomethyl: 8, 9, 10 |

# Detailed Protein Report

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**Protein 716:** **dystrotelin [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|157364926 | **Score:** | 23.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 65.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.5 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MDPDKQDALN SIENSIYRTA FKLQSVQTLC QLDLIDSSLI QQVLLRPSFW EARKHSLSVQ QLSQALQELF QKAREENPGQ
        90        100        110        120        130        140        150        160
VHPRAPELTL SLLTTMYNSK GTGFLQLMPA AAALITLSGD SPLSKYRALF QLYAENSRGG YDSGPRMTRR VLRKLLTDLQ
       170        180        190        200        210        220        230        240
QIPTFVGESR ALCPVESATR SCFQGVLSPA IKEEKFLSWV QSEPPILLWL PTCHRLSAAE RVTHPARCTL CRTFPITGLR
       250        260        270        280        290        300        310        320
YRCLKCLNFD ICQMCFLSGL HSKSHQKSHP VIEHCIQMSA MQNTKLLFRT LRNNLLQGRC RKKEAARRQQ LLDQVNPKGV
       330        340        350        360        370        380        390        400
PHHAQARLLK KQLNQYKDKL QAIYTSQEER ICRFETRIHK LKTNQDSLWT KLQQIRRDLQ ARLQPPGPSS SSFQNVGNKV
       410        420        430        440        450        460        470        480
DHSSTEKVPK GGDYLQIKNA TEDASTGEPL PKLDEVDRSH RSHTNAEHAL RNPESPETTL HSTRAQSQTQ KMPQKVISAL
       490        500        510        520        530        540        550        560
PSYQEGLKQD IPKMVPAEMS SPALAAVEKK EAGNIKERKD ELEEEELQEL LSKLMDAFNL ETPSGPESSV NMDLYSGAQR
       570        580
VCRAFSALVD QIALPNLK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 268 | 1 | 549.5949 | -25.82 | 3 | 33.0 | 13.5 | 0 | 494-509 | K.MVPAEMSSPALAAVEK.K | Oxidation: 1 |

# Detailed Protein Report

## Protein 717: DNA topoisomerase 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|11225260 | **Score:** | 23.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 90.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSGDHLHNDS | QIEADFRLND | SHKHKDKHKD | REHRHKEHKK | EKDREKSKHS | NSEHKDSEKK | HKEKEKTKHK | DGSSEKHKDK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HKDRDKEKRK | EEKVRASGDA | KIKKEKENGF | SSPPQIKDEP | EDDGYFVPPK | EDIKPLKRPR | DEDDADYKPK | KIKTEDTKKE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KKRKLEEEED | GKLKKPKNKD | KDKKVPEPDN | KKKKPKKEEE | QKWKWWEEER | YPEGIKWKFL | EHKGPVFAPP | YEPLPENVKF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YYDGKVMKLS | PKAEEVATFF | AKMLDHEYTT | KEIFRKNFFK | DWRKEMTNEE | KNIITNLSKC | DFTQMSQYFK | AQTEARKQMS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KEEKLKIKEE | NEKLLKEYGF | CIMDNHKERI | ANFKIEPPGL | FRGRGNHPKM | GMLKRRIMPE | DIIINCSKDA | KVPSPPPGHK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| WKEVRHDNKV | TWLVSWTENI | QGSIKYIMLN | PSSRIKGEKD | WQKYETARRL | KKCVDKIRNQ | YREDWKSKEM | KVRQRAVALY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FIDKLALRAG | NEKEEGETAD | TVGCCSLRVE | HINLHPELDG | QEYVVEFDFL | GKDSIRYYNK | VPVEKRVFKN | LQLFMENKQP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EDDLFDRLNT | GILNKHLQDL | MEGLTAKVFR | TYNASITLQQ | QLKELTAPDE | NIPAKILSYN | RANRAVAILC | NHQRAPPKTF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EKSMMNLQTK | IDAKKEQLAD | ARRDLKSAKA | DAKVMKDAKT | KKVVESKKKA | VQRLEEQLMK | LEVQATDREE | NKQIALGTSK |
| 730 | 740 | 750 | 760 | 770 | | | |
| LNYLDPRITV | AWCKKWGVPI | EKIYNKTQRE | KFAWAIDMAD | EDYEF | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1827 | 1 | 590.7884 | 2.35 | 2 | 53.2 | 13.5 | 2 | 463-471 | R.EDWKSKEMK.V | |
| 2688 | 1 | 484.7720 | 85.41 | 2 | 62.0 | 10.3 | 0 | 643-650 | K.SMMNLQTK.I | Oxidation: 2 |

# Detailed Protein Report

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## Protein 718: poly [ADP-ribose] polymerase 8 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|295844832 | **Score:** | 23.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 91.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 2.10 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGMCSRQERI | QKDIDVVIQK | SRAEKDCLFA | DFRYSDSTFT | FTYVGGPRSV | SYSVHVSEDY | PDNTYVSSSE | NDEDVLVTTE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PIPVIFHRIA | TELRKTNDIN | CCLSIKSKLQ | KENGEESRQN | STVEEDSEGD | NDSEEFYYGG | QVNYDGELHK | HPQLEADLSA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VREIYGPHAV | SLREYGAIDD | VDIDLHIDVS | FLDEEIAVAW | EVIRTEPIIV | RLHCSLTQYL | NGPVPTVDVF | QISTKERFGL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GHQLKKIMQT | FVTQQWKQSK | EKSNCLHNKK | LSEKKVKSPL | HLFSTLRRSP | SYPPPGCGKS | KSKLKSEQDG | ISKTHKLLRR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TCSSTVKTDD | VCVTKSHRTF | GRSLSSDPRA | EQAMTAIKSH | KLLNRPCPAA | VKSEECLTLK | SHRLLTRSCS | GDPRCEHNTN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LKPHKLLSRS | YSSNLRMEEL | YGLKNHKLLS | KSYSSAPKSS | KTELFKEPNA | EGRRLSLTSG | LIGILTPSSS | SSSQLAPNGA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KCIPVRDRGF | LVQTIEFAEQ | RIPVLNEYCV | VCDEPHVFQN | GPMLRPTVCE | RELCVFAFQT | LGVMNEAADE | IATGAQKKNY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DRVMKALDSI | TSIREMTQAP | YLEIKKQMDK | QDPLAHPLLQ | WVISSNRSHI | VKLPVNRQLK | FMHTPHQFLL | LSSPPAKESN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FRAAKKLFGS | TFAFHGSHIE | NWHSILRNGL | VVASNTRLQL | HGAMYGSGIY | LSPMSSISFG | YSGMNKKQKV | SAKDEPASSS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KSSNTSQSQK | KGQQSQFLQS | RNLKCIALCE | VITSSDLHKH | GEIWVVPNTD | HVCTRFFFVY | EDGQVGDANI | NTQEGGIHKE |
| 810 | 820 | | | | | | |
| ILRVIGNQTA | TG | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1355 | 1 | 719.8571 | 2.88 | 2 | 45.3 | 12.6 | 1 | 96-108 | K.TNDINCCLSIKSK.L | | WUP:QUP 2.10 |

# Detailed Protein Report

## Protein 719: histone-lysine N-methyltransferase 2C [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|91718902 | **Score:** | 23.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 541.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 0.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSEEDKSVE | QPQPPPPPPE | EPGAPAPSPA | AADKRPRGRP | RKDGASPFQR | ARKKPRSRGK | TAVEDEDSMD | GLETTETETI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VETEIKEQSA | EEDAEAEVDN | SKQLIPTLQR | SVSEESANSL | VSVGVEAKIS | EQLCAFCYCG | EKSSLGQGDL | KQFRITPGFI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LPWRNQPSNK | KDIDDNSNGT | YEKMQNSAPR | KQRGQRKERS | PQQNIVSCVS | VSTQTASDDQ | AGKLWDELSL | VGLPDAIDIQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ALFDSTGTCW | AHHRCVEWSL | GVCQMEEPLL | VNVDKAVVSG | STERCAFCKH | LGATIKCCEE | KCTQMYHYPC | AAGAGTFQDF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SHIFLLCPEH | IDQAPERSKE | DANCAVCDSP | GDLLDQFFCT | TCGQHYHGMC | LDIAVTPLKR | AGWQCPECKV | CQNCKQSGED |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SKMLVCDTCD | KGYHTFCLQP | VMKSVPTNGW | KCKNCRICIE | CGTRSSSQWH | HNCLICDNCY | QQQDNLCPFC | GKCYHPELQK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DMLHCNMCKR | WVHLECDKPT | DHELDTQLKE | EYICMYCKHL | GAEMDRLQPG | EEVEIAELTT | DYNNEMEVEG | PEDQMVFSEQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AANKDVNGQE | STPGIVPDAV | QVHTEEQQKS | HPSESLDTDS | LLIAVSSQHT | VNTELEKQIS | NEVDSEDLKM | SSEVKHICGE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DQIEDKMEVT | ENIEVVTHQI | TVQQEQLQLL | EEPETVVSRE | ESRPPKLVME | SVTLPLETLV | SPHEESISLC | PEEQLVIERL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QGEKEQKENS | ELSTGLMDSE | MTPTIEGCVK | DVSYQGGKSI | KLSSETESSF | SSSADISKAD | VSSSPTPSSD | LPSHDMLHNY |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PSALSSSAGN | IMPTTYISVT | PKIGMGKPAI | TKRKFSPGRP | RSKQGAWSTH | NTVSPPSWSP | DISEGREIFK | PRQLPGSAIW |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SIKVGRGSGF | PGKRRPRGAG | LSGRGGRGRS | KLKSGIGAVV | LPGVSTADIS | SNKDDEENSM | HNTVVLFSSS | DKFTLNQDMC |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VVCGSFGQGA | EGRLLACSQC | GQCYHPYCVS | IKITKVVLSK | GWRCLECTVC | EACGKATDPG | RLLLCDDCDI | SYHTYCLDPP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LQTVPKGGWK | CKWCVWCRHC | GATSAGLRCE | WQNNYTQCAP | CASLSSCPVC | YRNYREEDLI | LQCRQCDRWM | HAVCQNLNTE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EEVENVADIG | FDCSMCRPYM | PASNVPSSDC | CESSLVAQIV | TKVKELDPPK | TYTQDGVCLT | ESGMTQLQSL | TVTVPRRKRS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KPKLKLKIIN | QNSVAVLQTP | PDIQSEHSRD | GEMDDSREGE | LMDCDGKSES | SPEREAVDDE | TKGVEGTDGV | KKRKRKPYRP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| GIGGFMVRQR | SRTGQGKTKR | SVIRKDSSGS | ISEQLPCRDD | GWSEQLPDTL | VDESVSVTES | TEKIKKRYRK | RKNKLEETFP |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| AYLQEAFFGK | DLLDTSRQSK | ISLDNLSEDG | AQLLYKTNMN | TGFLDPSLDP | LLSSSSAPTK | SGTHGPADDP | LADISEVLNT |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DDDILGIISD | DLAKSVDHSD | IGPVTDDPSS | LPQPNVNQSS | RPLSEEQLDG | ILSPELDKMV | TDGAILGKLY | KIPELGGKDV |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| EDLFTAVLSP | ANTQPTPLPQ | PPPPTQLLPI | HNQDAFSRMP | LMNGLIGSSP | HLPHNSLPPG | SGLGTFSAIA | QSSYPDARDK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| NSAFNPMASD | PNNSWTSSAP | TVEGENDTMS | NAQRSTLKWE | KEEALGEMAT | VAPVLYTNIN | FPNLKEEFPD | WTTRVKQIAK |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LWRKASSQER | APYVQKARDN | RAALRINKVQ | MSNDSMKRQQ | QQDSIDPSSR | IDSELFKDPL | KQRESEHEQE | WKFRQQMRQK |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| SKQQAKIEAT | QKLEQVKNEQ | QQQQQQQFGS | QHLLVQSGSD | TPSSGIQSPL | TPQPGNGNMS | PAQSFHKELF | TKQPPSTPTS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| TSSDDVFVKP | QAPPPPPAPS | RIPIQDSLSQ | AQTSQPPSPQ | VFSPGSSNSR | PPSPMDPYAK | MVGTPRPPPV | GHSFSRRNSA |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| APVENCTPLS | SVSRPLQMNE | TTANRPSPVR | DLCSSSTTNN | DPYAKPPDTP | RPVMTDQFPK | SLGLSRSPVV | SEQTAKGPIA |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| AGTSDHFTKP | SPRADVFQRQ | RIPDSYARPL | LTPAPLDSGP | GPFKTPMQPP | PSSQDPYGSV | SQASRRLSVD | PYERPALTPR |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| PIDNFSHNQS | NDPYSQPPLT | PHPAVNESFA | HPSRAFSQPG | TISRPTSQDP | YSQPPGTPRP | VVDSYSQSSG | TARSNTDPYS |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 132 | 1 | 846.0298 | -52.12 | 3 | 31.6 | 13.7 | 1 | 4823-4845 | R.GVYMFRMDNDHVIDATLTGGPAR.Y | |

# Detailed Protein Report

**Protein 720:** **PREDICTED: TFIIH basal transcription factor complex helicase XPB subunit isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530369093 | **Score:** | 23.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 81.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.9 |
| | | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MPLKDDHTSR PLWVAPDGHI FLEAFSPVYK YAQDFLVAIA EPVCRPTHVH EYKLTAYSLY AAVSVGLQTS DITEYLRKLS

        90        100        110        120        130        140        150        160
KTGVPDGIMQ FIKLCTVSYG KVKLVLKHNR YFVESCHPDV IQHLLQDPVI RECRLRNSEG EATELITETF TSKSAISKTA

       170        180        190        200        210        220        230        240
ESSGGPSTSR VTDPQGKSDI PMDLFDFYEQ MDKDEEEEEE TQTVSFEVKQ EMIEELQKRC IHLEYPLLAE YDFRNDSVNP

       250        260        270        280        290        300        310        320
DINIDLKPTA VLRPYQEKSL RKMFGNGRAR SGVIVLPCGA GKSLVGVTAA CTVRKRCLVL GNSAVSVEQW KAQFKMWSTI

       330        340        350        360        370        380        390        400
DDSQICRFTS DAKDKPIGCS VAISTYSMLG HTTKRSWEAE RVMEWLKTQE WGLMILDEVH TIPAKMFRRV LTIVQAHCKL

       410        420        430        440        450        460        470        480
GLTATLVRED DKIVDLNFLI GPKLYEANWM ELQNNGYIAK VQCAEVWCPM SPEFYREYVA IKTKKRILLY TMNPNKFRAC

       490        500        510        520        530        540        550        560
QFLIKFHERR NDKIIVFADN VFALKEYAIR LNKPYIYGPT SQGERMQILQ NFKHNPKINT IFISKVGDTS FDLPEANVLI

       570        580        590        600        610        620        630        640
QISSHGGSRR QEAQRLGRVL RAKKGMVAEE YNAFFYSLVS QDTQEMAYST KRQRFLVDQG YSFKVITKLA GMEEEDLAFS

       650        660        670        680        690        700        710        720
TKEEQQQLLQ KVLAATDLDA EEEVVAGEFG SRSSQASRRF GTMSSMSGAD DTVYMEYHSS RSKAPSKHVH PLFKRFRK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 96 | 1 | 822.4073 | -35.25 | 2 | 30.1 | 11.8 | 2 | 612-624 | K.RQRFLVDQGYSFK.V | |

# Detailed Protein Report

## Protein 721: alpha-amylase 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|40254482 | **Score:** | 23.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| | | **Sequence Coverage [%]:** | 6.8 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578798954 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: alpha-amylase 1 isoform X3 [Homo sapiens] |
| gi\|578798952 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: alpha-amylase 1 isoform X3 [Homo sapiens] |
| gi\|578798950 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: alpha-amylase 1 isoform X2 [Homo sapiens] |
| gi\|530362403 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: alpha-amylase 1 isoform X2 [Homo sapiens] |
| gi\|530362397 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: alpha-amylase 1 isoform X2 [Homo sapiens] |
| gi\|530362391 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: alpha-amylase 1 isoform X1 [Homo sapiens] |
| gi\|56549664 | refseq_human(refseq_human_20140103.fasta) | alpha-amylase 1 precursor [Homo sapiens] |
| gi\|56549662 | refseq_human(refseq_human_20140103.fasta) | alpha-amylase 1 precursor [Homo sapiens] |
| gi\|56549660 | refseq_human(refseq_human_20140103.fasta) | alpha-amylase 1 precursor [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKLFWLLFTI | GFCWAQYSSN | TQQGRTSIVH | LFEWRWVDIA | LECERYLAPK | GFGGVQVSPP | NENVAIHNPF | RPWWERYQPV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SYKLCTRSGN | EDEFRNMVTR | CNNVGVRIYV | DAVINHMCGN | AVSAGTSSTC | GSYFNPGSRD | FPAVPYSGWD | FNDGKCKTGS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GDIENYNDAT | QVRDCRLSGL | LDLALGKDYV | RSKIAEYMNH | LIDIGVAGFR | IDASKHMWPG | DIKAILDKLH | NLNSNWFPEG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SKPFIYQEVI | DLGGEPIKSS | DYFGNGRVTE | FKYGAKLGTV | IRKWNGEKMS | YLKNWGEGWG | FMPSDRALVF | VDNHDNQRGH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GAGGASILTF | WDARLYKMAV | GFMLAHPYGF | TRVMSSYRWP | RYFENGKDVN | DWVGPPNDNG | VTKEVTINPD | TTCGNDWVCE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HRWRQIRNMV | NFRNVVDGQP | FTNWYDNGSN | QVAFGRGNRG | FIVFNNDDWT | FSLTLQTGLP | AGTYCDVISG | DKINGNCTGI |
| 490 | 500 | 510 | 520 | | | | |
| KIYVSDDGKA | HFSISNSAED | PFIAIHAESK | L | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1297 | 1 | 863.8565 | -56.34 | 2 | 45.8 | 11.6 | 0 | 368-383 | K.DVNDWVGPPNDNGVTK.E | |

# Detailed Protein Report

## Protein 722: PREDICTED: zinc finger protein DZIP1 isoform X7 [Homo sapiens]

**Accession:** gi|578825198
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 23.7
**MW [kDa]:** 70.2
**pI:** 6.0
**Sequence Coverage [%]:** 3.4
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQKTKEEDFL | KLFDRWKEEE | KEKLVDEMEK | VKEMFMKEFK | ELTSKNSALE | YQLSEIQKSN | MQIKSNIGTL | KDAHEFKEDR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SPYPQDFHNV | MQLLDSQESK | WTARVQAIHQ | EHKKEKGRLL | SHIEKLRTSM | IDDLNASNVF | YKKRIEELGQ | RLQEQNELII |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TQRQQIKDFT | CNPLNSISEP | KGNPLAWQAF | ESQPAAPAVP | MNAPALHTLE | TKSSLPMVHE | QAFSSHILEP | IEELSEEEKG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RENEQKLNNN | KMHLRKALKS | NSSLTKGLRT | MVEQNLMEKL | ETLGINADIR | GISSDQLHRV | LKSVESERHK | QEREIPNFHQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IREFLEHQVS | CKIEEKALLS | SDQCSVSQMD | TLSTGEVPKM | IQLPSKNRQL | IRQKAVSTDR | TSVPKIKKNV | MEDPFPRKSS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TITTPPFSSE | EEQEDDDLIR | AYASPGPLPV | PPPQNKGSFG | KNTVKSDADG | TEGSEIEDTD | DSPKPAGVAV | KTPTEKVEKM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FPHRKNVNKP | VGGTNVPEMF | IKKEELQELK | CADVEDEDWD | ISSLEEEISL | GKKSGKEQKE | PPPAKNEPHF | AHVLNAWGAF |
| 570 | 580 | 590 | 600 | 610 | 620 | | |
| NPKGPKGEGL | LLSPLIQARS | IFLLVVFHLY | KYLINLCWYI | IRQKSCQCFL | YVI | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2012 | 1 | 616.7504 | -93.75 | 2 | 55.5 | 10.3 | 1 | 389-398 | K.NVMEDPFPRK.S | |

# Detailed Protein Report

## Protein 723: zinc finger protein 483 isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|190014620 | **Score:** | 23.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 85.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.6 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MQAVVPLNKM | TAISPEPQTL | ASTEQNEVPR | VVTSGEQEAI | LRGNAADAES | FRQRFRWFCY | SEVAGPRKAL | SQLWELCNQW |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| LRPDIHTKEQ | ILELLVFEQF | LTILPGEIRI | WVKSQHPESS | EEVVTLIEDL | TQMLEEKDPV | SQDSTVSQEE | NSKEDKMVTV |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| CPNTESCESI | TLKDVAVNFS | RGEWKKLEPF | QKELYKEVLL | ENLRNLEFLD | FPVSKLELIS | QLKWVELPWL | LEEVSKSSRL |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| DESALDKIIE | RCLRDDDHGL | MEESQQYCGS | SEEDHGNQGN | SKGRVAQNKT | LGSGSRGKKF | DPDKSPFGHN | FKETSDLIKH |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| LRVYLRKKSR | RYNESKKPFS | FHSDLVLNRK | EKTAGEKSRK | SNDGGKVLSH | SSALTEHQKR | QKIHLGDRSQ | KCSKCGIIFI |
| **410** | **420** | **430** | **440** | **450** | **460** | **470** | **480** |
| RRSTLSRRKT | PMCEKCRKDS | CQEAALNKDE | GNESGEKTHK | CSKCGKAFGY | SASLTKHRRI | HTGEKPYMCN | ECGKAFSDSS |
| **490** | **500** | **510** | **520** | **530** | **540** | **550** | **560** |
| SLTPHHRTHS | GEKPFKCDDC | GKGFTLSAHL | IKHQRIHTGE | KPYKCKDCGR | PFSDSSSLIQ | HQRIHTGEKP | YTCSNCGKSF |
| **570** | **580** | **590** | **600** | **610** | **620** | **630** | **640** |
| SHSSSLSKHQ | RIHTGEKPYK | CGECGKAFRQ | NSCLTRHQRI | HTGEKPYLCN | DCGMTFSHFT | SVIYHQRLHS | GEKPYKCNQC |
| **650** | **660** | **670** | **680** | **690** | **700** | **710** | **720** |
| EKAFPTHSLL | SRHQRIHTGV | KPYKCKECGK | SFSQSSSLNE | HHRIHTGEKP | YECNYCGATF | SRSSILVEHL | KIHTGRREYE |
| **730** | **740** | **750** | | | | | |
| CNECEKTFKS | NSGLIRHRGF | HSAE | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 266 | 1 | 1318.5931 | -74.95 | 2 | 33.3 | 12.9 | 1 | 68-88 | R.KALSQLWELCNQWLRPDIHTK.E | Carbamidomethyl: 10 |
| 2671 | 2 | 741.8482 | -69.33 | 2 | 63.5 | 10.8 | 2 | 389-401 | R.SQKCSKCGIIFIR.R | |

# Detailed Protein Report

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## Protein 724: ataxin-1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|51479158 | **Score:** | 23.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 86.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| | | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|189491748 | refseq_human (refseq_human_20140103.fasta) | ataxin-1 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MKSNQERSNE CLPPKKREIP ATSRSSEEKA PTLPSDNHRV EGTAWLPGNP GGRGHGGGRH GPAGTSVELG LQQGIGLHKA

        90        100        110        120        130        140        150        160
LSTGLDYSPP SAPRSVPVAT TLPAAYATPQ PGTPVSPVQY AHLPHTFQFI GSSQYSGTYA SFIPSQLIPP TANPVTSAVA

       170        180        190        200        210        220        230        240
SAAGATTPSQ RSQLEAYSTL LANMGSLSQT PGHKAEQQQQ QQQQQQQQHQ HQQQQQQQQQ QQQQQHLSRA PGLITPGSPP

       250        260        270        280        290        300        310        320
PAQQNQYVHI SSSPQNTGRT ASPPAIPVHL HPHQTMIPHT LTLGPPSQVV MQYADSGSHF VPREATKKAE SSRLQQAIQA

       330        340        350        360        370        380        390        400
KEVLNGEMEK SRRYGAPSSA DLGLGKAGGK SVPHPYESRH VVVHPSPSDY SSRDPSGVRA SVMVLPNSNT PAADLEVQQA

       410        420        430        440        450        460        470        480
THREASPSTL NDKSGLHLGK PGHRSYALSP HTVIQTTHSA SEPLPVGLPA TAFYAGTQPP VIGYLSGQQQ AITYAGSLPQ

       490        500        510        520        530        540        550        560
HLVIPGTQPL LIPVGSTDME ASGAAPAIVT SSPQFAAVPH TFVTTALPKS ENFNPEALVT QAAYPAMVQA QIHLPVVQSV

       570        580        590        600        610        620        630        640
ASPAAAPPTL PPYFMKGSII QLANGELKKV EDLKTEDFIQ SAEISNDLKI DSSTVERIED SHSPGVAVIQ FAVGEHRAQV

       650        660        670        680        690        700        710        720
SVEVLVEYPF FVFGQGWSSC CPERTSQLFD LPCSKLSVGD VCISLTLKNL KNGSVKKGQP VDPASVLLKH SKADGLAGSR

       730        740        750        760        770        780        790        800
HRYAEQENGI NQGSAQMLSE NGELKFPEKM GLPAAPFLTK IEPSKPAATR KRRWSAPESR KLEKSEDEPP LTLPKPSLIP

       810        820
QEVKICIEGR SNVGK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1037 | 3 | 612.4575 | 170.02 | 2 | 42.5 | 13.3 | 0 | 698-709 | K.GQPVDPASVLLK.H | |
| 1970 | 1 | 696.2657 | -144.31 | 2 | 54.5 | 10.5 | 2 | 710-722 | K.HSKADGLAGSRHR.Y | |

# Detailed Protein Report

## Protein 725: 60S ribosomal protein L23a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|17105394 | **Score:** | 23.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 17.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.9 |
| | | **Sequence Coverage [%]:** | 17.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAPKAKKEAP | APPKAEAKAK | ALKAKKAVLK | GVHSHKKKKI | RTSPTFRRPK | TLRLRRQPKY | PRKSAPRRNK | LDHYAIIKFP |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| LTTESAMKKI | EDNNTLVFIV | DVKANKHQIK | QAVKKLYDID | VAKVNTLIRP | DGEKKAYVRL | APDYDALDVA | NKIGII |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2608 | 1 | 974.3100 | -249.41 | 1 | 60.9 | 10.8 | 2 | 60-67 | K.YPRKSAPR.R | |

# Detailed Protein Report

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## Protein 726: PREDICTED: brain-specific angiogenesis inhibitor 3 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578812890 | **Score:** | 23.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 168.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.43 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.34 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKAVRNLLIY | IFSTYLLVMF | GFNAAQDFWC | STLVKGVIYG | SYSVSEMFPK | NFTNCTWTLE | NPDPTKYSIY | LKFSKKDLSC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SNFSLLAYQF | DHFSHEKIKD | LLRKNHSIMQ | LCNSKNAFVF | LQYDKNFIQI | RRVFPTNFPG | LQKKGEEDQK | SFFEFLVLNK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VSPSQFGCHV | LCTWLESCLK | SENGRTESCG | IMYTKCTCPQ | HLGEWGIDDQ | SLILLNNVVL | PLNEQTEGCL | TQELQTTQVC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NLTREAKRPP | KEEFGMMGDH | TIKSQRPRSV | HEKRVPQEQA | DAAKFMAQTG | ESGVEEWSQW | STCSVTCGQG | SQVRTRTCVS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PYGTHCSGPL | RESRVCNNTA | LCPVHGVWEE | WSPWSLCSFT | CGRGQRTRTR | SCTPPQYGGR | PCEGPETHHK | PCNIALCPVD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GQWQEWSSWS | QCSVTCSNGT | QQRSRQCTAA | AHGGSECRGP | WAESRECYNP | ECTANGQWNQ | WGHWSGCSKS | CDGGWERRIR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TCQGAVITGQ | QCEGTGEEVR | RCNEQRCPAP | YEICPEDYLM | SMVWKRTPAG | DLAFNQCPLN | ATGTTSRRCS | LSLHGVAFWE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QPSFARCISN | EYRHLQHSIK | EHLAKGQRML | AGDGMSQVTK | TLLDLTQRKN | FYAGDLLMSV | EILRNVTDTF | KRASYIPASD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GVQNFFQIVS | NLLDEENKEK | WEDAQQIYPG | SIELMQVIED | FIHIVGMGMM | DFQNSYLMTG | NVVASIQKLP | AASVLTDINF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PMKGRKGMVD | WARNSEDRVV | IPKSIFTPVS | SKELDESSVF | VLGAVLYKNL | DLILPTLRNY | TVINSKIIVV | TIRPEPKTTD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SFLEIELAHL | ANGTLNPYCV | LWDDSKTNES | LGTWSTQGCK | TVLTDASHTK | CLCDRLSTFA | ILAQQPREII | MESSGTPSVT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LIVGSGLSCL | ALITLAVVYA | ALWRYIRSER | SIILINFCLS | IISSNILILV | GQTQTHNKSI | CTTTTAFLHF | FFLASFCWVL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TEAWQSYMAV | TGKIRTRLIR | KRFLCLGWGL | PALVVATSVG | FTRTKGYGTD | HYCWLSLEGG | LLYAFVGPAA | AVVLVNMVIG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ILVFNKLVSR | DGILDKKLKH | RAGASLWSSC | VVLPLLALTW | MSAVLAMTDK | RSILFQILFA | VFDSLQGFVI | VMVHCILRRE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| VQDAFRCRLR | NCQDPINADS | SSSFPNGHAQ | IMTDFEKDVD | IACRSVLHKD | IGPCRAATIT | GTLSRISLND | DEEEKGTNPE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| GLSYSTLPGN | VISKVIIQQP | TGLHMPMSMN | ELSNPCLKKE | NSELRRTVYL | CTDDNLRGAD | MDIVHPQERM | MESDYIVMPR |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SSVNNQPSMK | EESKMNIGME | TLPHERLLHY | KVNPEFNMNP | PVMDQFNMNL | EQHLAPQEHM | QNLPFEPRTA | VKNFMASELD |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| DNAGLSRSET | GSTISMSSLE | RRKSRYSDLD | FEKVMHTRKR | HMELFQELNQ | KFQTLDRFRD | IPNTSSMENP | APNKNPWDTF |
| 1450 | 1460 | 1470 | 1480 | 1490 | | | |
| KNPSEYPHYT | TINVLDTEAK | DALELRPAEW | EKCLNLPLDV | QEGDFQTEV | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1939 | 1 | 917.8148 | -134.17 | 2 | 54.6 | 10.2 | 1 | 315-331 | R.TRTCVSPYGTHCSGPLR.E | | |
| 1881 | 2 | 590.7746 | -9.21 | 2 | 53.4 | 13.5 | 1 | 1120-1128 | R.EVQDAFRCR.L | Carbamidomethyl: 8 | QU:MU 0.43<br>WUP:QUP 2.34 |

# Detailed Protein Report

## Protein 727: PREDICTED: multimerin-1 isoform X1 [Homo sapiens]

**Accession:** gi|530377406
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 23.7
**MW [kDa]:** 134.3
**pI:** 9.2
**Sequence Coverage [%]:** 2.7
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKGARLFVLL | SSLWSGGIGL | NNSKHSWTIP | EDGNSQKTMP | SASVPPNKIQ | SLQILPTTRV | MSAEIATTPE | ARTSEDSLLK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| STLPPSETSA | PAEGVRNQTL | TSTEKAEGVV | KLQNLTLPTN | ASIKFNPGAE | SVVLSNSTLK | FLQSFARKSN | EQATSLNTVG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GTGGIGGVGG | TGGVGNRAPR | ETYLSRGDSS | SSQRTDYQKS | NFETTRGKNW | CAYVHTRLSP | TVILDNQVTY | VPGGKGPCGW |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TGGSCPQRSQ | KISNPVYRMQ | HKIVTSLDWR | CCPGYSGPKC | QLREVMQKMT | DQVNYQAMKL | TLLQKKIDNI | SLTVNDVRNT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YSSLEGKVSE | DKSREFQSLL | KGLKSKSINV | LIRDIVREQF | KIFQNDMQET | VAQLFKTVSS | LSEDLESTRQ | IIQKVNESVV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SIAAQQKFVL | VQENRPTLTD | IVELRNHIVN | VRQEMTLTCE | KPIKELEVKQ | THLEGALEQE | HSRSILYYES | LNKTLSKLKE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VHEQLLSTEQ | VSDQKNAPAA | ESVSNNVTEY | MSTLHENIKK | QSLMMLQMFE | DLHIQESKIN | NLTVSLEMEK | ESLRGECEDM |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LSKCRNDFKF | QLKDTEENLH | VLNQTLAEVL | FPMDNKMDKM | SEQLNDLTYD | MEILQPLLEQ | GASLRQTMTY | EQPKEAIVIR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KKIENLTSAV | NSLNFIIKEL | TKRHNLLRNE | VQGRDDALER | RINEYALEME | DGLNKTMTII | NNAIDFIQDN | YALKETLSTI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KDNSEIHHKC | TSDMETILTF | IPQFHRLNDS | IQTLVNDNQR | YNFVLQVAKT | LAGIPRDEKL | NQSNFQKMYQ | MFNETTSQVR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KYQQNMSHLE | EKLLLTTKIS | KNFETRLQDI | ESKVTQTLIP | YYISVKKGSV | VTNERDQALQ | LQVLNSRFKA | LEAKSIHLSI |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| NFFSLNKTLH | EVLTMCHNAS | TSVSELNATI | PKWIKHSLPD | IQLLQKGLTE | FVEPIIQIKT | QAALSNLTCC | IDRSLPGSLA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NVVKSQKQVK | SLPKKINALK | KPTVNLTTVL | IGRTQRNTDN | IIYPEEYSSC | SRHPCQNGGT | CINGRTSFTC | ACRHPFTGDN |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| CTIKLVEENA | LAPDFSKGSY | RYAPMVAFFA | SHTYGMTIPG | PILFNNLDVN | YGASYTPRTG | KFRIPYLGVY | VFKYTIESFS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| AHISGFLVVD | GIDKLAFESE | NINSEIHCDR | VLTGDALLEL | NYGQEVWLRL | AKGTIPAKFP | PVTTFSGYLL | YRT |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1058 | 1 | 974.4611 | 39.05 | 2 | 41.5 | 12.5 | 0 | 997-1012 | R.NTDNIIYPEEYSSCSR.H | Carbamidomethyl: 14 |

# Detailed Protein Report

## Protein 728: protein FAM160A1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|158341646 | **Score:** | 23.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 116.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530378111 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein FAM160A1 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMSSVSTESK | LQQAVSLQGV | DPETCMIVFK | NHWAQVVKIL | EKHDPLKNTQ | AKYGSIPPDE | ASAVQNYVEH | MLFLLIEEQA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KDAAMGPILE | FVVSENIMEK | LFLWSLRREF | TDETKIEQLK | MYEMLVTQSH | QPLLHHKPIL | KPLMMLLSSC | SGTTTPTVEE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KLVVLLNQLC | SILAKDPSIL | ELFFHTSEDQ | GAANFLIFSL | LIPFIHREGS | VGQQARDALL | FIMSLSAENT | MVAHHIVENT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YFCPVLATGL | SGLYSSLPTK | LEEKGEEWHC | LLKDDWLLLP | SLVQFMNSLE | FCNAVIQVAH | PLIRNQLVNY | IYNGFLVPVL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| APALHKVTVE | EVMTTTAYLD | LFLRSISEPA | LLEIFLRFIL | LHQHENVHIL | DTLTSRINTP | FRLCVVSLAL | FRTLIGLHCE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DVMLQLVLRY | LIPCNHMMLS | QRWAVKERDC | YSVSAAKLLA | LTPVCCSSGI | TLTLGNQERD | YILWSKCMHD | TSGPVERPFP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EAFSESACIV | EYGKALDISY | LQYLWEAHTN | ILRCMRDCRV | WSALYDGDSP | DPEMFLQSLT | EEGSVSSACP | VFGLPQQLPR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KTGPQLAPRK | DKSQTELEWD | DSYDTGISSG | ADVGSPGPYD | DLEVSGPPAP | IDPPKHIQEM | KKNALLLFKG | SYIEESDFQD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DVMVYRLCAE | KDSEDMKDSQ | EEAARPPAEA | QAEVQSVPIN | NGPLLSTQPE | TDSEEEWNRD | NSDPFHSEPK | EPKQEREPEA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| APESNSELAS | PAPEAEHSSN | LTAAHPESEE | LIAQYDQIIK | ELDSGAEGLM | EQNYPTPDPL | LLTKEEEGKE | ESKGEKEKEG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KKELEDEEDD | FDSFIAEMPA | VETVPSPFVG | RDEAAFASRH | PVRTQSTPFT | GPFISVVLSK | LENMLENSLH | VNLLLIGIIT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QLASYPQPLL | RSFLLNTNMV | FQPSVRSLYQ | VLASVKNKIE | QFASVERDFP | GLLIQAQQYL | LFRVDMSDMT | PAALTKDPIQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| EASRTGSGKN | LLDGPPRVLQ | PFLTHRTKVA | EAPPNLPLPV | RNPMLAAALF | PEFLKELAAL | AQEHSILCYK | ILGDFEDSCC |
| 1050 | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 468 | 1 | 686.9223 | 31.03 | 2 | 35.5 | 11.6 | 0 | 989-1001 | K.VAEAPPNLPLPVR.N | |

# Detailed Protein Report

## Protein 729: brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|25306253 | **Score:** | 23.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 7.7 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|219842314 | refseq_human (refseq_human_20140103.fasta) | brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens] |
| gi\|219842309 | refseq_human (refseq_human_20140103.fasta) | brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens] |
| gi\|219842306 | refseq_human (refseq_human_20140103.fasta) | brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens] |
| gi\|219842303 | refseq_human (refseq_human_20140103.fasta) | brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens] |
| gi\|219842300 | refseq_human (refseq_human_20140103.fasta) | brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens] |
| gi\|219842294 | refseq_human (refseq_human_20140103.fasta) | brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens] |
| gi\|219842292 | refseq_human (refseq_human_20140103.fasta) | brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens] |
| gi\|219842290 | refseq_human (refseq_human_20140103.fasta) | brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens] |
| gi\|219842288 | refseq_human (refseq_human_20140103.fasta) | brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens] |
| gi\|25306267 | refseq_human (refseq_human_20140103.fasta) | brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens] |
| gi\|25306264 | refseq_human (refseq_human_20140103.fasta) | brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens] |
| gi\|25306257 | refseq_human (refseq_human_20140103.fasta) | brain-derived neurotrophic factor isoform a preproprotein [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTILFLTMVI | SYFGCMKAAP | MKEANIRGQG | GLAYPGVRTH | GTLESVNGPK | AGSRGLTSLA | DTFEHVIEEL | LDEDQKVRPN |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| EENNKDADLY | TSRVMLSSQV | PLEPPLLFLL | EEYKNYLDAA | NMSMRVRRHS | DPARRGELSV | CDSISEWVTA | ADKKTAVDMS |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| GGTVTVLEKV | PVSKGQLKQY | FYETKCNPMG | YTKEGCRGID | KRHWNSQCRT | TQSYVRALTM | DSKKRIGWRF | IRIDTSCVCT |
| **250** | | | | | | | |
| LTIKRGR | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2135 | 1 | 1149.9035 | -125.59 | 2 | 56.6 | 23.7 | 2 | 175-193 | K.GQLKQYFYETKCNPMGYTK.E | |

# Detailed Protein Report

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## Protein 730: protein unc-45 homolog A isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|89179321 | **Score:** | 23.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 101.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTASSVEQLR | KEGNELFKCG | DYGGALAAYT | QALGLDATPQ | DQAVLHRNRA | ACHLKLEDYD | KAETEASKAI | EKDGGDVKAL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YRRSQALEKL | GRLDQAVLDL | QRCVSLEPKN | KVFQEALRNI | GGQIQEKVRY | MSSTDAKVEQ | MFQILLDPEE | KGTEKKQKAS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QNLVVLARED | AGAEKIFRSN | GVQLLQRLLD | MGETDLMLAA | LRTLVGICSE | HQSRTVATLS | ILGTRRVVSI | LGVESQAVSL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AACHLLQVMF | DALKEGVKKG | FRGKEGAIIV | DPARELKVLI | SNLLDLLTEV | GVSGQGRDNA | LTLLIKAVPR | KSLKDPNNSL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TLWVIDQGLK | KILEVGGSLQ | DPPGELAVTA | NSRMSASILL | SKLFDDLKCD | AERENFHRLC | ENYIKSWFEG | QGLAGKLRAI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QTVSCLLQGP | CDAGNRALEL | SGVMESVIAL | CASEQEEEQL | VAVEALIHAA | GKAKRASFIT | ANGVSLLKDL | YKCSEKDSIR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IRALVGLCKL | GSAGGTDFSM | KQFAEGSTLK | LAKQCRKWLC | NDQIDAGTRR | WAVEGLAYLT | FDADVKEEFV | EDAAALKALF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QLSRLEERSV | LFAVASALVN | CTNSYDYEEP | DPKMVELAKY | AKQHVPEQHP | KDKPSFVRAR | VKKLLAAGVV | SAMVCMVKTE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SPVLTSSCRE | LLSRVFLALV | EEVEDRGTVV | AQGGGRALIP | LALEGTDVGQ | TKAAQALAKL | TITSNPEMTF | PGERIYEVVR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PLVSLLHLNC | SGLQNFEALM | ALTNLAGISE | RLRQKILKEK | AVPMIEGYMF | EEHEMIRRAA | TECMCNLAMS | KEVQDLFEAQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GNDRLKLLVL | YSGEDDELLQ | RAAAGGLAML | TSMRPTLCSR | IPQVTTHWLE | ILQALLLSSN | QELQHRGAVV | VLNMVEASRE |
| 890 | 900 | 910 | 920 | 930 | | | |
| IASTLMESEM | MEILSVLAKG | DHSPVTRAAA | ACLDKAVEYG | LIQPNQDGE | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2777 | 1 | 703.4893 | 208.47 | 2 | 63.3 | 10.5 | 1 | 50-61 | R.AACHLKLEDYDK.A | |

# Detailed Protein Report

## Protein 731: PAB-dependent poly(A)-specific ribonuclease subunit 2 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|188536112 | **Score:** | 23.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 134.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNFEGLDPGL | AEYAPAMHSA | LDPVLDAHLN | PSLLQNVELD | PEGVALEALP | VQESVHIMEG | VYSELHSVVA | EVGVPVSVSH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FDLHEEMLWV | GSHGGHATSF | FGPALERYSS | FQVNGSDDIR | QIQSLENGIL | FLTKNNLKYM | ARGGLIIFDY | LLDENEDMHS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLLTDSSTLL | VGGLQNHILE | IDLNTVQETQ | KYAVETPGVT | IMRQTNRFFF | CGHTSGKVSL | RDLRTFKVEH | EFDAFSGSLS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DFDVHGNLLA | ACGFSSRLTG | LACDRFLKVY | DLRMMRAITP | LQVHVDPAFL | RFIPTYTSRL | AIISQSGQCQ | FCEPTGLANP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ADIFHVNPVG | PLLMTFDVSA | SKQALAFGDS | EGCVHLWTDS | PEPSFNPYSR | ETEFALPCLV | DSLPPLDWSQ | DLLPLSLIPV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PLTTDTLLSD | WPAANSAPAP | RRAPPVDAEI | LRTMKKVGFI | GYAPNPRTRL | RNQIPYRLKE | SDSEFDSFSQ | VTESPVGREE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EPHLHMVSKK | YRKVTIKYSK | LGLEDFDFKH | YNKTLFAGLE | PHIPNAYCNC | MIQVLYFLEP | VRCLIQNHLC | QKEFCLACEL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GFLFHMLDLS | RGDPCQGNNF | LRAFRTIPEA | SALGLILADS | DEASGKGNLA | RLIQRWNRFI | LTQLHQDMQE | LEIPQAYRGA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GGSSFCSSGD | SVIGQLFSCE | MENCSLCRCG | SETVRASSTL | LFTLSYPDDK | TGKNYDFAQV | LKRSICLDQN | TQAWCDTCEK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YQPTIQTRNI | RHLPDILVIN | CEVNSSKEAD | FWRMQAEVAF | KMAVKKHGGE | ISKNKEFALA | DWKELGSPEG | VLVCPSIEEL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KNVWLPFSIR | MKMTKNKGLD | VCNWTDGDEM | QWGPARAEEE | HGVYVYDLMA | TVVHILDSRT | GGSLVAHIKV | GETYHQRKEG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VTHQQWYLFN | DFLIEPIDKH | EAVQFDMNWK | VPAILYYVKR | NLNSRYNLNI | KNPIEASVLL | AEASLARKQR | KTHTTFIPLM |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LNEMPQIGDL | VGLDAEFVTL | NEEEAELRSD | GTKSTIKPSQ | MSVARITCVR | GQGPNEGIPF | IDDYISTQEQ | VVDYLTQYSG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| IKPGDLDAKI | SSKHLTTLKS | TYLKLRFLID | IGVKFVGHGL | QKDFRVINLM | VPKDQVLDTV | YLFHMPRKRM | ISLRFLAWYF |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LDLKIQGETH | DSIEDARTAL | QLYRKYLELS | KNGTEPESFH | KVLKGLYEKG | RKMDWKVPEP | EGQTSPKNAA | VFSSVLAL |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1833 | 1 | 1010.9916 | -90.84 | 3 | 53.3 | 11.9 | 0 | 639-668 | R.GAGGSSFCSSGDSVIGQLFSCEMENCSLCR.C | |
| 1929 | 1 | 650.7900 | -100.99 | 2 | 54.5 | 11.7 | 2 | 762-773 | K.MAVKKHGGEISK.N | Oxidation: 1 |

# Detailed Protein Report

## Protein 732: CUB and sushi domain-containing protein 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|259013213 | **Score:** | 23.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 388.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MTAWRRFQSL LLLLGLLVLC ARLLTAAKGQ NCGGLVQGPN GTIESPGFPH GYPNYANCTW IIITGERNRI QLSFHTFALE
        90        100        110        120        130        140        150        160
EDFDILSVYD GQPQQGNLKV RLSGFQLPSS IVSTGSILTL WFTTDFAVSA QGFKALYEVL PSHTCGNPGE ILKGVLHGTR
       170        180        190        200        210        220        230        240
FNIGDKIRYS CLPGYILEGH AILTCIVSPG NGASWDFPAP FCRAEGACGG TLRGTSSSIS SPHFPSEYEN NADCTWTILA
       250        260        270        280        290        300        310        320
EPGDTIALVF TDFQLEEGYD FLEISGTEAP SIWLTGMNLP SPVISSKNWL RLHFTSDSNH RRKGFNAQFQ VKKAIELKSR
       330        340        350        360        370        380        390        400
GVKMLPSKDG SHKNSVLSQG GVALVSDMCP DPGIPENGRR AGSDFRVGAN VQFSCEDNYV LQGSKSITCQ RVTETLAAWS
       410        420        430        440        450        460        470        480
DHRPICRART CGSNLRGPSG VITSPNYPVQ YEDNAHCVWV ITTTDPDKVI KLAFEEFELE RGYDTLTVGD AGKVGDTRSV
       490        500        510        520        530        540        550        560
LYVLTGSSVP DLIVSMSNQM WLHLQSDDSI GSPGFKAVYQ EIEKGGCGDP GIPAYGKRTG SSFLHGDTLT FECPAAFELV
       570        580        590        600        610        620        630        640
GERVITCQQN NQWSGNKPSC VFSCFFNFTA SSGIILSPNY PEEYGNNMNC VWLIISEPGS RIHLIFNDFD VEPQFDFLAV
       650        660        670        680        690        700        710        720
KDDGISDITV LGTFSGNEVP SQLASSGHIV RLEFQSDHST TGRGFNITYT TFGQNECHDP GIPINGRRFG DRFLLGSSVS
       730        740        750        760        770        780        790        800
FHCDDGFVKT QGSESITCIL QDGNVVWSST VPRCEAPCGG HLTASSGVIL PPGWPGYYKD SLHCEWIIEA KPGHSIKITF
       810        820        830        840        850        860        870        880
DRFQTEVNYD TLEVRDGPAS SSPLIGEYHG TQAPQFLIST GNFMYLLFTT DNSRSSIGFL IHYESVTLES DSCLDPGIPV
       890        900        910        920        930        940        950        960
NGHRHGGDFG IRSTVTFSCD PGYTLSDDEP LVCERNHQWN HALPSCDALC GGYIQGKSGT VLSPGFPDFY PNSLNCTWTI
       970        980        990       1000       1010       1020       1030       1040
EVSHGKGVQM IFHTFHLESS HDYLLITEDG SFSEPVARLT GSVLPHTIKA GLFGNFTAQL RFISDFSISY EGFNITFSEY
      1050       1060       1070       1080       1090       1100       1110       1120
DLEPCDDPGV PAFSRRIGFH FGVGDSLTFS CFLGYRLEGA TKLTCLGGGR RVWSAPLPRC VAECGASVKG NEGTLLSPNF
      1130       1140       1150       1160       1170       1180       1190       1200
PSNYDNNHEC IYKIETEAGK GIHLRTRSFQ LFEGDTLKVY DGKDSSSRPL GTFTKNELLG LILNSTSNHL WLEFNTNGSD
      1210       1220       1230       1240       1250       1260       1270       1280
TDQGFQLTYT SFDLVKCEDP GIPNYGYRIR DEGHFTDTVV LYSCNPGYAM HGSNTLTCLS GDRRVWDKPL PSCIAECGGQ
      1290       1300       1310       1320       1330       1340       1350       1360
IHAATSGRIL SPGYPAPYDN NLHCTWIIEA DPGKTISLHF IVFDTEMAHD ILKVWDGPVD SDILLKEWSG SALPEDIHST
      1370       1380       1390       1400       1410       1420       1430       1440
FNSLTLQFDS DFFISKSGFS IQFSTSIAAT CNDPGMPQNG TRYGDSREAG DTVTFQCDPG YQLQGQAKIT CVQLNNRFFW
      1450       1460       1470       1480       1490       1500       1510       1520
QPDPPTCIAA CGGNLTGPAG VILSPNYPQP YPPGKECDWR VKVNPDFVIA LIFKSFNMEP SYDFLHIYEG EDSNSPLIGS
      1530       1540       1550       1560       1570       1580       1590       1600
YQGSQAPERI ESSGNSLFLA FRSDASVGLS GFAIEFKEKP REACFDPGNI MNGTRVGTDF KLGSTITYQC DSGYKILDPS
      1610       1620       1630       1640       1650       1660       1670       1680
SITCVIGADG KPSWDQVLPS CNAPCGGQYT GSEGVVLSPN YPHNYTAGQI CLYSITVPKE FVVFGQFAYF QTALNDLAEL
      1690       1700       1710       1720       1730       1740       1750       1760
FDGTHAQARL LSSLSGSHSG ETLPLATSNQ ILLRFSAKSG ASARGFHFVY QAVPRTSDTQ CSSVPEPRYG RRIGSEFSAG
      1770       1780       1790       1800       1810       1820       1830       1840
SIVRFECNPG YLLQGSTALH CQSVPNALAQ WNDTIPSCVV PCSGNFTQRR GTILSPGYPE PYGNNLNCIW KIIVTEGSGI
      1850       1860       1870       1880       1890       1900       1910       1920
QIQVISFATE QNWDSLEIHD GGDVTAPRLG SFSGTTVPAL LNSTSNQLYL HFQSDISVAA AGFHLEYKTV GLAACQEPAL
      1930       1940       1950       1960       1970       1980       1990       2000
PSNSIKIGDR YMVNDVLSFQ CEPGYTLQGR SHISCMPGTV RRWNYPSPLC IATCGGTLST LGGVILSPGF PGSYPNNLDC
      2010       2020       2030       2040       2050       2060       2070       2080
TWRISLPIGY GAHIQFLNFS TEANHDFLEI QNGPYHTSPM IGQFSGTDLP AALLSTTHET LIHFYSDHSQ NRQGFKLAYQ
      2090       2100       2110       2120       2130       2140       2150       2160
AYELQNCPDP PPFQNGYMIN SDYSVGQSVS FECYPGYILI GHPVLTCQHG INRNWNYPFP RCDAPCGYNV TSQNGTIYSP
      2170       2180       2190       2200       2210       2220       2230       2240
GFPDEYPILK DCIWLITVPP GHGVYINFTL LQTEAVNDYI AVWDGPDQNS PQLGVFSGNT ALETAYSSTN QVLLKFHSDF
      2250       2260       2270       2280       2290       2300       2310       2320
SNGGFFVLNF HAFQLKKCQP PPAVPQAEML TEDDDFEIGD FVKYQCHPGY TLVGTDILTC KLSSQLQFEG SLPTCEAQCP
      2330       2340       2350       2360       2370       2380       2390       2400
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 570 | 1 | 720.8066 | -10.56 | 2 | 36.7 | 12.0 | 0 | 1217-1228 | K.CEDPGIPNYGYR.I | Carbamidomethyl: 1 |

# Detailed Protein Report

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## Protein 733: PREDICTED: ectopic P granules protein 5 homolog isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530413907 | **Score:** | 23.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 252.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MNENALVELK KLFDAKSEHL HQTLALHSYT SVLSRLQVES YIYALLSSSA VLRSSAIHQQ GRASKQTESI PSDLCQLKEC
        90        100        110        120        130        140        150        160
ISVLFMFTRR VNEDTQFHDD ILLWLQKLVS VLQRVGCPGD HLFLLNHILR CPAGVSKWAV PFIQIKVLHN PSGVFHFMQS
       170        180        190        200        210        220        230        240
LALLMSPVKN RAEFMCHMKP SERKPSSSGP GSGTWTLVDE GGEEDEDPET SWILLNEDDL VTILAQFPFH ELFQHLLGFK
       250        260        270        280        290        300        310        320
AKGDYLPETT RPQEMMKIFA FANSLVELLA VGLETFNRAR YRQFVKRIGY MIRMTLGYVS DHWAQYVSHN QGSGLAQQPY
       330        340        350        360        370        380        390        400
SMEKLQVEFD ELFLRAVLHV LKAKRLGIWL FMSEMPFGTL SVQMLWKLFY LMHQVESENL QQLSSSLQPA QCKQQLQDPE
       410        420        430        440        450        460        470        480
HFTNFEKCLS SMNSSEEICL LTTFAQMAQA RRTNVDEDFI KIIVLEIYEV SYVTLSTRET FSKVGRELLG TITAVHPEII
       490        500        510        520        530        540        550        560
SVLLDRVQET IDQVGMVSLY LFKELPLYLW QPSASEIAVI RDWLLNYNLT VVKNKLACVI LEGLNWGFAK QATLHLDQAV
       570        580        590        600        610        620        630        640
HAEVALMVLE AYQKYLAQKP YAGILSESMK QVSYLASIVR YGETPETSFN QWAWNLILRL KLHKNDYGIQ PNCPAVPFSV
       650        660        670        680        690        700        710        720
TVPDMTESPT FHPLLKAVKA GMPIGCYLAL SMTAVGHSIE KFCAEGIPLL GILVQSRHLR TVVHVLDKIL PLFYPCQYYL
       730        740        750        760        770        780        790        800
LKNEQFLSHL LLFLHLDSGV PQGVTQQVTH KVAQHLTGAS HGDNVKLLNS MIQAHISVST QPNEVGPVAV LEFWVQALIS
       810        820        830        840        850        860        870        880
QHLWYREQPI LFLMDHLCKA AFQLMQEDCI QKLLYQQHKN ALGYHCDRSL LSSLVSWIVA GNITPSFVEG LATPTQVWFA
       890        900        910        920        930        940        950        960
WTVLNMESIF EEDSQLRRVI EGELVINSAF TPDQALKKAQ TQLKLPIVPS LQRLLIYRWA HQALVTPSDH PLLPLIWQKF
       970        980        990       1000       1010       1020       1030       1040
FLLYLHRPGP QYGLPIDGCI GRRFFQSPAH INLLKEMKRR LTEVADFHHA ASKALRVPAE GSEGLPESHS GTPGYLTSPE
      1050       1060       1070       1080       1090       1100       1110       1120
LHKELVRLFN VYILWLEDEN FQKGDTYIPS LPKHYDIHRL AKVMQNQQDL WMEYLNMERI YHEFQETVGL WTQAKLESHS
      1130       1140       1150       1160       1170       1180       1190       1200
TPCSLSVQLD FTDPLLAKER VLSNLRKHEA PQPPLALHPT KPPVPVISSA VLLSQKDATQ LVCTDLNLLQ QQARTAALRE
      1210       1220       1230       1240       1250       1260       1270       1280
SQQVALDGEL LDTMPKQYVN REEQTTLHLE CRGSSGKKCQ GAAVVTVQFE GMHKNEAISQ QLHVLRKEVK QLQAEAAKPP
      1290       1300       1310       1320       1330       1340       1350       1360
SLNIVEAAVH AENLITALVN AYKLQPTPGI QKVGISLFFT IVDYVSDETQ RHPPTRQFFT SCIEILGQVF ISGIKSECRK
      1370       1380       1390       1400       1410       1420       1430       1440
VLETILKNSR LCSLLSPFFT PNAAPAEFIQ LYEQVVKFLS EDNSDMIFML LTKFDLKQWL SATKPPLSDR TRLLESIHLA
      1450       1460       1470       1480       1490       1500       1510       1520
LTAWGLEPDE DILMPFNLFC KHWTYLLLYQ FPDQYSDILR LLMQSSAEQL LSPECWKATL RALGCCAPSC QQGAASTEGA
      1530       1540       1550       1560       1570       1580       1590       1600
VLPSSSDALL SDKQVMETIQ WLSDFFYKLR LSKMDFKSFG LFSKWSPYMA DVKTFLGYLV KRLIDLEMTC LAQDPTASRK
      1610       1620       1630       1640       1650       1660       1670       1680
TVLKSLHSVI IQLFKPWILV LEDNESSQQR HYPWLESDTV VASSIVQLFT DCIDSLHESF KDKLLPGDAG ALWLHLMHYC
      1690       1700       1710       1720       1730       1740       1750       1760
EACTAPKMPE FILYAFHSTY RKLPWKDLHP DQMLMEAFFK VERGSPKSCF LFLGSVLCEV NWVSVLSDAW NSSPHPETRS
      1770       1780       1790       1800       1810       1820       1830       1840
MIVCLLFMMI LLAKEVQLVD QTDSPLLSLL GQTSSLSWHL VDIVSYQSVL SYFSSHYPPS IILAKESYAE LIMKLLKVSA
      1850       1860       1870       1880       1890       1900       1910       1920
GLSIPTDSQK HLDAVPKCQA FTHQMVQFLS TLEQNGKITL AVLEQEMSKL LDDIIVFNPP DMDSQTRHMA LSSLFMEVLM
      1930       1940       1950       1960       1970       1980       1990       2000
MMNNATIPTA EFLRGSIRTW IGQKMHGLVV LPLLTAACQS LASVRHMAET TEACITAYFK ESPLNQNSGW GPILVSLQVP
      2010       2020       2030       2040       2050       2060       2070       2080
ELTMEEFLQE CLTLGSYLTL YVYLLQCLNS EQTLRNEMKV LLILSKWLEQ VYPSSVEEEA KLFLWWHQVL QLSLIQTEQN
      2090       2100       2110       2120       2130       2140       2150       2160
DSVLTESVIR ILLLVQSRQN LVAEERLSSG ILGAIGFGRK SPLSNRFRVV ARSMAAFLSV QVPMEDQIRL RPGSELHLTP
      2170       2180       2190       2200       2210       2220       2230
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1127 | 1 | 759.8346 | -55.87 | 2 | 44.2 | 10.1 | 0 | 66-78 | K.QTESIPSDLCQLK.E | Carbamidomethyl: 10 |

# Detailed Protein Report

## Protein 734: PREDICTED: dystonin isoform X15 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530382446 | **Score:** | 23.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 825.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 0.4 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | |
|---|---|---|---|
| ***WUP:QUP*** | **Median:** 2.30 | **CV:** 65.23 % | **No. of Peptides:** 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MHSSSYSYRS | SDSVFSNTTS | TRTSLDSNEN | LLLVHCGPTL | INSCISFGSE | SFDGHRLEML | QQIANRVQRD | SVICEDKLIL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AGNALQSDSK | RLESGVQFQN | EAEIAGYILE | CENLLRQHVI | DVQILIDGKY | YQADQLVQRV | AKLRDEIMAL | RNECSSVYSK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GRILTTEQTK | LMISGITQSL | NSGFAQTLHP | SLTSGLTQSL | TPSLTSSSMT | SGLSSGMTSR | LTPSVTPAYT | PGFPSGLVPN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FSSGVEPNSL | QTLKLMQIRK | PLLKSSLLDQ | NLTEEEINMK | FVQDLLNWVD | EMQVQLDRTE | WGSDLPSVES | HLENHKNVHR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AIEEFESSLK | EAKISEIQMT | APLKLTYAEK | LHRLESQYAK | LLNTSRNQER | HLDTLHNFVS | RATNELIWLN | EKEEEEVAYD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| WSERNTNIAR | KKDYHAELMR | ELDQKEENIK | SVQEIAEQLL | LENHPARLTI | EAYRAAMQTQ | WSWILQLCQC | VEQHIKENTA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YFEFFNDAKE | ATDYLRNLKD | AIQRKYSCDR | SSSIHKLEDL | VQESMEEKEE | LLQYKSTIAN | LMGKAKTIIQ | LKPRNSDCPL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KTSIPIKAIC | DYRQIEITIY | KDDECVLANN | SHRAKWKVIS | PTGNEAMVPS | VCFTVPPPNK | EAVDLANRIE | QQYQNVLTLW |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HESHINMKSV | VSWHYLINEI | DRIRASNVAS | IKTMLPGEHQ | QVLSNLQSRF | EDFLEDSQES | QVFSGSDITQ | LEKEVNVCKQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YYQELLKSAE | REEQEESVYN | LYISEVRNIR | LRLENCEDRL | IRQIRTPLER | DDLHESVFRI | TEQEKLKKEL | ERLKDDLGTI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TNKCEEFFSQ | AAASSSVPTL | RSELNVVLQN | MNQVYSMSST | YIDKLKTVNL | VLKNTQAAEA | LVKLYETKLC | EEEAVIADKN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| NIENLISTLK | QWRSEVDEKR | QVFHALEDEL | QKAKAISDEM | FKTYKERDLD | FDWHKEKADQ | LVERWQNVHV | QIDNRLRDLE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GIGKSLKYYR | DTYHPLDDWI | QQVETTQRKI | QENQPENSKT | LATQLNQQKM | LVSEIEMKQS | KMDECQKYAE | QYSATVKDYE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LQTMTYRAMV | DSQQKSPVKR | RRMQSSADLI | IQEFMDLRTR | YTALVTLMTQ | YIKFAGDSLK | RLEEEEKSLE | EEKKEHVEKA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KELQKWVSNI | SKTLKDAEKA | GKPPFSKQKI | SSEEISTKKE | QLSEALQTIQ | LFLAKHGDKM | TDEERNELEK | QVKTLQESYN |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LLFSESLKQL | QESQTSGDVK | VEEKLDKVIA | GTIDQTTGEV | LSVFQAVLRG | LIDYDTGIRL | LETQLMISGL | ISPELRKCFD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LKDAKSHGLI | DEQILCQLKE | LSKAKEIISA | ASPTTIPVLD | ALAQSMITES | MAIKVLEILL | STGSLVIPAT | GEQLTLQKAF |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| QQNLVSSALF | SKVLERQNMC | KDLIDPCTSE | KVSLIDMVQR | STLQENTGMW | LLPVRPQEGG | RITLKCGRNI | SILRAAHEGL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| IDRETMFRLL | SAQLLSGGLI | NSNSGQRMTV | EEAVREGVID | RDTASSILTY | QVQTGGIIQS | NPAKRLTVDE | AVQCDLITSS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| SALLVLEAQR | GYVGLIWPHS | GEIFPTSSSL | QQELITNELA | YKILNGRQKI | AALYIPESSQ | VIGLDAAKQL | GIIDNNTASI |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LKNITLPDKM | PDLGDLEACK | NARRWLSFCK | FQPSTVHDYR | QEEDVFDGEE | PVTTQTSEET | KKLFLSYLMI | NSYMDANTGQ |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| RLLLYDGDLD | EAVGMLLEGC | HAEFDGNTAI | KECLDVLSSS | GVFLNNASGR | EKDECTATPS | SFNKCHCGEP | EHEETPENRK |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| CAIDEEFNEM | RNTVINSEFS | QSGKLASTIS | IDPKVNSSPS | VCVPSLISYL | TQTELADISM | LRSDSENILT | NYENQSRVET |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| NERANECSHS | KNIQNFPSDL | IENPIMKSKM | SKFCGVNETE | NEDNTNRDSP | IFDYSPRLSA | LLSHDKLMHS | QGSFNDTHTP |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| ESNGNKCEAP | ALSFSDKTML | SGQRIGEKFQ | DQFLGIAAIN | ISLPGEQYGQ | KSLNMISSNP | QVQYHNDKYI | SNTSGEDEKT |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| HPGFQQMPED | KEDESEIEEY | SCAVTPGGDT | DNAIVSLTCA | TPLLDETISA | SDYETSLLND | QQNNTGTDTD | SDDDFYDTPL |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| FEDDDHDSLL | LDGDDRDCLH | PEDYDTLQEE | NDETASPADV | FYDVSKENEN | SMVPQGAPVG | SLSVKNKAHC | LQDFLMDVEK |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| DELDSGEKIH | LNPVGSDKVN | GQSLETGSER | ECTNILEGDE | SDSLTDYDIV | GGKESFTASL | KFDDSGSWRG | RKEEYVTGQE |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| FHSDTDHLDS | MQSEESYGDY | IYDSNDQDDD | DDDGIDEEGG | GIRDENGKPR | CQNVAEDMDI | QLCASILNEN | SDENENINTM |
| 2330 | 2340 | 2350 | 2360 | 2370 | 2380 | 2390 | 2400 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1902 | 1 | 805.7986 | -138.23 | 2 | 54.1 | 11.0 | 1 | 3171-3184 | R.TKQIMLAIDSEMSK.L | Oxidation: 12 | WUP:QUP 1.27 |
| 1793 | 6 | 781.2979 | -163.01 | 2 | 52.8 | 12.6 | 2 | 6444-6457 | R.SLKEKTSLADDNLK.L |  | WUP:QUP 4.17 |

# Detailed Protein Report

**Protein 735:** **fibrinogen alpha chain isoform alpha preproprotein [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|11761629 | **Score:** | 23.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| | | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFSMRIVCLV | LSVVGTAWTA | DSGEGDFLAE | GGGVRGPRVV | ERHQSACKDS | DWPFCSDEDW | NYKCPSGCRM | KGLIDEVNQD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FTNRINKLKN | SLFEYQKNNK | DSHSLTTNIM | EILRGDFSSA | NNRDNTYNRV | SEDLRSRIEV | LKRKVIEKVQ | HIQLLQKNVR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AQLVDMKRLE | VDIDIKIRSC | RGSCSRALAR | EVDLKDYEDQ | QKQLEQVIAK | DLLPSRDRQH | LPLIKMKPVP | DLVPGNFKSQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LQKVPPEWKA | LTDMPQMRME | LERPGGNEIT | RGGSTSYGTG | SETESPRNPS | SAGSWNSGSS | GPGSTGNRNP | GSSGTGGTAT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WKPGSSGPGS | TGSWNSGSSG | TGSTGNQNPG | SPRPGSTGTW | NPGSSERGSA | GHWTSESSVS | GSTGQWHSES | GSFRPDSPGS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GNARPNNPDW | GTFEEVSGNV | SPGTRREYHT | EKLVTSKGDK | ELRTGKEKVT | SGSTTTTRRS | CSKTVTKTVI | GPDGHKEVTK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EVVTSEDGSD | CPEAMDLGTL | SGIGTLDGFR | HRHPDEAAFF | DTASTGKTFP | GFFSPMLGEF | VSETESRGSE | SGIFTNTKES |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SSHHPGIAEF | PSRGKSSSYS | KQFTSSTSYN | RGDSTFESKS | YKMADEAGSE | ADHEGTHSTK | RGHAKSRPVR | GIHTSPLGKP |
| 650 | | | | | | | |
| SLSP | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1392 | 1 | 721.3777 | -27.06 | 2 | 47.6 | 12.5 | 0 | 226-238 | K.MKPVPDLVPGNFK.S | |

# Detailed Protein Report

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## Protein 736: trifunctional enzyme subunit alpha, mitochondrial precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|20127408 | **Score:** | 23.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 82.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVACRAIGIL | SRFSAFRILR | SRGYICRNFT | GSSALLTRTH | INYGVKGDVA | VVRINSPNSK | VNTLSKELHS | EFSEVMNEIW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ASDQIRSAVL | ISSKPGCFIA | GADINMLAAC | KTLQEVTQLS | QEAQRIVEKL | EKSTKPIVAA | INGSCLGGGL | EVAISCQYRI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ATKDRKTVLG | TPEVLLGALP | GAGGTQRLPK | MVGVPAALDM | MLTGRSIRAD | RAKKMGLVDQ | LVEPLGPGLK | PPEERTIEYL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EEVAITFAKG | LADKKISPKR | DKGLVEKLTA | YAMTIPFVRQ | QVYKKVEEKV | RKQTKGLYPA | PLKIIDVVKT | GIEQGSDAGY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LCESQKFGEL | VMTKESKALM | GLYHGQVLCK | KNKFGAPQKD | VKHLAILGAG | LMGAGIAQVS | VDKGLKTILK | DATLTALDRG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QQQVFKGLND | KVKKKALTSF | ERDSIFSNLT | GQLDYQGFEK | ADMVIEAVFE | DLSLKHRVLK | EVEAVIPDHC | IFASNTSALP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ISEIAAVSKR | PEKVIGMHYF | SPVDKMQLLE | IITTEKTSKD | TSASAVAVGL | KQGKVIIVVK | DGPGFYTTRC | LAPMMSEVIR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ILQEGVDPKK | LDSLTTSFGF | PVGAATLVDE | VGVDVAKHVA | EDLGKVFGER | FGGGNPELLT | QMVSKGFLGR | KSGKGFYIYQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EGVKRKDLNS | DMDSILASLK | LPPKSEVSSD | EDIQFRLVTR | FVNEAVMCLQ | EGILATPAEG | DIGAVFGLGF | PPCLGGPFRF |
| 730 | 740 | 750 | 760 | 770 | | | |
| VDLYGAQKIV | DRLKKYEAAY | GKQFTPCQLL | ADHANSPNKK | FYQ | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1343 | 2 | 652.4474 | 143.56 | 3 | 46.9 | 12.8 | 2 | 1-17 | -.MVACRAIGILSRFSAFR.I | Carbamidomethyl: 4 |
| 1289 | 1 | 1136.5599 | -53.35 | 2 | 46.3 | 10.8 | 2 | 188-208 | R.LPKMVGVPAALDMMLTGRSIR.A | Oxidation: 4 |

# Detailed Protein Report

## Protein 737: PREDICTED: WD repeat-containing protein 11 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530393962 | **Score:** | 23.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 108.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 3.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530393964 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: WD repeat-containing protein 11 isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLLLYPREIL | ILDLEVNQTV | GVIAIERTGV | PFLQVIPCFQ | RDGLFCLHEN | GCITLRVRRS | YNNIFTTSNE | EPDPDPVQEL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TYDLRSQCDA | IRVTKTVRPF | SMVCCPVNEN | AAALVVSDGR | VMIWELKSAV | CNRNSRNSSS | GVSPLYSPVS | FCGIPVGVLQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NKLPDLSLDN | MIGQSAIAGE | EHPRGSILRE | VHLKFLLTGL | LSGLPAPQFA | IRMCPPLTTK | NIKMYQPLLA | VGTSNGSVLV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YHLTSGLLHK | ELSIHSCEVK | GIEWTSLTSF | LSFATSTPNN | MGLVRNELQL | VDLPTGRSIA | FRGERGNDES | AIEMIKVSHL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KQYLAVVFRD | KPLELWDVRT | CTLLREMSKN | FPTITALEWS | PSHNLKSLRK | KQLATREAMA | RQTVVSDTEL | SIVESSVISL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LQEAESKSEL | SQNISAREHF | VFTDIDGQVY | HLTVEGNSVK | DSARIPPDGS | MGSITCIAWK | GDTLVLGDMD | GNLNFWDLKG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RVSRGIPTHR | SWVRKIRFAP | GKGNQKLIAM | YNDGAEVWDT | KEVQMVSSLR | SGRNVTFRIL | DVDWCTSDKV | ILASDDGCIR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VLEMSMKSAC | FRMDEQELTE | PVWCPYLLVP | RASLALKAFL | LHQPWNGQYS | LDISHVDYPE | NEEIKNLLQE | QLNSLSNDIK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KLLLDPEFTL | LQRCLLVSRL | YGDESELHFW | TVAAHYLHSL | SQEKSASTTA | PKEAAPRDKL | SNPLDICYDV | LCENAYFQKF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QLERVNLQEV | KRSTYDHTRK | CTDQLLLLGQ | TDRAVQLLLE | TSADNQHYYC | DSLKACLVTT | VTSSGPSQST | IKLVATNMIA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NGKLAEGVQL | LCLIDKAADA | CRYLQTYGEW | NRAAWLAKVR | LNPEECADVL | RRWVDHLCSP | QVNQKSKALL | VLLSLGCFFS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VAETLHSMRY | FDRAALFVEA | CLKYGAFEVT | EDTEKLITAI | YADYARSLKN | LGFKQGAVLF | ASKAGAAGKD | LLNELESPKE |
| 970 | | | | | | | |
| EPIEE | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2753 | 1 | 973.5005 | 10.37 | 2 | 62.9 | 11.5 | 1 | 42-58 | R.DGLFCLHENGCITLRVR.R | |

# Detailed Protein Report

## Protein 738: geranylgeranyl transferase type-2 subunit alpha [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|33469951 | **Score:** | 23.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 65.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.26 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.05 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|53828918 | refseq_human (refseq_human_20140103.fasta) | geranylgeranyl transferase type-2 subunit alpha [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MHGRLKVKTS EEQAEAKRLE REQKLKLYQS ATQAVFQKRQ AGELDESVLE LTSQILGANP DFATLWNCRR EVLQQLETQK
        90        100        110        120        130        140        150        160
SPEELAALVK AELGFLESCL RVNPKSYGTW HHRCWLLGRL PEPNWTRELE LCARFLEVDE RNFHCWDYRR FVATQAAVPP
       170        180        190        200        210        220        230        240
AEELAFTDSL ITRNFSNYSS WHYRSCLLPQ LHPQPDSGPQ GRLPEDVLLK ELELVQNAFF TDPNDQSAWF YHRWLLGRAD
       250        260        270        280        290        300        310        320
PQDALRCLHV SRDEACLTVS FSRPLLVGSR MEILLLMVDD SPLIVEWRTP DGRNRPSHVW LCDLPAASLN DQLPQHTFRV
       330        340        350        360        370        380        390        400
IWTAGDVQKE CVLLKGRQEG WCRDSTTDEQ LFRCELSVEK STVLQSELES CKELQELEPE NKWCLLTIIL LMRALDPLLY
       410        420        430        440        450        460        470        480
EKETLQYFQT LKAVDPMRAT YLDDLRSKFL LENSVLKMEY AEVRVLHLAH KDLTVLCHLE QLLLVTHLDL SHNRLRTLPP
       490        500        510        520        530        540        550        560
ALAALRCLEV LQASDNAIES LDGVTNLPRL QELLLCNNRL QQPAVLQPLA SCPRLVLLNL QGNPLCQAVG ILEQLAELLP
       570
SVSSVLT
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2475 | 1 | 817.4620 | -51.73 | 1 | 61.5 | 11.7 | 0 | 445-451 | R.VLHLAHK.D | | WUP:QUP 1.05<br>QU:MU 1.26 |

# Detailed Protein Report

**Protein 739:** **ras-associated and pleckstrin homology domains-containing protein 1 isoform 1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|47132519 | **Score:** | 23.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 135.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEQLSDEEID | HGAEEDSDKE | DQDLDKMFGA | WLGELDKLTQ | SLDSDKPMEP | VKRSPLRQET | NMANFSYRFS | IYNLNEALNQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GETVDLDALM | ADLCSIEQEL | SSIGSGNSKR | QITETKATQK | LPVSRHTLKH | GTLKGLSSSS | NRIAKPSHAS | YSLDDVTAQL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EQASLSMDEA | AQQSVLEDTK | PLVTNQHRRT | ASAGTVSDAE | VHSISNSSHS | SITSAASSMD | SLDIDKVTRP | QELDLTHQGQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PITEEEQAAK | LKAEKIRVAL | EKIKEAQVKK | LVIRVHMSDD | SSKTMMVDER | QTVRQVLDNL | MDKSHCGYSL | DWSLVETVSE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LQMERIFEDH | ENLVENLLNW | TRDSQNKLIF | MERIEKYALF | KNPQNYLLGK | KETAEMADRN | KEVLLEECFC | GSSVTVPEIE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GVLWLKDDGK | KSWKKRYFLL | RASGIYYVPK | GKAKVSRDLV | CFLQLDHVNV | YYGQDYRNKY | KAPTDYCLVL | KHPQIQKKSQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YIKYLCCDDV | RTLHQWVNGI | RIAKYGKQLY | MNYQEALKRT | ESAYDWTSLS | SSSIKSGSSS | SSIPESQSNH | SNQSDSGVSD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TQPAGHVRSQ | SIVSSVFSEA | WKRGTQLEES | SKARMESMNR | PYTSLVPPLS | PQPKIVTPYT | ASQPSPPLPP | PPPPPPPPPP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PPPPPPPPLP | SQSAPSAGSA | APMFVKYSTI | TRLQNASQHS | GALFKPPTPP | VMQSQSVKPQ | ILVPPNGVVP | PPPPPPPPPT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PGSAMAQLKP | APCAPSLPQF | SAPPPPLKIH | QVQHITQVAP | PTPPPPPPIP | APLPPQAPPK | PLVTIPAPTS | TKTVAPVVTQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AAPPTPTPPV | PPAKKQPAFP | ASYIPPSPPT | PPVPVPPPTL | PKQQSFCAKP | PPSPLSPVPS | VVKQIASQFP | PPPTPPAMES |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QPLKPVPANV | APQSPPAVKA | KPKWQPSSIP | VPSPDFPPPP | PESSLVFPPP | PPSPVPAPPP | PPPPTASPTP | DKSGSPGKKT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SKTSSPGGKK | PPPTPQRNSS | IKSSSGAEHP | EPKRPSVDSL | VSKFTPPAES | GSPSKETLPP | PAAPPKPGKL | NLSGVNLPGV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LQQGCVSAKA | PVLSGRGKDS | VVEFPSPPSD | SDFPPPPPET | ELPLPPIEIP | AVFSGNTSPK | VAVVNPQPQQ | WSKMSVKKAP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PPTRPKRNDS | TRLTQAEISE | QPTMATVVPQ | VPTSPKSSLS | VQPGFLADLN | RTLQRKSITR | HGSLSSRMSR | AEPTATMDDM |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | | |
| ALPPPPPELL | SDQQKAGYGG | SHISGYATLR | RGPPPAPPKR | DQNTKLSRDW | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2470 | 1 | 938.4630 | 79.49 | 1 | 61.4 | 13.0 | 0 | 372-379 | K.ETAEMADR.N | Oxidation: 5 |

## Protein 740: PREDICTED: LOW QUALITY PROTEIN: spidroin-1-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578798093 | **Score:** | 23.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 23.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.7 |
| | | **Sequence Coverage [%]:** | 4.4 |
| | | **No. of unique Peptides:** | 2 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.33 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.18 | **CV:** | 15.71 % | **No. of Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MRGLDQMEIR | GGPYLLLGEV | VGHSALGAQP | AQAADEVLEL | PALLQRPAGR | RPCASHRGRR | ITPATALLLL | SHRGRAEXAA |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| AAKAGSPGRR | RVGKGPPIRE | SWTRSAPQRC | PSQDAGRAGS | RVCRSRPQSR | GGQKAAASGA | KRRGVGGKEL | WRRGQRAATA |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | |
| KTRGGGGKKP | RGQKPQKATA | AGAKSRGGGG | KKPRRQKTAA | AGAKSRGGGG | NKPQKAAAAG | ICCYQR | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2067 | 1 | 643.2889 | -61.34 | 2 | 54.2 | 12.7 | 1 | 0-0 | .AEEAAAAKAGSPGR. | | WUP:QUP 2.55<br>QU:MU 0.33 |
| 1150 | 1 | 500.6507 | -270.14 | 2 | 44.0 | 10.8 | 2 | 74-83 | R.GRAERAAAAK.A | | WUP:QUP 1.87 |

# Detailed Protein Report

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## Protein 741: zinc finger protein 609 [Homo sapiens]

**Accession:** gi|71725360
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 23.5
**MW [kDa]:** 151.1
**pI:** 9.0
**Sequence Coverage [%]:** 1.5
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSLSSGASGG | KGVDANPVET | YDSGDEWDIG | VGNLIIDLDA | DLEKDQQKLE | MSGSKEVGIP | APNAVATLPD | NIKFVTPVPG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PQGKEGKSKS | KRSKSGKDTS | KPTPGTSLFT | PSEGAASKKE | VQGRSGDGAN | AGGLVAAIAP | KGSEKAAKAS | RSVAGSKKEK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ENSSSKSKKE | RSEGVGTCSE | KDPGVLQPVP | LGGRGGQYDG | SAGVDTGAVE | PLGSIAIEPG | AALNPLGTKP | EPEEGENECR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LLKKVKSEKM | ESPVSTPAVL | PIHLLVPVVN | NDISSPCEQI | MVRTRSVGVN | TCDVALATEP | ECLGPCEPGT | SVNLEGIVWQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ETEDGMLVVN | VTWRNKTYVG | TLLDCTRHDW | APPRFCDSPT | SDLEMRNGRG | RGKRMRPNSN | TPVNETATAS | DSKGTSNSSK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TRAGANSKGR | RGSQNSSEHR | PPASSTSEDV | KASPSSANKR | KNKPLSDMEL | NSSSEDSKGS | KRVRTNSMGS | ATGPLPGTKV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EPTVLDRNCP | SPVLIDCPHP | NCNKKYKHIN | GLKYHQAHAH | TDDDSKPEAD | GDSEYGEEPI | LHADLGSCNG | ASVSQKGSLS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PARSATPKVR | LVEPHSPSPS | SKFSTKGLCK | KKLSGEGDTD | LGALSNDGSD | DGPSVMDETS | NDAFDSLERK | CMEKEKCKKP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SSLKPEKIPS | KSLKSARPIA | PAIPPQQIYT | FQTATFTAAS | PGSSSGLTAT | VAQAMPNSPQ | LKPIQPKPTV | MGEPFTVNPA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LTPAKDKKKK | DKKKKESSKE | LESPLTPGKV | CRAEEGKSPF | RESSGDGMKM | EGLLNGSSDP | HQSRLASIKA | EADKIYSFTD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NAPSPSIGGS | SRLENTTPTQ | PLTPLHVVTQ | NGAEASSVKT | NSPAYSDISD | AGEDGEGKVD | SVKSKDAEQL | VKEGAKKTLF |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PPQPQSKDSP | YYQGFESYYS | PSYAQSSPGA | LNPSSQAGVE | SQALKTKRDE | EPESIEGKVK | NDICEEKKPE | LSSSSQQPSV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| IQQRPNMYMQ | SLYYNQYAYV | PPYGYSDQSY | HTHLLSTNTA | YRQQYEEQQK | RQSLEQQQRG | VDKKAEMGLK | EREAALKEEW |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KQKPSIPPTL | TKAPSLTDLV | KSGPGKAKEP | GADPAKSVII | PKLDDSSKLP | GQAPEGLKVK | LSDASHLSKE | ASEAKTGAEC |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GRQAEMDPIL | WYRQEAEPRM | WTYVYPAKYS | DIKSEDERWK | EERDRKLKEE | RSRSKDSVPK | EDGKESTSSD | CKLPTSEESR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LGSKEPRPSV | HVPVSSPLTQ | HQSYIPYMHG | YSYSQSYDPN | HPSYRSMPAV | MMQNYPGSYL | PSSYSFSPYG | SKVSGGEDAD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KARASPSVTC | KSSSESKALD | ILQQHASHYK | SKSPTISDKT | SQERDRGGCG | VVGGGGSCSS | VGGASGGERS | VDRPRTSPSQ |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | | |
| RLMSTHHHHH | HLGYSLLPAQ | YNLPYAAGLS | STAIVASQQG | STPSLYPPPR | R | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2845 | 1 | 657.3625 | 105.46 | 2 | 64.2 | 12.5 | 1 | 758-769 | K.SPFRESSGDGMK.M | Oxidation: 11 |

# Detailed Protein Report

## Protein 742: PREDICTED: transcriptional regulator ATRX isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578838421 | **Score:** | 23.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 211.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| | | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTAEPMSESK | LNTLVQKLHD | FLAHSSEESE | ETSSPPRLAM | NQNTDKISGS | GSNSDMMENS | KEEGTSSSEK | SKSSGSSRSK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RKPSIVTKYV | ESDDEKPLDD | ETVNEDASNE | NSENDITMQS | LPKGTVIVQP | EPVLNEDKDD | FKGPEFRSRS | KMKTENLKKR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GEDGLHGIVS | CTACGQQVNH | FQKDSIYRHP | SLQVLICKNC | FKYYMSDDIS | RDSDGMDEQC | RWCAEGGNLI | CCDFCHNAFC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KKCILRNLGR | KELSTIMDEN | NQWYCYICHP | EPLLDLVTAC | NSVFENLEQL | LQQNKKKIKV | DSEKSNKVYE | HTSRFSPKKT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SSNCNGEEKK | LDDSCSGSVT | YSYSALIVPK | EMIKKAKKLI | ETTANMNSSY | VKFLKQATDN | SEISSATKLR | QLKAFKSVLA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DIKKAHLALE | EDLNSEFRAM | DAVNKEKNTK | EHKVIDAKFE | TKARKGEKPC | ALEKKDISKS | EAKLSRKQVD | SEHMHQNVPT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EEQRTNKSTG | GEHKKSDRKE | EPQYEPANTS | EDLDMDIVSV | PSSVPEDIFE | NLETAMEVQS | SVDHQGDGSS | GTEQEVESSS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VKLNISSKDN | RGGIKSKTTA | KVTKELYVKL | TPVSLSNSPI | KGADCQEVPQ | DKDGYKSCGL | NPKLEKCGLG | QENSDNEHLV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ENEVSLLLEE | SDLRRSPRVK | TTPLRRPTET | NPVTSNSDEE | CNETVKEKQK | LSVPVRKKDK | RNSSDSAIDN | PKPNKLPKSK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QSETVDQNSD | SDEMLAILKE | VSRMSHSSSS | DTDINEIHTN | HKTLYDLKTQ | AGKDDKGKRK | RKSSTSGSDF | DTKKGKSAKS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SIISKKKRQT | QSESSNYDSE | LEKEIKSMSK | IGAARTTKKR | IPNTKDFDSS | EDEKHSKKGM | DNQGHKNLKT | SQEGSSDDAE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RKQERETFSS | AEGTVDKDTT | IMELRDRLPK | KQQASASTDG | VDKLSGKEES | FTSLEVRKVA | ETKEKSKHLK | TKTCKKVQDG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LSDIAEKFLK | KDQSDETSED | DKKQSKKGTE | EKKKPSDFKK | KVIKMEQQYE | SSSDGTEKLP | EREEICHFPK | GIKQIKNGTT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| DGEKKSKKIR | DKTSKKKDEL | SDYAEKSTGK | GDSCDSSEDK | KSKNGAYGRE | KKRCKLLGKS | SRKRQDCSSS | DTEKYSMKED |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GCNSSDKRLK | RIELRERRNL | SSKRNTKEIQ | SGSSSSDAEE | SSEDNKKKKQ | RTSSKKKAVI | VKEKKRNSLR | TSTKRKQADI |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TSSSSSDIED | DDQNSIGEGS | SDEQKIKPVT | ENLVLSSHTG | FCQSSGDEAL | SKSVPVTVDD | DDDDNDPENR | IAKKMLLEEI |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KANLSSDEDG | SSDDEPEEGK | KRTGKQNEEN | PGDEEAKNQV | NSESDSDSEE | SKKPRYRHRL | LRHKLTVSDG | ESGEEKKTKP |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KEHKEVKGRN | RRKVSSEDSE | DSDFQESGVS | EEVSESEDEQ | RPRTRSAKKA | ELEENQRSYK | QKKKRRRIKV | QEDSSSENKS |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| NSEEEEEEKE | EEEEEEEEEE | EEEEDENDDS | KSPGKGRKKI | RKILKDDKLR | TETQNALKEE | EERRKRIAER | EREREKLREV |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| IEIEDASPTK | CPITTKLVLD | EDEETKEPLV | QVHRNMVIKL | KPHQVDGVQF | MWDCCCESVK | KTKKSPGSGC | ILAHCMGLGK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| TLQVVSFLHT | VLLCDKLDFS | TALVVCPLNT | ALNWMNEFEK | WQEGLKDDEK | LEVSELATVK | RPQERSYMLQ | RWQEDGGVMI |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| IGYEMYRNLA | QGRNVKSRKL | KEIFNKALVD | PGPDFVVCDE | GHILKNEASA | VSKAMNSIRS | RRRIILTGTP | LQNNLIEYHC |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| MVNFIKENLL | GSIKEFRNRF | INPIQNGQCA | DSTMVDVRVM | KKRAHILYEM | LAGCVQRKDY | TALTKFLPPK | HEYVLAVRMT |
| 1850 | 1860 | 1870 | 1880 | | | | |
| SIQCKLYQYY | LDHLTVLHLN | KMGMLKSIKY | F | | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1627 | 1 | 1010.4939 | -28.29 | 1 | 50.6 | 13.2 | 2 | 71-80 | K.SKSSGSSRSK.R | |
| 2633 | 1 | 589.1691 | -335.46 | 1 | 61.2 | 10.3 | 1 | 572-577 | R.GGIKSK.T | |

# Detailed Protein Report

## Protein 743: zinc finger protein 600 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|156766086 | **Score:** | 23.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 83.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| | | **Sequence Coverage [%]:** | 4.4 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MMKEVLSTGQ | GNTEVIHTGT | LQRYQSYHIG | DFCFQEIEKE | IHDIEFQCQE | DERNGHEAPM | TKIKKLTGST | DQHDHRHAGN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KPIKDQLGSS | FYSHLPELHI | IQIKGKIGNQ | FEKSTSDAPS | VSTSQRISPR | PQIHISNNYG | NNSPNSSLLP | QKQEVYMREK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SFQCNESGKA | FNCSSLLRKH | QIPHLGDKQY | KCDVCGKLFN | HKQYLTCHRR | CHTGEKPYKC | NECGKSFSQV | SSLTCHRRLH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TAVKSHKCNE | CGKIFGQNSA | LVIHKAIHTG | EKPYKCNECD | KAFNQQSNLA | RHRRIHTGEK | PYKCEECDKV | FSRKSTLESH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KRIHTGEKPY | KCKVCDTAFT | WNSQLARHKR | IHTGEKTYKC | NECGKTFSHK | SSLVCHHRLH | GGEKSYKCKV | CDKAFAWNSH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LVRHTRIHSG | GKPYKCNECG | KTFGQNSDLL | IHKSIHTGEQ | PYKYEECEKV | FSCGSTLETH | KIIHTGEKPY | KCKVCDKAFA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CHSYLAKHTR | IHSGEKPYKC | NECSKTFRLR | SYLASHRRVH | SGEKPYKCNE | CSKTFSQRSY | LHCHRRLHSG | EKPYKCNECG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KTFSHKPSLV | HHRRLHTGEK | SYKCTVCDKA | FVRNSYLARH | TRIHTAEKPY | KCNECGKAFN | QQSQLSLHHR | IHAGEKLYKC |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ETCDKVFSRK | SHLKRHRRIH | PGKKPYKCKV | CDKTFGSDSH | LKQHTGLHTG | EKPYKCNECG | KAFSKQSTLI | HHQAVHGVGK |
| 730 | | | | | | | |
| LD | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 114 | 1 | 1234.5408 | -63.72 | 2 | 31.4 | 12.1 | 1 | 674-695 | K.TFGSDSHLKQHTGLHTGEKPYK.C | |

# Detailed Protein Report

## Protein 744: lysine-specific demethylase 5B [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|57242796 | **Score:** | 23.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 175.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEAATTLHPG | PRPALPLGGP | GPLGEFLPPP | ECPVFEPSWE | EFADPFAFIH | KIRPIAEQTG | ICKVRPPPDW | QPPFACDVDK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LHFTPRIQRL | NELEAQTRVK | LNFLDQIAKY | WELQGSTLKI | PHVERKILDL | FQLNKLVAEE | GGFAVVCKDR | KWTKIATKMG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FAPGKAVGSH | IRGHYERILN | PYNLFLSGDS | LRCLQKPNLT | TDTKDKEYKP | HDIPQRQSVQ | PSETCPPARR | AKRMRAEAMN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IKIEPEETTE | ARTHNLRRRM | GCPTPKCENE | KEMKSSIKQE | PIERKDYIVE | NEKEKPKSRS | KKATNAVDLY | VCLLCGSGND |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EDRLLLCDGC | DDSYHTFCLI | PPLHDVPKGD | WRCPKCLAQE | CSKPQEAFGF | EQAARDYTLR | TFGEMADAFK | SDYFNMPVHM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VPTELVEKEF | WRLVSTIEED | VTVEYGADIA | SKEFGSGFPV | RDGKIKLSPE | EEEYLDSGWN | LNNMPVMEQS | VLAHITADIC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GMKLPWLYVG | MCFSSFCWHI | EDHWSYSINY | LHWGEPKTWY | GVPGYAAEQL | ENVMKKLAPE | LFVSQPDLLH | QLVTIMNPNT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LMTHEVPVYR | TNQCAGEFVI | TFPRAYHSGF | NQGFNFAEAV | NFCTVDWLPL | GRQCVEHYRL | LHRYCVFSHD | EMICKMASKA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DVLDVVVAST | VQKDMAIMIE | DEKALRETVR | KLGVIDSERM | DFELLPDDER | QCVKCKTTCF | MSAISCSCKP | GLLVCLHHVK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ELCSCPPYKY | KLRYRYTLDD | LYPMMNALKL | RAESYNEWAL | NVNEALEAKI | NKKKSLVSFK | ALIEESEMKK | FPDNDLLRHL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RLVTQDAEKC | ASVAQQLLNG | KRQTRYRSGG | GKSQNQLTVN | ELRQFVTQLY | ALPCVLSQTP | LLKDLLNRVE | DFQQHSQKLL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SEETPSAAEL | QDLLDVSFEF | DVELPQLAEM | RIRLEQARWL | EEVQQACLDP | SSLTLDDMRR | LIDLGVGLAP | YSAVEKAMAR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LQELLTVSEH | WDDKAKSLLK | ARPRHSLNSL | ATAVKEIEEI | PAYLPNGAAL | KDSVQRARDW | LQDVEGLQAG | GRVPVLDTLI |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ELVTRGRSIP | VHLNSLPRLE | TLVAEVQAWK | ECAVNTFLTE | NSPYSLLEVL | CPRCDIGLLG | LKRKQRKLKE | PLPNGKKKST |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KLESLSDLER | ALTESKETAS | AMATLGEARL | REMEALQSLR | LANEGKLLSP | LQDVDIKICL | CQKAPAAPMI | QCELCRDAFH |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TSCVAVPSIS | QGLRIWLCPH | CRRSEKPPLE | KILPLLASLQ | RIRVRLPEGD | ALRYMIERTV | NWQHRAQQLL | SSGNLKFVQD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| RVGSGLLYSR | WQASAGQVSD | TNKVSQPPGT | TSFSLPDDWD | NRTSYLHSPF | STGRSCIPLH | GVSPEVNELL | MEAQLLQVSL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PEIQELYQTL | LAKPSPAQQT | DRSSPVRPSS | EKNDCCRGKR | DGINSLERKL | KRRLEREGLS | SERWERVKKM | RTPKKKKIKL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SHPKDMNNFK | LERERSYELV | RSAETHSLPS | DTSYSEQEDS | EDEDAICPAV | SCLQPEGDEV | DWVQCDGSCN | QWFHQVCVGV |
| 1530 | 1540 | 1550 | | | | | |
| SPEMAEKEDY | ICVRCTVKDA | PSRK | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 333 | 1 | 734.3935 | -67.03 | 2 | 34.1 | 13.3 | 0 | 1033-1045 | R.VPVLDTLIELVTR.G | |
| 1877 | 1 | 1059.3256 | -215.69 | 1 | 53.8 | 10.2 | 1 | 1400-1408 | K.RDGINSLER.K | |

# Detailed Protein Report

## Protein 745: kinesin-like protein KIF18B isoform 2 [Homo sapiens]

**Accession:** gi|387942371
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 23.5
**MW [kDa]:** 91.0
**pI:** 9.5
**Sequence Coverage [%]:** 3.2
**No. of unique Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAVEDSTLQV | VVRVRPPTPR | ELDSQRRPVV | QVVDERVLVF | NPEEPDGGFP | GLKWGGTHDG | PKKKGKDLTF | VFDRVFGEAA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TQQDVFQHTT | HSVLDSFLQG | YNCSVFAYGA | TGAGKTHTML | GREGDPGIMY | LTTVELYRRL | EARQQEKHFE | VLISYQEVYN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EQIHDLLEPK | GPLAIREDPD | KGVVVQGLSF | HQPASAEQLL | EILTRGNRNR | TQHPTDANAT | SSRSHAIFQI | FVKQQDRVPG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LTQAVQVAKM | SLIDLAGSER | ASSTHAKGER | LREGANINRS | LLALINVLNA | LADAKGRKTH | VPYRDSKLTR | LLKDSLGGNC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RTVMIAAISP | SSLTYEDTYN | TLKYADRAKE | IRLSLKSNVT | SLDCHISQYA | TICQQLQAEV | AALRKKLQVY | EGGGQPPPQD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LPGSPKSGPP | PEHLPSSPLP | PHPPSQPCTP | ELPAGPRALQ | EESLGMEAQV | ERAMEGNSSD | QEQSPEDEDE | GPAEEVPTQM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PEQNPTHALP | ESPRLTLQPK | PVVGHFSARE | LDGDRSKQLA | LKVLCVAQRQ | YSLLQAANLL | TPDMITEFET | LQQLVQEEKI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EPGAEALRTS | GLARGAPLAQ | ELCSESIPVP | SPLCPEPPGY | TGPVTRTMAR | RLSGPLHTLG | IPPGPNCTPA | QGSRWPMEKK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RRRPSALEAD | SPMAPKRGTK | RQRQSFLPCL | RRGSLPDTQP | SQGPSTPKGE | RASSPCHSPR | VCPATVIKSR | VPLGPSAMQN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CSTPLALPTR | DLNATFDLSE | EPPSKPSFHE | CIGWDKIPQE | LSRLDQPFIP | RAPVPLFTMK | GPKPTSSLPG | TSACKKKRVA |
| 810 | 820 | 830 | 840 | | | | |
| SSSVSHGRSR | IARLPSSTLK | RPAGPLVLPG | DWH | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2131 | 1 | 899.4303 | -47.52 | 2 | 55.0 | 10.7 | 2 | 642-657 | R.RRPSALEADSPMAPKR.G | Oxidation: 12 |

# Detailed Protein Report

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## Protein 746: multiple epidermal growth factor-like domains protein 8 isoform 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|145701025 | **Score:** | 23.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 295.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.96 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MALGKVLAMA LVLALAVLGS LSPGARAGDC KGQRQVLREA PGFVTDGAGN YSVNGNCEWL IEAPSPQHRI LLDFLFLDTE
        90        100        110        120        130        140        150        160
CTYDYLFVYD GDSPRGPLLA SLSGSTRPPP IEASSGKMLL HLFSDANYNL LGFNASFRFS LCPGGCQSHG QCQPPGVCAC
       170        180        190        200        210        220        230        240
EPGWGGPDCG LQECSAYCGS HGTCASPLGP CRCEPGFLGR ACDLHLWENQ GAGWWHNVSA RDPAFSARIG AAGAFLSPPG
       250        260        270        280        290        300        310        320
LLAVFGGQDL NNALGDLVLY NFSANTWESW DLSPAPAARH SHVAVAWAGS LVLMGGELAD GSLTNDVWAF SPLGRGHWEL
       330        340        350        360        370        380        390        400
LAPPASSSSG PPGLAGHAAA LVDDVWLYVS GGRTPHDLFS SGLFRFRLDS TSGGYWEQVI PAGGRPPAAT GHSMVFHAPS
       410        420        430        440        450        460        470        480
RALLVHGGHR PSTARFSVRV NSTELFHVDR HVWTTLKGRD GLQGPRERAF HTASVLGNYM VVYGGNVHTH YQEEKCYEDG
       490        500        510        520        530        540        550        560
IFFYHLGCHQ WVSGAELAPP GTPEGRAAPP SGRYSHVAAV LGGSVLLVAG GYSGRPRGDL MAYKVPPFVF QAPAPDYHLD
       570        580        590        600        610        620        630        640
YCSMYTDHSV CSRDPECSWC QGACQAAPPP GTPLGACPAA SCLGLGRLLG DCQACLAFSS PTAPPRGPGT LGWCVHNESC
       650        660        670        680        690        700        710        720
LPRPEQARCR GEQISGTVGW WGPAPVFVTS LEACVTQSFL PGLHLLTFQQ PPNTSQPDKE EVGRWVAHQE KETRRLQRPG
       730        740        750        760        770        780        790        800
SARLFPLPGR DHKYAVEIQG QLNGSAGPGH SELTLLWDRT GVPGGSEISF FFLEPYRSSS CTSYSSCLGC LADQGCGWCL
       810        820        830        840        850        860        870        880
TSATCHLRQG GAHCGDDGAG GSLLVLVPTL CPLCEEHRDC HACTQDPFCE WHQSTSRKGD AACSRRGRGR GALKSPEECP
       890        900        910        920        930        940        950        960
PLCSQRLTCE DCLANSSQCA WCQSTHTCFL FAAYLARYPH GGCRGWDDSV HSEPRCRSCD GFLTCHECLQ SHECGWCGNE
       970        980        990       1000       1010       1020       1030       1040
DNPTLGRCLQ GDFSGPLGGG NCSLWVGEGL GLPVALPARW AYARCPDVDE CRLGLARCHP RATCLNTPLS YECHCQRGYQ
      1050       1060       1070       1080       1090       1100       1110       1120
GDGISHCNRT CLEDCGHGVC SGPPDFTCVC DLGWTSDLPP PTPAPGPPAP RCSRDCGCSF HSHCRKRGPG FCDECQDWTW
      1130       1140       1150       1160       1170       1180       1190       1200
GEHCERCRPG SFGNATGSRG CRPCQCNGHG DPRRGHCDNL SGLCFCQDHT EGAHCQLCSP GYYGDPRAGG SCFRECGGRA
      1210       1220       1230       1240       1250       1260       1270       1280
LLTNVSSVAL GSRRVGGLLP PGGGAARAGP GLSYCVWVVS ATEELQPCAP GTLCPPLTLT FSPDSSTPCT LSYVLAFDGF
      1290       1300       1310       1320       1330       1340       1350       1360
PRFLDTGVVQ SDRSLIAAFC GQRRDRPLTV QALSGLLVLH WEANGSSSWG FNASVGSARC GSGGPGSCPV PQECVPQDGA
      1370       1380       1390       1400       1410       1420       1430       1440
AGAGLCRCPQ GWAGPHCRMA LCPENCNAHT GAGTCNQSLG VCICAEGFGG PDCATKLDGG QLVWETLMDS RLSADTASRF
      1450       1460       1470       1480       1490       1500       1510       1520
LHRLGHTMVD GPDATLWMFG GLGLPQGLLG NLYRYSVSER RWTQMLAGAE DGGPGPSPRS FHAAAYVPAG RGAMYLLGGL
      1530       1540       1550       1560       1570       1580       1590       1600
TAGGVTRDFW VLNLTTLQWR QEKAPQTVEL PAVAGHTLTA RRGLSLLLVG GYSPENGFNQ QLLEYQLATG TWVSGAQSGT
      1610       1620       1630       1640       1650       1660       1670       1680
PPTGLYGHSA VYHEATDSLY VFGGFRFHVE LAAPSPELYS LHCPDRTWSL LAPSQGAKRD RMRNVRGSSR GLGQVPGEQP
      1690       1700       1710       1720       1730       1740       1750       1760
GSWGFREVRK KMALWAALAG TGGFLEEISP HLKEPRPRLF HASALLGDTM VVLGGRSDPD EFSSDVLLYQ VNCNAWLLPD
      1770       1780       1790       1800       1810       1820       1830       1840
LTRSASVGPP MEESVAHAVA AVGSRLYISG GFGGVALGRL LALTLPPDPC RLLSSPEACN QSGACTWCHG ACLSGDQAHR
      1850       1860       1870       1880       1890       1900       1910       1920
LGCGGSPCSP MPRSPEECRR LRTCSECLAR HPRTLQPGDG EASTPRCKWC TNCPEGACIG RNGSCTSEND CRINQREVFW
      1930       1940       1950       1960       1970       1980       1990       2000
AGNCSEAACG AADCEQCTRE GKCMWTRQFK RTGETRRILS VQPTYDWTCF SHSLLNVSPM PVESSPPLPC PTPCHLLPNC
      2010       2020       2030       2040       2050       2060       2070       2080
TSCLDSKGAD GGWQHCVWSS SLQQCLSPSY LPLRCMAGGC GRLLRGPESC SLGCAQATQC ALCLRRPHCG WCAWGGQDGG
      2090       2100       2110       2120       2130       2140       2150       2160
GRCMEGGLSG PRDGLTCGRP GASWAFLSCP PEDECANGHH DCNETQNCHD QPHGYECSCK TGYTMDNMTG LCRPVCAQGC
      2170       2180       2190       2200       2210       2220       2230       2240
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2125 | 1 | 1023.8906 | -13.46 | 3 | 57.0 | 12.4 | 2 | 1-31 | -.<br>MALGKVLAMALVLALAVLGSLSPG<br>G | Carbamidomethyl: 30;<br>Oxidation: 1 | |
| 112 | 1 | 668.6652 | 6.60 | 3 | 31.1 | 11.1 | 0 | 608-626 | R.LLGDCQACLAFSSPTAPPR.G | Carbamidomethyl: 8 | QU:MU 1.96 |

# Detailed Protein Report

## Protein 747: vacuolar protein sorting-associated protein 13D isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|54607139 | **Score:** | 23.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 491.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLEGLVAWVL | NTYLGKYVNN | LNTDQLSVAL | LKGAVELENL | PLKKDALKEL | ELPFEVKAGF | IGKVTLQIPF | YRPHVDPWVI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SISSLHLIGA | PEKIQDFNDE | KEKLLERERK | KALLQALEEK | WKNDRQQKGE | SYWYSVTASV | VTRIVENIEL | KIQDVHLRFE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DGVTNPSHPF | AFGICIKNVS | MQNAVNEPVQ | KLMRKKQLDV | AEFSIYWDVD | CTLLGDLPQM | ELQEAMARSM | ESRSHHYVLE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PVFASALLKR | NCSKKPLRSR | HSPRIDCDIQ | LETIPLKLSQ | LQYRQIMEFL | KELERKERQV | KFRRWKPKVA | ISKNCREWWY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FALNANLYEI | REQRKRCTWD | FMLHRARDAV | SYTDKYFNKL | KGGLLSTDDK | EEMCRIEEEQ | SFEELKILRE | LVHDRFHKQE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ELAESLREPQ | FDSPGACPGA | PEPGGGSGML | QYLQSWFPGW | GGWYGQQTPE | GNVVEGLSAE | QQEQWIPEEI | LGTEEFFDPT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ADASCMNTYT | KRDHVFAKLN | LQLQRGTVTL | LHKEQGTPQM | NESAFMQLEF | SDVKLLAESL | PRRNSSLLSV | RLGGLFLRDL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ATEGTMFPLL | VFPNPQKEVG | RVSQSFGLQT | TSADRSDHYP | AADPDGPVFE | MLYERNPAHS | HFERRLNVST | RPLNIIYNPQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AIKKVADFFY | KGKVHTSGFG | YQSELELRVA | EAARRQYNKL | KMQTKAEIRQ | TLDRLLVGDF | IEESKRWTVR | LDISAPQVIF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PDDFKFKNPV | LVVVDLGRML | LTNTQDNSRR | KSRDGSASEE | TQFSDDEYKT | PLATPPNTPP | PESSSSNGEK | TPPFSGVEFS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EEQLQAHLMS | TKMYERYSLS | FMDLQIMVGR | VKDNWKHVQD | IDVGPTHVVE | KFNVHLQLER | RLIYTSDPKY | PGAVLSGNLP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DLKIHINEDK | ISALKNCFAL | LTTPEMKTSD | TQIKEKIFPQ | EEQRGSLQDS | VMNLTQSIVL | LEQHTREVLV | ESQLLLAEFK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VNCMQLGVES | NGRYISVLKV | FGTNAHFVKR | PYDAEVSLTV | HGLLLVDTMQ | TYGADFDLLM | ASHKNLSFDI | PTGSLRDSRA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QSPVSGPNVA | HLTDGATLND | RSATSVSLDK | ILTKEQESLI | KLEYQFVSSE | CPSMNLDSTL | QVISLQVNNL | DIILNPETIV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ELIGFLQKSF | PKEKDDLSPQ | PLMTDFERSF | REQGTYQSTY | EQNTEVAVEI | HRLNLLLLRT | VGMANREKYG | RKIATASIGG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TKVNVSMGST | FDMNGSLGCL | QLMDLTQDNV | KNQYVVSIGN | SVGYENIISD | IGYFESVFVR | MEDAALTEAL | SFTFVERSKQ |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| ECFLNLKMAS | LHYNHSAKFL | KELTLSMDEL | EENFRGMLKS | AATKVTTVLA | TKTAEYSEMV | SLFETPRKTR | EPFILEENEI |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| YGFDLASSHL | DTVKLILNIN | IESPVVSIPR | KPGSPELLVG | HLGQIFIQNF | VAGDDESRSD | RLQVEIKDIK | LYSLNCTQLA |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GREAVGSEGS | RMFCPPSGSG | SANSQEEAHF | TRHDFFESLH | RGQAFHILNN | TTIQFKLEKI | PIERESELTF | SLSPDDLGTS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| SIMKIEGKFV | NPVQVVLAKH | VYEQVLQTLD | NLVYSEDLNK | YPASATSSPC | PDSPLPPLST | CGESSVERKE | NGLFSHSSLS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| NTSQKSLSVK | EVKSFTQIQA | TFCISELQVQ | LSGDLTLGAQ | GLVSLKFQDF | EVEFSKDHPQ | TLSIQIALHS | LLMEDLLEKN |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| PDSKYKNLMV | SRGAPKPSSL | AQKEYLSQSC | PSVSNVEYPD | MPRSLPSHME | EAPNVFQLYQ | RPTSASRKKQ | KEVQDKDYPL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| TPPPSPTVDE | PKILVGKSKF | DDSLVHINIF | LVDKKHPEFS | SSYNRVNRSI | DVDFNCLDVL | ITLQTWVVIL | DFFGIGSTAD |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| NHAMRLPPEG | ILHNVKLEPH | ASMESGLQDP | VNTKLDLKVH | SLSLVLNKTT | SELAKANVSK | LVAHLEMIEG | DLALQGSIGS |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| LSLSDLTCHG | EFYRERFTTS | GEEALIFQTF | KYGRPDPLLR | REHDIRVSLR | MASVQYVHTQ | RFQAEVVAFI | QHFTQLQDVL |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| GRQRAAIEGQ | TVRDQAQRCS | RVLLDIEAGA | PVLLIPESSR | SNNLIVANLG | KLKVKNKFLF | AGFPGTFSLQ | DKESVPSASP |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| TGIPKHSLRK | TTSTEEPRGT | HSQGQFTMPL | AGMSLGSLKS | EFVPSTSTKQ | QGPQPTLSVG | QESSSPEDHV | CLLDCVVVDL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| QDMDIFAAER | HPREYSKAPE | DSSGDLIFPS | YFVRQTGGSL | LTEPCRLKLQ | VERNLDKEIS | HTVPDISIHG | NLSSVHCSLD |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| LYKYKLIRGL | LENNLGEPIE | EFMRPYDLQD | PRIHTVLSGE | VYTCMCFLID | MVNVSLELKD | PKRKEGAGSL | ARFDFKKCKL |
| 2330 | 2340 | 2350 | 2360 | 2370 | 2380 | 2390 | 2400 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2118 | 1 | 900.3217 | -110.13 | 3 | 54.8 | 10.2 | 0 | 2835-2858 | K.SEDWMGSSVDPPCFGQSLPLVYLR.T | Oxidation: 5 |

# Detailed Protein Report

## Protein 748: PREDICTED: protein SZT2 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578798759 | **Score:** | 23.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 345.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.23 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.39 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVGGVYSYDC | SFGHVPNVEL | MKFIAMATFG | SYLSTCPEPE | PGNLGLTVYH | RAFLLYSFLR | SGEALNPEYY | CGSQHRLFNE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HLVSASSNPA | LALRRKKHTE | KEVPADLVST | VSVRLREGYS | VREVTLAKGG | SQLEVKLVLL | WKHNMRIEYV | AMAPWPLEPE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GPRVTRVEVT | MEGGYDILHD | VSCALRQPIR | SLYRTHVIRR | FWNTLQSINQ | TDQMLAHLQS | FSSVPEHFTL | PDSTKSGVPL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FYIPPGSTTP | VLSLQPSGSD | SSHAQFAAYW | KPVLSMDANS | WQRWLHMHRL | VLILEHDTPI | PKHLHTPGSN | GRYSTIQCRI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SHSSLTSLLR | DWSSFVLVEG | YSYVKLLSSA | PDQPPNSFYM | VRIISKAPCM | VLRLGFPIGT | PAPARHKIVS | GLREEILRLR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FPHRVQSKEP | TPKVKRKGLG | GAGGGSSPSK | SPPVLGPQQA | LSDRPCLVVL | HKPLDKLLIR | YEKLPLDYRA | PFLLTLEPPG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PLPLVSGRSA | SSSLASLSRY | LYHQRWLWSV | PSGLAPALPL | SAIAQLLSIL | TEVRLSEGFH | FACSGEGIIN | MVLELPIQNE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PPGQAAAEEK | HTCVVQYILF | PPHSTSTKDS | FSTDDDNDVE | VEALEGDSEL | NLVTEVWVEP | QYGRVGPGPG | IWKHLQDLTY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SEIPQALHPR | DAACIGSMLS | FEYLIQLCQS | KEWGPLPPEP | RVSDGLDQGG | DTCVHEIPFH | FDLMGLLPQC | QQLQMFFLLL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AREPEGVPFA | EGSCPANDMV | LCLLHSCLGQ | ELSDREIPLT | PVDQAAFLSE | VLRRTCHVPG | AEGPLLGVHG | IPKEQAVGST |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QATGDSAFTS | LSVGLPETLK | PLISAQPPQW | RCYARLVNPQ | HVFLTFLPAT | FSDVQRLAAC | GLEGPPQEET | KPKFGDWSGA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PSLKDLGGTG | IKATKSHVPV | LSVTLASDNA | QNQGELSPPF | RRDLQAYAGR | QASQTESADG | PRTRCPVYIY | SCSLEALREQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| MVGMQPPQAP | RDLIFRTQFL | DHPSPSSAWM | EPRYKEAANH | CALLQEHAQR | CYVRGLFRSL | QQAQSVTSQD | LLTAVDACEE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LLQEIDITPF | LLALCGHTWG | LPHAPPSPGP | LSPGPFSSSM | EEGAEPRERA | ILASESSIET | EDLSEPEFQS | TRVPGIPDPG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PEISLTDVCQ | LRGEAHGALH | SVIQEKFLEI | SRLHFRTVPS | NPHYFFYCPP | SSRREDEGPR | DTVDRKISDL | EFSEAELMGE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EGDTSACCVV | TESDPELEVE | YRESRESDLG | PAGLDSASLS | DVDTVNPDED | SFSILGGDSP | TGPESFLHDL | PPLFLHLTCS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VRLRGQHSSV | PVCSLPTCLG | QVLSSLEGPP | VGGRVPLRDL | SVTLDVFMLT | LPLEVELPTA | SDPQHHRSTS | ESSASFPRSP |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| GQPSSLRSDD | GLGPPLPPPE | EERHPGLSNL | ATPHRLAIET | TMNEIRWLLE | DEMVGALRRG | GIPQSPALHR | AAAHIHSSPG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| RSTCLRQTLP | LSFVFGPERS | LTQFKEEFRR | LHLPGHVLLE | DPDSGFFFVA | AGQQPGGSHG | EPSSAAWAWH | SHEDRAEGIE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| GETLTASPQA | PGSPEDSEGV | PLISLPRVPQ | GGSQPGPSRG | LSLMSSQGSV | DSDHLGYDGG | SSGSDSEGPN | DTLGEKAPFT |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LRTPPGPAPP | QPSLSGLPGP | CLPDFWLIVR | VLQDRVEVYA | HARSLIREDG | GPGTECRHLQ | QLLVRRVGEI | CREVNQRLLL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| QDLHDSHVCN | SLLVAESEED | LWRSETPFHS | RQRAPLPSDD | YAADESCAPR | GYLAATMQFV | PGHFSCDVVW | GTVIRVHSRL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| KMGPSMGVSR | AIQALRSVLN | AFSVVNRKNM | FVYQERATKA | VYYLRLLETS | CSDRPWKGDA | LPPSLALSRS | QEPIYSEEAS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| GPRSPLDMVS | SRSSDAARPV | GQVDRHIQLL | VHGVGQAGPE | ITDELVRVLC | RRLDEATLDV | ITVMLVRNCK | LTPADVEFIQ |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| PPGSLPSEVL | HLALPTSCRP | WLPALAWYLR | QNLLIFLHSP | KYTDSNSRNH | FQHPLPPQGG | LPDLDIYLYN | KPGGQGTGGK |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| GVACITLAFV | DEGGAPLSLA | LWPPSSPGPP | DPLREEEFEQ | LTQVIRCPVV | VDSSSAQNGA | PRLRLDVWEK | GNISIVQLEE |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| KLRGAARQAL | ADAIIELQLL | PASLCTEDTP | TGSLRNGSLE | TKSSAGRAST | FPPAPVPGEP | VTPPSKAGRR | SFWDMLSKTE |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2181 | 1 | 952.3242 | -131.11 | 2 | 57.1 | 11.6 | 0 | 2746-2760 | R.DLMHVHSFSYDFHLR.L | | |
| 865 | 1 | 705.2586 | -198.51 | 2 | 40.9 | 11.8 | 1 | 2989-3000 | K.RLFLLEPPGPDR.L | | WUP:QUP 0.39<br>QU:MU 1.23 |

# Detailed Protein Report

## Protein 749: PREDICTED: cytosolic carboxypeptidase 3 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578814196 | **Score:** | 23.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 99.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 4.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.88 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.52 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSEDSEKEDY | SDRTISDEDE | SDEDMFMKFV | SEDLHRCALL | TADSFGDPFF | PRTTQILLEY | QLGRWVPRLR | EPRDLYGVSS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SGPLSPTRWP | YHCEVIDEKV | QHIDWTPSCP | EPVYIPTGLE | TEPLYPDSKE | ATVVYLAEDA | YKEPCFVYSR | VGGNRTPLKQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PVDYRDNTLM | FEARFESGNL | QKVVKVAEYE | YQLTVRPDLF | TNKHTQWYYF | QVTNMRAGIV | YRFTIVNFTK | PASLYSRGMR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PLFYSEKEAK | AHHIGWQRIG | DQIKYYRNNP | GQDGRHYFSL | TWTFQFPHNK | DTCYFAHCYP | YTYTNLQEYL | SGINNDPVRS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KFCKIRVLCH | TLARNMVYIL | TITTPLKNSD | SRKRKAVILT | ARVHPGETNS | SWIMKGFLDY | ILGNSSDAQL | LRDTFVFKVV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PMLNPDGVIV | GNYRCSLAGR | DLNRNYTSLL | KESFPSVWYT | RNMVHRLMEK | REVILYCDLH | GHSRKENIFM | YGCDGSDRSK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TLYLQQRIFP | LMLSKNCPDK | FSFSACKFNV | QKSKEGTGRV | VMWKMGIRNS | FTMEATFCGS | TLGNKRGTHF | STKDLESMGY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HFCDSLLDYC | DPDRTKYYRC | LKELEEMERH | ITLEKVFEDS | DTPVIDITLD | VESSSRGSDS | SESIDSLTYL | LKLTSQKKHL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KTKKERNSTI | ASHQNARGQE | VYDRGHLLQR | HTQSNSDVKD | TRPNEPDDYM | VDYFRRQLPN | QGLVKIPERA | PSWLLKKYLR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LNPATCRNIK | KYSTSWTAPR | NHPFVIQGDV | MANSSEWVQS | KPHRSLESLS | PLKGPKKNKH | SQIWAIKNED | IKPLSSKWET |
| 810 | 820 | 830 | 840 | 850 | 860 | | |
| ASSSFGMDAN | VLKYKSLQAE | ETNQQSSKHT | ALHLTKNKDE | QANKNDGQPT | LYLKFQRES | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1532 | 1 | 917.3273 | -136.49 | 2 | 49.4 | 13.3 | 1 | 839-854 | K.DEQANKNDGQPTLYLK.F | | WUP:QUP 0.52<br>QU:MU 0.88 |

# Detailed Protein Report

## Protein 750: acetylcholine receptor subunit delta isoform 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|375331911 | **Score:** | 23.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| | | **Sequence Coverage [%]:** | 5.4 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEGPVLTLGL | LAALAVCGSW | GLNEEERLIR | HLFQEKGYNK | ELRPVAHKEE | SVDVALALTL | SNLISLGWTD | NRLKWNAEEF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GNISVLRLPP | DMVWLPEIVL | ENNNDGSFQI | SYSCNVLVYH | YGFVYWLPPA | IFRSSCPISV | TYFPFDWQNC | SLKFSSLKYT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AKEITLSLKQ | DAKENRTYPV | EWIIIDPEGF | TENGEWEIVH | RPARVNVDPR | APLDSPSRQD | ITFYLIIRRK | PLFYIINILV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PCVLISFMVN | LVFYLPADSG | EKTSVAISVL | LAQSVFLLLI | SKRLPATSMA | IPLIGKFLLF | GMVLVTMVVV | ICVIVLNIHF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RTPSTHVLSE | GVKKLFLETL | PELLHMSRPA | EDGPSPGALV | RRSSSLGYIS | KAEEYFLLKS | RSDLMFEKQS | ERHGLARRLT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TARRPPASSE | QAQQELFNEL | KPAVDGANFI | VNHMRDQNNY | NEEKDSWNRV | ARTVDRLCLF | VVTPVMVVGT | AWIFLQGVYN |
| 490 | 500 | 510 | | | | | |
| QPPPQPFPGD | PYSYNVQDKR | FI | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1638 | 1 | 823.4155 | -56.77 | 2 | 48.8 | 12.6 | 2 | 28-40 | R.LIRHLFQEKGYNK.E | |
| 1931 | 1 | 734.3090 | -177.58 | 2 | 52.5 | 10.8 | 1 | 283-296 | K.RLPATSMAIPLIGK.F | |

# Detailed Protein Report

## Protein 751: PREDICTED: serine/arginine repetitive matrix protein 2 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530407861 | **Score:** | 23.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 281.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.6 |
| | | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MYNGIGLPTP | RGSGTNGYVQ | RNLSLVRGRR | GERPDYKGEE | ELRRLEAALV | KRPNPDILDH | ERKRRVELRC | LELEEMMEEQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GYEEQQIQEK | VATFRLMLLE | KDVNPGGKEE | TPGQRPAVTE | THQLAELNEK | KNERLRAAFG | ISDSYVDGSS | FDPQRRAREA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KQPAPEPPKP | YSLVRESSSS | RSPTPKQKKK | KKKKDRGRRS | ESSSPRRERK | KSSKKKKHRS | ESESKKRKHR | SPTPKSKRKS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KDKKRKRSRS | TTPAPKSRRA | HRSTSADSAS | SSDTSRSRSR | SAAAKTHTTA | LAGRSPSPAS | GRRGEGDAPF | SEPGTTSTQR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PSSPETATKQ | PSSPYEDKDK | DKKEKSATRP | SPSPERSSTG | PEPPAPTPLL | AERHGGSPQP | LATTPLSQEP | VNPPSEASPT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RDRSPPKSPE | KLPQSSSSES | SPPSPQPTKV | SRHASSSPES | PKPAPAPGSH | REISSSPTSK | NRSHGRAKRD | KSHSHTPSRR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| MGRSRSPATA | KRGRSRSRTP | TKRGHSRSRS | PQWRRSRSAQ | RWGRSRSPQR | RGRSRSPQRP | GWSRSRNTQR | RGRSRSARRG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RSHSRSPATR | GRSRSRTPAR | RGRSRSRTPA | RRRSRSRTPT | RRRSRSRTPA | RRGRSRSRTP | ARRRSRTRSP | VRRRSRSRSP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ARRSGRSRSR | TPARRGRSRS | RTPARRGRSR | SRTPARRSGR | SRSRTPARRG | RSRSRTPRRG | RSRSRSLVRR | GRSHSRTPQR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RGRSGSSSER | KNKSRTSQRR | SRSNSSPEMK | KSRISSRRSR | SLSSPRSKAK | SRLSLRRSLS | GSSPCPKQKS | QTPPRRSRSG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SSQPKAKSRT | PPRRSRSSSS | PPPKQKSKTP | SRQSHSSSSP | HPKVKSGTPP | RQGSITSPQA | NEQSVTPQRR | SCFESSPDPE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LKSRTPSRHS | CSGSSPPRVK | SSTPPRQSPS | RSSSPQPKVK | AIISPRQRSH | SGSSSPSPSR | VTSRTTPRRS | RSVSPCSNVE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SRLLPRYSHS | GSSSPDTKVK | PETPPRQSHS | GSISPYPKVK | AQTPPGPSLS | GSKSPCPQEK | SKDSLVQSCP | GSLSLCAGVK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SSTPPGESYF | GVSSLQLKGQ | SQTSPDHRSD | TSSPEVRQSH | SESPSLQSKS | QTSPKGGRSR | SSSPVTELAS | RSPIRQDRGE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| FSASPMLKSG | MSPEQSRFQS | DSSSYPTVDS | NSLLGQSRLE | TAESKEKMAL | PPQEDATASP | PRQKDKFSPF | PVQDRPESSL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VFKDTLRTPP | RERSGAGSSP | ETKEQNSALP | TSSQDEELME | VVEKSEEPAG | QILSHLSSEL | KEMSTSNFES | SPEVEERPAV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SLTLDQSQSQ | ASLEAVEVPS | MASSWGGPHF | SPEHKELSNS | PLRENSFGSP | LEFRNSGPLG | TEMNTGFSSE | VKEDLNGPFL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| NQLETDPSLD | MKEQSTRSSG | HSSSELSPDA | VEKAGMSSNQ | SISSPVLDAV | PRTPSRERSS | SASSPEMKDG | LPRTPSRRSR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SGSSPGLRDG | SGTPSRHSLS | GSSPGMKDIP | RTPSRGRSEC | DSSPEPKALP | QTPRPRSRSP | SSPELNNKCL | TPQRERSGSE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| SSVDQKTVAR | TPLGQRSRSG | SSQELDVKPS | ASPQERSESD | SSPDSKAKTR | TPLRQRSRSG | SSPEVDSKSR | LSPRRSRSGS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| SPEVKDKPRA | APRAQSGSDS | SPEPKAPAPR | ALPRRSRSGS | SSKGRGPSPE | GSSSTESSPE | HPPKSRTARR | GSRSSPEPKT |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| KSRTPPRRRS | SRSSPELTRK | ARLSRRSRSA | SSSPETRSRT | PPRHRRSPSV | SSPEPAEKSR | SSRRRRSASS | PRTKTTSRRG |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| RSPSPKPRGL | QRSRSRSRRE | KTRTTRRRDR | SGSSQSTSRR | RQRSRSRSRV | TRRRRGGSGY | HSRSPARQES | SRTSSRRRRG |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| RSRTPPTSRK | RSRSRTSPAP | WKRSRSRASP | ATHRRSRSRT | PLISRRRSRS | RTSPVSRRRS | RSRTSVTRRR | SRSRASPVSR |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| RRSRSRTPPV | TRRRSRSRTP | TTRRRSRSRT | PPVTRRRSRS | RTPPVTRRRS | RSRTSPITRR | RSRSRTSPVT | RRRSRSRTSP |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| VTRRRSRSRT | SPVTRRRSRS | RTPPAIRRRS | RSRTPLLPRK | RSRSRSPLAI | RRRSRSRTPR | TARGKRSLTR | SPPAIRRRSA |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| SGSSSDRSRS | ATPPATRNHS | GSRTPPVALN | SSRMSCFSRP | SMSPTPLDRC | RSPGMLEPLG | SSRTPMSVLQ | QAGGSMMDGP |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2872 | 4 | 703.3612 | -2.24 | 2 | 66.4 | 13.0 | 1 | 833-845 | R.QSHSSSSPHPKVK.S | |
| 2324 | 1 | 841.5088 | 116.64 | 2 | 57.3 | 10.3 | 1 | 1614-1630 | R.AQSGSDSSPEPKAPAPR.A | |

# Detailed Protein Report

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**Protein 752:** **PREDICTED: signal transducer and activator of transcription 2 isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530400750 | **Score:** | 23.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 60.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530400752 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: signal transducer and activator of transcription 2 isoform X4 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAASVGVAAG | NGGRSGLPLP | TTRGRVRGGL | AEVVGGARGS | STRAHTRDGK | SRPEPLEGAG | TATLIRAQMA | QWEMLQNLDS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PFQDQLHQLY | SHSLLPVDIR | QYLAVWIEDQ | NWQEAALGSD | DSKATMLFFH | FLDQLNYECG | RCSQDPESLL | LQHNLRKFCR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DIQPFSQDPT | QLAEMIFNLL | LEEKRILIQA | QRAQLEQGEP | VLETPVESQQ | HEIESRILDL | RAMMEKLVKS | ISQLKDQQDV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FCFRYKIQAK | GKTPSLDPHQ | TKEQKILQET | LNELDKRRKE | VLDASKALLG | RLTTLIELLL | PKLEEWKAQQ | QKACIRAPID |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HGLEQLETWF | TAGAKLLFHL | RQLLKELKGL | SCLVSYQDDP | LTKGVDLRNA | QVTELLQRLL | HRAFVVETQP | CMPQTPHRPL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ILKTGSKFTV | RTRLLVRLQE | GNESLTVEVS | IDRNPPQLQG | FRKFNILTSN | QKTLTPEKGQ | SQGLIWDFGY | LTLVEQRSGG |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| SGKGSNKGPL | GVTEELHIIS | FTVKYTYQGL | KQELKVSENG | GQGERKQLWK | KA | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 782 | 1 | 1105.5604 | -4.79 | 2 | 39.8 | 12.9 | 0 | 459-477 | K.GQSQGLIWDFGYLTLVEQR.S | |

# Detailed Protein Report

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**Protein 753:** **glutamyl aminopeptidase [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|132814467 | **Score:** | 23.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 109.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| | | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MNFAEREGSK | RYCIQTKHVA | ILCAVVVGVG | LIVGLAVGLT | RSCDSSGDGG | PGTAPAPSHL | PSSTASPSGP | PAQDQDICPA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SEDESGQWKN | FRLPDFVNPV | HYDLHVKPLL | EEDTYTGTVS | ISINLSAPTR | YLWLHLRETR | ITRLPELKRP | SGDQVQVRRC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FEYKKQEYVV | VEAEEELTPS | SGDGLYLLTM | EFAGWLNGSL | VGFYRTTYTE | NGQVKSIVAT | DHEPTDARKS | FPCFDEPNKK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ATYTISITHP | KEYGALSNMP | VAKEESVDDK | WTRTTFEKSV | PMSTYLVCFA | VHQFDSVKRI | SNSGKPLTIY | VQPEQKHTAE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YAANITKSVF | DYFEEYFAMN | YSLPKLDKIA | IPDFGTGAME | NWGLITYRET | NLLYDPKESA | SSNQQRVATV | VAHELVHQWF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GNIVTMDWWE | DLWLNEGFAS | FFEFLGVNHA | ETDWQMRDQM | LLEDVLPVQE | DDSLMSSHPI | IVTVTTPDEI | TSVFDGISYS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KGSSILRMLE | DWIKPENFQK | GCQMYLEKYQ | FKNAKTSDFW | AALEEASRLP | VKEVMDTWTR | QMGYPVLNVN | GVKNITQKRF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LLDPRANPSQ | PPSDLGYTWN | IPVKWTEDNI | TSSVLFNRSE | KEGITLNSSN | PSGNAFLKIN | PDHIGFYRVN | YEVATWDSIA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TALSLNHKTF | SSADRASLID | DAFALARAQL | LDYKVALNLT | KYLKREENFL | PWQRVISAVT | YIISMFEDDK | ELYPMIEEYF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QGQVKPIADS | LGWNDAGDHV | TKLLRSSVLG | FACKMGDREA | LNNASSLFEQ | WLNGTVSLPV | NLRLLVYRYG | MQNSGNEISW |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NYTLEQYQKT | SLAQEKEKLL | YGLASVKNVT | LLSRYLDLLK | DTNLIKTQDV | FTVIRYISYN | SYGKNMAWNW | IQLNWDYLVN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RYTLNNRNLG | RIVTIAEPFN | TELQLWQMES | FFAKYPQAGA | GEKPREQVLE | TVKNNIEWLK | QHRNTIREWF | FNLLESG |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 793 | 1 | 709.9203 | 61.50 | 2 | 38.3 | 10.6 | 0 | 541-553 | R.QMGYPVLNVNGVK.N | |

# Detailed Protein Report

## Protein 754: PREDICTED: zinc finger protein 263 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578827945 | **Score:** | 23.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 67.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.1 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASGPGSQER | EGLLIVKLEE | DCAWSQELPP | PDPGPSPEAS | HLRFRRFRFQ | EAAGPREALS | RLQELCHGWL | RPEMRTKEQI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LELLVLEQFL | TILPQEIQSR | VQELHPESGE | EAVTLVEDMQ | RELGRLRQQL | PESLEDVAMY | ISQEEWGHQD | PSKRALSRDT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VQESYENVDS | LESHIPSQEV | PGTQVGQGGK | LWDPSVQSCK | EGLSPRGPAP | GEEKFENLEG | VPSVCSENIH | PQVLLPDQAR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GEVPWSPELG | RPHDRSQGDW | APPPEGGMEQ | ALAGASSGRE | LGRPKELQPK | KLHLCPLCGK | NFSNNSNLIR | HQRIHAAERL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CMGVDCTEIF | GGNPRFLSLH | RAHLGEEAHK | CLECGKCFSQ | NTHLTRHQRT | HTGEKPYQCN | ICGKCFSCNS | NLHRHQRTHT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GEKPYKCPEC | GEIFAHSSNL | LRHQRIHTGE | RPYKCPECGK | SFSRSSHLVI | HERTHERERL | YPFSECGEAV | SDSTPFLTNH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GAHKAEKKLF | ECLTCGKSFR | QGMHLTRHQR | THTGEKPYKC | TLCGENFSHR | SNLIRHQRIH | TGEKPYTCHE | CGDSFSHSSN |
| 570 | 580 | 590 | 600 | | | | |
| RIRHLRTHTG | ERPYKCSECG | ESFSRSSRLM | SHQRTHTG | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1617 | 1 | 820.8186 | -162.40 | 2 | 50.5 | 10.3 | 1 | 2-17 | M.ASGPGSQEREGLLIVK.L | |

# Detailed Protein Report

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## Protein 755: PREDICTED: polycystic kidney disease protein 1-like 1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578813318 | **Score:** | 23.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 223.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.24 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.54 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAEEAAQNIS | DDQERCLQAA | CCLSFGGELS | VSTDKSWGLH | LCSCSPPGGG | LWVEVYANHV | LLMSDGKCGC | PWCALNGKAE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DRESQSPSSS | ASRQKNIWKT | TSEAALSVVN | EKTQAVVNEK | TQAPLDCDNS | ADRIPHKPFI | IIARAWSSGG | PRFHHRRLCA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TGTADSTFSA | LLQLQGTTSA | AAPCSLKMEA | SCCVLRLLCC | AEDVATGLLP | GTVTMETPTK | VARPTQTSSQ | RVPLWPISHF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PTSPRSSHGL | PPGIPRTPSF | TASQSGSEIL | YPPTQHPPVA | ILARNSDNFM | NPVLNCSLEV | EARAPPNLGF | RVHMASGEAL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CLMMDFGDSS | GVEMRLHNMS | EAMAVTAYHQ | YSKEDWQRNS | QEGVYMLKAV | IYNEFHGTEV | ELGPYYVEIG | HEAVSAFMNS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SSVHEDEVLV | FADSQVNQKS | TVVIHHFPSI | PSYNVSFISQ | TQVGDSQAWH | SMTVWYKMQS | VSVYTNGTVF | ATDTDITFTA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VTKETIPLEF | EWYFGEDPPV | RTTSRSIKKR | LSIPQWYRVM | VKASNRMSSV | VSEPHVIRVQ | KKIVANRLTS | PSSALVNASV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AFECWINFGT | DVAYLWDFGD | GTVSLGSSSS | SHVYSREGEF | TVEVLAFNNV | SASTLRQQLF | IVCEPCQPPL | VKNMGPGKVQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IWRSQPVRLG | VTFEAAVFCD | ISQGLSYTWN | LMDSEGLPVS | LPAAVDTHRQ | TLILPSHTLE | YGNYTALAKV | QIEGSVVYSN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YCVGLEVRAQ | APVSVISEGT | HLFFSRTTSS | PIVLRGTQSF | DPDDPGATLR | YHWECATAGS | PAHPCFDSST | AHQLDAAAPT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VSFEAQWLSD | SYDQFLVMLR | VSSGGRNSSE | TRVFLSPYPD | SAFRFVHISW | VSFKDTFVNW | NDELSLQAMC | EDCSEIPNLS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| YSWDLFLVNA | TEKNRIEVPF | CRVVGLLGSL | GLGAISESSQ | LNLLPTEPGT | ADPDATTTPF | SREPSPVTLG | QPATSAPRGT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PTEPMTGVYW | IPPAGDSAVL | GEAPEEGSLD | LEPGPQSKGS | LMTGRSERSQ | PTHSPDPHLS | DFEAYYSDIQ | EAIPSGGRQP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AKDTSFPGSG | PSLSAEESPG | DGDNLVDPSL | SAGRAEPVLM | IDWPKALLGR | AVFQGYSSSG | ITEQTVTIKP | YSLSSGETYV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LQVSVASKHG | LLGKAQLYLT | VNPAPRDMAC | QVQPHHGLEA | HTVFSVFCMS | GKPDFHYEFS | YQIGNTSKHT | LYHGRDTQYY |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| FVLPAGEHLD | NYKVMVSTEI | TDGKGSKVQP | CTVVVTVLPR | YHGNDCLGED | LYNSSLKNLS | TLQLMGSYTE | IRNYITVITR |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| ILSRLSKEDK | TASCNQWSRI | QDALISSVCR | LAFVDQEEMI | GSVLMLRDLV | SFSNKLGFMS | AVLILKYTRA | LLAQGQFSGP |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| FVIDKGVRLE | LIGLISRVWE | VSEQENSKEE | VYRHEEGITV | ISDLLLGCLS | LNHVSTGQME | FRTLLHYNLQ | SSVQSLGSVQ |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| VHLPGDLAGH | SPAGAETQSP | CYISQLILFK | KNPYPGSQAP | GQIGGVVGLN | LYTCSSRRPI | NRQWLRKPVM | VEFGEEDGLD |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| NRRNKTTFVL | LRDKVNLHQF | TELSENPQES | LQIEIEFSKP | VTRAFPVMLL | VRFSEKPTPS | DFLVKQIYFW | DESIVQIYIP |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| AASQKDASVG | YLSLLDADYD | RKPPNRYLAK | AVNYTVHFQW | IRCLFWDKRE | WKSERFSPQP | GTSPEKVNCS | YHRLAAFALL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| RRKLKASFEV | SDISKLQSHP | ENLLPSIFIM | GSVILYGFLV | AKSRQVDHHE | KKKAGYIFLQ | EASLPGHQLY | AVVIDTGFRA |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| PARLTSKVYI | VLCGDNGLSE | TKELSCPEKP | LFERNSRHTF | ILSAPAQLGL | LRKIRLWHDS | RGPSPGWFIS | HVMVKELHTG |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| QGWFFPAQCW | LSAGRHDGRV | ERELTCLQGG | LGFRKLFYCK | FTEYLEDFHV | WLSVYSRPSS | SRYLHTPRLT | VSFSLLCVYA |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| CLTALVAAGG | QEQPHLDVSP | TLGSFRVGLL | CTLLASPGAQ | LLSLLFRLSK | EAPGSARVEP | HSPLRGGAQT | EAPHGPNSWG |
| 2010 | 2020 | 2030 | | | | | |
| RIPDAQEPRK | VNQSLCAAAN | LLA | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 465 | 1 | 667.6915 | -184.62 | 2 | 34.3 | 10.3 | 0 | 1378-1388 | R.VWEVSEQENSK.E | | |
| 714 | 1 | 541.1775 | -140.74 | 3 | 37.4 | 13.0 | 0 | 1986-2001 | R.GGAQTEAPHGPNSWGR.I | | WUP:QUP 0.54<br>QU:MU 2.24 |

# Detailed Protein Report

## Protein 756: 2'-5'-oligoadenylate synthase 2 isoform 1 [Homo sapiens]

**Accession:** gi|74229019
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 23.3
**MW [kDa]:** 82.4
**pI:** 9.4
**Sequence Coverage [%]:** 3.1
**No. of unique Peptides:** 1

## Quantitation

***WUP:QUP*** **Median:** 1.34 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGNGESQLSS | VPAQKLGWFI | QEYLKPYEEC | QTLIDEMVNT | ICDVLQEPEQ | FPLVQGVAIG | GSYGRKTVLR | GNSDGTLVLF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FSDLKQFQDQ | KRSQRDILDK | TGDKLKFCLF | TKWLKNNFEI | QKSLDGFTIQ | VFTKNQRISF | EVLAAFNALS | LNDNPSPWIY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RELKRSLDKT | NASPGEFAVC | FTELQQKFFD | NRPGKLKDLI | LLIKHWHQQC | QKKIKDLPSL | SPYALELLTV | YAWEQGCRKD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NFDIAEGVRT | VLELIKCQEK | LCIYWMVNYN | FEDETIRNIL | LHQLQSARPV | ILDPVDPTNN | VSGDKICWQW | LKKEAQTWLT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SPNLDNELPA | PSWNVLPAPL | FTTPGHLLDK | FIKEFLQPNK | CFLEQIDSAV | NIIRTFLKEN | CFRQSTAKIQ | IVRGGSTAKG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TALKTGSDAD | LVVFHNSLKS | YTSQKNERHK | IVKEIHEQLK | AFWREKEEEL | EVSFEPPKWK | APRVLSFSLK | SKVLNESVSF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DVLPAFNALG | QLSSGSTPSP | EVYAGLIDLY | KSSDLPGGEF | STCFTVLQRN | FIRSRPTKLK | DLIRLVKHWY | KECERKLKPK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GSLPPKYALE | LLTIYAWEQG | SGVPDFDTAE | GFRTVLELVT | QYQQLCIFWK | VNYNFEDETV | RKFLLSQLQK | TRPVILDPAE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PTGDVGGGDR | WCWHLLAKEA | KEWLSSPCFK | DGTGNPIPPW | KVPTMQTPGS | CGARIHPIVN | EMFSSRSHRI | LNNNSKRNF |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1541 | 1 | 669.8176 | -79.84 | 2 | 49.5 | 10.7 | 2 | 707-717 | R.SHRILNNNSKR.N | | WUP:QUP 1.34 |

# Detailed Protein Report

## Protein 757: immunoglobulin superfamily member 22 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|253970427 | **Score:** | 23.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 147.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTTIHSRQML | QEHVSMEFSS | STTHVQTFSQ | TTKIVGEEVV | RRKSSSIVEF | FSLVTRSSNI | PAGDSVPEFV | EKPQPVTAPE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GDKAVFRARV | QGNAKPHISW | KRESGIPIKE | SAKIFYDSIN | KEHVLKLEPL | TSDDSDNYKC | IASNDHADAI | YTVSLLVTEG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QEKMDFKKML | KKRAPPAPKK | KQKKVANEKE | MLEILSKVPK | KDFEKVCMEY | GFTDFRGLLR | KLKEMKKKVE | VEAIRILKPL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EDKETKVDTT | VVFDCIMELK | DPNVKMIWIK | GTEPLRIQYS | LGKYDVKQMG | TKYMLVISNV | NMNDAGIYSL | SVGDKRMSAE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LTVLDEPLKF | LGEMKPVKVT | ERQTAVFEIR | LSKKEPNFVW | KFNGKELKRD | DKYEITVSED | GLTHTLKIKD | ARLSDSGEFS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AEAGNLVQKA | QLTIDRIPIK | FVSNLKNVRV | KERSRACLEC | ELTSKDVTLR | WKKDGQLLMH | GTKYSMNHEG | KRAELIIEDA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QLSDGGEYTV | VAMQDGDPTE | YYSTAIVTVE | ERLATVKSGM | SDVHAATGSP | AELCVVLNDE | KVEGVWLKDG | KEITDLPGMQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IVKQGAVHKL | IFPSMGPEHE | GKYTFRAKGT | ESEASVFIAD | PPTIDPSVLE | ALAAHAITVK | VGHTAHIKVP | FRGKPLPKVT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| WYKDGMEVTE | EERVSMERGE | DQALLTISNC | VREDSGLILL | KLKNDHGSAT | ATLHLSVLDR | PKPPQGRVEF | LELSGSCVHM |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KWKAPKDNGG | RPVTQFIVER | RAVGKKSWIK | IGEVDGKVTN | FSTNKVEEGK | AYQFRILAVN | SEGVSDPLET | EEVFAGNPIE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PPGFASQPQV | TDVTKEAVTI | TWNAPTQDGG | APVLGYIVER | RKKGSNLWVP | VNKDPIQGTK | CTVDGLLEDT | EYEFRVIAVN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KAGPGQPSVP | SSSVVAKDPV | KPPGLVQDLH | VSDSSNSSIS | LAWREPAEGD | PPSGYILEMR | AEDTKEWSKC | TKIPISGTCY |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TVGGLIERQK | YFFRIRAVNE | AGVGEPVELD | KGVRAMPPPA | APKFDLSARL | KSHMVVRAGT | ALCIHAAFSG | SPPPDVIWQK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| DGVPTKGRET | ITKSKNHSQF | LINSTKRSDS | GVYRILLQNE | FGEARYDIHV | RVADFPRPPT | NLRLFEEVPN | TVTLTWNHSP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DVQEDGEAHY | IIMKRDASTA | TWYTAAERVF | SNKYTVTGLL | PGRKYYFRVV | ARNEIGDSEP | LDSRDTWLIN | KDQIQDLSAK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LKPYEKKDWR | HAPRFVTPLK | PHTVLRGQDC | TMTCAFLGNP | RPTVTLYKGD | VNITANSKFW | YNSTSGVCTL | VIPTCTLKDS |
| 1290 | 1300 | 1310 | 1320 | 1330 | | | |
| GDYSVLVENE | LGKDRSSCTL | TVYDKDDKSV | VASITESLQK | KSKHLM | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2097 | 1 | 900.3887 | -98.78 | 3 | 56.6 | 12.0 | 2 | 977-1003 | R.AVNEAGVGEPVELDKGVRAMPPPAAPK.F | |

# Detailed Protein Report

## Protein 758: mediator of RNA polymerase II transcription subunit 13 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|102468717 | **Score:** | 23.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 239.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSASFVPNGA | SLEDCHCNLF | CLADLTGIKW | KKYVWQGPTS | APILFPVTEE | DPILSSFSRC | LKADVLGVWR | RDQRPGRREL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| WIFWWGEDPS | FADLIHHDLS | EEEDGVWENG | LSYECRTLLF | KAVHNLLERC | LMNRNFVRIG | KWFVKPYEKD | EKPINKSEHL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SCSFTFFLHG | DSNVCTSVEI | NQHQPVYLLS | EEHITLAQQS | NSPFQVILCP | FGLNGTLTGQ | AFKMSDSATK | KLIGEWKQFY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PISCCLKEMS | EEKQEDMDWE | DDSLAAVEVL | VAGVRMIYPA | CFVLVPQSDI | PTPSPVGSTH | CSSSCLGVHQ | VPASTRDPAM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SSVTLTPPTS | PEEVQTVDPQ | SVQKWVKFSS | VSDGFNSDST | SHHGGKIPRK | LANHVVDRVW | QECNMNRAQN | KRKYSASSGG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LCEEATAAKV | ASWDFVEATQ | RTNCSCLRHK | NLKSRNAGQQ | GQAPSLGQQQ | QILPKHKTNE | KQEKSEKPQK | RPLTPFHHRV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SVSDDVGMDA | DSASQRLVIS | APDSQVRFSN | IRTNDVAKTP | QMHGTEMANS | PQPPPLSPHP | CDVVDEGVTK | TPSTPQSQHF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YQMPTPDPLV | PSKPMEDRID | SLSQSFPPQY | QEAVEPTVYV | GTAVNLEEDE | ANIAWKYYKF | PKKKDVEFLP | PQLPSDKFKD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DPVGPFGQES | VTSVTELMVQ | CKKPLKVSDE | LVQQYQIKNQ | CLSAIASDAE | QEPKIDPYAF | VEGDEEFLFP | DKKDRQNSER |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EAGKKHKVED | GTSSVTVLSH | EEDAMSLFSP | SIKQDAPRPT | SHARPPSTSL | IYDSDLAVSY | TDLDNLFNSD | EDELTPGSKK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SANGSDDKAS | CKESKTGNLD | PLSCISTADL | HKMYPTPPSL | EQHIMGFSPM | NMNNKEYGSM | DTTPGGTVLE | GNSSSIGAQF |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KIEVDEGFCS | PKPSEIKDFS | YVYKPENCQI | LVGCSMFAPL | KTLPSQYLPP | IKLPEECIYR | QSWTVGKLEL | LSSGPSMPFI |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KEGDGSNMDQ | EYGTAYTPQT | HTSFGMPPSS | APPSNSGAGI | LPSPSTPRFP | TPRTPRTPRT | PRGAGGPASA | QGSVKYENSD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LYSPASTPST | CRPLNSVEPA | TVPSIPEAHS | LYVNLILSES | VMNLFKDCNF | DSCCICVCNM | NIKGADVGVY | IPDPTQEAQY |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RCTCGFSAVM | NRKFGNNSGL | FLEDELDIIG | RNTDCGKEAE | KRFEALRATS | AEHVNGGLKE | SEKLSDDLIL | LLQDQCTNLF |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SPFGAADQDP | FPKSGVISNW | VRVEERDCCN | DCYLALEHGR | QFMDNMSGGK | VDEALVKSSC | LHPWSKRNDV | SMQCSQDILR |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| MLLSLQPVLQ | DAIQKKRTVR | PWGVQGPLTW | QQFHKMAGRG | SYGTDESPEP | LPIPTFLLGY | DYDYLVLSPF | ALPYWERLML |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| EPYGSQRDIA | YVVLCPENEA | LLNGAKSFFR | DLTAIYESCR | LGQHRPVSRL | LTDGIMRVGS | TASKKLSEKL | VAEWFSQAAD |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GNNEAFSKLK | LYAQVCRYDL | GPYLASLPLD | SSLLSQPNLV | APTSQSLITP | PQMTNTGNAN | TPSATLASAA | SSTMTVTSGV |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| AISTSVATAN | STLTTASTSS | SSSSNLNSGV | SSNKLPSFPP | FGSMNSNAAG | SMSTQANTVQ | SGQLGGQQTS | ALQTAGISGE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| SSSLPTQPHP | DVSESTMDRD | KVGIPTDGDS | HAVTYPPAIV | VYIIDPFTYE | NTDESTNSSS | VWTLGLLRCF | LEMVQTLPPH |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| IKSTVSVQII | PCQYLLQPVK | HEDREIYPQH | LKSLAFSAFT | QCRRPLPTST | NVKTLTGFGP | GLAMETALRS | PDRPECIRLY |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| APPFILAPVK | DKQTELGETF | GEAGQKYNVL | FVGYCLSHDQ | RWILASCTDL | YGELLETCII | NIDVPNRARR | KKSSARKFGL |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| QKLWEWCLGL | VQMSSLPWRV | VIGRLGRIGH | GELKDWSCLL | SRRNLQSLSK | RLKDMCRMCG | ISAADSPSIL | SACLVAMEPQ |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| GSFVIMPDSV | STGSVFGRST | TLNMQTSQLN | TPQDTSCTHI | LVFPTSASVQ | VASATYTTEN | LDLAFNPNND | GADGMGIFDL |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| LDTGDDLDPD | IINILPASPT | GSPVHSPGSH | YPHGGDAGKG | QSTDRLLSTE | PHEEVPNILQ | QPLALGYFVS | TAKAGPLPDW |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| FWSACPQAQY | QCPLFLKASL | HLHVPSVQSD | ELLHSKHSHP | LDSNQTSDVL | RFVLEQYNAL | SWLTCDPATQ | DRRSCLPIHF |
| 2170 | 2180 | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1464 | 1 | 1006.5988 | 75.55 | 2 | 46.7 | 10.3 | 2 | 1251-1267 | K.VDEALVKSSCLHPWSKR.N | Carbamidomethyl: 10 |

# Detailed Protein Report

## Protein 759: PREDICTED: extended synaptotagmin-3 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578807790 | **Score:** | 23.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 91.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MRAEEPCAPG APSALGAQRT PGPELRLSSQ LLPELCTFVV RVLFYLGPVY LAGYLGLSIT WLLLGALLWM WWRRNRRGKL
        90        100        110        120        130        140        150        160
GRLAAAFEFL DNEREFISRE LRGQHLPAWI HFPDVERVEW ANKIISQTWP YLSMIMESKF REKLEPKIRE KSIHLRTFTF
       170        180        190        200        210        220        230        240
TKLYFGQKCP RVNGVKAHTN TCNRRRVTVD LQICYIGDCE ISVELQKIQA GVNGIQLQGT LRVILEPLLV DKPFVGAVTV
       250        260        270        280        290        300        310        320
FFLQKPHLQI NWTGLTNLLD APGINDVSDS LLEDLIATHL VLPNRVTVPV KKGLDLTNLR FPLPCGVIRV HLLEAEQLAQ
       330        340        350        360        370        380        390        400
KDNFLGLRGK SDPYAKVSIG LQHFRSRTIY RNLNPTWNEV FEFMVYEVPG QDLEVDLYDE DTDRDDFLGS LQICLGDVMT
       410        420        430        440        450        460        470        480
NRVVDEWFVL NDTTSGRLHL RLEWLSLLTD QEVLTEDHGG LSTAILVVFL ESACNLPRNP FDYLNGEYRA KKLSRFARNK
       490        500        510        520        530        540        550        560
VSKDPSSYVK LSVGKKTHTS KTCPHNKDPV WSQVFSFFVH NVATERLHLK VLDDDQECAL GMLEVPLCQI LPYADLTLEQ
       570        580        590        600        610        620        630        640
RFQLDHSGLD SLISMRLVLR FLQVEERELG SPYTGPEALK KGPLLIKKVA TNQGPKAQPQ EEGPTDLPCP PDPASDTKDV
       650        660        670        680        690        700        710        720
SRSTTTTTSA TTVATEPTSQ ETGPEPKGKD SAKRFCEPIG EKKSPATIFL TVPGPHSPGP IKSPRPMKCP ASPFAWPPKR
       730        740        750        760        770        780        790        800
LAPSMSSLNS LASSCFDLAD ISLNIEYAPL CLIFSKIACM KNTSLDGKVD MNLHFCASCF FTKYLPKRQH GVVERTQDKG
       810        820
ERAKQAVYGS SCVLTIK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 182 | 1 | 713.3577 | -22.73 | 2 | 32.3 | 11.8 | 0 | 805-817 | K.QAVYGSSCVLTIK.- | Carbamidomethyl: 8 |

# Detailed Protein Report

---

**Protein 760:** **GRINL1A combined protein isoform 3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|553726985 | **Score:** | 23.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 87.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 1.81 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLRSTSTVTL | LSGGAARTPG | APSRRANVCR | LRLTVPPESP | VPEQCEKKIE | RKEQLLDLSN | GEPTRKLPQG | VVYGVVRRSD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QNQQKEMVVY | GWSTSQLKEE | MNYIKDVRAT | LEKVRKRMYG | DYDEMRQKIR | QLTQELSVSH | AQQEYLENHI | QTQSSALDRF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NAMNSALASD | SIGLQKTLVD | VTLENSNIKD | QIRNLQQTYE | ASMDKLREKQ | RQLEVAQVEN | QLLKMKVESS | QEANAEVMRE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MTKKLYSQYE | EKLQEEQRKH | SAEKEALLEE | TNSFLKAIEE | ANKKMQAAEI | SLEEKDQRIG | ELDRLIERME | KERHQLQLQL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LEHETEMSGE | LTDSDKERYQ | QLEEASASLR | ERIRHLDDMV | HCQQKKVKQM | VEEIESLKKK | LQQKQLLILQ | LLEKISFLEG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ENNELQSRLD | YLTETQAKTE | VETREIGVGC | DLLPRKFICK | LPDKGKKIFD | SFAKLKAAIA | ECEEVRRKSE | LFNPVSLDCK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LRQKAIAEVD | VGTDKAQNSD | PILDTSSLVP | GCSSVDNIKS | SQTSQNQGLG | RPTLEGDEET | SEVEYTVNKG | PASSNRDRVP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PSSEASEHHP | RHRVSSQAED | TSSSFDNLFI | DRLQRITIAD | QGEQQSEENA | STKNLTGLSS | GTEKKPHYME | VLEMRAKNPV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PQLRKFKTNV | LPFRQNDSSS | HCQKSGSPIS | SEERRRRDKQ | HLDDITAARL | LPLHHMPTQL | LSIEESLALQ | KQQKQNYEEM |
| 730 | 740 | 750 | 760 | 770 | | | |
| QAKLAAQKLA | ERLNIKMRSY | NPEGESSGRY | REVRDEDDDW | SSDEF | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 205 | 1 | 854.9273 | -8.70 | 2 | 32.5 | 10.1 | 2 | 355-368 | R.HLDDMVHCQQKKVK.Q | | QU:MU 1.81 |

# Detailed Protein Report

## Protein 761: fibronectin type-III domain-containing protein 3A isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|118918397 | **Score:** | 23.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 125.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSGPAQVPMM | SPNGSVPPIY | VPPGYAPQVI | EDNGVRRVVV | VPQAPEFHPG | SHTVLHRSPH | PPLPGFIPVP | TMMPPPPRHM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YSPVTGAGDM | TTQYMPQYQS | SQVYGDVDAH | STHGRSNFRD | ERSSKTYERL | QKKLKDRQGT | QKDKMSSPPS | SPQKCPSPIN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EHNGLIKGQI | AGGINTGSAK | IKSGKGKGGT | QVDTEIEEKD | EETKAFEALL | SNIVKPVASD | IQARTVVLTW | SPPSSLINGE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TDESSVPELY | GYEVLISSTG | KDGKYKSVYV | GEETNITLND | LKPAMDYHAK | VQAEYNSIKG | TPSEAEIFTT | LSCEPDIPNP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PRIANRTKNS | LTLQWKAPSD | NGSKIQNFVL | EWDEGKGNGE | FCQCYMGSQK | QFKITKLSPA | MGCKFRLSAR | NDYGTSGFSE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EVLYYTSGCA | PSMPASPVLT | KAGITWLSLQ | WSKPSGTPSD | EGISYILEME | EETSGYGFKP | KYDGEDLAYT | VKNLRRSTKY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KFKVIAYNSE | GKSNPSEVVE | FTTCPDKPGI | PVKPSVKGKI | HSHSFKITWD | PPKDNGGATI | NKYVVEMAEG | SNGNKWEMIY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SGATREHLCD | RLNPGCFYRL | RVYCISDGGQ | SAVSESLLVQ | TPAVPPGPCL | PPRLQGRPKA | KEIQLRWGPP | LVDGGSPISC |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| YSVEMSPIEK | DEPREVYQGS | EVECTVSSLL | PGKTYSFRLR | AANKMGFGPF | SEKCDITTAP | GPPDQCKPPQ | VTCRSATCAQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VNWEVPLSNG | TDVTEYRLEW | GGVEGSMQIC | YCGPGLSYEI | KGLSPATTYY | CRVQALSVVG | AGPFSEVVAC | VTPPSVPGIV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TCLQEISDDE | IENPHYSPST | CLAISWEKPC | DHGSEILAYS | IDFGDKQSLT | VGKVTSYIIN | NLQPDTTYRI | RIQALNSLGA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GPFSHMIKLK | TKPLPPDPPR | LECVAFSHQN | LKLKWGEGTP | KTLSTDSIQY | HLQMEDKNGR | FVSLYRGPCH | TYKVQRLNES |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TSYKFCIQAC | NEAGEGPLSQ | EYIFTTPKSV | PAALKAPKIE | KVNDHICEIT | WECLQPMKGD | PVIYSLQVML | GKDSEFKQIY |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KGPDSSFRYS | SLQLNCEYRF | RVCAIRQCQD | SLGHQDLVGP | YSTTVLFISQ | RTEPPASTNR | DTVESTRTRR | ALSDEQCAAV |
| 1130 | 1140 | 1150 | | | | | |
| ILVLFAFFSI | LIAFIIQYFV | IK | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1739 | 1 | 626.2821 | -30.30 | 4 | 50.1 | 10.2 | 1 | 999-1018 | K.IEKVNDHICEITWECLQPMK.G | Carbamidomethyl: 15;<br>Oxidation: 19 |

# Detailed Protein Report

## Protein 762: cytoplasmic phosphatidylinositol transfer protein 1 isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|32307140 | **Score:** | 23.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 10.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLLKEYRICM | PLTVDEYKIG | QLYMISKHSH | EQSDRGEGVE | VVQNEPFEDP | HHGNGQFTEK | RVYLNSKLPS | WARAVVPKIF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YVTEKAWNYY | PYTITEYTCS | FLPKFSIHIE | TKYEDNKGSN | DTIFDNEAKD | VEREVCFIDI | ACDEIPERYY | KESEDPKHFK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SEKTGRGQLR | EGWRDSHQPI | MCSYKLVTVK | FEVWGLQTRV | EQFVHKVVRD | ILLIGHRQAF | AWVDEWYDMT | MDEVREFERA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TQEATNKKIG | IFPPAISISS | IPLLPSSVRS | APSSAPSTPL | STDAPEFLSV | PKDRPRKKSA | PETLTLPDPE | KKATLNLPGM |
| 330 | 340 | | | | | | |
| HSSDKPCRPK | SE | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 26 | 2 | 712.9803 | -81.39 | 3 | 29.3 | 11.2 | 1 | 312-330 | K.KATLNLPGMHSSDKPCRPK.S | Carbamidomethyl: 16 |

# Detailed Protein Report

## Protein 763: PREDICTED: F-box/LRR-repeat protein 17 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530380083 | **Score:** | 23.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 53.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 7.1 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MGHLLSKEPR NRPSQKRPRC CSWCRRRRPL LRLPRRTPAK VPPQPAAPRS RDCFFRGPCM LCFIVHSPGA PAPAGPEEEP

        90        100        110        120        130        140        150        160
PLSPPPRDGA YAAASSSQHL ARRYAALAAE DCAAAARRFL LSSAAAAAAA AASASSPASC CKELGLAAAA AWEQQGRSLF

       170        180        190        200        210        220        230        240
LASLGPVRFL GPPAAVQLFR GPTPSPAELP TPPEMVCKRK GAGVPACTPC KQPRCGGGGC GGGGGGGGGG GPAGGGASPP

       250        260        270        280        290        300        310        320
RPPDAGCCQA PEQPPQPLCP PPSSPTSEGA PTEAGGDAVR AGGTAPLSAQ QQHECGDADC RESPENPCDC HREPPPETPD

       330        340        350        360        370        380        390        400
INQLPPSILL KIFSNLSLDE RCLSASLVCK YWRDLCLDFQ FWKQLDLSSR QQVTDELLEK IASRSQNIIE INISDCRSMS

       410        420        430        440        450        460        470        480
DNGVCVLAFK CPGLLRYTAY RCKQLSDTSI IAVASHCPLL QKVHVGNQDK LTDEGLKQLG SKCRELKDIH FGQCYKISDE

       490        500        510
GMIVIAKGCL KLQRIYMQEN KLILD
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 191 | 1 | 879.7026 | -94.05 | 3 | 32.1 | 12.5 | 2 | 465-487 | R.ELKDIHFGQCYKISDEGMIVIAK.G | |

# Detailed Protein Report

## Protein 764: PREDICTED: stabilin-1 isoform X5 [Homo sapiens]

**Accession:** gi|578805875
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 23.1
**MW [kDa]:** 162.4
**pI:** 9.7
**Sequence Coverage [%]:** 1.6
**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MAGPRGLLPL CLLAFCLAGF SFVRGQVLFK GCDVKTTFVT HVPCTSCAAI KKQTCPSGWL RELPDQITQD CRYEVQLGGS
        90        100        110        120        130        140        150        160
MVSMSGCRRK CRKQVVQKAC CPGYWGSRCH ECPGGAETPC NGHGTCLDGM DRNGTCVCQE NFRGSACQEC QDPNRFGPDC
       170        180        190        200        210        220        230        240
QSVCSCVHGV CNHGPRGDGS CLCFAGYTGP HCDQELPVCQ ELRCPQNTQC SAEAPSCRCL PGYTQQGSEC RAPNPCWPSP
       250        260        270        280        290        300        310        320
CSLLAQCSVS PKGQAQCHCP ENYHGDGMVC LPKDPCTDNL GGCPSNSTLC VYQKPGQAFC TCRPGLVSIN SNASAGCFAF
       330        340        350        360        370        380        390        400
CSPFSCDRSA TCQVTADGKT SCVCRESEVG DGRACYGHLL HEVQKATQTG RVFLQLRVAV AMMDQGCREI LTTAGPFTVL
       410        420        430        440        450        460        470        480
VPSVSSFSSR TMNASLAQQL CRQHIIAGQH ILEDTRTQQT RRWWTLAGQE ITVTFNQFTK YSYKYKDQPQ QTFNIYKANN
       490        500        510        520        530        540        550        560
IAANGVFHVV TGLRWQAPSG TPGDPKRTIG QILASTEAFS RFETILENCG LPSILDGPGP FTVFAPSNEA VDSLRDGRLI
       570        580        590        600        610        620        630        640
YLFTAGLSKL QELVRYHIYN HGQLTVEKLI SKGRILTMAN QVLAVNISEE GRILLGPEGV PLQRVDVMAA NGVIHMLDGI
       650        660        670        680        690        700        710        720
LLPPTILPIL PKHCSEEQHK IVAGSCVDCQ ALNTSTCPPN SVKLDIFPKE CVYIHDPTGL NVLKKGCASY CNQTIMEQGC
       730        740        750        760        770        780        790        800
CKGFFGPDCT QCPGGFSNPC YGKGNCSDGI QGNGACLCFP DYKGIACHIC SNPNKHGEQC QEDCGCVHGL CDNRPGSGGV
       810        820        830        840        850        860        870        880
CQQGTCAPGF SGRFCNESMG DCGPTGLAQH CHLHARCVSQ EGVARCRCLD GFEGDGFSCT PSNPCSHPDR GGCSENAECV
       890        900        910        920        930        940        950        960
PGSLGTHHCT CHKGWSGDGR VCVAIDECEL DMRGGCHTDA LCSYVGPGQS RCTCKLGFAG DGYQCSPIDP CRAGNGGCHG
       970        980        990       1000       1010       1020       1030       1040
LATCRAVGGG QRVCTCPPGF GGDGFSCYGD IFRELEANAH FSIFYQWLKS AGITLPADRR VTALVPSEAA VRQLSPEDRA
      1050       1060       1070       1080       1090       1100       1110       1120
FWLQPRTLPN LVRAHFLQGA LFEEELARLG GQEVATLNPT TRWEIRNISG RVWVQNASVD VADLLATNGV LHILSQVLLP
      1130       1140       1150       1160       1170       1180       1190       1200
PRGDVPGGQG LLQQLDLVPA FSLFRELLQH HGLVPQIEAA TAYTIFVPTN RSLEAQGNSS HLDADTVRHH VVLGEALSME
      1210       1220       1230       1240       1250       1260       1270       1280
TLRKGGHRNS LLGPAHWIVF YNHSGQPEVN HVPLEGPMLE APGRSLIGLS GVLTVGSSRC LHSHAEALRE KCVNCTRRFR
      1290       1300       1310       1320       1330       1340       1350       1360
CTQGFQLQDT PRKSCVYRSG FSFSRGCSYT CAKKIQCVTV PMGCARRGCK GTEAVSVTWA GRASAVTRKS PALSALGSAT
      1370       1380       1390       1400       1410       1420       1430       1440
PMPTACRTRP EPPPAPVLRD TPAMASSVQR WTPAPTAMGA APLMPTVPRW HLGSGHAPAR MATWATGSCA RKLTAVSSTT
      1450       1460       1470       1480       1490       1500       1510       1520
GAATFTPSAS PLAPSRSPAA AVRVTAGMAS GPASSWTPAL RTMEDAAHMP PAKAQGMARG HVPATQPTPW GTASPAVPES
      1530
A
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2603 | 1 | 637.1527 | -199.59 | 2 | 60.8 | 12.7 | 0 | 953-965 | R.AGNGGCHGLATCR.A | Carbamidomethyl: 12 |

# Detailed Protein Report

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## Protein 765: tyrosine-protein phosphatase non-receptor type 11 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|18375644 | **Score:** | 23.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 52.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.2 |
| | | **Sequence Coverage [%]:** | 5.2 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 0.76 | **CV:** 0.00 % | **No. of Peptides:** 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTSRRWFHPN | ITGVEAENLL | LTRGVDGSFL | ARPSKSNPGD | FTLSVRRNGA | VTHIKIQNTG | DYYDLYGGEK | FATLAELVQY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YMEHHGQLKE | KNGDVIELKY | PLNCADPTSE | RWFHGHLSGK | EAEKLLTEKG | KHGSFLVRES | QSHPGDFVLS | VRTGDDKGES |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NDGKSKVTHV | MIRCQELKYD | VGGGERFDSL | TDLVEHYKKN | PMVETLGTVL | QLKQPLNTTR | INAAEIESRV | RELSKLAETT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DKVKQGFWEE | FETLQQQECK | LLYSRKEGQR | QENKNKNRYK | NILPFDHTRV | VLHDGDPNEP | VSDYINANII | MPEFETKCNN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SKPKKSYIAT | QGCLQNTVND | FWRMVFQENS | RVIVMTTKEV | ERGKSKCVKY | WPDEYALKEY | GVMRVRNVKE | SAAHDYTLRE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | |
| LKLSKVGQGN | TERTVWQYHF | RTWPDHGVPS | DPGGVLDFLE | EVHHKQESIM | DAGPVVVHCR | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 797 | 1 | 534.6313 | -263.66 | 2 | 40.0 | 11.7 | 0 | 112-120 | R.WFHGHLSGK.E | | |
| 1576 | 1 | 820.8084 | -108.92 | 2 | 49.9 | 11.5 | 0 | 446-460 | K.QESIMDAGPVVVHCR.- | | QU:MU 0.76 |

# Detailed Protein Report

## Protein 766: UPF0598 protein C8orf82 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|49169841 | **Score:** | 23.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 23.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| | | **Sequence Coverage [%]:** | 14.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 1.00 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MWPPCGTLRT LALARSRGAR ACSGDGGVSY TQGQSPEPRT REYFYYVDHQ GQLFLDDSKM KNFITCFKDP QFLVTFFSRL
         90        100        110        120        130        140        150        160
RPNRSGRYEA AFPFLSPCGR ERNFLRCEDR PVVFTHLLTA DHGPPRLSYC GGGEALAVPF EPARLLPLAA NGRLYHPAPE
        170        180        190        200        210        220
RAGGVGLVRS ALAFELSACF EYGPGAPALP SHVRWQGRRL ALTMDLAPLL LAARSP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 367 | 1 | 846.3873 | -98.49 | 2 | 34.2 | 12.6 | 1 | 154-169 | R.LYHPAPERAGGVGLVR.S | | QU:MU 1.00 |

# Detailed Protein Report

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## Protein 767: PREDICTED: lactosylceramide alpha-2,3-sialyltransferase isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578803239 | **Score:** | 23.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 43.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 6.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.89 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.47 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MRTKAAGCAE | RRPLQPRTEA | AAAPAGRAMP | SEYTYVKLRS | DCSRPSLQWY | TRAQSKMRRP | SLLLKDILKC | TLLVFGVWIL |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| YILKLNYTTE | ECDMKKMHYV | DPDHVKKAPK | DSEAESKYDP | PFGFRKFSSK | VQTLLELLPE | HDLPEHLKAK | TCRRCVVIGS |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| GGILHGLELG | HTLNQFDVVI | RLNSAPVEGY | SEHVGNKTTI | RMTYPEGAPL | SDLEYYSNDL | FVAVLFKSVD | FNWLQAMVKK |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| ETLPFWVRLF | FWKQVAEKIP | LQPKHFRILN | PVIIKETAFD | ILQYSEPQSR | FWGRDKNVPT | IGVIAVVLAT | HLCDEVSLAG |
| **330** | **340** | **350** | **360** | **370** | **380** | | |
| FGYDLNQPRT | PLHYFDSQCM | AAMNFQTMHN | VTTETKFLLK | LVKEGVVKDL | SGGIDREF | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1485 | 1 | 850.8758 | -46.71 | 2 | 48.7 | 10.4 | 0 | 182-197 | R.LNSAPVEGYSEHVGNK.T | | WUP:QUP 0.47<br>QU:MU 2.89 |

# Detailed Protein Report

## Protein 768: spectrin beta chain, non-erythrocytic 5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|485837026 | **Score:** | 23.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 416.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 0.7 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.09 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.75 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAGQPHSPRE | LLGAAGHRSR | RPSTELRVPP | SPSLTMDSQY | ETGHIRKLQA | RHMQMQEKTF | TKWINNVFQC | GQAGIKIRNL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YTELADGIHL | LRLLELISGE | ALPPPSRGRL | RVHFLENSSR | ALAFLRAKVP | VPLIGPENIV | DGDQTLILGL | IWVIILRFQI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SHISLDKEEF | GASAALLSTK | EALLVWCQRK | TASYTNVNIT | DFSRSWSDGL | GFNALIHAHR | PDLLDYGSLR | PDRPLHNLAF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AFLVAEQELG | IAQLLDPEDV | AAAQPDERSI | MTYVSLYYHY | CSRLHQGQTV | QRRLTKILLQ | LQETELLQTQ | YEQLVADLLR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WIAEKQMQLE | ARDFPDSLPA | MRQLLAAFTI | FRTQEKPPRL | QQRGAAEALL | FRLQTALQAQ | NRRPFLPHEG | LGLAELSQCW |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AGLEWAEAAR | SQALQQRLLQ | LQRLETLARR | FQHKAALRES | FLKDAEQVLD | QARAPPASLA | TVEAAVQRLG | MLEAGILPQE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GRFQALAEIA | DILRQEQYHS | WADVARRQEE | VTVRWQRLLQ | HLQGQRKQVA | DMQAVLSLLQ | EVEAASHQLE | ELQEPARSTA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| CGQQLAEVVE | LLQRHDLLEA | QVSAHGAHVS | HLAQQTAELD | SSLGTSVEVL | QAKARTLAQL | QQSLVALVRA | RRALLEQTLQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RAEFLRNCEE | EEAWLKECGQ | RVGNAALGRD | LSQIAGALQK | HKALEAEVHR | HQAVCVDLVR | RGRDLSARRP | PTQPDPGERA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EAVQGGWQLL | QTRVVGRGAR | LQTALLVLQY | FADAAEAASW | LRERRSSLER | ASCGQDQAAA | ETLLRRHVRL | ERVLRAFAAE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LRRLEEQGRA | ASARASLFTV | NSALSPPGES | LRNPGPWSEA | SCHPGPGDAW | KMALPAEPDP | DFDPNTILQT | QDHLSQDYES |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LRALAQLRRA | RLEEAMALFG | FCSSCGELQL | WLEKQTVLLQ | RVQPQADTLE | VMQLKYENFL | TALAVGKGLW | AEVSSSAEQL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RQRYPGNSTQ | IQRQQEELSQ | RWGQLEALKR | EKAVQLAHSV | EVCSFLQECG | PTQVQLRDVL | LQLEALQPGS | SEDTCHALQL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AQKKTLVLER | RVHFLQSVVV | KVEEPGYAES | QPLQGQVETL | QGLLKQVQEQ | VAQRARRQAE | TQARQSFLQE | SQQLLLWAES |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| VQAQLRSKEV | SVDVASAQRL | LREHQDLLEE | IHLWQERLQQ | LDAQSQPMAA | LDCPDSQEVP | NTLRVLGQQG | QELKVLWEQR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| QQWLQEGLEL | QKFGREVDGF | TATCANHQAW | LHLDNLGEDV | REALSLLQQH | REFGRLLSTL | GPRAEALRAH | GEKLVQSQHP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| AAHTVREQLQ | SIQAQWTRLQ | GRSEQRRRQL | LASLQLQEWK | QDVAELMQWM | EEKGLMAAHE | PSGARRNILQ | TLKRHEAAES |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ELLATRRHVE | ALQQVGRELL | SRRPCGQEDI | QTRLQGLRSK | WEALNRKMTE | RGDELQQAGQ | QEQLLRQLQD | AKEQLEQLEG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ALQSSETGQD | LRSSQRLQKR | HQQLESESRT | LAAKMAALAS | MAHGMAASPA | ILEETQKHLR | RLELLQGHLA | IRGLQLQASV |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ELHQFCHLSN | MELSWVAEHM | PHGSPTSYTE | CLNGAQSLHR | KHKELQVEVK | AHQGQVQRVL | SSGRSLAASG | HPQAQHIVEQ |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| CQELEGHWAE | LERACEARAQ | CLQQAVTFQQ | YFLDVSELEG | WVEEKRPLVS | SRDYGRDEAA | TLRLINKHQA | LQEELAIYWS |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| SMEELDQTAQ | TLTGPEVPEQ | QRVVQERLRE | QLRALQELAA | TRDRELEGTL | RLHEFLREAE | DLQGWLASQK | QAAKGGESLG |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| EDPEHALHLC | TKFAKFQHQV | EMGSQRVAAC | RLLAESLLER | GHSAGPMVRQ | RQQDLQTAWS | ELWELTQARG | HALRDTETTL |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| RVHRDLLEVL | TQVQEKATSL | PNNVARDLCG | LEAQLRSHQG | LERELVGTER | QLQELLETAG | RVQKLCPGPQ | AHAVQQRQQA |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| VTQAWAVLQR | RMEQRRAQLE | RARLLARFRT | AVRDYASWAA | RVRQDLQVEE | SSQEPSSGPL | KLSAHQWLRA | ELEAREKLWQ |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| QATQLGQQAL | LAAGTPTKEV | QEELRALQDQ | RDQVYQTWAR | KQERLQAEQQ | EQLFLRECGR | LEEILAAQEV | SLKTSALGSS |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| VEEVEQLIRK | HEVFLKVLTA | QDKKEAALRE | RLKTLRRPRV | RDRLPILLQR | RMRVKELAES | RGHALHASLL | MASFTQAATQ |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1262 | 1 | 598.7915 | -6.95 | 2 | 45.9 | 11.3 | 0 | 1334-1345 | K.GLMAAHEPSGAR.R | | WUP:QUP 0.75<br>QU:MU 1.09 |
| 2799 | 2 | 665.3651 | -30.72 | 2 | 65.4 | 11.8 | 0 | 3278-3291 | R.LGQLHPAAPGGLAK.V | | |

# Detailed Protein Report

**Protein 769:** **ribosome biogenesis regulatory protein homolog [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|14719402 | **Score:** | 23.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEGQSVEELL | AKAEQDEAEK | LQRITVHKEL | ELQFDLGNLL | ASDRNPPTGL | RCAGPTPEAE | LQALARDNTQ | LLINQLWQLP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TERVEEAIVA | RLPEPTTRLP | REKPLPRPRP | LTRWQQFARL | KGIRPKKKTN | LVWDEVSGQW | RRRWGYQRAR | DDTKEWLIEV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PGNADPLEDQ | FAKRIQAKKE | RVAKNELNRL | RNLARAHKMQ | LPSAAGLHPT | GHQSKEELGR | AMQVAKVSTA | SVGRFQERLP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KEKVPRGSGK | KRKFQPLFGD | FAAEKKNQLE | LLRVMNSKKP | QLDVTRATNK | QMREEDQEEA | AKRRKMSQKG | KRKGGRQGPG |
| 330 | 340 | 350 | 360 | 370 | | | |
| GKRKGGPPSQ | GGKRKGGLGG | KMNSGPPGLG | GKRKGGQRPG | GKRRK | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 448 | 1 | 593.8428 | 66.22 | 2 | 35.2 | 10.6 | 1 | 342-353 | K.MNSGPPGLGGKR.K | Oxidation: 1 |

## Protein 770: dnaJ homolog subfamily B member 12 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|194306640 | **Score:** | 23.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| | | **Sequence Coverage [%]:** | 6.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530393899 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: dnaJ homolog subfamily B member 12 isoform X2 [Homo sapiens] |
| gi\|194306642 | refseq_human (refseq_human_20140103.fasta) | dnaJ homolog subfamily B member 12 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSLRARLPA | TRRRVAQPFA | RPASPSLVPR | SGSAMESNKD | EAERCISIAL | KAIQSNQPDR | ALRFLEKAQR | LYPTPRVRAL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IESLNQKPQT | AGDQPPPTDT | THATHRKAGG | TDAPSANGEA | GGESTKGYTA | EQVAAVKRVK | QCKDYYEILG | VSRGASDEDL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KKAYRRLALK | FHPDKNHAPG | ATEAFKAIGT | AYAVLSNPEK | RKQYDQFGDD | KSQAARHGHG | HGDFHRGFEA | DISPEDLFNM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FFGGGFPSSN | VHVYSNGRMR | YTYQQRQDRR | DNQGDGGLGV | FVQLMPILIL | ILVSALSQLM | VSSPPYSLSP | RPSVGHIHRR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VTDHLGVVYY | VGDTFSEEYT | GSSLKTVERN | VEDDYIANLR | NNCWKEKQQK | EGLLYRARYF | GDTDMYHRAQ | KMGTPSCSRL |
| 410 | | | | | | | |
| SEVQASLHG | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2330 | 1 | 557.1827 | -147.66 | 3 | 59.0 | 11.1 | 1 | 212-226 | K.SQAARHGHGHGDFHR.G | |

# Detailed Protein Report

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**Protein 771:** **PREDICTED: peptidase M20 domain-containing protein 2 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530383022 | **Score:** | 23.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 8.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.64 **CV:** 0.00 % **No. of Peptides:** 1

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530383024 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: peptidase M20 domain-containing protein 2 isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAHPSQENAA | YLPDMAEHDV | TVKYYGKASH | SASYPWEGLN | ALDAAVLAYN | NLSVFRQQMK | PTWRVHGIIK | NGGVKPNIIP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SYSELIYYFR | APSMKELQVL | TKKAEDCFRA | AALASGCTVE | IKGGAHDYYN | VLPNKSLWKA | YMENGRKLGI | EFISEDTMLN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GPSGSTDFGN | VSFVVPGIHP | YFHIGSNALN | HTEQYTEAAG | SQEAQFYTLR | TAKALAMTAL | DVIFKPELLE | GIREDFKLKL |
| 250 | 260 | | | | | | |
| QEEQFVNAVE | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 151 | 1 | 773.9066 | -3.42 | 2 | 31.9 | 12.7 | 1 | 238-250 | K.LKLQEEQFVNAVE.- | | WUP:QUP 0.64 |

# Detailed Protein Report

## Protein 772: collagen alpha-3(VI) chain isoform 4 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|240255535 | **Score:** | 23.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 278.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| | | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRKHRHLPLV | AVFCLFLSGF | PTTHAQQQQA | VIEVNKRDIV | FLVDGSSALG | LANFNAIRDF | IAKVIQRLEI | GQDLIQVAVA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QYADTVRPEF | YFNTHPTKRE | VITAVRKMKP | LDGSALYTGS | ALDFVRNNLF | TSSAGYRAAE | GIPKLLVLIT | GGKSLDEISQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PAQELKRSSI | MAFAIGNKGA | DQAELEEIAF | DSSLVFIPAE | FRAAPLQGML | PGLLAPLRTL | SGTPEESKRD | ILFLFDGSAN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LVGQFPVVRD | FLYKIIDELN | VKPEGTRIAV | AQYSDDVKVE | SRFDEHQSKP | EILNLVKRMK | IKTGKALNLG | YALDYAQRYI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FVKSAGSRIE | DGVLQFLVLL | VAGRSSDRVD | GPASNLKQSG | VVPFIFQAKN | ADPAELEQIV | LSPAFILAAE | SLPKIGDLHP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QIVNLLKSVH | NGAPAPVSGE | KDVVFLLDGS | EGVRSGFPLL | KEFVQRVVES | LDVGQDRVRV | AVVQYSDRTR | PEFYLNSYMN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KQDVVNAVRQ | LTLLGGPTPN | TGAALEFVLR | NILVSSAGSR | ITEGVPQLLI | VLTADRSGDD | VRNPSVVVKR | GGAVPIGIGI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GNADITEMQT | ISFIPDFAVA | IPTFRQLGTV | QQVISERVTQ | LTREELSRLQ | PVLQPLPSPG | VGGKRDVVFL | IDGSQSAGPE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FQYVRTLIER | LVDYLDVGFD | TTRVAVIQFS | DDPKVEFLLN | AHSSKDEVQN | AVQRLRPKGG | RQINVGNALE | YVSRNIFKRP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LGSRIEEGVP | QFLVLISSGK | SDDEVDDPAV | ELKQFGVAPF | TIARNADQEE | LVKISLSPEY | VFSVSTFREL | PSLEQKLLTP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ITTLTSEQIQ | KLLASTRYPP | PAVESDAADI | VFLIDSSEGV | RPDGFAHIRD | FVSRIVRRLN | IGPSKVRVGV | VQFSNDVFPE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| FYLKTYRSQA | PVLDAIRRLR | LRGGSPLNTG | KALEFVARNL | FVKSAGSRIE | DGVPQHLVLV | LGGKSQDDVS | RFAQVIRSSG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| IVSLGVGDRN | IDRTELQTIT | NDPRLVFTVR | EFRELPNIEE | RIMNSFGPSA | ATPAPPGVDT | PPPSRPEKKK | ADIVFLLDGS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| INFRRDSFQE | VLRFVSEIVD | TVYEDGDSIQ | VGLVQYNSDP | TDEFFLKDFS | TKRQIIDAIN | KVVYKGGRHA | NTKVGLEHLR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| VNHFVPEAGS | RLDQRVPQIA | FVITGGKSVE | DAQDVSLALT | QRGVKVFAVG | VRNIDSEEVG | KIASNSATAF | RVGNVQELSE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LSEQVLETLH | DAMHETLCPG | VTDAAKACNL | DVILGFDGSR | DQNVFVAQKG | FESKVDAILN | RISQMHRVSC | SGGRSPTVRV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SVVANTPSGP | VEAFDFDEYQ | PEMLEKFRNM | RSQHPYVLTE | DTLKVYLNKF | RQSSPDSVKV | VIHFTDGADG | DLADLHRASE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| NLRQEGVRAL | ILVGLERVVN | LERLMHLEFG | RGFMYDRPLR | LNLLDLDYEL | AEQLDNIAEK | ACCGVPCKCS | GQRGDRGPIG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SIGPKGIPGE | DGYRGYPGDE | GGPGERGPPG | VNGTQGFQGC | PGQRGVKGSR | GFPGEKGEVG | EIGLDGLDGE | DGDKGLPGSS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| GEKGNPGRRG | DKGPRGEKGE | RGDVGIRGDP | GNPGQDSQER | GPKGETGDLG | PMGVPGRDGV | PGGPGETGKN | GGFGRRGPPG |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| AKGNKGGPGQ | PGFEGEQGTR | GAQGPAGPAG | PPGLIGEQGI | SGPRGSGGAA | GAPGERGRTG | PLGRKGEPGE | PGPKGGIGNR |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| GPRGETGDDG | RDGVGSEGRR | GKKGERGFPG | YPGPKGNPGE | PGLNGTTGPK | GIRGRRGNSG | PPGIVGQKGD | PGYPGPAGPK |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| GNRGDSIDQC | ALIQSIKDKC | PCCYGPLECP | VFPTELAFAL | DTSEGVNQDT | FGRMRDVVLS | IVNDLTIAES | NCPRGARVAV |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| VTYNNEVTTE | IRFADSKRKS | VLLDKIKNLQ | VALTSKQQSL | ETAMSFVARN | TFKRVRNGFL | MRKVAVFFSN | TPTRASPQLR |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| EAVLKLSDAG | ITPLFLTRQE | DRQLINALQI | NNTAVGHALV | LPAGRDLTDF | LENVLTCHVC | LDICNIDPSC | GFGSWRPSFR |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| DRRAAGSDVD | IDMAFILDSA | ETTTLFQFNE | MKKYIAYLVR | QLDMSPDPKA | SQHFARVAVV | QHAPSESVDN | ASMPPVKVEF |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| SLTDYGSKEK | LVDFLSRGMT | QLQGTRALGS | AIEYTIENVF | ESAPNPRDLK | IVVLMLTGEV | PEQQLEEAQR | VILQAKCKGY |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 605 | 1 | 472.1588 | -273.18 | 2 | 37.1 | 12.8 | 1 | 99-106 | K.REVITAVR.K | |

# Detailed Protein Report

## Protein 773: PR domain zinc finger protein 15 isoform 3 [Homo sapiens]

**Accession:** gi|544710466
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 23.0
**MW [kDa]:** 135.6
**pI:** 9.4
**Sequence Coverage [%]:** 3.9
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPRRRPPASG | AAQFPERIAT | RSPDPIPLCT | FQRQVSEMAE | DGSEEIMFIW | CEDCSQYHDS | ECPELGPVVM | VKDSFVLSRA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RSSLPPNLEI | RRLEDGAEGV | FAITQLVKRT | QFGPFESRRV | AKWEKESAFP | LKVFQKDGHP | VCFDTSNEDD | CNWMMLVRPA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AEAEHQNLTA | YQHGSDVYFT | TSRDIPPGTE | LRVWYAAFYA | KKMDKPMLKQ | AGSGVHAAGT | PENSAPVESE | PSQWACKVCS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ATFLELQLLN | EHLLGHLEQA | KSLPPGSQSE | AAAPEKEQDT | PRGEPPAVPE | SENVATKEQK | KKPRRGRKPK | VSKAEQPLVI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VEDKEPTEQV | AEIITEVPPD | EPVSATPDER | IMELVLGKLA | TTTTDTSSVP | KFTHHQNNTI | TLKRSLILSS | RHGIRRKLIK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QLGEHKRVYQ | CNICSKIFQN | SSNLSRHVRS | HGDKLFKCEE | CAKLFSRKES | LKQHVSYKHS | RNEVDGEYRY | RCGTCEKTFR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IESALEFHNC | RTGLIAHPGE | GGPGGSRLRD | LPDDKTFQCE | MCFRFFSTNS | NLSKHKKKHG | DKKFACEVCS | KMFYRKDVML |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DHQRRHLEGV | RRVKREDLEA | GGENLVRYKK | EPSGCPVCGK | VFSCRSNMNK | HLLTHGDKKY | TCEICGRKFF | RVDVLRDHIH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VHFKDIALMD | DHQREEFIGK | IGISSEENDD | NSDESADSEP | HKYSCKRCQL | TFGRGKEYLK | HIMEVHKEKG | YGCSICNRRF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ALKATYHAHM | VIHRENLPDP | NVQKYIHPCE | ICGRIFNSIG | NLERHKLIHT | GVKSHACEQC | GKSFARKDML | KEHMRVHDNV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| REYLCAECGK | GMKTKHALRH | HMKLHKGIKE | YECKECHRRF | AQKVNMLKHC | KRHTGIKDFM | CELCGKTFSE | RNTMETHKLI |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| HTVGKQWTCS | VCDKKYVTEY | MLQKHVQLTH | DKVEAQSCQL | CGTKVSTRAS | MSRHMRRKHP | EVLAVRIDDL | DHLPETTTID |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ASSIGIVQPE | LTLEQEDLAE | GKHGKAAKRS | HKRKQKPEEE | AGAPVPEDAT | FSEYSEKETE | FTGSVGDETN | SAVQSIQQVV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VTLGDPNVTT | PSSSVGLTNI | TVTPITTAAA | TQFTNLQPVA | VGHLTTPERQ | LQLDNSILTV | TFDTVSGSAM | LHNRQNDVQI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| HPQPEASNPQ | SVAHFINLTT | LVNSITPLGS | QLSDQHPLTW | RAVPQTDVLP | PSQPQAPPQQ | AAQPQVQAEQ | QQQQMYSY |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1744 | 1 | 1030.2489 | 59.15 | 3 | 51.6 | 11.7 | 2 | 481-509 | R.IESALEFHNCRTGLIAHPGEGGPGGSRLR.D | Carbamidomethyl: 10 |

# Detailed Protein Report

**Protein 774:** **PREDICTED: kinesin-like protein KIF7 isoform X4 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578826899 | **Score:** | 23.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 146.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGLEAQRLPG | AEEAPVRVAL | RVRPLLPKEL | LHGHQSCLQV | EPGLGRVTLG | RDRHFGFHVV | LAEDAGQEAV | YQACVQPLLE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AFFEGFNATV | FAYGQTGSGK | TYTMGEASVA | SLLEDEQGIV | PRAMAEAFKL | IDENDLLDCL | VHVSYLEVYK | EEFRDLLEVG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TASRDIQLRE | DERGNVVLCG | VKEVDVEGLD | EVLSLLEMGN | AARHTGATHL | NHLSSRSHTV | FTVTLEQRGR | APSRLPRPAP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GQLLVSKFHF | VDLAGSERVL | KTGSTGERLK | ESIQINSSLL | ALGNVISALG | DPQRRGSHIP | YRDSKITRIL | KDSLGGNAKT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VMIACVSPSS | SDFDETLNTL | NYASRAQNIR | NRATVNWRPE | AERPPEETAS | GARGPPRHRS | ETRIIHRGRR | APGPATASAA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AAMRLGAECA | RYRACTDAAY | SLLRELQAEP | GLPGAAARKV | RDWLCAVEGE | RSALSSASGP | DSGIESASVE | DQAAQGAGGR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KEDEGAQQLL | TLQNQVARLE | EENRDFLAAL | EDAMEQYKLQ | SDRLREQQEE | MVELRLRLEL | VRPGWGGPRL | LNGLPPGSFV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PRPHTAPLGG | AHAHVLGMVP | PACLPGDEVG | SEQRGEQVTN | GREAGAELLT | EVNRLGSGSS | AASEEEEEEE | EPPRRTLHLR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RNRISNCSQR | AGARPGSLPE | RKGPELCLEE | LDAAIPGSRA | VGGSKARVQA | RQVPPATASE | WRLAQAQQKI | RELAINIRMK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EELIGELVRT | GKAAQALNRQ | HSQRIRELEQ | EAEQVRAELS | EGQRQLRELE | GKELQDAGER | SRLQEFRRRV | AAAQSQVQVL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KEKKQATERL | VSLSAQSEKR | LQELERNVQL | MRQQQGQLQR | RLREETEQKR | RLEAEMSKRQ | HRVKELELKH | EQQQKILKIK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TEEIAAFQRK | RRSGSNGSVV | SLEQQQKIEE | QKKWLDQEME | KVLQQRRALE | ELGEELHKRE | AILAKKEALM | QEKTGLESKR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LRSSQALNED | IVRVSSRLEH | LEKELSEKSG | QLRQGSAQSQ | QQIRGEIDSL | RQEKDSLLKQ | RLEIDGKLRQ | GSLLSPEEER |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TLFQLDEAIE | ALDAAIEYKN | EAITCRQRVL | RASASLLSQC | EMNLMAKLSY | LSSSETRALL | CKYFDKVVTL | REEQHQQQIA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| FSELEMQLEE | QQRLVYWLEV | ALERQRLEMD | RQLTLQQKEH | EQNMQLLLQQ | SRDHLGEGLA | DSRRQYEARI | QALEKELGRY |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| MWINQELKQK | LGGVNAVGHS | RGGEKRSLCS | EGRQAPGNED | ELHLAPELLW | LSPLTEGAPR | TREETRDLVH | APLPLTWKRS |
| 1290 | 1300 | 1310 | 1320 | | | | |
| SLCGDSSTTP | ISGPGSEDLE | EPHAQGLLHT | TCN | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2376 | 1 | 847.3981 | -71.01 | 2 | 60.2 | 11.0 | 2 | 1209-1225 | K.QKLGGVNAVGHSRGGEK.R | |

# Detailed Protein Report

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## Protein 775: NACHT, LRR and PYD domains-containing protein 12 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21955154 | **Score:** | 23.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 120.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLRTAGRDGL | CRLSTYLEEL | EAVELKKFKL | YLGTATELGE | GKIPWGSMEK | AGPLEMAQLL | ITHFGPEEAW | RLALSTFERI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NRKDLWERGQ | REDLVRDTPP | GGPSSLGNQS | TCLLEVSLVT | PRKDPQETYR | DYVRRKFRLM | EDRNARLGEC | VNLSHRYTRL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLVKEHSNPM | QVQQQLLDTG | RGHARTVGHQ | ASPIKIETLF | EPDEERPEPP | RTVVMQGAAG | IGKSMLAHKV | MLDWADGKLF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QGRFDYLFYI | NCREMNQSAT | ECSMQDLIFS | CWPEPSAPLQ | ELIRVPERLL | FIIDGFDELK | PSFHDPQGPW | CLCWEEKRPT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ELLLNSLIRK | KLLPELSLLI | TTRPTALEKL | HRLLEHPRHV | EILGFSEAER | KEYFYKYFHN | AEQAGQVFNY | VRDNEPLFTM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CFVPLVCWVV | CTCLQQQLEG | GGLLRQTSRT | TTAVYMLYLL | SLMQPKPGAP | RLQPPPNQRG | LCSLAADGLW | NQKILFEEQD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LRKHGLDGED | VSAFLNMNIF | QKDINCERYY | SFIHLSFQEF | FAAMYYILDE | GEGGAGPDQD | VTRLLTEYAF | SERSFLALTS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RFLFGLLNEE | TRSHLEKSLC | WKVSPHIKMD | LLQWIQSKAQ | SDGSTLQQGS | LEFFSCLYEI | QEEEFIQQAL | SHFQVIVVSN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IASKMEHMVS | SFCLKRCRSA | QVLHLYGATY | SADGEDRARC | SAGAHTLLVQ | LPERTVLLDA | YSEHLAAALC | TNPNLIELSL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YRNALGSRGV | KLLCQGLRHP | NCKLQNLRLK | RCRISSSACE | DLSAALIANK | NLTRMDLSGN | GVGFPGMMLL | CEGLRHPQCR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LQMIQLRKCQ | LESGACQEMA | SVLGTNPHLV | ELDLTGNALE | DLGLRLLCQG | LRHPVCRLRT | LWLKICRLTA | AACDELASTL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SVNQSLRELD | LSLNELGDLG | VLLLCEGLRH | PTCKLQTLRL | GICRLGSAAC | EGLSVVLQAN | HNLRELDLSF | NDLGDWGLWL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LAEGLQHPAC | RLQKLWLDSC | GLTAKACENL | YFTLGINQTL | TDLYLTNNAL | GDTGVRLLCK | RLSHPGCKLR | VLWLFGMDLN |
| 1050 | 1060 | 1070 | | | | | |
| KMTHSRLAAL | RVTKPYLDIG | C | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2724 | 2 | 973.5090 | 17.10 | 2 | 64.4 | 12.7 | 2 | 144-159 | R.NARLGECVNLSHRYTR.L | Carbamidomethyl: 7 |

# Detailed Protein Report

## Protein 776: CCR4-NOT transcription complex subunit 1 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|388454220 | **Score:** | 23.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 266.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNLDSLSLAL | SQISYLVDNL | TKKNYRASQQ | EIQHIVNRHG | PEADRHLLRC | LFSHVDFSGD | GKSSGKDFHQ | TQFLIQECAL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LITKPNFIST | LSYAIDNPLH | YQKSLKPAPH | LFAQLSKVLK | LSKVQEVIFG | LALLNSSSSD | LRGFAAQFIK | QKLPDLLRSY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IDADVSGNQE | GGFQDIAIEV | LHLLLSHLLF | GQKGAFGVGQ | EQIDAFLKTL | RRDFPQERCP | VVLAPLLYPE | KRDILMDRIL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PDSGGVAKTM | MESSLADFMQ | EVGYGFCASI | EECRNIIVQF | GVREVTAAQV | ARVLGMMART | HSGLTDGIPL | QSISAPGSGI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WSDGKDKSDG | AQAHTWNVEV | LIDVLKELNP | SLNFKEVTYE | LDHPGFQIRD | SKGLHNVVYG | IQRGLGMEVF | PVDLIYRPWK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HAEGQLSFIQ | HSLINPEIFC | FADYPCHTVA | TDILKAPPED | DNREIATWKS | LDLIESLLRL | AEVGQYEQVK | QLFSFPIKHC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PDMLVLALLQ | INTSWHTLRH | ELISTLMPIF | LGNHPNSAII | LHYAWHGQGQ | SPSIRQLIMH | AMAEWYMRGE | QYDQAKLSRI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LDVAQDLKAL | SMLLNGTPFA | FVIDLAALAS | RREYLKLDKW | LTDKIREHGE | PFIQACMTFL | KRRCPSILGG | LAPEKDQPKS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AQLPPETLAT | MLACLQACAG | SVSQELSETI | LTMVANCSNV | MNKARQPPPG | VMPKGRPPSA | SSLDAISPVQ | IDPLAGMTSL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SIGGSAAPHT | QSMQGFPPNL | GSAFSTPQSP | AKAFPPLSTP | NQTTAFSGIG | GLSSQLPVGG | LGTGSLTGIG | TGALGLPAVN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NDPFVQRKLG | TSGLNQPTFQ | QTDLSQVWPE | ANQHFSKEID | DEANSYFQRI | YNHPPHPTMS | VDEVLEMLQR | FKDSTIKRER |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EVFNCMLRNL | FEEYRFFPQY | PDKELHITAC | LFGGIIEKGL | VTYMALGLAL | RYVLEALRKP | FGSKMYYFGI | AALDRFKNRL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KDYPQYCQHL | ASISHFMQFP | HHLQEYIEYG | QQSRDPPVKM | QGSITTPGSI | ALAQAQAQAQ | VPAKAPLAGQ | VSTMVTTSTT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TTVAKTVTVT | RPTGVSFKKD | VPPSINTTNI | DTLLVATDQT | ERIVEPPENI | QEKIAFIFNN | LSQSNMTQKV | EELKETVKEE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| FMPWVSQYLV | MKRVSIEPNF | HSLYSNFLDT | LKNPEFNKMV | LNETYRNIKV | LLTSDKAAAN | FSDRSLLKNL | GHWLGMITLA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KNKPILHTDL | DVKSLLLEAY | VKGQQELLYV | VPFVAKVLES | SIRSVVFRPP | NPWTMAIMNV | LAELHQEHDL | KLNLKFEIEV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LCKNLALDIN | ELKPGNLLKD | KDRLKNLDEQ | LSAPKKDVKQ | PEELPPITTT | TTSTTPATNT | TCTATVPPQP | QYSYHDINVY |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| SLAGLAPHIT | LNPTIPLFQA | HPQLKQCVRQ | AIERAVQELV | HPVVDRSIKI | AMTTCEQIVR | KDFALDSEES | RMRIAAHHMM |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| RNLTAGMAMI | TCREPLLMSI | STNLKNSFAS | ALRTASPQQR | EMMDQAAAQL | AQDNCELACC | FIQKTAVEKA | GPEMDKRLAT |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| EFELRKHARQ | EGRRYCDPVV | LTYQAERMPE | QIRLKVGGVD | PKQLAVYEEF | ARNVPGFLPT | NDLSQPTGFL | AQPMKQAWAT |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| DDVAQIYDKC | ITELEQHLHA | IPPTLAMNPQ | AQALRSLLEV | VVLSRNSRDA | IAALGLLQKA | VEGLLDATSG | ADADLLLRYR |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| ECHLLVLKAL | QDGRAYGSPW | CNKQITRCLI | ECRDEYKYNV | EAVELLIRNH | LVNMQQYDLH | LAQSMENGLN | YMAVAFAMQL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| VKILLVDERS | VAHVTEADLF | HTIETLMRIN | AHSRGNAPEG | LPQLMEVVRS | NYEAMIDRAH | GGPNFMMHSG | ISQASEYDDP |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| PGLREKAEYL | LREWVNLYHS | AAAGRDSTKA | FSAFVGQMHQ | QGILKTDDLI | TRFFRLCTEM | CVEISYRAQA | EQQHNPAANP |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| TMIRAKCYHN | LDAFVRLIAL | LVKHSGEATN | TVTKINLLNK | VLGIVVGVLL | QDHDVRQSEF | QQLPYHRIFI | MLLLELNAPE |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| HVLETINFQT | LTAFCNTFHI | LRPTKAPGFV | YAWLELISHR | IFIARMLAHT | PQQKGWPMYA | QLLIDLFKYL | APFLRNVELT |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| KPMQILYKGT | LRVLLVLLHD | FPEFLCDYHY | GFCDVIPPNC | IQLRNLILSA | FPRNMRLPDP | FTPNLKVDML | SEINIAPRIL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1883 | 1 | 946.8565 | -104.22 | 2 | 53.4 | 12.0 | 0 | 1908-1924 | R.AQAEQQHNPAANPTMIR.A | Oxidation: 15 |

# Detailed Protein Report

## Protein 777: tripartite motif-containing protein 38 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5454014 | **Score:** | 23.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 53.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 7.3 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530381362 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: tripartite motif-containing protein 38 isoform X2 [Homo sapiens] |
| gi\|530381360 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: tripartite motif-containing protein 38 isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MASTTSTKKM | MEEATCSICL | SLMTNPVSIN | CGHSYCHLCI | TDFFKNPSQK | QLRQETFCCP | QCRAPFHMDS | LRPNKQLGSL |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| IEALKETDQE | MSCEEHGEQF | HLFCEDEGQL | ICWRCERAPQ | HKGHTTALVE | DVCQGYKEKL | QKAVTKLKQL | EDRCTEQKLS |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| TAMRITKWKE | KVQIQRQKIR | SDFKNLQCFL | HEEEKSYLWR | LEKEEQQTLS | RLRDYEAGLG | LKSNELKSHI | LELEEKCQGS |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| AQKLLQNVND | TLSRSWAVKL | ETSEAVSLEL | HTMCNVSKLY | FDVKKMLRSH | QVSVTLDPDT | AHHELILSED | RRQVTRGYTQ |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| ENQDTSSRRF | TAFPCVLGCE | GFTSGRRYFE | VDVGEGTGWD | LGVCMENVQR | GTGMKQEPQS | GFWTLRLCKK | KGYVALTSPP |
| **410** | **420** | **430** | **440** | **450** | **460** | **470** | |
| TSLHLHEQPL | LVGIFLDYEA | GVVSFYNGNT | GCHIFTFPKA | SFSDTLRPYF | QVYQYSPLFL | PPPGD | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1325 | 1 | 991.5878 | 113.64 | 2 | 46.7 | 11.2 | 2 | 149-164 | K.QLEDRCTEQKLSTAMR.I | Carbamidomethyl: 6;<br>Oxidation: 15 |

# Detailed Protein Report

## Protein 778: DNA repair protein XRCC1 [Homo sapiens]

**Accession:** gi|190684675
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 22.9
**MW [kDa]:** 69.5
**pI:** 5.9
**Sequence Coverage [%]:** 5.5
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPEIRLRHVV | SCSSQDSTHC | AENLLKADTY | RKWRAAKAGE | KTISVVLQLE | KEEQIHSVDI | GNDGSAFVEV | LVGSSAGGAG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EQDYEVLLVT | SSFMSPSESR | SGSNPNRVRM | FGPDKLVRAA | AEKRWDRVKI | VCSQPYSKDS | PFGLSFVRFH | SPPDKDEAEA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PSQKVTVTKL | GQFRVKEEDE | SANSLRPGAL | FFSRINKTSP | VTASDPAGPS | YAAATLQASS | AASSASPVSR | AIGSTSKPQE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SPKGKRKLDL | NQEEKKTPSK | PPAQLSPSVP | KRPKLPAPTR | TPATAPVPAR | AQGAVTGKPR | GEGTEPRRPR | AGPEELGKIL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QGVVVVLSGF | QNPFRSELRD | KALELGAKYR | PDWTRDSTHL | ICAFANTPKY | SQVLGLGGRI | VRKEWVLDCH | RMRRRLPSQR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YLMAGPGSSS | EEDEASHSGG | SGDEAPKLPQ | KQPQTKTKPT | QAAGPSSPQK | PPTPEETKAA | SPVLQEDIDI | EGVQSEGQDN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GAEDSGDTED | ELRRVAEQKE | HRLPPGQEEN | GEDPYAGSTD | ENTDSEEHQE | PPDLPVPELP | DFFQGKHFFL | YGEFPGDERR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KLIRYVTAFN | GELEDYMSDR | VQFVITAQEW | DPSFEEALMD | NPSLAFVRPR | WIYSCNEKQK | LLPHQLYGVV | PQA |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2390 | 1 | 767.3810 | -70.91 | 2 | 58.1 | 11.1 | 0 | 257-271 | K.TPSKPPAQLSPSVPK.R | |

# Detailed Protein Report

**Protein 779:** **PREDICTED: rootletin-like [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578805488 | **Score:** | 22.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 147.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| | | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRAAIERRWR | REQELCLQLK | SSQALVASLQ | EQLSESRREL | WAAQKLQQER | AREQAREREA | LRGQLEAQRL | EVQQCRASCK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LLGREKAALE | MVVEELKGKA | DAADAEKQGL | EAEAAELQRS | LLLQAERREE | LALRRERSCR | ALETSQGRLQ | QLEEKVSGLR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EELASVREAL | STAQLQRDVV | ESEREGLRSA | LARAECSNAD | LELLVRRLKS | EGVEQRDSLA | AMAALMEGLA | QDKSALNHLA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LQLEQERDQL | REQRKTLEQE | RARAGEQLAQ | AEQQLALERA | ERRGLQQACG | RLEQRQEQLE | GQAALLGREK | AQLQEQVGQV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TCQKQALEEQ | LAQSLQDQEA | QMGTLQQALQ | GKDALSEERA | QLLAKQEALE | RQGRLAAEEA | ADLRVERDSL | ESSLLEAQQL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ATKLQEQLEE | EARSAGLARQ | ALQVEMEQLQ | SDWEVQEMKL | RQDTVRLQRQ | VAQQEREAQR | ALESQALAHR | EALAQLQREK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ETLSLTLAEE | KEVARCQLEQ | EKELVTKSAA | EREALKGEIQ | SLKQERDESL | LQLEHKMQQA | LSLKETERSL | LSEELSRARR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TLERVQQEAQ | SQQEQAQATI | SATTEELKAL | QAQFEDAITA | HQRETTALRE | SLQDLAAERG | DVEREVRGRA | GGLLGMPEDR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RKQGRRKVSF | QQISKSGPVS | DHTGKQNEIA | KLGAAGGGGG | GGVERAERLR | AQLTVAQEGL | AALRQELQGV | EESREGLHRE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AQEARRALSD | EAREKDVLLL | FNSELRATIC | RAEQEKASFK | RSKEEKEQKL | LILEEAQAAL | QQEASALRAH | LWELEQAGGD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ARQELRELHR | QVLGLQRKLA | EVEAAGEAHG | QRLQEHLRES | RGAEQTLRAE | LHSVTRKLQE | ASGVADALQA | RLDQACHRIH |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SLEQELAQAE | GARQDAEAQL | GRLCSTLRRG | LGLQRQSPWA | SPEQPGSPTK | GSDSSQALPG | QQGTSPPARP | HSPLRWPSPT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PGGRSSELMD | VATVQDILRD | FVQKLREAQR | ERDDSRIQMA | TLSSRLSEAE | CRCARAQSRV | GQLQKALAEA | EEGQRRVEGA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LSSARAARAL | QKEALRRLEL | EHLASVRAAG | QEKRRLQEQL | ETLRQALEES | RRHSQGLAKQ | GKLLEEQLTN | LEHRCQKAEV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SLEPLRQVLC | RPQRLSGGQE | AAEAQAERRV | LQEQTAALRT | ERARLQGELA | ALRAQLAQME | QETLKREEDV | ARLGAEKEQL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DQSLNSLHQE | VDGALRQNQQ | LQAQMTEMEQ | AHTQRLQDLT | AQHQRDLATE | AERLHGARPQ | ATQALESQEW | THQQQVKVLE |
| 1290 | 1300 | 1310 | 1320 | | | | |
| EQVASLKEQL | DQEVQWRQQA | HLGQAFQTGQ | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2839 | 3 | 973.5111 | -15.00 | 2 | 64.1 | 12.2 | 2 | 479-495 | R.EKETLSLTLAEEKEVAR.C | |
| 1510 | 1 | 899.4718 | 8.92 | 2 | 47.2 | 10.7 | 1 | 666-685 | K.QNEIAKLGAAGGGGGGGVER.A | |

# Detailed Protein Report

**Protein 780:** **gamma-tubulin complex component 6 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|56788364 | **Score:** | 22.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 200.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASITQLFDD | LCEALLPAAK | THLGQRSVNR | KRAKRSLKKV | AYNALFTNLF | QDETQQLQPD | MSKLPARNKI | LMLSFDLRVG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GLGPKADRLE | ELVEELEAAP | CCPLLEVGSV | LDLLVQLAGS | GPPQVLPRKR | DYFLNNKHVG | RNVPYSGYDC | DDLSVFEMDV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QSLISREECL | CHSMIQETLQ | VMEAAPGTGL | PTVGLFSFGD | PCGDRFERDT | RVSLFGALVH | SRTYDMDVRL | GLPPVPDNAD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LSGLAIKVPP | SVDQWEDEGF | QSASNLTPDS | QSEPSVTPDV | DLWEAALTYE | ASKRRCWERV | GCPPGHREEP | YLTEAGRDAF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DKFCRLHQGE | LQLLAGGVLQ | APQPVLVKEC | ELVKDVLNVL | IGVVSATFSL | CQPAQAFVVK | RGVHVSGASP | ESISSLLSEV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AEYGTCYTRL | SHFSLQPVLD | SLYSKGLVFQ | AFTSGLRRYL | QYYRACVLST | PPTLSLLTIG | FLFKKLGRQL | RYLAELCGVG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AVLPGTCGGG | PRAAFPTGVK | LLSYLYQEAL | HNCSNEHYPV | LLSLLKTSCE | PYTRFIHDWV | YSGVFRDAYG | EFMIQVNHEY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LSFRDKLYWT | HGYVLISKEV | EDCVPVFLKH | IAHDIYVCGK | TINLLKLCCP | RHYLCWSDVP | VPRISVIFSL | EELKEIEKDC |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AVYVGRMERV | ARHSSVSKEE | KELRMEIAKQ | ELIAHAREAA | SRVLSALSDR | QMSERMALDA | RKREQFQRLK | EQFVKDQERR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QAARQEELDD | DFSYARELRD | RERRLKSLEE | ELERKARQAL | VDHYSKLSAE | AARREQKALW | RIQRHRLESA | RLRFLLEDEK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| HIQEMLKAVS | EAHQPQEPPD | VLLSVHPQVT | SPGPEHPEGG | QGCDSGSAEQ | HSPAWDGWNR | PGLLTPQPLK | PLAVGAGGRG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LQQAEGARPF | SDSLSIGDFL | PVGPGAEPSV | QTGMVPLLEV | ALQTINLDLP | PSAPGEAPAA | ASTQPSRPQE | YDFSTVLRPA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VATSPAPGPL | QAAECSLGSS | GLQLWEDSCG | KMDACGSASR | ETLLPSHPPR | RAALEEGSSQ | PTERLFGQVS | GGGLPTGDYA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SEIAPTRPRW | NTHGHVSDAS | IRVGENVSDV | APTQPRWNTH | GHVSNASISL | GESVSDVAPT | RPRWNIHGHV | SNASIRVGEN |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| VSDVAPTRPR | WNTHGHVSNA | SIRVGENVSD | VAPTRPRWNT | HGHVSDASIS | LGESVSDMAP | ARPRWNTHGH | VSDASISLGE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SVSDMAPTRP | RWNTHGHVSD | TSIRVGENVS | DVAPIRSRCN | THGHVSDASI | SLGEPVSDVV | STRPRWNTHV | PIPPPHMVLG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| ALSPEAEPNT | PRPQQSPPGH | TSQSALSLGA | QSTVLDCGPR | LPVEVGPSLS | SPSSGCGEGS | ISVGENVSDV | APTQPWWPNT |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PGDSVSEELG | PGRSGDTEDL | SPNWPLNSQE | DTAAQSSPGR | GEEAEASAAE | AQGGEQAYLA | GLAGQYHLER | YPDSYESMSE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| PPIAHLLRPV | LPRAFAFPVD | PQVQSAADET | AVQLSELLTL | PVLMKRSITA | PLAAHISLVN | KAAVDYFFVE | LHLEAHYEAL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| RHFLLMEDGE | FAQSLSDLLF | EKLGAGQTPG | ELLNPLVLNS | VLSKALQCSL | HGDTPHASNL | SLALKYLPEV | FAPNAPDVLS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| CLELRYKVDW | PLNIVITEGC | LSKYSGVFSF | LLQLKLMMWA | LKDVCFHLKR | TALLSHMAGS | VQFRQLQLFK | HEMQHFVKVI |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| QGYIANQILH | VTWCEFRARL | ATVGDLEEIQ | RAHAEYLHKA | VFRGLLTEKA | APVMNVIHSI | FSLVLKFRSQ | LISQAWGPPG |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | | |
| GPRGAEHPNF | ALMQQSYNTF | KYYSHFLFKV | VTKLVNRGYQ | PHLEDFLLRI | NFNNYYQDA | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2334 | 1 | 1023.8623 | -142.84 | 2 | 59.1 | 12.7 | 0 | 472-492 | R.YLAELCGVGAVLPGTCGGGPR.A | Carbamidomethyl: 6 |

# Detailed Protein Report

## Protein 781: protein TALPID3 isoform 6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|346644669 | **Score:** | 22.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 149.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.08 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.98 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPVFKEVKVH | LLEDAGIEKD | AVTQETRISP | SGIDSATTVA | AATAAAIATA | APLIKVQSDL | EAKVNSVTEL | LSKLQETDKH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LQRVTEQQTS | IQRKQEKLHC | HDHEKQMNVF | MEQHIRHLEK | LQQQQIDIQT | HFISAALKTS | SFQPVSMPSS | RAVEKYSVKP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EHPNLGSCNP | SLYNTFASKQ | APLKEVEDTS | FDKQKSPLET | PAPRRFAPVP | VSRDDELSKR | ENLLEEKENM | EVSCHRGNVR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LLEQILNNND | SLTRKSESSN | TTSLTRSKIG | WTPEKTNRFP | SCEELETTKV | TMQKSDDVLH | DLGQKEKETN | SMVQPKESLS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MLKLPDLPQN | SVKLQTTNTT | RSVLKDAEKI | LRGVQNNKKV | LEENLEAIIR | AKDGAAMYSL | INALSTNREM | SEKIRIRKTV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DEWIKTISAE | IQDELSRTDY | EQKRFDQKNQ | RTKKGQNMTK | DIRTNTQDKT | VNKSVIPRKH | SQKQIEEHFR | NLPMRGMPAS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SLQKERKEGL | LKATTVIQDE | DYMLQVYGKP | VYQGHRSTLK | KGPYLRFNSP | SPKSRPQRPK | VIERVKGTKV | KSIRTQTDFY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ATKPKKMDSK | MKHSVPVLPH | GDQQYLFSPS | REMPTFSGTL | EGHLIPMAIL | LGQTQSNSDT | MPPAGVIVSK | PHPVTVTTSI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PPSSRKVETG | VKKPNIAIVE | MKSEKKDPPQ | LTVQVLPSVD | IDSISNSSAD | VLSPLSSPKE | ASLPPVQTWI | KTPEIMKVDE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EEVKFPGTNF | DEIIDVIQEE | EKCDEIPDSE | PILEFNRSVK | ADSTKYNGPP | FPPVASTFQP | TADILDKVIE | RKETLENSLI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QWVEQEIMSR | IISGLFPVQQ | QIAPSISVSV | SETSEPLTSD | IVEGTSSGAL | QLFVDAGVPV | NSNVIKHFVN | EALAETIAVM |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LGDREAKKQG | PVATGVSGDA | STNETYLPAR | VCTPLPTPQP | TPPCSPSSPA | KECVLVKTPD | SSPCDSDHDM | AFPVKEICAE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KGDDMPAIML | VNTPTVTPTT | TPPPAAAVFT | PTLSDISIDK | LKVSSPELPK | PWGDGDLPLE | EENPNSPQEE | LHPRAIVMSV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AKDEEPESMD | FPAQPPPPEP | VPFMPFPAGT | KAPSPSQMPG | SDSSTLESTL | SVTVTETETL | DKPISEGEIL | FSCGQKLAPK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ILEDIGLYLT | NLNDSLSSTL | HDAVEMEDDP | PSEGQVIRMS | HKKFHADAIL | SFAKQNQESA | VSQQAVYHSE | DLENSVGELS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EGQRPQLTAA | AENILMGHSL | YMQPPVTNTQ | SLDQQCDPKP | LSRQFDTVSG | SIYEDSCASH | GPMSLGELEL | EPNSKLVLPT |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | |
| TLLTAQENDV | NLPVAAEDFS | QYQLKQNQDV | KQVEHKPSQS | YLRVRNKSDI | APSQQQVLIS | RIKNCKN | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2296 | 1 | 653.8345 | 23.68 | 2 | 58.6 | 11.0 | 1 | 306-316 | K.EKETNSMVQPK.E | Oxidation: 7 | QU:MU 1.08<br>WUP:QUP 1.98 |

# Detailed Protein Report

**Protein 782:** **histone-lysine N-methyltransferase SETD1B [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|210032580 | **Score:** | 22.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 208.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| | | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MENSHPPHHH | HQQPPPQPGP | SGERRNHHWR | SYKLMIDPAL | KKGHHKLYRY | DGQHFSLAMS | SNRPVEIVED | PRVVGIWTKN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KELELSVPKF | KIDEFYVGPV | PPKQVTFAKL | NDNIRENFLR | DMCKKYGEVE | EVEILYNPKT | KKHLGIAKVV | FATVRGAKDA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VQHLHSTSVM | GNIIHVELDT | KGETRMRFYE | LLVTGRYTPQ | TLPVGELDAV | SPIVNETLQL | SDALKRLKDG | GLSAGCGSGS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SSVTPNSGGT | PFSQDTAYSS | CRLDTPNSYG | QGTPLTPRLG | TPFSQDSSYS | SRQPTPSYLF | SQDPAVTFKA | RRHESKFTDA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YNRRHEHHYV | HNSPAVTAVA | GATAAFRGSS | DLPFGAVGGT | GGSSGPPFKA | QPQDSATFAH | TPPPAQATPA | PGFKSAFSPY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QTPVAHFPPP | PEEPTATAAF | GARDSGEFRR | APAPPPLPPA | EPLAKEKPGT | PPGPPPPDTN | SMELGGRPTF | GWSPEPCDSP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GTPTLESSPA | GPEKPHDSLD | SRIEMLLKEQ | RTKLLFLREP | DSDTELQMEG | SPISSSSSQL | SPLAPFGTNS | QPGFRGPTPP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SSRPSSTGLE | DISPTPLPDS | DEDEELDLGL | GPRPPPEPGP | PDPAGLLSQT | AEVALDLVGD | RTPTSEKMDE | GQQSSGEDME |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ISDDEMPSAP | ITSADCPKPM | VVTPGAAAVA | APSVLAPTLP | LPPPPGFPPL | PPPPPPPPPQ | PGFPMPPPLP | PPPPPPPPAH |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PAVTVPPPPL | PAPPGVPPPP | ILPPLPPFPP | GLFPVMQVDM | SHVLGGQWGG | MPMSFQMQTQ | VLSRLMTGQG | ACPYPPFMAA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AAAAASAGLQ | FVNLPPYRGP | FSLSNSGPGR | GQHWPPLPKF | DPSVPPPGYM | PRQEDPHKAT | VDGVLLVVLK | ELKAIMKRDL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| NRKMVEVVAF | RAFDEWWDKK | ERMAKASLTP | VKSGEHKDED | RPKPKDRIAS | CLLESWGKGE | GLGYEGLGLG | IGLRGAIRLP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SFKVKRKEPP | DTTSSGDQKR | LRPSTSVDEE | DEESERERDR | DMADTPCELA | KRDPKGVGVR | RRPARPLELD | SGGEEDEKES |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LSEEQESTEE | EEEAEEEEEE | EDDDDDDSDD | RDESENDDED | TALSEASEKD | EGDSDEEETV | SIVTSKAEAT | SSSESSESSE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| FESSSESSPS | SSEDEEEVVA | REEEEEEEEE | EMVAEESMAS | AGPEDFEQDG | EEAALAPGAP | AVDSLGMEEE | VDIETEAVAP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EERPSMLDEP | PLPVGVEEPA | DSREPPEEPG | LSQEGAMLLS | PEPPAKEVEA | RPPLSPERAP | EHDLEVEPEP | PMMLPLPLQP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PLPPPRPPRP | PSPPPEPETT | DASHPSVPPE | PLAEDHPPHT | PGLCGSLAKS | QSTETVPATP | GGEPPLSGGS | SGLSLSSPQV |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PGSPFSYPAP | SPSLSSGGLP | RTPGRDFSFT | PTFSEPSGPL | LLPVCPLPTG | RRDERSGPLA | SPVLLETGLP | LPLPLPLPLP |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LALPAVLRAQ | ARAPTPLPPL | LPAPLASCPP | PMKRKPGRPR | RSPPSMLSLD | GPLVRPPAGA | ALGRELLLLP | GQPQTPVFPS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| THDPRTVTLD | FRNAGIPAPP | PPLPPQPPPP | PPPPPVEPTK | LPFKELDNQW | PSEAIPPGPR | GRDEVTEEYM | ELAKSRGPWR |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| RPPKKRHEDL | VPPAGSPELS | PPQPLFRPRS | EFEEMTILYD | IWNGGIDEED | IRFLCVTYER | LLQQDNGMDW | LNDTLWVYHP |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| STSLSSAKKK | KRDDGIREHV | TGCARSEGFY | TIDKKDKLRY | LNSSRASTDE | PPADTQGMSI | PAQPHASTRA | GSERRSEQRR |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| LLSSFTGSCD | SDLLKFNQLK | FRKKKLKFCK | SHIHDWGLFA | MEPIAADEMV | IEYVGQNIRQ | VIADMREKRY | EDEGIGSSYM |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| FRVDHDTIID | ATKCGNFARF | INHSCNPNCY | AKVITVESQK | KIVIYSKQHI | NVNEEITYDY | KFPIEDVKIP | CLCGSENCRG |
| 1930 | | | | | | | |
| TLN | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 837 | 1 | 801.1846 | -354.77 | 1 | 40.0 | 10.6 | 2 | 878-883 | K.RDLNRK.M | |

# Detailed Protein Report

---

**Protein 783:** **septin-7 isoform 3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|339639597 | **Score:** | 22.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| | | **Sequence Coverage [%]:** | 5.7 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.60 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.91 | **CV:** | 24.21 % | **No. of Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSVSARSAAA | EERSVNSSTM | GESGLGKSTL | INSLFLTDLY | SPEYPGPSHR | IKKTVQVEQS | KVLIKEGGVQ | LLLTIVDTPG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FGDAVDNSNC | WQPVIDYIDS | KFEDYLNAES | RVNRRQMPDN | RVQCCLYFIA | PSGHGLKPLD | IEFMKRLHEK | VNIIPLIAKA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DTLTPEECQQ | FKKQIMKEIQ | EHKIKIYEFP | ETDDEEENKL | VKKIKDRLPL | AVVGSNTIIE | VNGKRVRGRQ | YPWGVAEVEN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GEHCDFTILR | NMLIRTHMQD | LKDVTNNVHY | ENYRSRKLAA | VTYNGVDNNK | NKGQLTKSPL | AQMEEERREH | VAKMKKMEME |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MEQVFEMKVK | EKVQKLKDSE | AELQRRHEQM | KKNLEAQHKE | LEEKRRQFED | EKANWEAQQR | ILEQQNSSRT | LEKNKKKGKI |
| 410 | | | | | | | |
| F | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1252 | 1 | 918.2353 | -276.27 | 1 | 45.8 | 10.9 | 0 | 54-61 | K.TVQVEQSK.V | | WUP:QUP 0.72 |
| 150 | 1 | 894.4204 | -71.26 | 2 | 31.8 | 11.9 | 2 | 381-395 | R.ILEQQNSSRTLEKNK.K | | QU:MU 1.60<br>WUP:QUP 1.15 |

# Detailed Protein Report

---

**Protein 784:** **PREDICTED: xin actin-binding repeat-containing protein 2 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578803637 | **Score:** | 22.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 375.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.54 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.27 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMEESEMCAV | PGGLAKVKKQ | FEDEITSSRN | TFAQYQYQHQ | NRSEQEAIHS | SQVGTSRSSQ | EMARNEQEGS | KVQKIDVHGT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EMVSHLEKHT | EEVNQASQFH | QYVQETVIDT | PEDEEIPKVS | TKLLKEQFEK | SAQEKILYSD | KEMTTPAKQI | KTESEYEETF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KPSSVVSTSS | TSCVSTSQRK | ETSTTRYSDH | SVTSSTLAQI | NATSSGMTEE | FPPPPPDVLQ | TSVDVTAFSQ | SPELPSPPRR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LPVPKDVYSK | QRNLYELNRL | YKHIHPELRK | NLEKDYISEV | SEIVSSQMNS | GSSVSADVQQ | ARYVFENTND | SSQKDLNSER |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EYLEWDEILK | GEVQSIRWIF | ENQPLDSINN | GSPDEGDISR | GIADQEIIAG | GDVKYTTWMF | ETQPIDTLGA | YSSDTVENAE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KIPELARGDV | CTARWMFETR | PLDSMNKMHQ | SQEESAVTIS | KDITGGDVKT | VRYMFETQHL | DQLGQLHSVD | EVHLLQLRSE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LKEIKGNVKR | SIKCFETQPL | YVIRDGSGQM | LEIKTVHRED | VEKGDVRTAR | WMFETQPLDT | INKDITEIKV | VRGISMEENV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KGGVSKAKWL | FETQPLEKIK | ESEEVIIEKE | KIIGTDVSRK | CWMFETQPLD | ILKEVPDADS | LQREEIIGGD | VQTTKHLFET |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LPIEALKDSP | DIGKLQKITA | SEEEKGDVRH | QKWIFETQPL | EDIRKDKKEY | TRTVKLEEVD | RGDVKNYTHI | FESNNLIKFD |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ASHKIEVEGV | TRGAVELNKS | LFETTPLYAI | QDPLGKYHQV | KTVQQEEIVR | GDVRSCRWLF | ETRPIDQFDE | SIHKFQIIRG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ISAQEIQTGN | VKSAKWLFET | QPLDSIKYFS | DVEETESKTE | QTRDIVKGDV | KTCKWLFETQ | PMESLYEKVS | LMTSSEEIHK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GDVKTCTWLF | ETQPLDTIKD | DSETAVKLQT | VKQEEIQGGD | VRTACFLFET | ENLDSIQGEE | VKEIKPVEMD | IQAGDVSSMR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| YKFENQSLDS | ISSSSEEVLK | KIKTLKTEDI | QKGNVLNCRW | LFENQPIDKI | KESQEGDECV | KTVTDIQGGD | VRKGCFIFET |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| FSLDEIKEES | DYISTKKTIT | EEVIQGDVKS | YRMLFETQPL | YAIQDREGSY | HEVTTVKKEE | VIHGDVRGTR | WLFETKPLDS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| INKSETVYVI | KSVTQEDIQK | GDVSSVRYRF | ETQPLDQISE | ESHNIMPSID | HIQGGNVKTS | RQFFESENFD | KNNYIRTVSV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| NEIQKGNVKT | STWLFETHTM | DELRGEGLEY | ENIKTVTQED | VQKGDVKQAV | WLFENRTFDS | IMEAHKGITK | MTKEEIPPSD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VKTTTWLFET | TPLHEFNETR | VEKIEIIGKS | IKETLEDLYS | QKVIQAPGII | IEADEIGDVR | MAKYKLMNQA | SPEIQKEEII |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| RADLRNIMVN | LLSKRDCTER | EILISEEEKG | NVNLTKTQLL | NRSTEFHAEK | EEIVKGDVQQ | AIKNLFSEER | SVKKGILIQE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DEKGDINMTI | YCLLHENDGD | TIEREEVIGG | DVKRTIHNLL | SSTSNNKISE | RAKIDASERG | NVQFFTTCIE | AGALDYLKQL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| HTESNETLTA | KKQEGEKEII | GGDVEGTKLL | LKKRQSLVER | TVSETDIIPG | DVHNTVKVFM | TEPQSTFGKI | PKEEIIKGDL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| TSTLNSLSQA | VNQKTVTKTE | EIIKGNMLAT | LKSLKESSHR | WKESKQPDAI | PGDIEKAIEC | LEKATNTKTE | ILKKELLKDD |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LETSLRSLKE | AQRSFKEVHK | EGVIKKDAKA | VMAGSSGEQK | TDIHQVAVQR | NKNSLLQPKP | GPFEPAAKWQ | GGADTLSQTM |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| GKSCHGNLVE | ERTEVNLPKA | PKGTVKIVID | REQNNDALEK | SLRRLSNSHH | KSNVLESGDK | TGVWTDTTGE | QHLRDEYMSR |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| QLTSTVSVKN | NLTTKESDRA | VRELKKDDVF | NSIQSAGKTV | GKQQTYELRN | DHQKMEGFHI | KSPKKTKNIK | ILTDTQSSKP |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| SPTQHPVSMP | VGGTYDLSGD | FQKQTLLKQE | TKYSNKDIKK | KNINLQPMWQ | LLPVEQDTSN | VTEMKVSEKS | HNTFKATNKK |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| RETDVHLKSQ | DFLMKTNTST | GLKMAMERSL | NPINFNPENN | VKESECPLPP | PSPPPPPPSN | ASSEIEFPLP | PPPPLMMFPE |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| KNGFLPSLST | EKIKAEFESF | PGLPLPPPPV | DEKSERESSS | MFLPPPPPPT | PSQKPAHLLS | SSAPEKHSGD | FMQQYSQKEA |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2325 | 1 | 805.7815 | -141.84 | 2 | 58.9 | 11.2 | 0 | 75-88 | K.IDVHGTEMVSHLEK.H | Oxidation: 8 | WUP:QUP 1.27<br>QU:MU 2.54 |

# Detailed Protein Report

## Protein 785: tyrosine-protein kinase BTK isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|565324227 | **Score:** | 22.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 55.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.9 |
| | | **Sequence Coverage [%]:** | 5.4 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MAAVILESIF LKRSQQKKKT SPLNFKKRLF LLTVHKLSYY EYDFERGRRG SKKGSIDVEK ITCVETVVPE KNPPPERQIP

        90        100        110        120        130        140        150        160
RRGEESSEME QISIIERFPY PFQVVYDEGP LYVFSPTEEL RKRWIHQLKN VIRYNSDLVQ KYHPCFWIDG QYLCCSQTAK

       170        180        190        200        210        220        230        240
NAMGCQILEN RNGSLKPGSS HRKTKKPLPP TPEEDQILKK PLPPEPAAAP VSTSELKKVV ALYDYMPMNA NDLQLRKGDE

       250        260        270        280        290        300        310        320
YFILEESNLP WWRARDKNGQ EGYIPSNYVT EAEDSIEMYE WYSKHMTRSQ AEQLLKQEGK EGGFIVRDSS KAGKYTVSVF

       330        340        350        360        370        380        390        400
AKSTGDPQGV IRHYVVCSTP QSQYYLAARN CLVNDQGVVK VSDFGLSRYV LDDEYTSSVG SKFPVRWSPP EVLMYSKFSS

       410        420        430        440        450        460        470        480
KSDIWAFGVL MWEIYSLGKM PYERFTNSET AEHIAQGLRL YRPHLASEKV YTIMYSCWHE KADERPTFKI LLSNILDVMD

       490
EES
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1867 | 1 | 918.3491 | -141.72 | 2 | 53.2 | 12.2 | 1 | 383-397 | K.FPVRWSPPEVLMYSK.F | |

# Detailed Protein Report

## Protein 786: ephrin type-A receptor 5 isoform e [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|528881091 | **Score:** | 22.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 110.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.16 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.93 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MRGSGPRGAG RRRPPSGGGD TPITPASLAG CYSAPRRAPL WTCLLLCAAL RTLLASPSNE VNLLDSRTVM GDLGWIAFPK
        90        100        110        120        130        140        150        160
NGWEEIGEVD ENYAPIHTYQ VCKVMEQNQN NWLLTSWISN EGASRIFIEL KFTLRDCNSL PGGLGTCKET FNMYYFESDD
       170        180        190        200        210        220        230        240
QNGRNIKENQ YIKIDTIAAD ESFTELDLGD RVMKLNTEVR DVGPLSKKGF YLAFQDVGAC IALVSVRVYY KKCPSVVRHL
       250        260        270        280        290        300        310        320
AVFPDTITGA DSSQLLEVSG SCVNHSVTDE PPKMHCSAEG EWLVPIGKCM CKAGYEEKNG TCQVCRPGFF KASPHIQSCG
       330        340        350        360        370        380        390        400
KCPPHSYTHE EASTSCVCEK DYFRRESDPP TMACTRPPSA PRNAISNVNE TSVFLEWIPP ADTGGRKDVS YYIACKKCNS
       410        420        430        440        450        460        470        480
HAGVCEECGG HVRYLPRQSG LKNTSVMMVD LLAHTNYTFE IEAVNGVSDL SPGARQYVSV NVTTNQAAPS PVTNVKKGKI
       490        500        510        520        530        540        550        560
AKNSISLSWQ EPDRPNGIIL EYEIKYFEKD QETSYTIIKS KETTITAEGL KPASVYVFQI RARTAAGYGV FSRRFEFETT
       570        580        590        600        610        620        630        640
PVSVAASSDQ SQIPVIAVSV TVGVILLAVV IGVLLSGSCC ECGCGRASSL CAVAHPSLIW RCGYSKAKQD PEEEKMHFHN
       650        660        670        680        690        700        710        720
GHIKLPGVRT YIDPHTYEDP NQAVHEFAKE IEASCITIER VIGAGEFGEV CSGRLKLPGK RELPVAIKTL KVGYTEKQRR
       730        740        750        760        770        780        790        800
DFLGEASIMG QFDHPNIIHL EGVVTKSKPV MIVTEYMENG SLDTFLKKND GQFTVIQLVG MLRGISAGMK YLSDMGYVHR
       810        820        830        840        850        860        870        880
DLAARNILIN SNLVCKVSDF GLSRVLEDDP EAAYTTRGGK IPIRWTAPEA IAFRKFTSAS DVWSYGIVMW EVVSYGERPY
       890        900        910        920        930        940        950        960
WEMTNQDVIK AVEEGYRLPS PMDCPAALYQ LMLDCWQKER NSRPKFDEIV NMLDKLIRNP SSLKTLVNAS CRVSNLLAEH
       970        980        990       1000       1010
SPLGSGAYRS VGEWLEAIKM GRYTEIFMEN GYSSMDAVAQ VTLE
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2043 | 1 | 661.2613 | -54.57 | 2 | 53.9 | 10.7 | 0 | 136-148 | R.DCNSLPGGLGTCK.E | Carbamidomethyl: 2 | WUP:QUP<br>QU:MU | 0.93<br>1.16 |

# Detailed Protein Report

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## Protein 787: PREDICTED: transcription initiation factor TFIID subunit 6 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578814558 | **Score:** | 22.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 71.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 6.3 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578814560 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: transcription initiation factor TFIID subunit 6 isoform X3 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAEEKKLKLS | NTVLPSESMK | VVAESMGIAQ | IQEETCQLLT | DEDALKFMHM | GKRQKLTTSD | IDYALKLKNV | EPLYGFHAQE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FIPFRFASGG | GRELYFYEEK | EVDLSDIINT | PLPRVPLDVC | LKAHWLSIEG | CQPAIPENPP | PAPKEQQKAE | ATEPLKSAKP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GQEEDGPLKG | KGQGATTADG | KGKEKKAPPL | LEGAPLRLKP | RSIHELSVEQ | QLYYKEITEA | CVGSCEAKRA | EALQSIATDP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GLYQMLPRFS | TFISEGVRVN | VVQNNLALLI | YLMRMVKALM | DNPTLYLEKY | VHELIPAVMT | CIVSRQLCLR | PDVDNHWALR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DFAARLVAQI | CKHFSTTTNN | IQSRITKTFT | KSWVDEKTPW | TTRYGSIAGL | AELGHDVIKT | LILPRLQQEG | ERIRSVLDGP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VLSNIDRIGA | DHVQSLLLKH | CAPVLAKLRP | PPDNQDAYRA | EFGSLGPLLC | SQVVKARAQA | ALQAQQVNRT | TLTITQPRPT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LTLSQAPQPG | PRTPGLLKVP | GSIALPVQTL | VSARAAAPPQ | PSPPPTKFIV | MSSSSSAPST | QQVLSLSTSA | PGSGSTTTSP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VTTTVPSVQP | IVKLVSTATT | APPSTAPSGP | GSVQKYIVVS | LPPTGEGKGG | PTSHPSPVPP | PASSPSPLSG | SALCGGKQEA |
| 650 | 660 | 670 | | | | | |
| GDSPPPAPGT | PKANGSQPNS | GSPQPAP | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2147 | 1 | 753.2605 | -149.09 | 2 | 57.2 | 10.4 | 1 | 352-363 | K.SWVDEKTPWTTR.Y | |
| 868 | 1 | 946.6986 | -87.24 | 3 | 39.3 | 12.4 | 1 | 638-667 | K.QEAGDSPPPAPGTPKANGSQPNSGSPQPAP.- | |

# Detailed Protein Report

## Protein 788: ubiquitin carboxyl-terminal hydrolase 22 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|150010639 | **Score:** | 22.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 5.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVSRPEPEGE | AMDAELAVAP | PGCSHLGSFK | VDNWKQNLRA | IYQCFVWSGT | AEARKRKAKS | CICHVCGVHL | NRLHSCLYCV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FFGCFTKKHI | HEHAKAKRHN | LAIDLMYGGI | YCFLCQDYIY | DKDMEIIAKE | EQRKAWKMQG | VGEKFSTWEP | TKRELELLKH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NPKRRKITSN | CTIGLRGLIN | LGNTCFMNCI | VQALTHTPLL | RDFFLSDRHR | CEMQSPSSCL | VCEMSSLFQE | FYSGHRSPHI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PYKLLHLVWT | HARHLAGYEQ | QDAHEFLIAA | LDVLHRHCKG | DDNGKKANNP | NHCNCIIDQI | FTGGLQSDVT | CQVCHGVSTT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IDPFWDISLD | LPGSSTPFWP | LSPGSEGNVV | NGESHVSGTT | TLTDCLRRFT | RPEHLGSSAK | IKCSGCHSYQ | ESTKQLTMKK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LPIVACFHLK | RFEHSAKLRR | KITTYVSFPL | ELDMTPFMAS | SKESRMNGQY | QQPTDSLNND | NKYSLFAVVN | HQGTLESGHY |
| 490 | 500 | 510 | 520 | 530 | | | |
| TSFIRQHKDQ | WFKCDDAIIT | KASIKDVLDS | EGYLLFYHKQ | FLEYE | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1841 | 1 | 785.8992 | 58.70 | 2 | 51.4 | 11.0 | 1 | 381-394 | K.IKCSGCHSYQESTK.Q | |

# Detailed Protein Report

## Protein 789: PREDICTED: rho GTPase-activating protein SYDE2 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530363440 | **Score:** | 22.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 105.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.6 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKGRELEELK | DNIEFRGHKP | LNSITVSKKR | NWLYQSTLRP | LNLEEENKKC | QDRSHLSISP | VSLPKHQLSQ | SFLKSSKEYC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TYVVCNATNS | SLSKNCALDF | NEENDADDEG | EIWYNPIPED | DDLGISSALS | FGEADSAVLK | LPAVNLSMLS | GSDLMKAERH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TEDSLCSSEH | AGDIQTTRSN | GMNPIHPAHS | TEFVQQYKQK | LGHKTQEGIM | VEDSPMLKSP | FAGSGILAAT | NSTELGIMEP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SSPNPSPVKK | GSSINWSLPD | KIKSPRTVRK | LSMKMKKLPE | FSRKLSVKGT | LNYINSPDNT | PSLSKYNCRE | VHHTDILPSG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NTTTAAKRNV | ISRYHLDTSV | SSQQSYQKKN | SMSSKYSCKG | GYLSDGDSPE | LTTKASKHGS | ENKFGKGKEI | ISNSCSKNEI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DIDAFRHYSF | SDQPKCSQYI | SGLMSVHFYG | AEDLKPPRID | SKDVFCAIQV | DSVNKARTAL | LTCRTTFLDM | DHTFNIEIEN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AQHLKLVVFS | WEPTPRKNRV | CCHGTVVLPT | LFRVTKTHQL | AVKLEPRGLI | YVKVTLMEQW | ENSLHGLDIN | QEPIIFGVDI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QKVVEKENIG | LMVPLLIQKC | IMEIEKRGCQ | VVGLYRLCGS | AAVKKELREA | FERDSKAVGL | CENQYPDINV | ITGVLKDYLR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ELPSPLITKQ | LYEAVLDAMA | KSPLKMSSNG | CENDPGDSKY | TVDLLDCLPE | IEKATLKMLL | DHLKLVASYH | EVNKMTCQNL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AVCFGPVLLS | QRQEPSTHNN | RVFTDSEELA | SALDFKKHIE | VLHYLLQLWP | VQRLTVKKST | DNLFPEQKSS | LNYLRQKKER |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PHMLNLSGTD | SSGVLRPRQN | RLDSPLSNRY | AGDWSSCGEN | YFLNTKENLN | DVDYDDVPSE | DRKIGENYSK | MDGPEVMIEQ |
| 890 | 900 | 910 | 920 | 930 | 940 | | |
| PIPMSKECTF | QTYLTMQTVE | STVDRKNNLK | DLQESIDTLI | GNLERELNKN | KLNMSF | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2968 | 1 | 964.7824 | -62.98 | 3 | 65.9 | 11.8 | 2 | 50-74 | K.CQDRSHLSISPVSLPKHQLSQSFLK.S | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 790: PREDICTED: lysosomal-trafficking regulator isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530365992 | **Score:** | 22.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 313.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSTDSNSLAR | EFLTDVNRLC | NAVVQRVEAR | EEEEEETHMA | TLGQYLVHGR | GFLLLTKLNS | IIDQALTCRE | ELLTLLLSLL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PLVWKIPVQE | EKATDFNLPL | SADIILTKEK | NSSSQRSTQE | KLHLEGSALS | SQVSAKVNVF | RKSRRQRKIT | HRYSVRDARK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TQLSTSDSEA | NSDEKGIAMN | KHRRPHLLHH | FLTSFPKQDH | PKAKLDRLAT | KEQTPPDAMA | LENSREIIPR | QGSNTDILSE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PAALSVISNM | NNSPFDLCHV | LLSLLEKVCK | FDVTLNHNSP | LAASVVPTLT | EFLAGFGDCC | SLSDNLESRV | VSAGWTEEPV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ALIQRMLFRT | VLHLLSVDVS | TAEMMPENLR | KNLTELLRAA | LKIRICLEKQ | PDPFAPRQKK | TLQEVQEDFV | FSKYRHRALL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LPELLEGVLQ | ILICCLQSAA | SNPFYFSQAM | DLVQEFIQHH | GFNLFETAVL | QMEWLVLRDG | VPPEASEHLK | ALINSVMKIM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| STVKKVKSEQ | LHHSMCTRKR | HRRCEYSHFM | HHHRDLSGLL | VSAFKNQVSK | NPFEETADGD | VYYPERCCCI | AVCAHQCLRL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LQQASLSSTC | VQILSGVHNI | GICCCMDPKS | VIIPLLHAFK | LPALKNFQQH | ILNILNKLIL | DQLGGAEISP | KIKKAACNIC |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TVDSDQLAQL | EETLQGNLCD | AELSSSLSSP | SYRFQGILPS | SGSEDLLWKW | DALKAYQNFV | FEEDRLHSIQ | IANHICNLIQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KGNIVVQWKL | YNYIFNPVLQ | RGVELAHHCQ | HLSVTSAQSH | VCSHHNQCLP | QDVLQIYVKT | LPILLKSRVI | RDLFLSCNGV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SQIIELNCLN | GIRSHSLKAF | ETLIISLGEQ | QKDASVPDID | GIDIEQKELS | SVHVGTSFHH | QQAYSDSPQS | LSKFYAGLKE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| AYPKRRKTVN | QDVHINTINL | FLCVAFLCVS | KEAESDRESA | NDSEDTSGYD | STASEPLSHM | LPCISLESLV | LPSPEHMHQA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ADIWSMCRWI | YMLSSVFQKQ | FYRLGGFRVC | HKLIFMIIQK | LFRSHKEEQG | KKEGDTSVNE | NQDLNRISQP | KRTMKEDLLS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LAIKSDPIPS | ELGSLKKSAD | SLGKLELQHI | SSINVEEVSA | TEAAPEEAKL | FTSQESETSL | QSIRLLEALL | AICLHGARTS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QQKMELELPN | QNLSVESILF | EMRDHLSQSK | VIETQLAKPL | FDALLRVALG | NYSADFEHND | AMTEKSHQSA | EELSSQPGDF |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SEEAEDSQCC | SFKLLVEEEG | YEADSESNPE | DGETQDDGVD | LKSETEGFSA | SSSPNDLLEN | LTQGEIIYPE | ICMLELNLLS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| ASKAKLDVLA | HVFESFLKII | RQKEKNVFLL | MQQGTVKNLL | GGFLSILTQD | DSDFQACQRV | LVDLLVSLMS | SRTCSEELTL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LLRIFLEKSP | CTKILLLGIL | KIIESDTTMS | PSQYLTFPLL | HAPNLSNGVS | SQKYPGILNS | KAMGLLRRAR | VSRSKKEADR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ESFPHRLLSS | WHIAPVHLPL | LGQNCWPHLS | EGFSVSLWFN | VECIHEAEST | TEKGKKIKKR | NKSLILPDSS | FDGTESDRPE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| GAEYINPGER | LIEEGCIHII | SLGSKALMIQ | VWADPHNATL | IFRVCMDSND | DMKAVLLAQV | ESQENIFLPS | KWQHLVLTYL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QQPQGKRRIH | GKISIWVSGQ | RKPDVTLDFM | LPRKTSLSSD | SNKTFCMIGH | CLSSQEEFLQ | LAGKWDLGNL | LLFNGAKVGS |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| QEAFYLYACG | PNHTSVMPCK | YGKPVNDYSK | YINKEILRCE | QIRELFMTKK | DVDIGLLIES | LSVVYTTYCP | AQYTIYEPVI |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| RLKGQMKTQL | SQRPFSSKEV | QSILLEPHHL | KNLQPTEYKT | IQGILHEIGG | TGIFVFLFAR | VVELSSCEET | QALALRVILS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| LIKYNQQRVH | ELENCNGLSM | IHQVLIKQKC | IVGFYILKTL | LEGCCGEDII | YMNENGEFKL | DVDSNAIIQD | VKLLEELLLD |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| WKIWSKAEQG | VWETLLAALE | VLIRADHHQQ | MFNIKQLLKA | QVVHHFLLTC | QVLQEYKEGQ | LTPMPREVCR | SFVKIIAEVL |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| GSPPDLELLT | IIFNFLLAVH | PPTNTYVCHN | PTNFYFSLHI | DGKIFQEKVR | SIMYLRHSSS | GGRSLMSPGF | MVISPSGFTA |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| SPYEGENSSN | IIPQQMAAHM | LRSRSLPAFP | TSSLLTQSQK | LTGSLGCSID | RLQNIADTYV | ATQSKKQNSL | GSSDTLKKGK |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

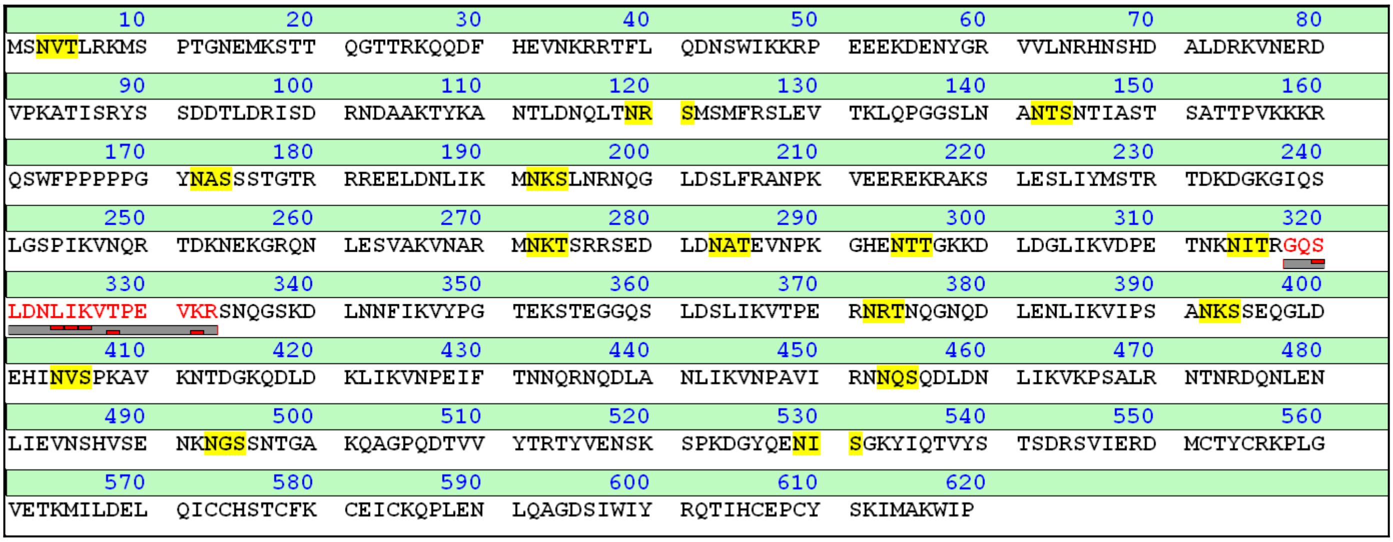
# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1683 | 1 | 853.4016 | -89.30 | 2 | 49.4 | 11.6 | 1 | 515-530 | R.DLSGLLVSAFKNQVSK.N | |

# Detailed Protein Report

## Protein 791: PREDICTED: sciellin isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578825065 | **Score:** | 22.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |



| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSNVTLRKMS | PTGNEMKSTT | QGTTRKQQDF | HEVNKRRTFL | QDNSWIKKRP | EEEKDENYGR | VVLNRHNSHD | ALDRKVNERD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VPKATISRYS | SDDTLDRISD | RNDAAKTYKA | NTLDNQLTNR | SMSMFRSLEV | TKLQPGGSLN | ANTSNTIAST | SATTPVKKKR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QSWFPPPPPG | YNASSSTGTR | RREELDNLIK | MNKSLNRNQG | LDSLFRANPK | VEEREKRAKS | LESLIYMSTR | TDKDGKGIQS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LGSPIKVNQR | TDKNEKGRQN | LESVAKVNAR | MNKTSRRSED | LDNATEVNPK | GHENTTGKKD | LDGLIKVDPE | TNKNITRGQS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LDNLIKVTPE | VKRSNQGSKD | LNNFIKVYPG | TEKSTEGGQS | LDSLIKVTPE | RNRTNQGNQD | LENLIKVIPS | ANKSSEQGLD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EHINVSPKAV | KNTDGKQDLD | KLIKVNPEIF | TNNQRNQDLA | NLIKVNPAVI | RNNQSQDLDN | LIKVKPSALR | NTNRDQNLEN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LIEVNSHVSE | NKNGSSNTGA | KQAGPQDTVV | YTRTYVENSK | SPKDGYQENI | SGKYIQTVYS | TSDRSVIERD | MCTYCRKPLG |
| 570 | 580 | 590 | 600 | 610 | 620 | | |
| VETKMILDEL | QICCHSTCFK | CEICKQPLEN | LQAGDSIWIY | RQTIHCEPCY | SKIMAKWIP | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 501 | 1 | 599.6854 | 10.39 | 3 | 35.9 | 11.0 | 2 | 318-333 | R.GQSLDNLIKVTPEVKR.S | |

# Detailed Protein Report

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**Protein 792:** **tetratricopeptide repeat protein 39C isoform 3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|343478167 | **Score:** | 22.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 8.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| | | **Sequence Coverage [%]:** | 14.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAGSEQQRPR | RRDDGDSDAA | AAAAAPLQDA | ELALAGINML | LNNGFRESDQ | LFKQYRKSFL | TSEKTSALPG | ETQRRL |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2678 | 1 | 693.8667 | -8.26 | 2 | 64.6 | 22.7 | 2 | 54-64 | K.QYRKSFLTSEK.T | |

# Detailed Protein Report

## Protein 793: PREDICTED: protein FAM57B isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530409233 | **Score:** | 22.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 25.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 11.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASTAGYIVS | TSCKHIIDDQ | HWLSSAYTQF | AVPYFIYDIY | AMFLCHWHKH | QVKGHGGDDG | AARAPGSTWA | IARGYLHKEF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LMVLHHAAMV | LVCFPLSVVW | RQGKGDFFLG | CMLMAEVSTP | FVCLGKILIQ | YKQQHTLLHK | VNGALMLLSF | LCCRVLLFPY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | |
| LYWAYGRHAG | LPLLAVPLAI | PAHVNLGAAL | LLAPQLYWFF | LICRGACRLF | WPRSRPPPAC | QAQD | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 207 | 1 | 613.7832 | 0.80 | 2 | 32.6 | 10.1 | 0 | 214-224 | R.SRPPPACQAQD.- | Carbamidomethyl: 7 |

# Detailed Protein Report

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**Protein 794:** **ankyrin repeat domain-containing protein 62 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|472339087 | **Score:** | 22.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 106.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEVRGSFLAA | CRRRMATWRK | NRDKDGFSNP | GYRVRQKDLG | MIHKAAIAGD | VNKVMESILL | RLNDLNDRDK | KNRTALLLAC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AHGRPGVVAD | LVARKCQLNL | TDSENRTALI | KAVQCQEEVC | ASILLEHGAN | PNVRDMYGNT | ALHYAIDNEN | ISMARKLLAY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GADIEARSQD | GHTSLLLAVN | RKKEQMVAFL | LKKKPDLTAI | DNFGRTALIL | AARNGSTSVV | YQLLQHNIDV | FCQDISGWTA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EDYAVASKFQ | AIRGMISEYK | ANKRCKSLQN | SNSEQDLEMT | SEGEQERLEG | CESSQPQVEE | KMKKCRNKKM | EVSRNVHADD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SDNYNDDVDE | LIHKIKNRKP | DNHQSPGKEN | GEFDRLARKT | SNEKSKVKSQ | IYFTDDLNDI | SGSSEKTSED | DELPYSDDEN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FMLLIEQSGM | ECKDFVSLSK | SKNATAACGR | SIEDQKCYCE | RLKVKFQKMK | NNISVLQKVL | SETDKTKSQS | EHQNLQGKKK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LCNLRFILQQ | QEEERIKAEE | LYEKDIEELK | IMEEQYRTQT | EVKKQSKLTL | KSLEVELKTV | RSNSNQNFHT | HERERDLWQE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NHLMRDEIAR | LRLEIDTIKH | QNQETENKYF | KDIEIIKENN | EDLEKTLKRN | EEALTKTITR | YSKELNVLMD | ENTMLNSELQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KEKQSMSRLE | TEMESYRCRL | AAALCDHDQR | QSSKRDLQLA | FQSTVNEWCH | LQEDTNSHIQ | ILSQQLSKAE | STSSGLETEL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HYEREALKEK | TLHIEHMQGV | LSRTQRRLED | IEHMYQNDQP | ILEKYVRKQQ | SVEDGLFQLQ | SQNLLYQQQC | NDARKKADNQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EKTIINIQVK | CEDTVEKLQA | ECRKLEENNK | GLMKECTLLK | ERQCQYEKEK | EEREVVRRQL | QREVDDALNK | QLLLEAMLEI |
| 890 | 900 | 910 | 920 | | | | |
| SSERRINLED | EAQSLKKKLG | QMRSQVCMKL | SMSTVTL | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2195 | 1 | 900.3616 | -160.41 | 2 | 57.3 | 12.4 | 1 | 45-61 | K.AAIAGDVNKVMESILLR.L | |

# Detailed Protein Report

## Protein 795: seizure 6-like protein 2 isoform 4 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|166235140 | **Score:** | 22.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 86.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGTPRAQHPP | PPQLLFLILL | SCPWIQGLPL | KEEEILPEPG | SETPTVASEA | LAELLHGALL | RRGPEMGYLP | GSDRDPTLAT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PPAGQTLAVP | SLPRATEPGT | GPLTTAVTPN | GVRGAGPTAP | ELLTPPPGTT | APPPPSPASP | GPPLGPEGGE | EETTTTIITT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TTVTTTVTSP | AYLLSCGFPP | RPAHGDVSVT | DLHPGGTATF | HCDSGYQLQG | EETLICLNGT | RPSWNGETPS | CMASCGGTIH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NATLGRIVSP | EPGGAVGPNL | TCRWVIEAAE | GRRLHLHFER | VSLDEDNDRL | MVRSGGSPLS | PVIYDSDMDD | VPERGLISDA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QSLYVELLSE | TPANPLLLSL | RFEAFEEDRC | FAPFLAHGNV | TTTDPEYRPG | ALATFSCLPG | YALEPPGPPN | AIECVDPTEP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HWNDTEPACK | AMCGGELSEP | AGVVLSPDWP | QSYSPGQDCV | WGVHVQEEKR | ILLQVEILNV | REGDMLTLFD | GDGPSARVLA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QLRGPQPRRR | LLSSGPDLTL | QFQAPPGPPN | PGLGQGFVLH | FKEVPRNDTC | PELPPPEWGW | RTASHGDLIR | GTVLTYQCEP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GYELLGSDIL | TCQWDLSWSA | APPACQKIMT | CADPGEIANG | HRTASDAGFP | VGSHVQYRCL | PGYSLEGAAM | LTCYSRDTGT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PKWSDRVPKC | ALKYEPCLNP | GVPENGYQTL | YKHHYQAGES | LRFFCYEGFE | LIGEVTITCV | PGHPSQWTSQ | PPLCKVAYEE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LLDNRKLEVT | QTTDPSRQLE | GGNLALAILL | PLGLVIVLGS | GVYIYYTKLQ | GKSLFGFSGS | HSYSPITVES | DFSNPLYEAG |
| 810 | | | | | | | |
| DTREYEVSI | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 516 | 1 | 717.8729 | 41.21 | 2 | 36.4 | 10.2 | 1 | 62-74 | R.RGPEMGYLPGSDR.D | |
| 2089 | 2 | 862.3060 | -159.34 | 2 | 56.0 | 12.4 | 0 | 247-263 | R.IVSPEPGGAVGPNLTCR.W | Carbamidomethyl: 16 |

# Detailed Protein Report

## Protein 796: sphingosine 1-phosphate receptor 4 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4503459 | **Score:** | 22.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.8 |
| | | **Sequence Coverage [%]:** | 7.3 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MNATGTPVAP | ESCQQLAAGG | HSRLIVLHYN | HSGRLAGRGG | PEDGGLGALR | GLSVAASCLV | VLENLLVLAA | ITSHMRSRRW |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| VYYCLVNITL | SDLLTGAAYL | ANVLLSGART | FRLAPAQWFL | REGLLFTALA | ASTFSLLFTA | GERFATMVRP | VAESGATKTS |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| RVYGFIGLCW | LLAALLGMLP | LLGWNCLCAF | DRCSSLLPLY | SKRYILFCLV | IFAGVLATIM | GLYGAIFRLV | QASGQKAPRP |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| AARRKARRLL | KTVLMILLAF | LVCWGPLFGL | LLADVFGSNL | WAQEYLRGMD | WILALAVLNS | AVNPIIYSFR | SREVCRAVLS |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | |
| FLCCGCLRLG | MRGPGDCLAR | AVEAHSGAST | TDSSLRPRDS | FRGSRSLSFR | MREPLSSISS | VRSI | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1600 | 1 | 853.3743 | -147.58 | 2 | 48.3 | 12.4 | 2 | 229-244 | R.LVQASGQKAPRPAARR.K | |
| 94 | 1 | 707.7845 | -110.73 | 2 | 30.1 | 10.1 | 2 | 359-370 | R.DSFRGSRSLSFR.M | |

# Detailed Protein Report

---

## Protein 797: PREDICTED: short transient receptor potential channel 7 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530380051 | **Score:** | 22.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 55.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 8.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKFVAHAVSF | TIFLGLLVVN | ASDRFEGVKT | LPNETFTDYP | KQIFRVKTTQ | FSWTEMLIMK | WVLGMIWSEC | KEIWEEGPRE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YVLHLWNLLD | FGMLSIFVAS | FTARFMAFLK | ATEAQLYVDQ | HVQDDTLHNV | SLPPEVAYFT | YARDKWWPSD | PQIISEGLYA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IAVVLSFSRI | AYILPANESF | GPLQISLGRT | VKDIFKFMVI | FIMVFVAFMI | GMFNLYSYYR | GAKYNPAFTT | VEESFKTLFW |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SIFGLSEVIS | VVLKYDHKFI | ENIGYVLYGV | YNVTMVVVLL | NMLIAMINNS | YQEIEEDADV | EWKFARAKLW | LSYFDEGRTL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PAPFNLVPSP | KSFYYLIMRI | KMCLIKLCKS | KAKSCENDLE | MGMLNSKFKK | TRYQAGMRNS | ENLTANNTLS | KPTRYQKIMK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RLIKRYVLKA | QVDRENDEVN | EGELKEIKQD | ISSLRYELLE | EKSQATGELA | DLIQQLSEKF | GKNLNKDHLR | VNKGKDI |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 398 | 1 | 879.0703 | -93.51 | 3 | 35.0 | 10.2 | 1 | 1-24 | -.MKFVAHAVSFTIFLGLLVVNASDR.F | |

# Detailed Protein Report

## Protein 798: PREDICTED: LIM and calponin homology domains-containing protein 1 isoform X14 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530376597 | **Score:** | 22.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 147.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MACPALGLEA LQPLQPEPPP EPAFSEAQKW IEQVTGRSFG DKDFRTGLEN GILLCELLNA IKPGLVKKIN RLPTPIAGLD

        90        100        110        120        130        140        150        160
NIILFLRGCK ELGLKESQLF DPSDLQDTSN RVTVKSLDYS RKLKNVLVTI YWLGKAANSC TSYSGTTLNL KEFEGLLAQM

       170        180        190        200        210        220        230        240
RKDTDDIESP KRSIRDSGYI DCWDSERSDS LSPPRHGRDD SFDSLDSFGS RSRQTPSPDV VLRGSSDGRG SDSESDLPHR

       250        260        270        280        290        300        310        320
KLPDVKKDDM SARRTSHGEP KSAVPFNQYL PNKSNQTAYV PAPLRKKKAE REEYRKSWST ATSPLGGERP FSFPETIEEE

       330        340        350        360        370        380        390        400
GSEVGSAGED NPAGQMNPGW KPSDGGCELP DGSGKEHPSS DGAVVAPAPK SEEKDAAEIQ KRKRLEQAGI KVMPAAQRFA

       410        420        430        440        450        460        470        480
SQKQLSEEKE AIRDIVLRKE NSFLTHQHGN DSEAEGEVVC RLPDLEKDDF AARRARMNQT KPMVPLNQLL YGPYPKKGAE

       490        500        510        520        530        540        550        560
KSDGSKQLSK GISKKRSLEY KRNQGHTEEV KLIVTCNMRA QESEPVEGGL RKVPDLHKDD LAQQRIQGSL APHREPPSFI

       570        580        590        600        610        620        630        640
TLSNITEADL ETWERLKVSE KARDGDVQHI CASEPSPEIK AETAIRDDFA NRKARASKKA SSPRQKFVHF GPVTELDQQK

       650        660        670        680        690        700        710        720
WKRLSIGKAG PREDEEEVIC HGSKIQMDSV SPVSAATSSL KGHQIFNRQN DCRTMNCGRG DYCRRASWLA PVPESQEEWV

       730        740        750        760        770        780        790        800
CSLGECPRGT EEVTSKQLPQ DGKEETESAP RDSERLSKAE RSEDSSQPLV CPLASECEAS GTEEKLEKMT APAWSGSGLK

       810        820        830        840        850        860        870        880
GQRKLDDSRK DDMMARRTGM SLRHTGSNPN QFLPVPFAKQ QDVEESSKGL PMKDQRYGPR TPVSDDAEST SMFDMRCEEE

       890        900        910        920        930        940        950        960
AAVQPHSRAR QEQLQLINNQ LREEDDKWQD DLARWKSRRR SVSQDLIKKE EERKKMEKLL AGEDGTSERR KSIKTYREIV

       970        980        990       1000       1010       1020       1030       1040
QEKERREREL HEAYKNARSQ EEAEGILQQY IERFTISEAV LERLEMPKIL ERSHSTEPNL SSFLNDPNPM KYLRQQSLPP

      1050       1060       1070       1080       1090       1100       1110       1120
PKFTATVETT IARASVLDTS MSAGSGSPSK TVTPKAVPML TPKPYSQPKN SQDVLKTFKV DGKVSVNGET VHREEEKERE

      1130       1140       1150       1160       1170       1180       1190       1200
CPTVAPAHSL TKSQMFEGVA RVHGSPLELK QDNGSIEINI KKPNSVPQEL AATTEKTEPN SQEDKNDGGK SRKGNIELAS

      1210       1220       1230       1240       1250       1260       1270       1280
SEPQHFTTTV TRCSPTVAFV EFPSSPQLKN DVSEEKDQKK PENEMSGKVE LVLSQKVVKP KSPEPEATLT FPFLDKMPEA

      1290       1300       1310       1320       1330
NQLHLPNLNS QESPGTASVP LRVQNSWRRS QFFSQSGKLH TG
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 259 | 1 | 898.4195 | -32.39 | 3 | 33.2 | 12.1 | 2 | 582-606 | K.ARDGDVQHICASEPSPEIKAETAIR.D | |

# Detailed Protein Report

## Protein 799: laminin subunit alpha-5 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21264602 | **Score:** | 22.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 399.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MAKRLCAGSA LCVRGPRGPA PLLLVGLALL GAARAREEAG GGFSLHPPYF NLAEGARIAA SATCGEEAPA RGSPRPTEDL
        90        100        110        120        130        140        150        160
YCKLVGGPVA GGDPNQTIRG QYCDICTAAN SNKAHPASNA IDGTERWWQS PPLSRGLEYN EVNVTLDLGQ VFHVAYVLIK
       170        180        190        200        210        220        230        240
FANSPRPDLW VLERSMDFGR TYQPWQFFAS SKRDCLERFG PQTLERITRD DAAICTTEYS RIVPLENGEI VVSLVNGRPG
       250        260        270        280        290        300        310        320
AMNFSYSPLL REFTKATNVR LRFLRTNTLL GHLMGKALRD PTVTRRYYYS IKDISIGGRC VCHGHADACD AKDPTDPFRL
       330        340        350        360        370        380        390        400
QCTCQHNTCG GTCDRCCPGF NQQPWKPATA NSANECQSCN CYGHATDCYY DPEVDRRRAS QSLDGTYQGG GVCIDCQHHT
       410        420        430        440        450        460        470        480
TGVNCERCLP GFYRSPNHPL DSPHVCRRCN CESDFTDGTC EDLTGRCYCR PNFSGERCDV CAEGFTGFPS CYPTPSSSND
       490        500        510        520        530        540        550        560
TREQVLPAGQ IVNCDCSAAG TQGNACRKDP RVGRCLCKPN FQGTHCELCA PGFYGPGCQP CQCSSPGVAD DRCDPDTGQC
       570        580        590        600        610        620        630        640
RCRVGFEGAT CDRCAPGYFH FPLCQLCGCS PAGTLPEGCD EAGRCLCQPE FAGPHCDRCR PGYHGFPNCQ ACTCDPRGAL
       650        660        670        680        690        700        710        720
DQLCGAGGLC RCRPGYTGTA CQECSPGFHG FPSCVPCHCS AEGSLHAACD PRSGQCSCRP RVTGLRCDTC VPGAYNFPYC
       730        740        750        760        770        780        790        800
EAGSCHPAGL APVDPALPEA QVPCMCRAHV EGPSCDRCKP GFWGLSPSNP EGCTRCSCDL RGTLGGVAEC QPGTGQCFCK
       810        820        830        840        850        860        870        880
PHVCGQACAS CKDGFFGLDQ ADYFGCRSCR CDIGGALGQS CEPRTGVCRC RPNTQGPTCS EPARDHYLPD LHHLRLELEE
       890        900        910        920        930        940        950        960
AATPEGHAVR FGFNPLEFEN FSWRGYAQMA PVQPRIVARL NLTSPDLFWL VFRYVNRGAM SVSGRVSVRE EGRSATCANC
       970        980        990       1000       1010       1020       1030       1040
TAQSQPVAFP PSTEPAFITV PQRGFGEPFV LNPGTWALRV EAEGVLLDYV VLLPSAYYEA ALLQLRVTEA CTYRPSAQQS
      1050       1060       1070       1080       1090       1100       1110       1120
GDNCLLYTHL PLDGFPSAAG LEALCRQDNS LPRPCPTEQL SPSHPPLITC TGSDVDVQLQ VAVPQPGRYA LVVEYANEDA
      1130       1140       1150       1160       1170       1180       1190       1200
RQEVGVAVHT PQRAPQQGLL SLHPCLYSTL CRGTARDTQD HLAVFHLDSE ASVRLTAEQA RFFLHGVTLV PIEEFSPEFV
      1210       1220       1230       1240       1250       1260       1270       1280
EPRVSCISSH GAFGPNSAAC LPSRFPKPPQ PIILRDCQVI PLPPGLPLTH AQDLTPAMSP AGPRPRPPTA VDPDAEPTLL
      1290       1300       1310       1320       1330       1340       1350       1360
REPQATVVFT THVPTLGRYA FLLHGYQPAH PTFPVEVLIN AGRVWQGHAN ASFCPHGYGC RTLVVCEGQA LLDVTHSELT
      1370       1380       1390       1400       1410       1420       1430       1440
VTVRVPKGRW LWLDYVLVVP ENVYSFGYLR EEPLDKSYDF ISHCAAQGYH ISPSSSSLFC RNAAASLSLF YNNGARPCGC
      1450       1460       1470       1480       1490       1500       1510       1520
HEVGATGPTC EPFGGQCPCH AHVIGRDCSR CATGYWGFPN CRPCDCGARL CDELTGQCIC PPRTIPPDCL LCQPQTFGCH
      1530       1540       1550       1560       1570       1580       1590       1600
PLVGCEECNC SGPGIQELTD PTCDTDSGQC KCRPNVTGRR CDTCSPGFHG YPRCRPCDCH EAGTAPGVCD PLTGQCYCKE
      1610       1620       1630       1640       1650       1660       1670       1680
NVQGPKCDQC SLGTFSLDAA NPKGCTRCFC FGATERCRSS SYTRQEFVDM EGWVLLSTDR QVVPHERQPG TEMLRADLRH
      1690       1700       1710       1720       1730       1740       1750       1760
VPEAVPEAFP ELYWQAPPSY LGDRVSSYGG TLRYELHSET QRGDVFVPME SRPDVVLQGN QMSITFLEPA YPTPGHVHRG
      1770       1780       1790       1800       1810       1820       1830       1840
QLQLVEGNFR HTETRNTVSR EELMMVLASL EQLQIRALFS QISSAVFLRR VALEVASPAG QGALASNVEL CLCPASYRGD
      1850       1860       1870       1880       1890       1900       1910       1920
SCQECAPGFY RDVKGLFLGR CVPCQCHGHS DRCLPGSGVC VDCQHNTEGA HCERCQAGFV SSRDDPSAPC VSCPCPLSVP
      1930       1940       1950       1960       1970       1980       1990       2000
SNNFAEGCVL RGGRTQCLCK PGYAGASCER CAPGFFGNPL VLGSSCQPCD CSGNGDPNLL FSDCDPLTGA CRGCLRHTTG
      2010       2020       2030       2040       2050       2060       2070       2080
PRCEICAPGF YGNALLPGNC TRCDCTPCGT EACDPHSGHC LCKAGVTGRR CDRCQEGHFG FDGCGGCRPC ACGPAAEGSE
      2090       2100       2110       2120       2130       2140       2150       2160
CHPQSGQCHC RPGTMGPQCR ECAPGYWGLP EQGCRRCQCP GGRCDPHTGR CNCPPGLSGE RCDTCSQQHQ VPVPGGPVGH
      2170       2180       2190       2200       2210       2220       2230       2240
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1502 | 1 | 1052.1977 | 73.86 | 3 | 48.4 | 12.0 | 0 | 782-812 | R.GTLGGVAECQPGTGQCFCKPHVCGQACASCK.D | Carbamidomethyl: 16, 18 |

# Detailed Protein Report

## Protein 800: testis-expressed sequence 30 protein isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|557948022 | **Score:** | 22.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 25.8 |
| | | **No. of unique Peptides:** | 1 |

```
         10         20         30         40         50         60         70         80
MNLPHLMSLA SHLASHGFFC LRFTCKGLNI VHRIKAYKSV LNYLKTSGEY KLAGVFLGGR SMGSRAAASV MCHIEPDDGD
         90        100        110        120        130        140        150        160
DFVRGLICIS YPLHHPKQQH KLRDEDLFRL KEPVLFVSGS ADEMCEKNLL EKVAQKMQAP HKIHWIEKAN HSMAVKGRST
        170        180        190
NDVFKEINTQ ILFWIQEITE MDKKCH
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1136 | 1 | 1207.6290 | 45.30 | 3 | 44.3 | 11.4 | 1 | 66-97 | R.AAASVMCHIEPDDGDDFVRGLICISYPLHHPK.Q | Carbamidomethyl: 7, 23 |

# Detailed Protein Report

## Protein 801: zinc finger and SCAN domain-containing protein 16 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|13376834 | **Score:** | 22.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 4.6 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTTALEPEDQ | KGLLIIKAED | HYWGQDSSSQ | KCSPHRRELY | RQHFRKLCYQ | DAPGPREALT | QLWELCRQWL | RPECHTKEQI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LDLLVLEQFL | SILPKDLQAW | VRAHHPETGE | EAVTVLEDLE | RELDEPGKQV | PGNSERRDIL | MDKLAPLGRP | YESLTVQLHP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KKTQLEQEAG | KPQRNGDKTR | TKNEELFQKE | DMPKDKEFLG | EINDRLNKDT | PQHPKSKDII | ENEGRSEWQQ | RERRRYKCDE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CGKSFSHSSD | LSKHRRTHTG | EKPYKCDECG | KAFIQRSHLI | GHHRVHTGVK | PYKCKECGKD | FSGRTGLIQH | QRIHTGEKPY |
| 330 | 340 | 350 | | | | | |
| ECDECGRPFR | VSSALIRHQR | IHTANKLY | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2161 | 2 | 1022.8836 | -107.34 | 2 | 57.4 | 22.5 | 2 | 218-233 | K.DIIENEGRSEWQQRER.R | |

# Detailed Protein Report

## Protein 802: transmembrane protein 194A isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|195972881 | **Score:** | 22.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 50.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAGGMKVAVS | PAVGPGPWGS | GVGGGGTVRL | LLILSGCLVY | GTAETDVNVV | MLQESQVCEK | RASQQFCYTN | VLIPKWHDIW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TRIQIRVNSS | RLVRVTQVEN | EEKLKELEQF | SIWNFFSSFL | KEKLNDTYVN | VGLYSTKTCL | KVEIIEKDTK | YSVIVIRRFD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PKLFLVFLLG | LMLFFCGDLL | SRSQIFYYST | GMTVGIVASL | LIIIFILSKF | MPKKSPIYVI | LVGGWSFSLY | LIQLVFKNLQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EIWRCYWQYL | LSYVLTVGFM | SFAVCYKYGP | LENERSINLL | TWTLQLMGLC | FMYSGIQIPH | IALAIIIIAL | CTKNLEHPIQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WLYITCRKVC | KGAEKPVPPR | LLTEEEYRIQ | GEVETRKALE | ELREFCNSPD | CSAWKTVSRI | QSPKRFADFV | EGSSHLTPNE |
| 410 | 420 | 430 | 440 | 450 | | | |
| VSVHEQEYGL | GSIIAQDEIY | EEASSEEEDS | YSRCPAITQN | NFLT | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1826 | 1 | 1045.0325 | -2.71 | 2 | 51.2 | 10.5 | 1 | 124-141 | K.LNDTYVNVGLYSTKTCLK.V | Carbamidomethyl: 16 |

# Detailed Protein Report

**Protein 803:** **translation factor GUF1, mitochondrial [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|157426893 | **Score:** | 22.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 74.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MWTLVGRGWG | CARALAPRAT | GAALLVAPGP | RSAPTLGAAP | ESWATDRLYS | SAEFKEKLDM | SRFPVENIRN | FSIVAHVDHG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KSTLADRLLE | LTGTIDKTKN | NKQVLDKLQV | ERERGITVKA | QTASLFYNCE | GKQYLLNLID | TPGHVDFSYE | VSRSLSACQG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VLLVVDANEG | IQAQTVANFF | LAFEAQLSVI | PVINKIDLKN | ADPERVENQI | EKVFDIPSDE | CIKISAKLGT | NVESVLQAII |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ERIPPPKVHR | KNPLRALVFD | STFDQYRGVI | ANVALFDGVV | SKGDKIVSAH | TQKTYEVNEV | GVLNPNEQPT | HKLYAGQVGY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LIAGMKDVTE | AQIGDTLCLH | KQPVEPLPGF | KSAKPMVFAG | MYPLDQSEYN | NLKSAIEKLT | LNDSSVTVHR | DSSLALGAGW |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RLGFLGLLHM | EVFNQRLEQE | YNASVILTTP | TVPYKAVLSS | SKLIKEHREK | EITIINPAQF | PDKSKVTEYL | EPVVLGTIIT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PDEYTGKIMM | LCEARRAVQK | NMIFIDQNRV | MLKYLFPLNE | IVVDFYDSLK | SLSSGYASFD | YEDAGYQTAE | LVKMDILLNG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NTVEELVTVV | HKDKAHSIGK | AICERLKDSL | PRQLFEIAIQ | AAIGSKIIAR | ETVKAYRKNV | LAKCYGGDIT | RKMKLLKRQA |
| 650 | 660 | 670 | | | | | |
| EGKKKLRKIG | NVEVPKDAFI | KVLKTQSSK | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2764 | 1 | 821.8813 | -33.54 | 2 | 65.0 | 10.3 | 0 | 327-341 | K.DVTEAQIGDTLCLHK.Q | |

# Detailed Protein Report

## Protein 804: retinol dehydrogenase 14 [Homo sapiens]

**Accession:** gi|10190746
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 22.4
**MW [kDa]:** 36.8
**pI:** 9.9
**Sequence Coverage [%]:** 10.4
**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MAVATAAAVL AALGGALWLA ARRFVGPRVQ RLRRGGDPGL MHGKTVLITG ANSGLGRATA AELLRLGARV IMGCRDRARA
        90        100        110        120        130        140        150        160
EEAAGQLRRE LRQAAECGPE PGVSGVGELI VRELDLASLR SVRAFCQEML QEEPRLDVLI NNAGIFQCPY MKTEDGFEMQ
       170        180        190        200        210        220        230        240
FGVNHLGHFL LTNLLLGLLK SSAPSRIVVV SSKLYKYGDI NFDDLNSEQS YNKSFCYSRS KLANILFTRE LARRLEGTNV
       250        260        270        280        290        300        310        320
TVNVLHPGIV RTNLGRHIHI PLLVKPLFNL VSWAFFKTPV EGAQTSIYLA SSPEVEGVSG RYFGDCKEEE LLPKAMDESV
       330        340
ARKLWDISEV MVGLLK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1653 | 1 | 698.3330 | -119.22 | 3 | 50.9 | 11.2 | 1 | 2-23 | M.AVATAAAVLAALGGALWLAARR.F | |

# Detailed Protein Report

**Protein 805:** **PREDICTED: centrosomal protein of 164 kDa isoform X10 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530397903 | **Score:** | 22.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 151.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGPAGNPPTG | LAPRLRLQAL | GSSLAPVHVP | LGGLAPLRGL | VDTPPSALRG | SQSVSLGSSV | ESGRQLGELM | LPSQGLKTSA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YTKGLLGSIY | EDKTALSLLG | LGEETNEEDE | EESDNQSVHS | SSEPLRNLHL | DIGALGGDFE | YEESLRTSQP | EEKKDVSLDS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DAAGPPTPCK | PSSPGADSSL | SSAVGKGRQG | SGARPGLPEK | EENEKSEPKI | CRNLVTPKAD | PTGSEPAKAS | EKEAPEDTVD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AGEEGSRREE | AAKEPKKKAS | ALEEGSSDAS | QELEISEHMK | EPQLSDSIAS | DPKSFHGLDF | GFRSRISEHL | LDVDVLSPVL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GGACRQAQQP | LGIEDKDDSQ | SSQDELQSKQ | SKGLEERYHR | LSPPLPHEER | AQSPPRSLAT | EEEPPQGPEG | QPEWKEAEEL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GEDSAASLSL | QLSLQREQAP | SPPAACEKGK | EQHSQAEELG | PGQEEAEDPE | EKVAVSPTPP | VSPEVRSTEP | VAPPEQLSEA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ALKAMEEAVA | QVLEQDQRHL | LESKQEKMQQ | LREKLCQEEE | EEILRLHQQK | EQSLSSLRER | LQKAIEEEEA | RMREEESQRL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SWLRAQVQSS | TQADEDQIRA | EQEASLQKLR | EELESQQKAE | RASLEQKNRQ | MLEQLKEEIE | ASEKSEQAAL | NAAKEKALQQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LREQLEGERK | EAVATLEKEH | SAELERLCSS | LEAKHREVVS | SLQKKIQEAQ | QKEEAQLQKC | LGQVEHRVHQ | KSYHVAGYEH |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ELSSLLREKR | QEVEGEHERR | LDKMKEEHQQ | VMAKAREQYE | AEERKQRAEL | LGHLTGELER | LQRAHERELE | TVRQEQHKRL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EDLRRRHREQ | ERKLQDLELD | LETRAKDVKA | RLALLEVQEE | TARREKQQLL | DVQRQVALKS | EEATATHQQL | EEAQKEHTHL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LQSNQQLREI | LDELQARKLK | LESQVDLLQA | QSQQLQKHFS | SLEAEAQKKQ | HLLREVTVEE | NNASPHFEPD | LHIEDLRKSL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GTNQTKEVSS | SLSQSKEDLY | LDSLSSHNVW | HLLSAEGVAL | RSAKEFLVQQ | TRSMRRRQTA | LKAAQQHWRH | ELASAQEVAK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| DPPGIKALED | MRKNLEKETR | HLDEMKSAMR | KGHNLLKKKE | EKLNQLESSL | WEEASDEGTL | GGSPTKKAVT | FDLSDMDSLS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SESSESFSPP | HREWWRQQRI | DSTPSLTSRK | IHGLSHSLRQ | ISSQLSSVLS | ILDSLNPQSP | PPLLASMPAQ | LPPRDPKSTP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TPTYYGSLAR | FSALSSATPT | STQWAWDSGQ | GPRLPSSVAQ | TVDDFLLEKW | RKYFPSGIPL | LSNSPTPLES | RLGYMSASEQ |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LRLLQHSHSQ | VPEAGSTTFQ | GIIEANRRWL | ERVKNDPRLP | LFSSTPKPKA | TLSLLQLGLD | EHNRVKVYRF | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 142 | 1 | 797.3752 | -80.90 | 2 | 31.7 | 10.3 | 2 | 1017-1029 | R.RQTALKAAQQHWR.H | |

# Detailed Protein Report

## Protein 806: E3 ubiquitin-protein ligase Topors isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|307344673 | **Score:** | 22.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 112.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MIMASAAKEF | KMDNFSPKAG | TSKLQQTVPA | DASPDSKCPI | CLDRFDNVSY | LDRCLHKFCF | RCVQEWSKNK | AECPLCKQPF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DSIFHSVRAE | DDFKEYVLRP | SYNGSFVTPD | RRFRYRTTLT | RERNASVYSP | SGPVNRRTTT | PPDSGVLFEG | LGISTRPRDV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EIPQFMRQIA | VRRPTTADER | SLRKIQEQDI | INFRRTLYRA | GARVRNIEDG | GRYRDISAEF | FRRNPACLHR | LVPWLKRELT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VLFGAHGSLV | NIVQHIIMSN | VTRYDLESQA | FVSDLRPFLL | NRTEHFIHEF | ISFARSPFNM | AAFDQHANYD | CPAPSYEEGS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HSDSSVITIS | PDEAETQELD | INVATVSQAP | WDDETPGPSY | SSSEQVHVTM | SSLLNTSDSS | DEELVTGGAT | SQIQGVQTND |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DLNNDSDDSS | DNCVIVGFVK | PLAERTPELV | ELSSDSEDLG | SYEKMETVKT | QEQEQSYSSG | DSDVSRCSSP | HSVLGKDEQI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NKGHCDSSTR | IKSKKEEKRS | TSLSSPRNLN | SSVRGDRVYS | PYNHRHRKRG | RSRSSDSRSQ | SRSGHDQKNH | RKHHGKKRMK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SKRSRSRESS | RPRGRRDKKR | SRTRDSSWSR | RSQTLSLSSE | STSRSRSRSS | DHGKRRSRSR | NRDRYYLRNN | YGSRYKWEYT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| YYSRNKDRDG | YESSYRRRTL | SRAHYSRQSS | SPEFRVQSFS | ERTNARKKNN | HSERKYYYYE | RHRSRSLSSN | RSRTASTGTD |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RVRNEKPGGK | RKYKTRHLEG | TNEVAQPSRE | FASKAKDSHY | QKSSSKLDGN | YKNESDTFSD | SRSSDRETKH | KRRKRKTRSL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SVEIVYEGKA | TDTTKHHKKK | KKKHKKKHKK | HHGDNASRSP | VVITIDSDSD | KDSEVKEDTE | CDNSGPQDPL | QNEFLAPSLE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PFETKDVVTI | EAEFGVLDKE | CDIATLSNNL | NNANKTVDNI | PPLAASVEQT | LDVREESTFV | SDLENQPSNI | VSLQTEPSRQ |
| 970 | 980 | 990 | | | | | |
| LPSPRTSLMS | VCLGRDCDMS | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2563 | 1 | 625.3176 | 42.38 | 2 | 62.7 | 10.1 | 1 | 696-703 | K.YYYYERHR.S | |

# Detailed Protein Report

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## Protein 807: RNA-binding protein MEX3A [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|147902746 | **Score:** | 22.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 6.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPSLVVSGIM | ERNGGFGELG | CFGGSAKDRG | LLEDERALQL | ALDQLCLLGL | GEPPAPTAGE | DGGGGGGGAP | AQPAAPPQPA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PPPPPAAPPA | APTAAPAAQT | PQPPTAPKGA | SDAKLCALYK | EAELRLKGSS | NTTECVPVPT | SEHVAEIVGR | QGCKIKALRA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KTNTYIKTPV | RGEEPVFMVT | GRREDVATAR | REIISAAEHF | SMIRASRNKS | GAAFGVAPAL | PGQVTIRVRV | PYRVVGLVVG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PKGATIKRIQ | QQTNTYIITP | SRDRDPVFEI | TGAPGNVERA | REEIETHIAV | RTGKILEYNN | ENDFLAGSPD | AAIDSRYSDA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WRVHQPGCKP | LSTFRQNSLG | CIGECGVDSG | FEAPRLGEQG | GDFGYGGYLF | PGYGVGKQDV | YYGVAETSPP | LWAGQENATP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TSVLFSSASS | SSSSSAKARA | GPPGAHRSPA | TSAGPELAGL | PRRPPGEPLQ | GFSKLGGGGL | RSPGGGRDCM | VCFESEVTAA |
| 490 | 500 | 510 | 520 | 530 | | | |
| LVPCGHNLFC | MECAVRICER | TDPECPVCHI | TATQAIRIFS | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1760 | 1 | 1273.5603 | 8.38 | 3 | 51.8 | 22.3 | 1 | 462-496 | R.SPGGGRDCMVCFESEVTAALVPCGHNLFCMECAVR.I | Carbamidomethyl: 8, 11;<br>Oxidation: 9 |

## Protein 808: PREDICTED: A-kinase anchor protein 12 isoform X3 [Homo sapiens]

**Accession:** gi|530384249
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 22.3
**MW [kDa]:** 180.9
**pI:** 4.3
**Sequence Coverage [%]:** 1.6
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVGQRDSEDV | SKRDSDKEMA | TKSAVVHDIT | DDGQEETPEI | IEQIPSSESN | LEELTQPTES | QANDIGFKKV | FKFVGFKFTV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KKDKTEKPDT | VQLLTVKKDE | GEGAAGAGDH | KDPSLGAGEA | ASKESEPKQS | TEKPEETLKR | EQSHAEISPP | AESGQAVEEC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KEEGEEKQEK | EPSKSAESPT | SPVTSETGST | FKKFFTQGWA | GWRKKTSFRK | PKEDEVEASE | KKKEQEPEKV | DTEEDGKAEV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ASEKLTASEQ | AHPQEPAESA | HEPRLSAEYE | KVELPSEEQV | SGSQGPSEEK | PAPLATEVFD | EKIEVHQEEV | VAEVHVSTVE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ERTEEQKTEV | EETAGSVPAE | ELVEMDAEPQ | EAEPAKELVK | LKETCVSGED | PTQGADLSPD | EKVLSKPPEG | VVSEVEMLSS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QERMKVQGSP | LKKLFTSTGL | KKLSGKKQKG | KRGGGDEESG | EHTQVPADSP | DSQEEQKGES | SASSPEEPEE | ITCLEKGLAE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VQQDGEAEEG | ATSDGEKKRE | GVTPWASFKK | MVTPKKRVRR | PSESDKEDEL | DKVKSATLSS | TESTASEMQE | EMKGSVEEPK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PEEPKRKVDT | SVSWEALICV | GSSKKRARRG | SSSDEEGGPK | AMGGDHQKAD | EAGKDKETGT | DGILAGSQEH | DPGQGSSSPE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QAGSPTEGEG | VSTWESFKRL | VTPRKKSKSK | LEEKSEDSIA | GSGVEHSTPD | TEPGKEESWV | SIKKFIPGRR | KKRPDGKQEQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| APVEDAGPTG | ANEDDSDVPA | VVPLSEYDAV | EREKMEAQQA | QKSAEQPEQK | AATEVSKELS | ESQVHMMAAA | VADGTRAATI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IEERSPSWIS | ASVTEPLEQV | EAEAALLTEE | VLEREVIAEE | EPPTVTEPLP | ENREARGDTV | VSEAELTPEA | VTAAETAGPL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GAEEGTEASA | AEETTEMVSA | VSQLTDSPDT | TEEATPVQEV | EGGVPDIEEQ | ERRTQEVLQA | VAEKVKEESQ | LPGTGGPEDV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LQPVQRAEAE | RPEEQAEASG | LKKETDVVLK | VDAQEAKTEP | FTQGKVVGQT | TPESFEKAPQ | VTESIESSEL | VTTCQAETLA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GVKSQEMVME | QAIPPDSVET | PTDSETDGST | PVADFDAPGT | TQKDEIVEIH | EENEVASGTQ | SGGTEAEAVP | AQKERPPAPS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SFVFQEETKE | QSKMEDTLEH | TDKEVSVETV | SILSKTEGTQ | EADQYADEKT | KDVPFFEGLE | GSIDTGITVS | REKVTEVALK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| GEGTEEAECK | KDDALELQSH | AKSPPSPVER | EMVVQVEREK | TEAEPTHVNE | EKLEHETAVT | VSEEVSKQLL | QTVNVPIIDG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| AKEVSSLEGS | PPPCLGQEEA | VCTKIQVQSS | EASFTLTAAA | EEEKVLGETA | NILETGETLE | PAGAHLVLEE | KSSEKNEDFA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| AHPGEDAVPT | GPDCQAKSTP | VIVSATTKKG | LSSDLEGEKT | TSLKWKSDEV | DEQVACQEVK | VSVAIEDLEP | ENGILELETK |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SSKLVQNIIQ | TAVDQFVRTE | ETATEMLTSE | LQTQAHVIKA | DSQDAGQETE | KEGEEPQASA | QDETPITSAK | EESESTAVGQ |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| AHSDISKDMS | EASEKTMTVE | VEGSTVNDQQ | LEEVVLPSEE | EGGGAGTKSV | PEDDGHALLA | ERIEKSLVEP | KEDEKGDDVD |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| DPENQNSALA | DTDASGGLTK | ESPDTNGPKQ | KEKEDAQEVE | LQEGKVHSES | DKAITPQAQE | ELQKQERESA | KSELTES |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2874 | 2 | 703.3652 | -25.20 | 2 | 66.5 | 11.9 | 2 | 498-509 | K.KREGVTPWASFK.K | |

# Detailed Protein Report

## Protein 809: PREDICTED: nuclear body protein SP140 isoform X7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530369725 | **Score:** | 22.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 77.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAQQGQQGQM | ASGDSNLNFR | MVAEIQNVEG | QNLQEQVCPE | PIFRFFRENK | VEIASAITRP | FPFLMGLRDR | SFISEQMYEH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FQEAFRNLVP | VTRVMYCVLS | ELEKTFGWSH | LEALFSRINL | MAYPDLNEIY | RSFQNVCYEH | SPLQMNNVND | LEDRPRLLPY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GKQENSNACH | EMDDIAVPQE | ALSSSPRCEP | GFSSESCEQL | ALPKAGGGDA | EDAPSLLPGG | GVSSELENHP | MNEEGESEEL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ASSLLYDNVP | GAEQSAYENE | KCSCVMCFSE | EVPGSPEART | ESDQACGTMD | TVDIANNSTL | GKPKRKRRKK | RGHGWSRMRM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RRQENSQQND | NSKADGQVVS | SEKKANVNLK | DLSKIRGRKR | GKPGTRFTQS | DRAAQKRVRS | RASRKHKDET | VDFKAPLLPV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TCGGVKGILH | KKKLQQGILV | KCIQTEDGKW | FTPTEFEIKG | GHARSKNWRL | SVRCGGWPLR | WLMENGFLPD | PPRIRYRKKK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RILKSQNNSS | VDPCMRNLDE | CEVCRDGGEL | FCCDTCSRVF | HEDCHIPPVE | AERTPWNCIF | CRMKESPGSQ | QCCQESEVLE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RQMCPEEQLK | CEFLLLKVYC | CSESSFFAKI | PYYYYIREAC | QGLKEPMWLD | KIKKRLNEHG | YPQVEGFVQD | MRLIFQNHRA |
| 650 | 660 | 670 | 680 | | | | |
| SYKYKDFGQM | GFRLEAEFEK | NFKEVFAIQE | TNGNN | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2587 | 1 | 941.5681 | 155.71 | 2 | 62.4 | 10.3 | 0 | 188-204 | R.CEPGFSSESCEQLALPK.A | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 810: testis-specific protein 10-interacting protein [Homo sapiens]

**Accession:** gi|154759273
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 22.3
**MW [kDa]:** 62.3
**pI:** 10.9
**Sequence Coverage [%]:** 4.3
**No. of unique Peptides:** 2

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.10 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.25 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGQDTDMLNT | YQQLVRTPSV | RPGQDVRLQA | PGTRTGLLKL | LSTVSQDKQG | CLGSGDGVPN | QDLQQRSQSS | RQTAKKDRKP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RGQSKKGQGS | EESEDHFPLL | PRKPSFPFQW | AWESIATDVR | AVLQPSSPTP | GHQALPMPSS | FSQRQSRRKS | TANLPEAHGC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CWKTEAQNLK | ARQQLGAWGG | VSIPTGKGEL | GSEPPSGLQL | PGRRPGSGSA | SDKQVQLQSL | GAEEAERGLS | SGVLPQRPRR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GSISEEEQFS | EATEEAEEGE | HRTPCRRRAG | CQRKGQISGE | EASDEGEVQG | QSQGSSPSFN | NLRRRQWRKT | RAKELQGPWD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LEKLHRQLQR | DLDCGPQKLP | WKTLRAAFQA | SKRNGKAYAS | GYDETFVSAN | LPNRTFHKRQ | EATRSLLQAW | ERQRQEERQQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AELRRARTQH | VQRQVAHCLA | AYAPRGSRGP | GAAQRKLEEL | RRQERQRFAE | YQAELQGIQH | RVQARPFLFQ | QAMQANARLT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VTRRFSQVLS | ALGLDEEQLL | SEAGKVDREG | TPRKPRSHRS | MGVRMEHSPQ | RPPRTEPTGS | QPDRHYNPSL | DPECSP |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2105 | 1 | 707.2250 | -208.16 | 2 | 54.7 | 11.8 | 1 | 312-323 | R.AKELQGPWDLEK.L | | |
| 467 | 1 | 708.1877 | -156.38 | 2 | 34.3 | 10.4 | 0 | 545-556 | R.HYNPSLDPECSP.- | Carbamidomethyl: 10 | WUP:QUP 1.25<br>QU:MU 1.10 |

# Detailed Protein Report

## Protein 811: 7SK snRNA methylphosphate capping enzyme isoform A [Homo sapiens]

**Accession:** gi|47271406
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 22.3
**MW [kDa]:** 74.3
**pI:** 10.3
**Sequence Coverage [%]:** 4.4
**No. of unique Peptides:** 1

## Quantitation

***QU:MU*** **Median:** 0.49 **CV:** 0.00 % **No. of Peptides:** 1
***WUP:QUP*** **Median:** 1.96 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MIEMAAEKEP | FLVPAPPPPL | KDESGGGGGP | TVPPHQEAAS | GELRGGTERG | PGRCAPSAGS | PAAAVGRESP | GAAATSSSGP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QAQQHRGGGP | QAQSHGEARL | SDPPGRAAPP | DVGEERRGGG | GTELGPPAPP | RPRNGYQPHR | PPGGGGGKRR | NSCNVGGGGG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GFKHPAFKRR | RRVNSDCDSV | LPSNFLLGGN | IFDPLNLNSL | LDEEVSRTLN | AETPKSSPLP | AKGRDPVEIL | IPKDITDPLS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LNTCTDEGHV | VLASPLKTGR | KRHRHRGQHH | QQQQAAGGSE | SHPVPPTAPL | TPLLHGEGAS | QQPRHRGQNR | DAPQPYELNT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AINCRDEVVS | PLPSALQGPS | GSLSAPPAAS | VISAPPSSSS | RHRKRRRTSS | KSEAGARGGG | QGSKEKGRGS | WGGRHHHHHP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LPAAGFKKQQ | RKFQYGNYCK | YYGYRNPSCE | DGRLRVLKPE | WFRGRDVLDL | GCNVGHLTLS | IACKWGPSRM | VGLDIDSRLI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HSARQNIRHY | LSEELRLPPQ | TLEGDPGAEG | EEGTTTVRKR | SCFPASLTAS | RGPIAAPQVP | LDGADTSVFP | NNVVFVTGNY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VLDRDDLVEA | QTPEYDVVLC | LSLTKWVHLN | WGDEGLKRMF | RRIYRHLRPG | GILVLEPQPW | SSYGKRKTLT | ETIYKNYYRI |
| 650 | 660 | 670 | 680 | 690 | | | |
| QLKPEQFSSY | LTSPDVGFSS | YELVATPHNT | SKGFQRPVYL | FHKARSPSH | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1179 | 1 | 1070.0301 | 2.64 | 2 | 43.0 | 11.4 | 2 | 45-67 | R. GGTERGPGRCAPSAGSPAAAVG E | Carbamidomethyl: 10 | QU:MU 0.49<br>WUP:QUP 1.96 |

# Detailed Protein Report

## Protein 812: polypeptide N-acetylgalactosaminyltransferase 9 isoform A [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|169790926 | **Score:** | 22.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 68.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 3.8 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.38 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.94 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAVARKIRTL | LTVNILVFVG | IVLFSVYCRL | QGRSQELVRI | VSGDRRVRSR | HAKVGTLGDR | EAILQRLDHL | EEVVYNQLNG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LAKPIGLVEG | PGGLGQGGLA | ATLRDDGQEA | EGKYEEYGYN | AQLSDRISLD | RSIPDYRPRK | CRQMSYAQDL | PQVSVVFIFV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NEALSVILRS | VHSVVNHTPS | QLLKEVILVD | DNSDNVELKF | NLDQYVNKRY | PGLVKIVRNS | RREGLIRARL | QGWKAATAPV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VGFFDAHVEF | NTGWAEPALS | RIREDRRRIV | LPAIDNIKYS | TFEVQQYANA | AHGYNWGLWC | MYIIPPQDWL | DRGDESAPIR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TPAMIGCSFV | VDREYFGDIG | LLDPGMEVYG | GENVELGMRV | WQCGGSMEVL | PCSRVAHIER | TRKPYNNDID | YYAKRNALRA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AEVWMDDFKS | HVYMAWNIPM | SNPGVDFGDV | SERLALRQRL | KCRSFKWYLE | NVYPEMRVYN | NTLTYGEVRN | SKASAYCLDQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GAEDGDRAIL | YPCHGMSSQL | VRYSADGLLQ | LGPLGSTAFL | PDSKCLVDDG | TGRMPTLKKC | EDVARPTQRL | WDFTQSGPIV |
| 570 | 580 | 590 | 600 | 610 | | | |
| SRATGRCLEV | EMSKDANFGL | RLVVQRCSGQ | KWMIRNWIKH | ARH | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 393 | 1 | 548.2880 | -98.86 | 2 | 34.9 | 10.8 | 0 | 269-278 | R.IVLPAIDNIK.Y | | QU:MU 1.38<br>WUP:QUP 0.94 |
| 2013 | 2 | 698.2912 | -72.12 | 2 | 55.1 | 11.4 | 0 | 321-333 | R.TPAMIGCSFVVDR.E | | |

# Detailed Protein Report

## Protein 813: zinc finger and BTB domain-containing protein 1 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|182509180 | **Score:** | 22.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 82.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530403260 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger and BTB domain-containing protein 1 isoform X2 [Homo sapiens] |
| gi\|530403258 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger and BTB domain-containing protein 1 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAKPSHSSYV | LQQLNNQREW | GFLCDCCIAI | DDIYFQAHKA | VLAACSSYFR | MFFMNHQHST | AQLNLSNMKI | SAECFDLILQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FMYLGKIMTA | PSSFEQFKVA | MNYLQLYNVP | DCLEDIQDAD | CSSSKCSSSA | SSKQNSKMIF | GVRMYEDTVA | RNGNEANRWC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AEPSSTVNTP | HNREADEESL | QLGNFPEPLF | DVCKKSSVSK | LSTPKERVSR | RFGRSFTCDS | CGFGFSCEKL | LDEHVLTCTN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RHLYQNTRSY | HRIVDIRDGK | DSNIKAEFGE | KDSSKTFSAQ | TDKYRGDTSQ | AADDSASTTG | SRKSSTVESE | IASEEKSRAA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ERKRIIIKME | PEDIPTDELK | DFNIIKVTDK | DCNESTDNDE | LEDEPEEPFY | RYYVEEDVSI | KKSGRKTLKP | RMSVSADERG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GLENMRPPNN | SSPVQEDAEN | ASCELCGLTI | TEEDLSSHYL | AKHIENICAC | GKCGQILVKG | RQLQEHAQRC | GEPQDLTMNG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LGNTEEKMDL | EENPDEQSEI | RDMFVEMLDD | FRDNHYQINS | IQKKQLFKHS | ACPFRCPNCG | QRFETENLVV | EHMSSCLDQD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MFKSAIMEEN | ERDHRRKHFC | NLCGKGFYQR | CHLREHYTVH | TKEKQFVCQT | CGKQFLRERQ | LRLHNDMHKG | MARYVCSICD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QGNFRKHDHV | RHMISHLSAG | ETICQVCFQI | FPNNEQLEQH | MDVHLYTCGI | CGAKFNLRKD | MRSHYNAKHL | KRT |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 83 | 1 | 809.4031 | 121.71 | 2 | 31.0 | 10.5 | 0 | 215-229 | R.SFTCDSCGFGFSCEK.L | |

# Detailed Protein Report

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## Protein 814: abnormal spindle-like microcephaly-associated protein isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|332205965 | **Score:** | 22.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 217.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.44 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.14 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MANRRVGRGC WEVSPTERRP PAGLRGPAAE EEASSPPVLS LSHFCRSPFL CFGDVLLGAS RTLSLALDNP NEEVAEVKIS
        90        100        110        120        130        140        150        160
HFPAADLGFS VSQRCFVLQP KEKIVISVNW TPLKEGRVRE IMTFLVNDVL KHQAILLGNA EEQKKKKRSL WDTIKKKKIS
       170        180        190        200        210        220        230        240
ASTSHNRRVS NIQNVNKTFS VSQKVDRVRS PLQACENLAM NEGGPPTENN SLILEENKIP ISPISPAFNE CHGATCLPLS
       250        260        270        280        290        300        310        320
VRRSTTYSSL HASENRELLN VHSANVSKVS FNEKAVTETS FNSVNVNGQR GENSKLSLTP NCSSTLNITQ SQIHFLSPDS
       330        340        350        360        370        380        390        400
FVNNSHGANN ELELVTCLSS DMFMKDNSQP VHLESTIAHE IYQKILSPDS FIKDNYGLNQ DLESESVNPI LSPNQFLKDN
       410        420        430        440        450        460        470        480
MAYMCTSQQT CKVPLSNENS QVPQSPEDWR KSEVSPRIPE CQGSKSPKAI FEELVEMKSN YYSFIKQNNP KFSAVQDISS
       490        500        510        520        530        540        550        560
HSHNKQPKRR PILSATVTKR KATCTRENQT EINKPKAKRC LNSAVGEHEK VINNQKEKED FHSYLPIIDP ILSKSKSYKN
       570        580        590        600        610        620        630        640
EVTPSSTTAS VARKRKSDGS MEDANVRVAI TEHTEVREIK RIHFSPSEPK TSAVKKTKNV TTPISKRISN REKLNLKKKT
       650        660        670        680        690        700        710        720
DLSIFRTPIS KTNKRTKPII AVAQSSLTFI KPLKTDIPRH PMPFAAKNMF YDERWKEKQE QGFTWWLNFI LTPDDFTVKT
       730        740        750        760        770        780        790        800
NISEVNAATL LLGIENQHKI SVPRAPTKEE MSLRAYTARC RLNRLRRAAC RLFTSEKMVK AIKKLEIEIE ARRLIVRKDR
       810        820        830        840        850        860        870        880
HLWKDVGERQ KVLNWLLSYN PLWLRIGLET TYGELISLED NSDVTGLAMF ILNRLLWNPD IAAEYRHPTV PHLYRDGHEE
       890        900        910        920        930        940        950        960
ALSKFTLKKL LLLVCFLDYA KISRLIDHDP CLFCKDAEFK ASKEILLAFS RDFLSGEGDL SRHLGLLGLP VNHVQTPFDE
       970        980        990       1000       1010       1020       1030       1040
FDFAVTNLAV DLQCGVRLVR TMELLTQNWD LSKKLRIPAI SRLQKMHNVD IVLQVLKSRG IELSDEHGNT ILSKDIVDRH
      1050       1060       1070       1080       1090       1100       1110       1120
REKTLRLLWK IAFAFQVDIS LNLDQLKEEI AFLKHTKSIK KTISLLSCHS DDLINKKKGK RDSGSFEQYS ENIKLLMDWV
      1130       1140       1150       1160       1170       1180       1190       1200
NAVCAFYNKK VENFTVSFSD GRVLCYLIHH YHPCYVPFDA ICQRTTQTVE CTQTGSVVLN SSSESDDSSL DMSLKAFDHE
      1210       1220       1230       1240       1250       1260       1270       1280
NTSELYKELL ENEKKNFHLV RSAVRDLGGI PAMINHSDMS NTIPDEKVVI TYLSFLCARL LDLRKEIRAA RLIQTTWRKY
      1290       1300       1310       1320       1330       1340       1350       1360
KLKTDLKRHQ EREKAARIIQ LAVINFLAKQ RLRKRVNAAL VIQKYWRRVL AQRKLLMLKK EKLEKVQNKA ASLIQAMWRR
      1370       1380       1390       1400       1410       1420       1430       1440
YRAKKYLCKV KAACKIQAWY RCWRAHKEYL AILKAVKIIQ GCFYTKLERT RFLNVRASAI IIQRKWRAIL PAKIAHEHFL
      1450       1460       1470       1480       1490       1500       1510       1520
MIKRHRAACL IQAHYRGYKG RQVFLRQKSA ALIIQKYIRA REAGKHERIK YIEFKKSTVI LQALVRGWLV RKRFLEQRAK
      1530       1540       1550       1560       1570       1580       1590       1600
IRLLHFTAAA YYHLNAVRIQ RAYKLYLAVK NANKQVNSVI CIQRWFRARL QEKRFIQKYH SIKKIEHEGQ ECLSQRNRAA
      1610       1620       1630       1640       1650       1660       1670       1680
SVIQKAVRHF LLRKKQEKFT SGIIKIQALW RGYSWRKKND CTKIKAIRLS LQVVNREIRE ENKLYKRTAL ALHYLLTYKH
      1690       1700       1710       1720       1730       1740       1750       1760
LSAILEALKH LEVVTRLSPL CCENMAQSGA ISKIFVLIRS CNRSIPCMEV IRYAVQVLLN VSKYEKTTSA VYDVENCIDI
      1770       1780       1790       1800       1810       1820       1830       1840
LLELLQIYRE KPGNKVADKG GSIFTKTCCL LAILLKTTNR ASDVRSRSKV VDRIYSLYKL TAHKHKMNTE RILYKQKKNS
      1850       1860       1870       1880       1890       1900
SISIPFIPET PVRTRIVSRL KPDWVLRRDN MEEITNPLQA IQMVMDTLGI PY
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1490 | 1 | 719.8392 | -53.72 | 2 | 48.8 | 11.2 | 1 | 1445-1456 | R.HRAACLIQAHYR.G | | |
| 1961 | 1 | 656.7950 | -150.69 | 2 | 54.9 | 11.0 | 2 | 1597-1608 | R.NRAASVIQKAVR.H | | WUP:QUP 2.14<br>QU:MU 0.44 |

# Detailed Protein Report

## Protein 815: PREDICTED: protein FAM188A isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530392461 | **Score:** | 22.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 30.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 14.3 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530392465 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein FAM188A isoform X5 [Homo sapiens] |
| gi\|530392463 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein FAM188A isoform X4 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MWGNKFGVLL FLYSVLLTKG IENIKNEIED ASEPLIDPVY GHGSQSLINL LLTGHAVSNV WDGDRECSGM KLLGIHEQAA
        90        100        110        120        130        140        150        160
VGFLTLMEAL RYCKVGSYLK SPKFPIWIVG SETHLTVFFA KDMALVAPEA PSEQARRVFQ TYDPEDNGFI PDSLLEDVMK
       170        180        190        200        210        220        230        240
ALDLVSDPEY INLMKNKLDP EGLGIILLGP FLQEFFPDQG SSGPESFTVY HYNGLKQSNY NEKVMYVEGT AVVMGFEDPM
       250        260        270        280
LQTDDTPIKR CLQTKWPYIE LLWTTDRSPS LN
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1733 | 1 | 1030.7459 | -72.31 | 3 | 51.5 | 11.5 | 1 | 224-250 | K.VMYVEGTAVVMGFEDPMLQTDDTPIKR.C | Oxidation: 2, 11, 17 |

BRUKER

# Detailed Protein Report

## Protein 816: mitogen-activated protein kinase kinase kinase kinase 5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|14589909 | **Score:** | 22.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 95.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578825438 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: mitogen-activated protein kinase kinase kinase kinase 5 isoform X1 [Homo sapiens] |
| gi\|38570135 | refseq_human (refseq_human_20140103.fasta) | mitogen-activated protein kinase kinase kinase kinase 5 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEAPLRPAAD | ILRRNPQQDY | ELVQRVGSGT | YGDVYKARNV | HTGELAAVKI | IKLEPGDDFS | LIQQEIFMVK | ECKHCNIVAY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FGSYLSREKL | WICMEYCGGG | SLQDIYHVTG | PLSELQIAYV | CRETLQGLAY | LHTKGKMHRD | IKGANILLTD | HGDVKLADFG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VAAKITATIA | KRKSFIGTPY | WMAPEVAAVE | KNGGYNQLCD | IWAVGITAIE | LGELQPPMFD | LHPMRALFLM | SKSNFQPPKL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KDKTKWSSTF | HNFVKIALTK | NPKKRPTAER | LLTHTFVAQP | GLSRALAVEL | LDKVNNPDNH | AHYTEADDDD | FEPHAIIRHT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IRSTNRNARA | ERTASEINFD | KLQFEPPLRK | ETEARDEMGL | SSDPNFMLQW | NPFVDGANTG | KSTSKRAIPP | PLPPKPRISS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YPEDNFPDEE | KASTIKHCPD | SESRAPQILR | RQSSPSCGPV | AETSSIGNGD | GISKLMSENT | EGSAQAPQLP | RKKDKRDFPK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PAINGLPPTP | KVLMGACFSK | VFDGCPLKIN | CATSWIHPDT | KDQYIIFGTE | DGIYTLNLNE | LHEATMEQLF | PRKCTWLYVI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NNTLMSLSEG | KTFQLYSHNL | IALFEHAKKP | GLAAHIQTHR | FPDRILPRKF | ALTTKIPDTK | GCHKCCIVRN | PYTGHKYLCG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ALQSGIVLLQ | WYEPMQKFML | IKHFDFPLPS | PLNVFEMLVI | PEQEYPMVCV | AISKGTESNQ | VVQFETINLN | SASSWFTEIG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AGSQQLDSIH | VTQLERDTVL | VCLDKFVKIV | NLQGKLKSSK | KLASELSFDF | RIESVVCLQD | SVLAFWKHGM | QGKSFKSDEV |
| 810 | 820 | 830 | 840 | 850 | | | |
| TQEISDETRV | FRLLGSDRVV | VLESRPTENP | TAHSNLYILA | GHENSY | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2211 | 1 | 1023.8566 | -120.36 | 2 | 57.5 | 10.8 | 1 | 71-87 | K.ECKHCNIVAYFGSYLSR.E | Carbamidomethyl: 2 |

# Detailed Protein Report

## Protein 817: histone-lysine N-methyltransferase PRDM9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|147905620 | **Score:** | 22.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 103.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSPEKSQEES | PEEDTERTER | KPMVKDAFKD | ISIYFTKEEW | AEMGDWEKTR | YRNVKRNYNA | LITIGLRATR | PAFMCHRRQA |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| IKLQVDDTED | SDEEWTPRQQ | VKPPWMALRV | EQRKHQKGMP | KASFSNESSL | KELSRTANLL | NASGSEQAQK | PVSPSGEAST |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| SGQHSRLKLE | LRKKETERKM | YSLRERKGHA | YKEVSEPQDD | DYLYCEMCQN | FFIDSCAAHG | PPTFVKDSAV | DKGHPNRSAL |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| SLPPGLRIGP | SGIPQAGLGV | WNEASDLPLG | LHFGPYEGRI | TEDEEAANNG | YSWLITKGRN | CYEYVDGKDK | SWANWMRYVN |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| CARDDEEQNL | VAFQYHRQIF | YRTCRVIRPG | CELLVWYGDE | YGQELGIKWG | SKWKKELMAG | REPKPEIHPC | PSCCLAFSSQ |
| **410** | **420** | **430** | **440** | **450** | **460** | **470** | **480** |
| KFLSQHVERN | HSSQNFPGPS | ARKLLQPENP | CPGDQNQEQQ | YPDPHSRNDK | TKGQEIKERS | KLLNKRTWQR | EISRAFSSPP |
| **490** | **500** | **510** | **520** | **530** | **540** | **550** | **560** |
| KGQMGSCRVG | KRIMEEESRT | GQKVNPGNTG | KLFVGVGISR | IAKVKYGECG | QGFSVKSDVI | THQRTHTGEK | LYVCRECGRG |
| **570** | **580** | **590** | **600** | **610** | **620** | **630** | **640** |
| FSWKSHLLIH | QRIHTGEKPY | VCRECGRGFS | WQSVLLTHQR | THTGEKPYVC | RECGRGFSRQ | SVLLTHQRRH | TGEKPYVCRE |
| **650** | **660** | **670** | **680** | **690** | **700** | **710** | **720** |
| CGRGFSRQSV | LLTHQRRHTG | EKPYVCRECG | RGFSWQSVLL | THQRTHTGEK | PYVCRECGRG | FSWQSVLLTH | QRTHTGEKPY |
| **730** | **740** | **750** | **760** | **770** | **780** | **790** | **800** |
| VCRECGRGFS | NKSHLLRHQR | THTGEKPYVC | RECGRGFRDK | SHLLRHQRTH | TGEKPYVCRE | CGRGFRDKSN | LLSHQRTHTG |
| **810** | **820** | **830** | **840** | **850** | **860** | **870** | **880** |
| EKPYVCRECG | RGFSNKSHLL | RHQRTHTGEK | PYVCRECGRG | FRNKSHLLRH | QRTHTGEKPY | VCRECGRGFS | DRSSLCYHQR |
| **890** | **900** | | | | | | |
| THTGEKPYVC | REDE | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2778 | 1 | 941.4753 | -36.22 | 2 | 63.3 | 12.1 | 1 | 99-113 | R.QQVKPPWMALRVEQR.K | Oxidation: 8 |
| 2592 | 1 | 673.3616 | 27.18 | 2 | 63.1 | 10.0 | 1 | 629-639 | R.RHTGEKPYVCR.E | |

# Detailed Protein Report

**Protein 818:** **transcription factor NF-E2 45 kDa subunit [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5453774 | **Score:** | 22.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| | | **Sequence Coverage [%]:** | 5.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530400324 | refseq_human<br>(refseq_human_20140103.fasta) | PREDICTED: transcription factor NF-E2 45 kDa subunit isoform X2 [Homo sapiens] |
| gi\|530400322 | refseq_human<br>(refseq_human_20140103.fasta) | PREDICTED: transcription factor NF-E2 45 kDa subunit isoform X1 [Homo sapiens] |
| gi\|387848979 | refseq_human<br>(refseq_human_20140103.fasta) | transcription factor NF-E2 45 kDa subunit [Homo sapiens] |
| gi\|209862847 | refseq_human<br>(refseq_human_20140103.fasta) | transcription factor NF-E2 45 kDa subunit [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSPCPPQQSR | NRVIQLSTSE | LGEMELTWQE | IMSITELQGL | NAPSEPSFEP | QAPAPYLGPP | PPTTYCPCSI | HPDSGFPLPP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PPYELPASTS | HVPDPPYSYG | NMAIPVSKPL | SLSGLLSEPL | QDPLALLDIG | LPAGPPKPQE | DPESDSGLSL | NYSDAESLEL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EGTEAGRRRS | EYVEMYPVEY | PYSLMPNSLA | HSNYTLPAAE | TPLALEPSSG | PVRAKPTARG | EAGSRDERRA | LAMKIPFPTD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KIVNLPVDDF | NELLARYPLT | ESQLALVRDI | RRRGKNKVAA | QNCRKRKLET | IVQLERELER | LTNERERLLR | ARGEADRTLE |
| 330 | 340 | 350 | 360 | 370 | 380 | | |
| VMRQQLTELY | RDIFQHLRDE | SGNSYSPEEY | ALQQAADGTI | FLVPRGTKME | ATD | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 366 | 1 | 800.8792 | -39.89 | 2 | 34.5 | 10.8 | 2 | 214-228 | R.AKPTARGEAGSRDER.R | |

# Detailed Protein Report

## Protein 819: PREDICTED: ubiquilin-4 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530365094 | **Score:** | 22.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 7.0 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAEPSGAETR | PPIRVTVKTP | KDKEEIVICD | RASVKEFKEE | ISRRFKAQQD | QLVLIFAGKI | LKDGDTLNQH | GIKDGLTVHL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VIKTPQKAQD | PAAATASSPS | TPDPASAPST | TPASPATPAQ | PSTSGSASSD | AGSGSRRSSG | GGPSPGAGEG | SPSATASILS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GFGGILGLGS | LGLGSANFME | LQQQMQRQLM | SNPEMLSQIM | ENPLVQDMMS | NPDLMRHMIM | ANPQMQQLME | RNPEISHMLN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NPELMRQTME | LARNPAMMQE | MMRNQDRALS | NLESIPGGYN | ALRRMYTDIQ | EPMFSAAREQ | FGNNPFSSLA | GNSDSSSSQP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LRTENREPLP | NPWSPSPPTS | QAPGSGGEGT | GGSGTSQVHP | TVSNPFGINA | ASLGSGMFNS | PEMQALLQQI | SENPQLMQNV |
| 410 | 420 | 430 | | | | | |
| ISAPYMRSMM | QTLAQNPDFA | AQAFRIL | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1812 | 1 | 916.3298 | -105.96 | 2 | 53.0 | 10.4 | 1 | 284-298 | R.RMYTDIQEPMFSAAR.E | Oxidation: 2 |

# Detailed Protein Report

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**Protein 820:** **PREDICTED: zinc finger protein 85 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578833573 | **Score:** | 22.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.7 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***WUP:QUP*** | **Median:** | 0.32 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578840631 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 85 isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGPLTFRDVA | IEFSLKEWQC | LDTAQRNLYR | NVMLENYRNL | VFLGITVSKP | DLITCLEQGK | EAWSMKRHEI | MVAKPTGCLS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KRMSYELLRK | VYILMLLRSV | LYASVRIMCS | HFAQDLWPEQ | NIKDSFQKVT | LKRYGKCRHE | NLPLRKGCES | MDECKMHKGG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CNGLNQCLTA | TQSKIFQCDK | YVKVAHKFSN | SNRHEIRHTK | KKPFKCTKCG | KSFGMISCLT | EHSRIHTRVN | FYKCEECGKA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FNWSSTLTKH | KRIHTGEKPY | KCEECGKAFN | QSSNLIKHKK | IHTGEKPYKC | EECGKTFNRF | STLTTHKIIH | TGEKPYKCKE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CGKAFNRSST | LTTHRKIHTG | EKPYKCEECG | KAFKQSSNLT | THKIIHTGEK | PYKCKKCGKA | FNQSAHLTTH | EVIHTGEKPY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KCEKCGKAFN | HFSHLTTHKI | IHTGEKPYKC | KECGKAFKHS | STLTKHKIIH | TGEKPYKCKE | CEKAFNQSSK | LTEHKKIHTG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EKPYECEKCG | KAFNQSSNLT | RHKKSHTEEK | PYKCEECGKA | FNQSSKLTKH | KKIHTGEKPY | TCEECGKAFN | QSSNLTKHKR |
| 570 | 580 | 590 | 600 | | | | |
| IHTGEKPYKC | EECDKAFKWS | SVLTKHKIIH | TGEKLQI | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2769 | 1 | 863.9639 | 6.63 | 2 | 65.0 | 11.0 | 1 | 68-82 | R.HEIMVAKPTGCLSKR.M | Carbamidomethyl: 11 | WUP:QUP 0.32 |
| 2022 | 1 | 765.7797 | -170.72 | 2 | 55.7 | 11.2 | 2 | 548-560 | K.AFNQSSNLTKHKR.I | | |

# Detailed Protein Report

## Protein 821: activator of apoptosis harakiri [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4504493 | **Score:** | 22.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 9.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 34.1 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MCPCPLHRGR GPPAVCACSA GRLGLRSSAA QLTAARLKAL GDELHQRTMW RRRARSRRAP APGALPTYWP WLCAAAQVAA
        90        100
LAAWLLGRRN L
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1505 | 1 | 599.9721 | -16.93 | 3 | 47.2 | 10.9 | 2 | 9-26 | R.GRGPPAVCACSAGRLGLR.S | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 822: TBC1 domain family member 8B isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|38570103 | **Score:** | 22.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 72.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWLKPEEVLL | KNALKLWLME | RSNDYFVLQR | RRGYGEEGGG | GLTGLLVGTL | DSVLDSTAKV | APFRILHQTP | DSQVYLSIAC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GANREEITKH | WDWLEQNIMK | TLSVFDSNED | ITNFVQGKIR | GLIAEEGKHC | FAKEDDPEKF | REALLKFEKC | FGLPEKEKLV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TYYSCSYWKG | RVPCQGWLYL | STNFLSFYSF | LLGSEIKLII | SWDEVSKLEK | TSNVILTESI | HVCSQGENHY | FSMFLHINQT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YLLMEQLANY | AIRRLFDKET | FDNDPVLYNP | LQITKRGLEN | RAHSEQFNAF | FRLPKGESLK | EVHECFLWVP | FSHFNTHGKM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CISENYICFA | SQDGNQCSVI | IPLREVLAID | KTNDSSKSVI | ISIKGKTAFR | FHEVKDFEQL | VAKLRLRCGA | ASTQYHDIST |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ELAISSESTE | PSDNFEVQSL | TSQRECSKTV | NTEALMTVFH | PQNLETLNSK | MLKEKMKEQS | WKILFAECGR | GVSMFRTKKT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RDLVVRGIPE | TLRGELWMLF | SGAVNDMATN | PDYYTEVVEQ | SLGTCNLATE | EIERDLRRSL | PEHPAFQSDT | GISALRRVLT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AYAYRNPKIG | YCQAMNILTS | VLLLYAKEEE | AFWLLVAVCE | RMLPDYFNRR | IIGSDDFMPL | VRIQGQCVIG | EK |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2720 | 1 | 941.9748 | 14.19 | 2 | 62.5 | 10.1 | 2 | 157-171 | K.EKLVTYYSCSYWKGR.V | |

# Detailed Protein Report

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**Protein 823:** **olfactory receptor 2T27 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|49227791 | **Score:** | 22.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 35.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 10.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEQSNYSVYA | DFILLGLFSN | ARFPWLLFAL | ILLVFLTSIA | SNVVKIILIH | IDSRLHTPMY | FLLSQLSLRD | ILYISTIVPK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MLVDQVMSQR | AISFAGCTAQ | HFLYLTLAGA | EFFLLGLMSY | DRYVAICNPL | HYPVLMSRKI | CWLIVAAAWL | GGSIDGFLLT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PVTMQFPFCA | SREINHFFCE | VPALLKLSCT | DTSAYETAMY | VCCIMMLLIP | FSVISGSYTR | ILITVYRMSE | AEGRGKAVAT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CSSHMVVVSL | FYGAAMYTYV | LPHSYHTPEQ | DKAVSAFYTI | LTPMLNPLIY | SLRNKDVTGA | LQKVVGRCVS | SGKVTTF |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 128 | 1 | 1319.6098 | 4.84 | 3 | 30.5 | 22.1 | 0 | 187-220 | K.LSCTDTSAYETAMYVCCIMMLLIPFSVISGSYTR.I | Carbamidomethyl: 3, 16, 17; Oxidation: 13 |

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# Detailed Protein Report

## Protein 824: pancreatic lipase-related protein 3 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|190341077 | **Score:** | 22.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 52.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.03 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.08 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MLGIWIVAFL FFGTSRGKEV CYERLGCFKD GLPWTRTFST ELVGLPWSPE KINTRFLLYT IHNPNAYQEI SAVNSSTIQA
        90        100        110        120        130        140        150        160
SYFGTDKITR INIAGWKTDG KWQRDMCNVL LQLEDINCIN LDWINGSREY IHAVNNLRVV GAEVAYFIDV LMKKFEYSPS
       170        180        190        200        210        220        230        240
KVHLIGHSLG AHLAGEAGSR IPGLGRITGL DPAGPFFHNT PKEVRLDPSD ANFVDVIHTN AARILFELGV GTIDACGHLD
       250        260        270        280        290        300        310        320
FYPNGGKHMP GCEDLITPLL KFNFNAYKKE MASFFDCNHA RSYQFYAESI LNPDAFIAYP CRSYTSFKAG NCFFCSKEGC
       330        340        350        360        370        380        390        400
PTMGHFADRF HFKNMKTNGS HYFLNTGSLS PFARWRHKLS VKLSGSEVTQ GTVFLRVGGA VRKTGEFAIV SGKLEPGMTY
       410        420        430        440        450        460        470
TKLIDADVNV GNITSVQFIW KKHLFEDSQN KLGAEMVINT SGKYGYKSTF CSQDIMGPNI LQNLKPC
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 261 | 1 | 528.1590 | -186.43 | 2 | 32.0 | 10.3 | 0 | 394-402 | K.LEPGMTYTK.L | Oxidation: 5 | QU:MU 2.03<br>WUP:QUP 1.08 |

# Detailed Protein Report

## Protein 825: zinc finger protein 676 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|111548668 | **Score:** | 22.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 67.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLENYRNLVF | LGIAAFKPDL | IIFLEQGKEP | WNMKRHEMVE | EPPVICSHFS | QEFWPEQGIE | DSFQKMILRR | YDKCGHENLH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LKISCTNVDE | CNVHKEGYNK | LNQSLTTTQS | KVFQCGKYAN | VFHKCSNSNR | HKIRHTGEKG | LKCKEYVRSF | CMLSHLSQHE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RIYTRENSYK | CEENGKAFNW | SSTLTYYKSI | HTGEKPYKCE | ECGKAFSKFS | ILTKHKVIHT | GEKPYKCEEC | GKAFNRSSIL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TKHKIIHTGE | KPYKCEECGK | GFSSVSTLNT | HKAIHAEEKP | YKCEECGKAS | NSSSKLMEHK | RIHTGEKPYK | CEECGKAFSW |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SSSLTEHKRI | HAGEKPYKCE | ECGKAFNRSS | ILTKHKIIHT | GEKPYKCEGC | GKAFSKVSTL | NTHKAIHAEE | KPYKCEECGK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ASNSSSKLME | HKRIHTGEKP | YKCEECGKAF | SWSSSLTEHK | RIHAGEKPYK | CEECGKAFTW | SSSFTKHKRI | HAAEKPYKCE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ECGKGFSTFS | ILTKHKIIHT | GEKRYKCEEC | GKAFSWSSIL | TEHKIIHTGE | KPYKCEECGK | AFSRSSSLTR | HKRIHTGEKP |
| 570 | 580 | 590 | | | | | |
| YKCEECGKAF | KSSSTVSYHK | KIHTGENP | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2120 | 1 | 924.3321 | -133.13 | 2 | 56.4 | 11.9 | 2 | 199-214 | K.CEECGKAFSKFSILTK.H | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 826: synaptonemal complex protein 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|38373673 | **Score:** | 22.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 175.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530417767 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: synaptonemal complex protein 2 isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPIRPDLQQL | EKCIDDALRK | NDFKPLKTLL | QIDICEDVKI | KCSKQFFHKV | DNLICRELNK | EDIHNVSAIL | VSVGRCGKNI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SVLGQAGLLT | MIKQGLIQKM | VAWFEKSKDI | IQSQGNSKDE | AVLNMIEDLV | DLLLVIHDVS | DEGKKQVVES | FVPRICSLVI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DSRVNICIQQ | EIIKKMNAML | DKMPQDARKI | LSNQEMLILM | SSMGERILDA | GDYDLQVGIV | EALCRMTTEK | QRQELAHQWF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SMDFIAKAFK | RIKDSEFETD | CRIFLNLVNG | MLGDKRRVFT | FPCLSAFLDK | YELQIPSDEK | LEEFWIDFNL | GSQTLSFYIA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GDNDDHQWEA | VTVPEEKVQI | YSIEVRESKK | LLTIILKNTV | KISKREGKEL | LLYFDASLEI | TNVTQKIFGA | TKHRESIRKQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GISVAKTSLH | ILFDASGSQI | LVPESQISPV | GEELVSLKEK | SKSPKEFAKP | SKYIKNSDKG | NRNNSQLEKT | TPSKRKMSEA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SMIVSGADRY | TMRSPVLFSN | TSIPPRRRRI | KPPLQMTSSA | EKPSVSQTSE | NRVDNAASLK | SRSSEGRHRR | DNIDKHIKTA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KCVENTENKN | VEFPNQNFSE | LQDVIPDSQA | AEKRDHTILP | GVLDNICGNK | IHSKWACWTP | VTNIELCNNQ | RASTSSGDTL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NQDIVINKKL | TKQKSSSSIS | DHNSEGTGKV | KYKKEQTDHI | KIDKAEVEVC | KKHNQQQNHP | KYSGQKNTEN | AKQSDWPVES |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ETTFKSVLLN | KTIEESLIYR | KKYILSKDVN | TATCDKNPSA | SKNVQSHRKA | EKELTSELNS | WDSKQKKMRE | KSKGKEFTNV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AESLISQINK | RYKTKDDIKS | TRKLKESLIN | SGFSNKPVVQ | LSKEKVQKKS | YRKLKTTFVN | VTSECPVNDV | YNFNLNGADD |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PIIKLGIQEF | QATAKEACAD | RSIRLVGPRN | HDELKSSVKT | KDKKIITNHQ | KKNLFSDTET | EYRCDDSKTD | ISWLREPKSK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PQLIDYSRNK | NVKNHKSGKS | RSSLEKGQPS | SKMTPSKNIT | KKMDKTIPEG | RIRLPRKATK | TKKNYKDLSN | SESECEQEFS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| HSFKENIPVK | EENIHSRMKT | VKLPKKQQKV | FCAETEKELS | KQWKNSSLLK | DAIRDNCLDL | SPRSLSGSPS | SIEVTRCIEK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ITEKDFTQDY | DCITKSISPY | PKTSSLESLN | SNSGVGGTIK | SPKNNEKNFL | CASESCSPIP | RPLFLPRHTP | TKSNTIVNRK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KISSLVLTQE | TQNSNSYSDV | SSYSSEERFM | EIESPHINEN | YIQSKREESH | LASSLSKSSE | GREKTWFDMP | CDATHVSGPT |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| QHLSRKRIYI | EDNLSNSNEV | EMEEKGERRA | NLLPKKLCKI | EDADHHIHKM | SESVSSLSTN | DFSIPWETWQ | NEFAGIEMTY |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ETYERLNSEF | KRRNNIRHKM | LSYFTTQSWK | TAQQHLRTMN | HQSQDSRIKK | LDKFQFIIIE | ELENFEKDSQ | SLKDLEKEFV |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DFWEKIFQKF | SAYQKSEQQR | LHLLKTSLAK | SVFCNTDSEE | TVFTSEMCLM | KEDMKVLQDR | LLKDMLEEEL | LNVRRELMSV |
| 1530 | 1540 | | | | | | |
| FMSHERNANV | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 423 | 1 | 1294.0056 | -68.64 | 2 | 35.3 | 11.4 | 1 | 1265-1286 | K.TWFDMPCDATHVSGPTQHLSRK.R | Carbamidomethyl: 7; Oxidation: 5 |

# Detailed Protein Report

## Protein 827: PREDICTED: serine protease 23 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530396226 | **Score:** | 22.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 51.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 7.5 |
| | | **No. of unique Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MCSGAGGVRA ASPRPEAGRA GLGWRGGRTR QLPALLASLL ALGCAAGQAW EPRALSRRPH LSERRSEPRP GRAARRGTVL
        90        100        110        120        130        140        150        160
GMAGIPGLLF LLFFLLCAVG QVSPYSAPWK PTWPAYRLPV VLPQSTLNLA KPDFGAEAKL EVSSSCGPQC HKGTPLPTYE
       170        180        190        200        210        220        230        240
EAKQYLSYET LYANGSRTET QVGIYILSSS GDGAQHRDSG SSGKSRRKRQ IYGYDSRFSI FGKDFLLNYP FSTSVKLSTG
       250        260        270        280        290        300        310        320
CTGTLVAEKH VLTAAHCIHD GKTYVKGTQK LRVGFLKPKF KDGGRGANDS TSAMPEQMKF QWIRVKRTHV PKGWIKGNAN
       330        340        350        360        370        380        390        400
DIGMDYDYAL LELKKPHKRK FMKIGVSPPA KQLPGGRIHF SGYDNDRPGN LVYRFCDVKD ETYDLLYQQC DAQPGASGSG
       410        420        430        440        450        460        470
VYVRMWKRQQ QKWERKIIGI FSGHQWVDMN GSPQDFNVAV RITPLKYAQI CYWIKGNYLD CREG
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2331 | 1 | 1175.1968 | 47.50 | 2 | 59.6 | 11.4 | 0 | 31-53 | R.QLPALLASLLALGCAAGQAWEPR.A | |
| 123 | 1 | 659.8121 | -104.66 | 2 | 30.5 | 10.7 | 2 | 340-351 | R.KFMKIGVSPPAK.Q | Oxidation: 3 |

# Detailed Protein Report

## Protein 828: PHD and RING finger domain-containing protein 1 isoform 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|557440810 | **Score:** | 22.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 178.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDDDSLDELV | ARSPGPDGHP | QVGPADPAES | SVGSSGDSGD | DSDSEHGDGT | DGEDEGASEE | EDLEDRSGSE | DSEDDGETLL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EVAGTQGKLE | AAGSFNSDDD | AESCPICLNA | FRDQAVGTPE | NCAHYFCLDC | IVEWSKNANS | CPVDRTLFKC | ICIRAQFGGK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ILRKIPVENT | KASEEEEDPT | FCEVCGRSDR | EDRLLLCDGC | DAGYHMECLD | PPLQEVPVDE | WFCPECAAPG | VVLAADAGPV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SEEEVSLLLA | DVVPTTSRLR | PRAGRTRAIA | RTRQSERVRA | TVNRNRISTA | RRVQHTPGRL | GSSLLDEAIE | AVATGLSTAV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YQRPLTPRTP | ARRKRKTRRR | KKVPGRKKTP | SGPSAKSKSS | ATRSKKRQHR | VKKRRGKKVK | SEATTRSRIA | RTLGLRRPVH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SSCIPSVLKP | VEPSLGLLRA | DIGAASLSLF | GDPYELDPFD | SSEELSANPL | SPLSAKRRAL | SRSALQSHQP | VARPVSVGLS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RRRLPAAVPE | PDLEEEPVPD | LLGSILSGQS | LLMLGSSDVI | IHRDGSLSAK | RAAPVSFQRN | SGSLSRGEEG | FKGCLQPRAL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PSGSPAQGPS | GNRPQSTGLS | CQGRSRTPAR | TAGAPVRLDL | PAAPGAVQAR | NLSNGSVPGF | RQSHSPWFNG | TNKHTLPLAS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AASKISSRDS | KPPCRSVVPG | PPLKPAPRRT | DISELPRIPK | IRRDDGGGRR | DAAPAHGQSI | EIPSACISRL | TGREGTGQPG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RGTRAESEAS | SRVPREPGVH | TGSSRPPAPS | SHGSLAPLGP | SRGKGVGSTF | ESFRINIPGN | MAHSSQLSSP | GFCNTFRPVD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DKEQRKENPS | PLFSIKKTKQ | LRSEVYDPSD | PTGSDSSAPG | SSPERSGPGL | LPSEITRTIS | INSPKAQTVQ | AVRCVTSYTV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ESIFGTEPEP | PLGPSSAMSK | LRGAVAAEGA | SDTEREEPTE | SQGLAARLRR | PSPPEPWDEE | DGASCSTFFG | SEERTVTCVT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VVEPEAPPSP | DVLQAATHRV | VELRPPSRSR | STSSSRSRKK | AKRKRVSREH | GRTRSGTRSE | SRDRSSRSAS | PSVGEERPRR |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QRSKAKSRRS | SSDRSSSRER | AKRKKAKDKS | REHRRGPWGH | SRRTSRSRSG | SPGSSSYEHY | ESRKKKKRRS | ASRPRGRECS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PTSSLERLCR | HKHQRERSHE | RPDRKESVAW | PRDRRKRRSR | SPSSEHRARE | HRRPRSREKW | PQTRSHSPER | KGAVREASPA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PLAQGEPGRE | DLPTRLPALG | EAHVSPEVAT | ADKAPLQAPP | VLEVAAECEP | DDLDLDYGDS | VEAGHVFDDF | SSDAVFIQLD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DMSSPPSPES | TDSSPERDFP | LKPALPPASL | AVAAIQREVS | LMHDEDPSQP | PPLPEGTQEP | HLLRPDAAEK | AEAPSSPDVA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PAGKEDSPSA | SGRVQEAARP | EEVVSQTPLL | RSRALVKRVT | WNLQESESSA | PAEDRAPRAP | LHRPQKPREG | AWDMEDVAPT |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GVRQVFSELP | FPSHVLPEPG | FPDTDPSQVY | SPGLPPAPAQ | PSSIPPCALV | SQPTVQFILQ | GSLPLVGCGA | AQTLAPVPAA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| LTPASEPASQ | ATAASNSEEK | TPAPRLAAEK | TKKEEYMKKL | HMQERAVEEV | KLAIKPFYQK | REVTKEEYKD | ILRKAVQKIC |
| 1610 | 1620 | 1630 | 1640 | 1650 | | | |
| HSKSGEINPV | KVANLVKAYV | DKYRHMRRHK | KPEAGEEPPT | QGAEG | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2635 | 1 | 644.4948 | 273.66 | 1 | 63.7 | 10.4 | 0 | 1599-1603 | K.ICHSK.S | Carbamidomethyl: 2 |

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# Detailed Protein Report

## Protein 829: PREDICTED: mitochondrial Rho GTPase 2 isoform X9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578828338 | **Score:** | 22.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 52.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| | | **Sequence Coverage [%]:** | 6.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.54 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.79 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MGGPRRGPVG NKSDLRSGSS MEAVLPIMSQ FPEIETCVEC SAKNLRNISE LFYYAQKAVL HPTAPLYDPE AKQKSCFGHP

        90        100        110        120        130        140        150        160
LAPQALEDVK TVVCRNVAGG VREDRLTLDG FLFLNTLFIQ RGRHETTWTI LRRFGYSDAL ELTADYLSPL IHVPPGCSTE

       170        180        190        200        210        220        230        240
LNHLGYQFVQ RVFEKHDQDR DGALSPVELQ SLFSVFPAAP WGPELPRTVR TEAGRLPLHG YLCQWTLVTY LDVRSCLGHL

       250        260        270        280        290        300        310        320
GYLGYPTLCE QDQAHAITVT REKRLDQEKG QTQRSVLLCK VVGARGVGKS AFLQAFLGRG LGHQDTREQP PGYAIDTVQV

       330        340        350        360        370        380        390        400
NGQEKYLILC EVGTDGLLAT SLDATCDVAC LMFDGSDPKS FAHCASVYKH HYMDGQTPCL FVSSKADLPE GVAVSGPSPA

       410        420        430        440        450        460        470        480
EFCRKHRLPA PVPFSCAGPA EPSTTIFTQL ATMAAFPHLV HAELHPSSFW LRGLLGVVGA AVAAVLSFSL YRVLVKSQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2170 | 1 | 951.3588 | -102.94 | 2 | 57.0 | 10.3 | 0 | 386-404 | K.ADLPEGVAVSGPSPAEFCR.K | | WUP:QUP 0.79<br>QU:MU 1.54 |

# Detailed Protein Report

## Protein 830: PREDICTED: mucin-6 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578840955 | **Score:** | 22.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 141.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 4.63 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVQRWLLLSC | CGALLSAGLA | NTSYTSPGLQ | RLKDSPQTAP | DKGQCSTWGA | GHFSTFDHHV | YDFSGTCNYI | FAATCKDAFP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TFSVQLRRGP | DGSISRIIVE | LGASVVTVSE | AIISVKDIGV | ISLPYTSNGL | QITPFGQSVR | LVAKQLELEL | EVVWGPDSHL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MVLVERKYMG | QMCGLCGNFD | GKVTNEFVSE | EGKFLEPHKF | AALQKLDDPG | EICTFQDIPS | THVRQAQHAR | ICTQLLTLVA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PECSVSKEPF | VLSCQADVAA | APQPGPQNSS | CATLSEYSRQ | CSMVGQPVRR | WRSPGLCSVG | QCPANQVYQE | CGSACVKTCS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NPQHSCSSSC | TFGCFCPEGT | VLNDLSNNHT | CVPVTQCPCV | LHGAMYAPGE | VTIAACQTCR | CTLGRWVCTE | RPCPGHCSLE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GGSFVTTFDA | RPYRFHGTCT | YILLQSPQLP | EDGALMAVYD | KSGVSHSETS | LVAVVYLSRQ | DKIVISQDEV | VTNNGEAKWL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PYKTRNITVF | RQTSTHLQMA | TSFGLELVVQ | LRPIFQAYVT | VGPQFRGQTR | GLCGNFNGDT | TDDFTTSMGI | AEGTASLFVD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SWRAGNCPAA | LERETDPCSM | SQLNKVCAET | HCSMLLRTGT | VFERCHATVN | PAPFYKRCMY | QACNYEETFP | HICAALGDYV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HACSLRGVLL | WGWRSSVDNC | TIPCTGNTTF | SYNSQACERT | CLSLSDRATE | CHHSAVPVDG | CNCPDGTYLN | QKGECVRKAQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CPCILEGYKF | ILAEQSTVIN | GITCHCINGR | LSCPQRPQMF | LASCQAPKTF | KSCSQSSENK | FGAACAPTCQ | MLATGVACVP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TKCEPGCVCA | EGLYENADGQ | CVPPEECPCE | FSGVSYPGGA | ELHTDCRTCS | CSRGRWACQQ | GTHCPSTCTL | YGEGHVITFD |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GQRFVFDGNC | EYILATDVCG | VNDSQPTFKI | LTENVICGNS | GVTCSRAIKI | FLGGLSVVLA | DRNYTVTGEE | PHVQLGVTPG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ALSLVVDISI | PGRYNLTLIW | NRHMTILIRI | ARASQDPLCG | LCGNFNGNMK | DDFETRSRYV | ASSELELVNS | WKESPLCGDV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SFVTDPCSLN | AFRRSWAERK | CSVINSQTFA | TCHSKVYHLP | YYEACVRDAC | GCDSGGDCEC | LCDAVAAYAQ | ACLDKGVCVD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| WRTPAFCPIY | CGFYNTHTQD | GHGEYQYTQE | ANCTWHYQPC | LCPSQPQSVP | GSNIEGCYNC | SQDEYFDHEE | GVCVPCMPPT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TPQPPTTPQL | PTTGSRPTQV | WPMTGTSTTI | GLLSSTGPSP | SSNHTPASPT | QTPLLPATLT | SSKPTASSGG | KEPPAEPMER |
| 1290 | 1300 | 1310 | 1320 | | | | |
| AAAGGPRYTS | GVGLGMALLP | GSHLPLSRFP | A | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2052 | 1 | 840.8203 | -18.08 | 2 | 56.0 | 10.4 | 0 | 168-182 | K.YMGQMCGLCGNFDGK.V | Carbamidomethyl: 6 | QU:MU 4.63 |

# Detailed Protein Report

## Protein 831: mothers against decapentaplegic homolog 3 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5174513 | **Score:** | 21.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 48.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 6.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSILPFTPP | IVKRLLGWKK | GEQNGQEEKW | CEKAVKSLVK | KLKKTGQLDE | LEKAITTQNV | NTKCITIPRS | LDGRLQVSHR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KGLPHVIYCR | LWRWPDLHSH | HELRAMELCE | FAFNMKKDEV | CVNPYHYQRV | ETPVLPPVLV | PRHTEIPAEF | PPLDDYSHSI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PENTNFPAGI | EPQSNIPETP | PPGYLSEDGE | TSDHQMNHSM | DAGSPNLSPN | PMSPAHNNLD | LQPVTYCEPA | FWCSISYYEL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NQRVGETFHA | SQPSMTVDGF | TDPSNSERFC | LGLLSNVNRN | AAVELTRRHI | GRGVRLYYIG | GEVFAECLSD | SAIFVQSPNC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NQRYGWHPAT | VCKIPPGCNL | KIFNNQEFAA | LLAQSVNQGF | EAVYQLTRMC | TIRMSFVKGW | GAEYRRQTVT | STPCWIELHL |
| 410 | 420 | 430 | | | | | |
| NGPLQWLDKV | LTQMGSPSIR | CSSVS | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2171 | 1 | 862.9449 | 30.12 | 2 | 57.5 | 11.0 | 1 | 410-425 | K.VLTQMGSPSIRCSSVS.- | Carbamidomethyl: 12;<br>Oxidation: 5 |

# Detailed Protein Report

## Protein 832: CD177 antigen precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|110735433 | **Score:** | 21.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSAVLLLALL | GFILPLPGVQ | ALLCQFGTVQ | HVWKVSDLPR | QWTPKNTSCD | SGLGCQDTLM | LIESGPQVSL | VLSKGCTEAK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DQEPRVTEHR | MGPGLSLISY | TFVCRQEDFC | NNLVNSLPLW | APQPPADPGS | LRCPVCLSME | GCLEGTTEEI | CPKGTTHCYD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GLLRLRGGGI | FSNLRVQGCM | PQPVCNLLNG | TQEIGPVGMT | ENCDMKDFLT | CHRGTTIMTH | GNLAQEPTDW | TTSNTEMCEV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GQVCQETLLL | LDVGLTSTLV | GTKGCSTVGA | QNSQKTTIHS | APPGVLVASY | THFCSSDLCN | SASSSSVLLN | SLPPQAAPVP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GDRQCPTCVQ | PLGTCSSGSP | RMTCPRGATH | CYDGYIHLSG | GGLSTKMSIQ | GCVAQPSSFL | LNHTRQIGIF | SAREKRDVQP |
| 410 | 420 | 430 | 440 | | | | |
| PASQHEGGGA | EGLESLTWGV | GLALAPALWW | GVVCPSC | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1857 | 1 | 939.3363 | -87.80 | 2 | 53.1 | 21.9 | 0 | 324-341 | R.QCPTCVQPLGTCSSGSPR.M | Carbamidomethyl: 5 |

# Detailed Protein Report

## Protein 833: partitioning defective 3 homolog B isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|119120907 | **Score:** | 21.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 121.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKVTVCFGRT | GIVVPCKEGQ | LRVGELTQQA | LQRYLKTREK | GPGYWVKIHH | LEYTDGGILD | PDDVLADVVE | DKDKLIAVFE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EQEPLHKIES | PSGNPADRQS | PDAFETEVAA | QLAAFKPIGG | EIEVTPSALK | LGTPLLVRRS | SDPVPGPPAD | TQPSASHPGG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QSLKLVVPDS | TQNLEDREVL | NGVQTELLTS | PRTKDTLSDM | TRTVEISGEG | GPLGIHVVPF | FSSLSGRILG | LFIRGIEDNS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RSKREGLFHE | NECIVKINNV | DLVDKTFAQA | QDVFRQAMKS | PSVLLHVLPP | QNREQYEKSV | IGSLNIFGNN | DGVLKTKVPP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PVHGKSGLKT | ANLTGTDSPE | TDASASLQQN | KSPRVPRLGG | KPSSPSLSPL | MGFGSNKNAK | KIKIDLKKGP | EGLGFTVVTR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DSSIHGPGPI | FVKNILPKGA | AIKDGRLQSG | DRILEVNGRD | VTGRTQEELV | AMLRSTKQGE | TASLVIARQE | GHFLPRELKG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EPDCCALSLE | TSEQLTFEIP | LNDSGSAGLG | VSLKGNKSRE | TGTDLGIFIK | SIIHGGAAFK | DGRLRMNDQL | IAVNGESLLG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KSNHEAMETL | RRSMSMEGNI | RGMIQLVILR | RPERPMEDPA | ECGAFSKPCF | ENCQNAVTTS | RRNDNSILHP | LGTCSPQDKQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KGLLLPNDGW | AESEVPPSPT | PHSALGLGLE | DYSHSSGVDS | AVYFPDQHIN | FRSVTPARQP | ESINLKASKS | MDLVPDESKV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HSLAGQKSES | PSKDFGPTLG | LKKSSSLESL | QTAVAEVRKN | DLPFHRPRPH | MVRGRGCNES | FRAAIDKSYD | GPEEIEADGL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SDKSSHSGQG | ALNCESAPQG | NSELEDMENK | ARKVKKTKEK | EKKKEKGKLK | VKEKKRKEEN | EDPERKIKKK | GFGAMLRFGK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KKEDKGGKAE | QKGTLKHGGL | REEELEKMKE | ERESGRPTGG | STDRIQKLRK | EYYQARREGF | PLYEDDEGRA | RPSEYDLLWV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PGRGPDGNAH | NLRFEGMERQ | YASLPRGGPA | DPVDYLPAAP | RGLYKERELP | YYPGAHPMHP | PKGSYPRPTE | LRVADLRYPQ |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | |
| HYPPPPAPQH | KGPFRQDVPP | SPPQHQRMPA | YQETGRPGPR | GGSPDQYPYR | TQDSRQKNPM | TAAV | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2561 | 1 | 913.4593 | -55.63 | 2 | 62.7 | 11.7 | 2 | 693-709 | R.SVTPARQPESINLKASK.S | |

# Detailed Protein Report

## Protein 834: complement C4-A isoform 2 preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|356582273 | **Score:** | 21.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 187.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRLLWGLIWA | SSFFTLSLQK | PRLLLFSPSV | VHLGVPLSVG | VQLQDVPRGQ | VVKGSVFLRN | PSRNNVPCSP | KVDFTLSSER |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DFALLSLQVP | LKDAKSCGLH | QLLRGPEVQL | VAHSPWLKDS | LSRTTNIQGI | NLLFSSRRGH | LFLQTDQPIY | NPGQRVRYRV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FALDQKMRPS | TDTITVMVEN | SHGLRVRKKE | VYMPSSIFQD | DFVIPDISEP | GTWKISARFS | DGLESNSSTQ | FEVKKYVLPN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FEVKITPGKP | YILTVPGHLD | EMQLDIQARY | IYGKPVQGVA | YVRFGLLDED | GKKTFFRGLE | SQTKLVNGQS | HISLSKAEFQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DALEKLNMGI | TDLQGLRLYV | AAAIIESPGG | EMEEAELTSW | YFVSSPFSLD | LSKTKRHLVP | GAPFLLQALV | REMSGSPASG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IPVKVSATVS | SPGSVPEVQD | IQQNTDGSGQ | VSIPIIIPQT | ISELQLSVSA | GSPHPAIARL | TVAAPPSGGP | GFLSIERPDS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RPPRVGDTLN | LNLRAVGSGA | TFSHYYYMIL | SRGQIVFMNR | EPKRTLTSVS | VFVDHHLAPS | FYFVAFYYHG | DHPVANSLRV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DVQAGACEGK | LELSVDGAKQ | YRNGESVKLH | LETDSLALVA | LGALDTALYA | AGSKSHKPLN | MGKVFEAMNS | YDLGCGPGGG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DSALQVFQAA | GLAFSDGDQW | TLSRKRLSCP | KEKTTRKKRN | VNFQKAINEK | LGQYASPTAK | RCCQDGVTRL | PMMRSCEQRA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ARVQQPDCRE | PFLSCCQFAE | SLRKKSRDKG | QAGLQRALEI | LQEEDLIDED | DIPVRSFFPE | NWLWRVETVD | RFQILTLWLP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DSLTTWEIHG | LSLSKTKGLC | VATPVQLRVF | REFHLHLRLP | MSVRRFEQLE | LRPVLYNYLD | KNLTVSVHVS | PVEGLCLAGG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GGLAQQVLVP | AGSARPVAFS | VVPTAAAAVS | LKVVARGSFE | FPVGDAVSKV | LQIEKEGAIH | REELVYELNP | LDHRGRTLEI |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PGNSDPNMIP | DGDFNSYVRV | TASDPLDTLG | SEGALSPGGV | ASLLRLPRGC | GEQTMIYLAP | TLAASRYLDK | TEQWSTLPPE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TKDHAVDLIQ | KGYMRIQQFR | KADGSYAAWL | SRDSSTWLTA | FVLKVLSLAQ | EQVGGSPEKL | QETSNWLLSQ | QQADGSFQDP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| CPVLDRSMQG | GLVGNDETVA | LTAFVTIALH | HGLAVFQDEG | AEPLKQRVEA | SISKANSFLG | EKASAGLLGA | HAAAITAYAL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TLTKAPVDLL | GVAHNNLMAM | AQETGDNLYW | GSVTGSQSNA | VSPTPAPRNP | SDPMPQAPAL | WIETTAYALL | HLLLHEGKAE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| MADQASAWLT | RQGSFQGGFR | STQDTVIALD | ALSAYWIASH | TTEERGLNVT | LSSTGRNGFK | SHALQLNNRQ | IRGLEEELQF |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| SLGSKINVKV | GGNSKGTLKV | LRTYNVLDMK | NTTCQDLQIE | VTVKGHVEYT | MEANEDYEDY | EYDELPAKDD | PDAPLQPVTP |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LQLFEGRRNR | RRREAPKLTS | LSDRYVSHFE | TEGPHVLLYF | DSVPTSRECV | GFEAVQEVPV | GLVQPASATL | YDYYNPERRC |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| SVFYGAPSKS | RLLATLCSAE | VCQCAEGKCP | RQRRALERGL | QDEDGYRMKF | ACYYPRVEYG | FQVKVLREDS | RAAFRLFETK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| ITQVLHFTKD | VKAAANQMRN | FLVRASCRLR | LEPGKEYLIM | GLDGATYDLE | GHPQYLLDSN | SWIEEMPSER | LCRSTRQRAA |
| 1690 | 1700 | | | | | | |
| CAQLNDFLQE | YGTQGCQV | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1263 | 1 | 714.0054 | -48.05 | 3 | 45.9 | 10.2 | 1 | 138-155 | R.RGHLFLQTDQPIYNPGQR.V | |
| 894 | 1 | 872.4102 | 17.32 | 2 | 39.6 | 11.7 | 0 | 730-743 | R.EPFLSCCQFAESLR.K | Carbamidomethyl: 6, 7 |

# Detailed Protein Report

**Protein 835:** **PREDICTED: probable E3 ubiquitin-protein ligase HERC1 isoform X6 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530406610 | **Score:** | 21.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 524.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 0.7 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MATMIPPVKL KWLEHLNSSW ITEDSESIAT REGVAVLYSK LVSNKEVVPL PQQVLCLKGP QLPDFERESL SSDEQDHYLD
        90        100        110        120        130        140        150        160
ALLSSQLALA KMVCSDSPFA GALRKRLLVL QRVFYALSNK YHDKGKVKQQ QHSPESSSGS ADVHSVSERP RSSTDALIEM
       170        180        190        200        210        220        230        240
GVRTGLSLLF ALLRQSWMMP VSGPGLSLCN DVIHTAIEVV SSLPPLSLAN ESKIPPMGLD CLSQVTTFLK GVTIPNSGAD
       250        260        270        280        290        300        310        320
TLGRRLASEL LLGLAAQRGS LRYLLEWIEM ALGASAVVHT MEKGKLLSSQ EGMISFDCFM TILMQMRRSL GSSADRSQWR
       330        340        350        360        370        380        390        400
EPTRTSDGLC SLYEAALCLF EEIEAGQYCT FVISTDGSVR ACGKGSYGRL GLGDSNNQST LKKLTFEPHR SIKKVSSSKG
       410        420        430        440        450        460        470        480
SDGHTLAFTT EGEVFSWGDG DYGKLGHGNS STQKYPKLIQ GPLQGKVVVC VSAGYRHSAA VTEDGELYTW GEGDFGRLGH
       490        500        510        520        530        540        550        560
GDSNSRNIPT LVKDISNVGE VSCGSSHTIA LSKDGRTVWS FGGGDNGKLG HGDTNRVYKP KVIEALQGMF IRKVCAGSQS
       570        580        590        600        610        620        630        640
SLALTSTGQV YAWGCGACLG CGSSEATALR PKLIEELAAT RIVDVSIGDS HCLALSHDNE VYAWGNNSMG QCGQGNSTGP
       650        660        670        680        690        700        710        720
ITKPKKVSGL DGIAIQQISA GTSHSLAWTA LPRDRQVVAW HRPYCVDLEE STFSHLRSFL ERYCDKINSE IPPLPFPSSR
       730        740        750        760        770        780        790        800
EHHSFLKLCL KLLSNHLALA LAGGVATSIL GRQAGPLRNL LFRLMDSTVP DEIQEVVIET LSVGATMLLP PLRERMELLH
       810        820        830        840        850        860        870        880
SLLPQGPDRW ESLSKGQRMQ LDIILTSLQD HTHVASLLGY SSPSDAADLS SVCTGYGNLS DQPYGTQSCH PDTHLAEILM
       890        900        910        920        930        940        950        960
KTLLRNLGFY TDQAFGELEK NSDKFLLGTS SSENSQPAHL HELLCSLQKQ LLAFCHINNI SENSSSVALL HKHLQLLLPH
       970        980        990       1000       1010       1020       1030       1040
ATDIYSRSAN LLKESPWNGS VGEKLRDVIY VSAAGSMLCQ IVNSLLLLPV SVARPLLSYL LDLLPPLDCL NRLLPAADLL
      1050       1060       1070       1080       1090       1100       1110       1120
EDQELQWPLH GGPELIDPAG LPLPQPAQSW VWLVDLERTI ALLIGRCLGG MLQGSPVSPE EQDTAYWMKT PLFSDGVEMD
      1130       1140       1150       1160       1170       1180       1190       1200
TPQLDKCMSC LLEVALSGNE EQKPFDYKLR PEIAVYVDLA LGCSKEPARS LWISMQDYAV SKDWDSATLS NESLLDTVSR
      1210       1220       1230       1240       1250       1260       1270       1280
FVLAALLKHT NLLSQACGES RYQPGKHLSE VYRCVYKVRS RLLACKNLEL IQTRSSSRDR WISENQDSAD VDPQEHSFTR
      1290       1300       1310       1320       1330       1340       1350       1360
TIDEEAEMEE QAERDREEGH PEPEDEEEER EHEVMTAGKI FQCFLSAREV ARSRDRDRMN SGAGSGARAD DPPPQSQQER
      1370       1380       1390       1400       1410       1420       1430       1440
RVSTDLPEGQ DVYTAACNSV IHRCALLILG VSPVIDELQK RREEGQLQQP STSASEGGGL MTRSESLTAE SRLVHTSPNY
      1450       1460       1470       1480       1490       1500       1510       1520
RLIKSRSESD LSQPESDEEG YALSGRRNVD LDLAASHRKR GPMHSQLESL SDSWARLKHS RDWLCNSSYS FESDFDLTKS
      1530       1540       1550       1560       1570       1580       1590       1600
LGVHTLIENV VSFVSGDVGN APGFKEPEES MSTSPQASII AMEQQQLRAE LRLEALHQIL VLLSGMEEKG SISLAGSRLS
      1610       1620       1630       1640       1650       1660       1670       1680
SGFQSSTLLT SVRLQFLAGC FGLGTVGHTG GKGESGRLHH YQDGIRAAKR NIQIEIQVAV HKIYQQLSAT LERALQANKH
      1690       1700       1710       1720       1730       1740       1750       1760
HIEAQQRLLL VTVFALSVHY QPVDVSLAIS TGLLNVLSQL CGTDTMLGQP LQLLPKTGVS QLSTALKVAS TRLLQILAIT
      1770       1780       1790       1800       1810       1820       1830       1840
TGTYADKLSP KVVQSLLDLL CSQLKNLLSQ TGVLHMASFG EGEQEDGEEE EKKVDSSGET EKKDFRAALR KQHAAELHLG
      1850       1860       1870       1880       1890       1900       1910       1920
DFLVFLRRVV SSKAIQSKMA SPKWTEVLLN IASQKCSSGI PLVGNLRTRL LALHVLEAVL PACESGVEDD QMAQIVERLF
      1930       1940       1950       1960       1970       1980       1990       2000
SLLSDCMWET PIAQAKHAIQ IKEKEQEIKL QKQGELEEED ENLPIQEVSF DPEKAQCCLV ENGQILTHGS GGKGYGLAST
      2010       2020       2030       2040       2050       2060       2070       2080
GVTSGCYQWK FYIVKENRGN EGTCVGVSRW PVHDFNHRTT SDMWLYRAYS GNLYHNGEQT LTLSSFTQGD FITCVLDMEA
      2090       2100       2110       2120       2130       2140       2150       2160
RTISFGKNGE EPKLAFEDVD AAELYPCVMF YSSNPGEKVK ICDMQMRGTP RDLLPGDPIC SPVAAVLAEA TIQLIRILHR
      2170       2180       2190       2200       2210       2220       2230       2240
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1613 | 1 | 954.4635 | -82.64 | 2 | 49.9 | 11.5 | 1 | 537-552 | R.VYKPKVIEALQGMFIR.K | Oxidation: 13 |

# Detailed Protein Report

## Protein 836: PREDICTED: transportin-1 isoform X2 [Homo sapiens]

**Accession:** gi|530379292
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 21.8
**MW [kDa]:** 98.6
**pI:** 4.7
**Sequence Coverage [%]:** 2.3
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVWDRQTKME | YEWKPDEQGL | QQILQLLKES | QSPDTTIQRT | VQQKLEQLNQ | YPDFNNYLIF | VLTKLKSEDE | PTRSLSGLIL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KNNVKAHFQN | FPNGVTDFIK | SECLNNIGDS | SPLIRATVGI | LITTIASKGE | LQNWPDLLPK | LCSLLDSEDY | NTCEGAFGAL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QKICEDSAEI | LDSDVLDRPL | NIMIPKFLQF | FKHSSPKIRS | HAVACVNQFI | ISRTQALMLH | IDSFIENLFA | LAGDEEPEVR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KNVCRALVML | LEVRMDRLLP | HMHNIVEYML | QRTQDQDENV | ALEACEFWLT | LAEQPICKDV | LVRHLPKLIP | VLVNGMKYSD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IDIILLKGDV | EEDETIPDSE | QDIRPRFHRS | RTVAQQHDED | GIEEEDDDDD | EIDDDDTISD | WNLRKCSAAA | LDVLANVYRD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ELLPHILPLL | KELLFHHEWV | VKESGILVLG | AIAEGCMQGM | IPYLPELIPH | LIQCLSDKKA | LVRSITCWTL | SRYAHWVVSQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PPDTYLKPLM | TELLKRILDS | NKRVQEAACS | AFATLEEEAC | TELVPYLAYI | LDTLVFAFSK | YQHKNLLILY | DAIGTLADSV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GHHLNKPEYI | QMLMPPLIQK | WNMLKDEDKD | LFPLLECLSS | VATALQSGFL | PYCEPVYQRC | VNLVQKTLAQ | AMLNNAQPDQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| YEAPDKDFMI | VALDLLSGLA | EGLGGNIEQL | VARSNILTLM | YQCMQDKMPE | VRQSSFALLG | DLTKACFQHV | KPCIADFMPI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LGTNLNPEFI | SVCNNATWAI | GEISIQMAIT | IGRLGYVCPQ | EVAPMLQQFI | RPWCTSLRNI | RDNEEKDSAF | RGICTMISVN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | |
| PSGVIQDFIF | FCDAVASWIN | PKDDLRDMFC | KILHGFKNQV | GDENWRRFSD | QFPLPLKERL | AAFYGV | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2076 | 1 | 753.4131 | -4.44 | 2 | 56.3 | 10.0 | 1 | 460-472 | K.ALVRSITCWTLSR.Y | |

# Detailed Protein Report

## Protein 837: cancer/testis antigen family 45 member A5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|56090473 | **Score:** | 21.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 15.9 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 4.95 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.60 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578847149 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: cancer/testis antigen family 45 member A2-like isoform X4 [Homo sapiens] |
| gi\|578847147 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: cancer/testis antigen family 45 member A2-like isoform X3 [Homo sapiens] |
| gi\|578847145 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: cancer/testis antigen family 45 member A2-like isoform X2 [Homo sapiens] |
| gi\|578847143 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: cancer/testis antigen family 45 member A2-like isoform X1 [Homo sapiens] |
| gi\|578838786 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: cancer/testis antigen family 45 member A5-like isoform X3 [Homo sapiens] |
| gi\|578838784 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: cancer/testis antigen family 45 member A5-like isoform X2 [Homo sapiens] |
| gi\|578838782 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: cancer/testis antigen family 45 member A5-like isoform X1 [Homo sapiens] |
| gi\|288683726 | refseq_human (refseq_human_20140103.fasta) | cancer/testis antigen family 45 member A5 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKKLMT GHAIPPSQLD SQIDDFTGFS
        90        100        110        120        130        140        150        160
KDGMMQKPGS NAPVGGNVTS NFSGDDLECR GIASSPKSQQ EINADIKCQV VKEIRCLGRK YEKIFEMLEG VQGPTAVRKR
       170        180        190
FFESIIKEAA RCMRRDFVKH LKKKLKRMI
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 309 | 1 | 704.8671 | 37.75 | 2 | 33.9 | 11.6 | 0 | 40-54 | K.QGAGDSLIAGSAMSK.E | Oxidation: 13 | |
| 267 | 1 | 823.8888 | -52.68 | 2 | 33.0 | 10.2 | 0 | 144-158 | K.IFEMLEGVQGPTAVR.K | | QU:MU 4.95<br>WUP:QUP 0.60 |

# Detailed Protein Report

## Protein 838: inositol hexakisphosphate kinase 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|55769530 | **Score:** | 21.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530381448 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: inositol hexakisphosphate kinase 3 isoform X1 [Homo sapiens] |
| gi\|218777830 | refseq_human(refseq_human_20140103.fasta) | inositol hexakisphosphate kinase 3 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVVQNSADAG | DMRAGVQLEP | FLHQVGGHMS | VMKYDEHTVC | KPLVSREQRF | YESLPLAMKR | FTPQYKGTVT | VHLWKDSTGH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LSLVANPVKE | SQEPFKVSTE | SAAVAIWQTL | QQTTGSNGSD | CTLAQWPHAQ | LARSPKESPA | KALLRSEPHL | NTPAFSLVED |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TNGNQVERKS | FNPWGLQCHQ | AHLTRLCSEY | PENKRHRFLL | LENVVSQYTH | PCVLDLKMGT | RQHGDDASEE | KKARHMRKCA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QSTSACLGVR | ICGMQVYQTD | KKYFLCKDKY | YGRKLSVEGF | RQALYQFLHN | GSHLRRELLE | PILHQLRALL | SVIRSQSSYR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FYSSSLLVIY | DGQEPPERAP | GSPHPHEAPQ | AAHGSSPGGL | TKVDIRMIDF | AHTTYKGYWN | EHTTYDGPDP | GYIFGLENLI |
| 410 | 420 | | | | | | |
| RILQDIQEGE | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2325 | 1 | 713.3471 | 54.08 | 2 | 57.3 | 11.3 | 0 | 1-13 | -.MVVQNSADAGDMR.A | Oxidation: 1, 12 |

# Detailed Protein Report

## Protein 839: PREDICTED: glycylpeptide N-tetradecanoyltransferase 1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530412338 | **Score:** | 21.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 61.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPGGRPVPKG | TPHVVGRGAL | LSQLKMADES | ETAVKPPAPP | LPQMMEGNGN | GHEHCSDCEN | EEDNSYNRGG | LSPANDTGAK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KKKKKQKKKK | EKGSETDSAQ | DQPVKMNSLP | AERIQEIQKA | IELFSVGQGP | AKTMEEASKR | SYQFWDTQPV | PKLGEVVNTH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GPVEPDKDNI | RQEPYTLPQG | FTWDALDLGD | RGVLKELYTL | LNENYVEDDD | NMFRFDYSPE | FLLWALRPPG | WLPQWHCGVR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VVSSRKLVGF | ISAIPANIHI | YDTEKKMVEI | NFLCVHKKLR | SKRVAPVLIR | EITRRVHLEG | IFQAVYTAGV | VLPKPVGTCR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YWHRSLNPRK | LIEVKFSHLS | RNMTMQRTMK | LYRLPETPKT | AGLRPMETKD | IPVVHQLLTR | YLKQFHLTPV | MSQEEVEHWF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YPQENIIDTF | VVENANGEVT | DFLSFYTLPS | TIMNHPTHKS | LKAAYSFYNV | HTQTPLLDLM | SDALVLAKMV | RSRRGGLWRC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | |
| AGKRQWSHGE | HSSRDAASHG | LEALSPPHLF | CLGRVPAVFR | QKLKTWREQG | ASEVKALNSS | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 653 | 1 | 820.5245 | 82.19 | 1 | 37.7 | 10.3 | 2 | 469-474 | K.MVRSRR.G | Oxidation: 1 |

# Detailed Protein Report

**Protein 840:** **PREDICTED: LIM and senescent cell antigen-like-containing domain protein 1 isoform X7 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578804328 | **Score:** | 21.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 13.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPSQSSNMAN | ALASATCERC | KGGFAPAEKI | VNSNGELYHE | QCFVCAQCFQ | QFPEGLFYEF | EGRKYCEHDF | QMLFAPCCHQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CGEFIIGRVI | KAMNNSWHPE | CFRCDLCQEV | LADIGFVKNA | GRHLCRPCHN | REKARGLGKY | ICQKCHAIID | EQPLIFKNDP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YHPDHFNCAN | CGKELTADAR | ELKGELYCLP | CHDKMGVPIC | GACRRPIEGR | VVNAMGKQWH | VEHFVCAKCE | KPFLGHRHYE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RKGLAYCETH | YNQLFGDVCF | HCNRVIEGDV | VSALNKAWCV | NCFACSTCNT | KLTLKDKFVE | IDLKPVCKHC | YEKMPEEFKR |
| 330 | 340 | 350 | | | | | |
| RLAKREREAK | DKDKQKKKKP | VCL | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1542 | 1 | 978.1217 | 1.51 | 3 | 49.0 | 11.6 | 1 | 265-291 | R.VIEGDVVSALNKAWCVNCFACSTCNTK.L | Carbamidomethyl: 21 |

# Detailed Protein Report

## Protein 841: PREDICTED: HHIP-like protein 1 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578826190 | **Score:** | 21.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 78.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.8 |
| | | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKIARCLPSE | ECSPYAAHLY | DAEDPFTPLR | TVPGLCQDYC | LDMWHKCRGL | FRHLSTDQEL | WALEGNLARF | CRYLSLDDTD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YCFPYLLVNK | NLNSNLGHVV | ADAKGCLQLC | LEEVANGLRN | PVAMVHARDG | THRFFVAEQV | GLVWAYLPDR | SRLGKPFLNI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SRVVLTSPWE | GDERGFLGIA | FHPSFQHNRR | LYVYYSVGIR | SSEWIRISEF | RVSEDDENAV | DHSSERIILE | VKEPASNHNG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GQLLFGDDGY | LYIFTGDGGM | AGDPFGTFGN | AQNKSALLGK | VLRIDVDRKE | RGLPYGIPPD | NPFVGDPAAQ | PEVYALGVRN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MWRCSFDRGD | PSSGTGRGRL | FCGDVGQNKF | EEVDVVERGG | NYGWRAREGF | ECYDRSLCAN | TSLNDLLPIF | AYPHTVGKSV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TGGYVYRGCE | YPNLNGLYIF | GDFMSGRLMS | LQENPGTGQW | QYSEICMGHG | QTCEFPGLIN | NYYPYIISFG | EDEAGELYFM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| STGEPSATAP | RGVVYKIIDA | SRRAPPGKCQ | IQPAQVKIRS | RLIPFVPKEK | FIPKTRSTPR | PTARAPTRAP | RRGRPTAAPP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| APTPRPARPT | QQPGSRRGGG | RRRGRLNSAS | RAFRDGEVRL | VRPAGLSSGS | GRVEVFVGGR | WGTVCDDSWN | ISGAAVVCRQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | |
| LGFAYAVRAV | KRAEFGQGGS | LPILLDDVRC | AGWERNLLEC | QHNGVGTHNC | EHDEDAGVVC | SHQNPDL | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1490 | 1 | 670.7423 | 81.50 | 3 | 48.3 | 11.7 | 0 | 134-150 | R.FFVAEQVGLVWAYLPDR.S | |

# Detailed Protein Report

## Protein 842: nuclear mitotic apparatus protein 1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|557440899 | **Score:** | 21.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 236.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.94 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.33 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578821456 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: nuclear mitotic apparatus protein 1 isoform X9 [Homo sapiens] |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTLHATRGAA | LLSWVNSLHV | ADPVEAVLQL | QDCSIFIKII | DRIHGTEEGQ | QILKQPVSER | LDFVCSFLQK | NRKHPSSPEC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LVSAQKVLEG | SELELAKMTM | LLLYHSTMSS | KSPRDWEQFE | YKIQAELAVI | LKFVLDHEDG | LNLNEDLENF | LQKAPVPSTC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SSTFPEELSP | PSHQAKREIR | FLELQKVASS | SSGNNFLSGS | PASPMGDILQ | TPQFQMRRLK | KQLADERSNR | DELELELAEN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RKLLTEKDAQ | IAMMQQRIDR | LALLNEKQAA | SPLEPKELEE | LRDKNESLTM | RLHETLKQCQ | DLKTEKSQMD | RKINQLSEEN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GDLSFKLREF | ASHLQQLQDA | LNELTEEHSK | ATQEWLEKQA | QLEKELSAAL | QDKKCLEEKN | EILQGKLSQL | EEHLSQLQDN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PPQEKGEVLG | DVLQLETLKQ | EAATLAANNT | QLQARVEMLE | TERGQQEAKL | LAERGHFEEE | KQQLSSLITD | LQSSISNLSQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AKEELEQASQ | AHGARLTAQV | ASLTSELTTL | NATIQQQDQE | LAGLKQQAKE | KQAQLAQTLQ | QQEQASQGLR | HQVEQLSSSL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KQKEQQLKEV | AEKQEATRQD | HAQQLATAAE | EREASLRERD | AALKQLEALE | KEKAAKLEIL | QQQLQVANEA | RDSAQTSVTQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AQREKAELSR | KVEELQACVE | TARQEQHEAQ | AQVAELELQL | RSEQQKATEK | ERVAQEKDQL | QEQLQALKES | LKVTKGSLEE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EKRRAADALE | EQQRCISELK | AETRSLVEQH | KRERKELEEE | RAGRKGLEAR | LQQLGEAHQA | ETEVLRRELA | EAMAAQHTAE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SECEQLVKEV | AAWRERYEDS | QQEEAQYGAM | FQEQLMTLKE | ECEKARQELQ | EAKEKVAGIE | SHSELQISRQ | QNELAELHAN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LARALQQVQE | KEVRAQKLAD | DLSTLQEKMA | ATSKEVARLE | TLVRKAGEQQ | ETASRELVKE | PARAGDRQPE | WLEEQQGRQF |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| CSTQAALQAM | EREAEQMGNE | LERLRAALME | SQGQQQEERG | QQEREVARLT | QERGRAQADL | ALEKAARAEL | EMRLQNALNE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QRVEFATLQE | ALAHALTEKE | GKDQELAKLR | GLEAAQIKEL | EELRQTVKQL | KEQLAKKEKE | HASGSGAQSE | AAGRTEPTGP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KLEALRAEVS | KLEQQCQKQQ | EQADSLERSL | EAERASRAER | DSALETLQGQ | LEEKAQELGH | SQSALASAQR | ELAAFRTKVQ |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DHSKAEDEWK | AQVARGRQEA | ERKNSLISSL | EEEVSILNRQ | VLEKEGESKE | LKRLVMAESE | KSQKLEERLR | LLQAETASNS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| ARAAERSSAL | REEVQSLREE | AEKQRVASEN | LRQELTSQAE | RAEELGQELK | AWQEKFFQKE | QALSTLQLEH | TSTQALVSEL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LPAKHLCQQL | QAEQAAAEKR | HREELEQSKQ | AAGGLRAELL | RAQRELGELI | PLRQKVAEQE | RTAQQLRAEK | ASYAEQLSML |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KKAHGLLAEE | NRGLGERANL | GRQFLEVELD | QAREKYVQEL | AAVRADAETR | LAEVQREAQS | TARELEVMTA | KYEGAKVKVL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| EERQRFQEER | QKLTAQVEEL | SKKLADSDQA | SKVQQQKLKA | VQAQGGESQQ | EAQRLQAQLN | ELQAQLSQKE | QAAEHYKLQM |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| EKAKTHYDAK | KQQNQELQEQ | LRSLEQLQKE | NKELRAEAER | LGHELQQAGL | KTKEAEQTCR | HLTAQVRSLE | AQVAHADQQL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| RDLGKFQVAT | DALKSREPQA | KPQLDLSIDS | LDLSCEEGTP | LSITSKLPRT | QPDGTSVPGE | PASPISQRLP | PKVESLESLY |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| FTPIPARSQA | PLESSLDSLG | DVFLDSGRKT | RSARRRTTQI | INITMTKKLD | VEEPDSANSS | FYSTRSAPAS | QASLRATSST |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| QSLARLGSPD | YGNSALLSLP | GYRPTTRSSA | RRSQAGVSSG | APPGRNSFYM | GTCQDEPEQL | DDWNRIAELQ | QRNRVCPPHL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| KTCYPLESRP | SLSLGTITDE | EMKTGDPQET | LRRASMQPIQ | IAEGTGITTR | QQRKRVSLEP | HQGPGTPESK | KATSCFPRPM |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| TPRDRHEGRK | QSTTEAQKKA | APASTKQADR | RQSMAFSILN | TPKKLGNSLL | RRGASKKALS | KASPNTRSGT | RRSPRIATTT |
| 2090 | 2100 | 2110 | | | | | |
| ASAATAAAIG | ATPRAKGKAK | H | | | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 500 | 1 | 630.6311 | -18.35 | 3 | 36.2 | 11.0 | 1 | 984-999 | R.LRAALMESQGQQQEER.G | Oxidation: 6 | QU:MU 1.94<br>WUP:QUP 0.33 |
| 1859 | 1 | 682.2687 | -75.42 | 3 | 53.6 | 10.7 | 1 | 1808-1825 | K.KLDVEEPDSANSSFYSTR.S | | |

# Detailed Protein Report

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## Protein 843: PR domain zinc finger protein 15 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|94536868 | **Score:** | 21.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 133.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPRRRPPASG | AAQFPERIAT | RSPDPIPLCT | FQRQVSEMAE | DGSEEIMFIW | CEDCSQYHDS | ECPELGPVVM | VKDSFVLSRA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RSSLPPNLEI | RRLEDGAEGV | FAITQLVKRT | QFGPFESRRV | AKWEKESAFP | LKVFQKDGHP | VCFDTSNEDD | CNWMMLVRPA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AEAEHQNLTA | YQHGSDVYFT | TSRDIPPGTE | LRVWYAAFYA | KKMDKPMLKQ | AGSGVHAAGT | PENSAPVESE | PSQWACKVCS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ATFLELQLLN | EHLLGHLEQA | KSLPPGSQSE | AAAPEKEQDT | PRGEPPAVPE | SENVATKEQK | KKPRRGRKPK | VSKAEQPLVI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VEDKEPTEQV | AEIITEVPPD | EPVSATPDER | IMELVLGKLA | TTTTDTSSVP | KFTHHQNNTI | TLKRSLILSS | RHGIRRKLIK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QLGEHKRVYQ | CNICSKIFQN | SSNLSRHVRS | HGDKLFKCEE | CAKLFSRKES | LKQHVSYKHS | RNEVDGEYRY | RCGTCEKTFR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IESALEFHNC | RTDDKTFQCE | MCFRFFSTNS | NLSKHKKKHG | DKKFACEVCS | KMFYRKDVML | DHQRRHLEGV | RRVKREDLEA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GGENLVRYKK | EPSGCPVCGK | VFSCRSNMNK | HLLTHGDKKY | TCEICGRKFF | RVDVLRDHIH | VHFKDIALMD | DHQREEFIGK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IGISSEENDD | NSDESADSEP | HKYSCKRCQL | TFGRGKEYLK | HIMEVHKEKG | YGCSICNRRF | ALKATYHAHM | VIHRENLPDP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NVQKYIHPCE | ICGRIFNSIG | NLERHKLIHT | GVKSHACEQC | GKSFARKDML | KEHMRVHDNV | REYLCAECGK | GMKTKHALRH |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| HMKLHKGIKE | YECKECHRRF | AQKVNMLKHC | KRHTGIKDFM | CELCGKTFSE | RNTMETHKLI | HTVGKQWTCS | VCDKKYVTEY |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| MLQKHVQLTH | DKVEAQSCQL | CGTKVSTRAS | MSRHMRRKHP | EVLAVRIDDL | DHLPETTTID | ASSIGIVQPE | LTLEQEDLAE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GKHGKAAKRS | HKRKQKPEEE | AGAPVPEDAT | FSEYSEKETE | FTGSVGDETN | SAVQSIQQVV | VTLGDPNVTT | PSSSVGLTNI |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TVTPITTAAA | TQFTNLQPVA | VGHLTTPERQ | LQLDNSILTV | TFDTVSGSAM | LHNRQNDVQI | HPQPEASNPQ | SVAHFINLTT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | | |
| LVNSITPLGS | QLSDQHPLTW | RAVPQTDVLP | PSQPQAPPQQ | AAQPQVQAEQ | QQQQMYSY | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1553 | 1 | 1018.4978 | 58.27 | 3 | 49.1 | 10.5 | 2 | 481-504 | R.IESALEFHNCRTDDKTFQCEMCFR.F | Carbamidomethyl: 19, 22; Oxidation: 21 |

# Detailed Protein Report

## Protein 844: kinesin-like protein KIF1B isoform alpha [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|41393559 | **Score:** | 21.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 130.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
|  |  | **Sequence Coverage [%]:** | 2.4 |
|  |  | **No. of unique Peptides:** | 2 |

## Quantitation

***WUP:QUP*** **Median:** 0.10 **CV:** 0.00 % **No. of Peptides:** 1

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSGASVKVAV | RVRPFNSRET | SKESKCIIQM | QGNSTSIINP | KNPKEAPKSF | SFDYSYWSHT | SPEDPCFASQ | NRVYNDIGKE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MLLHAFEGYN | VCIFAYGQTG | AGKSYTMMGK | QEESQAGIIP | QLCEELFEKI | NDNCNEEMSY | SVEVSYMEIY | CERVRDLLNP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KNKGNLRVRE | HPLLGPYVED | LSKLAVTSYT | DIADLMDAGN | KARTVAATNM | NETSSRSHAV | FTIVFTQKKH | DNETNLSTEK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VSKISLVDLA | GSERADSTGA | KGTRLKEGAN | INKSLTTLGK | VISALAEVSK | KKKKTDFIPY | RDSVLTWLLR | ENLGGNSRTA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MVAALSPADI | NYDETLSTLR | YADRAKQIKC | NAVINEDPNA | KLVRELKEEV | TRLKDLLRAQ | GLGDIIDTSM | GSLTSSPSSC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SLSSQVGLTS | VTSIQERIMS | TPGGEEAIER | LKESEKIIAE | LNETWEEKLR | KTEAIRMERE | ALLAEMGVAI | REDGGTLGVF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SPKKTPHLVN | LNEDPLMSEC | LLYYIKDGIT | RVGQADAERR | QDIVLSGAHI | KEEHCIFRSE | RSNSGEVIVT | LEPCERSETY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VNGKRVSQPV | QLRSGNRIIM | GKNHVFRFNH | PEQARAEREK | TPSAETPSEP | VDWTFAQREL | LEKQGIDMKQ | EMEKRLQEME |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ILYKKEKEEA | DLLLEQQRLD | ADSDSGDDSD | KRSCEESWKL | ITSLREKLPP | SKLQTIVKKC | GLPSSGKKRE | PIKMYQIPQR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RRLSKDSKWV | TISDLKIQAV | KEICYEVALN | DFRHSRQEIE | ALAIVKMKEL | CAMYGKKDPN | ERDSWRAVAR | DVWDTVGVGD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EKIEDVMATG | KGSTDVDDLK | VHIDKLEDIL | QEVKKQNNMK | DEEIKVLRNK | MLKMEKVLPL | IGSQEQKSPG | SHKAKEPVGA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GVSSTSENNV | SKGDNGELAK | EERVSQLMNG | DPAFRRGRLR | WMRQEQIRFK | NLQQQEITKQ | LRRQNVPHRF | IPPENRKPRF |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PFKSNPKHRN | SWSPGTHIII | TEDEVIELRI | PKDDEARKGN | KEESQEKGGK | GAFKDPQFPW | GSQGMRSQDH | IQVSKQHINN |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QQQPPQLRWR | SNSLNNGQPK | STRCQASASA | ESLNSHSGHP | TADVQTFQAK | RHIHQHRQSY | CNYNTGGQLE | GNAATSYQKQ |
| 1130 | 1140 | 1150 | 1160 |  |  |  |  |
| TDKPSHCSQF | VTPPRMRRQF | SAPNLKAGRE | TTV |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2531 | 1 | 701.8609 | -26.11 | 2 | 61.6 | 11.2 | 1 | 710-720 | R.EPIKMYQIPQR.R |  |  |
| 1501 | 1 | 671.0963 | 120.59 | 3 | 48.4 | 10.5 | 1 | 737-753 | K.IQAVKEICYEVALNDFR.H |  | WUP:QUP 0.10 |

# Detailed Protein Report

## Protein 845: smad nuclear-interacting protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21314720 | **Score:** | 21.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| | | **Sequence Coverage [%]:** | 6.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKAVKSERER | GSRRRHRDGD | VVLPAGVVVK | QERLSPEVAP | PAHRRPDHSG | GSPSPPTSEP | ARSGHRGNRA | RGVSRSPPKK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KNKASGRRSK | SPRSKRNRSP | HHSTVKVKQE | REDHPRRGRE | DRQHREPSEQ | EHRRARNSDR | DRHRGHSHQR | RTSNERPGSG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QGQGRDRDTQ | NLQAQEEERE | FYNARRREHR | QRNDVGGGGS | ESQELVPRPG | GNNKEKEVPA | KEKPSFELSG | ALLEDTNTFR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GVVIKYSEPP | EARIPKKRWR | LYPFKNDEVL | PVMYIHRQSA | YLLGRHRRIA | DIPIDHPSCS | KQHAVFQYRL | VEYTRADGTV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GRRVKPYIID | LGSGNGTFLN | NKRIEPQRYY | ELKEKDVLKF | GFSSREYVLL | HESSDTSEID | RKDDEDEEEE | EEVSDS |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1941 | 1 | 695.2967 | -132.94 | 2 | 54.6 | 10.4 | 2 | 97-108 | R.NRSPHHSTVKVK.Q | |

# Detailed Protein Report

## Protein 846: oxysterol-binding protein-related protein 8 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|51243032 | **Score:** | 21.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 96.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578823270 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: oxysterol-binding protein-related protein 8 isoform X6 [Homo sapiens] |
| gi\|530399711 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: oxysterol-binding protein-related protein 8 isoform X3 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSQRQGKEAY | PTPTKDLHQP | SLSPASPHSQ | GFERGKEDIS | QNKDESSLSM | SKSKSESKLY | NGSEKDSSTS | SKLTKKESLK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VQKKNYREEK | KRATKELLST | ITDPSVIVMA | DWLKIRGTLK | SWTKLWCVLK | PGVLLIYKTQ | KNGQWVGTVL | LNACEIIERP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SKKDGFCFKL | FHPLEQSIWA | VKGPKGEAVG | SITQPLPSSY | LIIRATSESD | GRCWMDALEL | ALKCSSLLKR | TMIREGKEHD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LSVSSDSTHV | TFYGLLRANN | LHSGDNFQLN | DSEIERQHFK | DQDMYSDKSD | KENDQEHDES | DNEVMGKSEE | SDTDTSERQD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DSYIEPEPVE | PLKETTYTEQ | SHEELGEAGE | ASQTETVSEE | NKSLIWTLLK | QVRPGMDLSK | VVLPTFILEP | RSFLDKLSDY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YYHADFLSEA | ALEENPYFRL | KKVVKWYLSG | FYKKPKGLKK | PYNPILGETF | RCLWIHPRTN | SKTFYIAEQV | SHHPPISAFY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VSNRKDGFCL | SGSILAKSKF | YGNSLSAILE | GEARLTFLNR | GEDYVMTMPY | AHCKGILYGT | MTLELGGTVN | ITCQKTGYSA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ILEFKLKPFL | GSSDCVNQIS | GKLKLGKEVL | ATLEGHWDSE | VFITDKKTDN | SEVFWNPTPD | IKQWRLIRHT | VKFEEQGDFE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SEKLWQRVTR | AINAKDQTEA | TQEKYVLEEA | QRQAARDRKT | KNEEWSCKLF | ELDPLTGEWH | YKFADTRPWD | PLNDMIQFEK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DGVIQTKVKH | RTPMVSVPKM | KHKPTRQQKK | VAKGYSSPEP | DIQDSSGSEA | QSVKPSTRRK | KGIELGDIQS | SIESIKQTQE |
| 810 | 820 | 830 | 840 | 850 | | | |
| EIKRNIMALR | NHLVSSTPAT | DYFLQQKDYF | IIFLLILLQV | IINFMFK | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2118 | 1 | 938.2839 | -90.14 | 2 | 56.9 | 10.3 | 0 | 292-307 | K.ENDQEHDESDNEVMGK.S | |

# Detailed Protein Report

## Protein 847: pantetheinase precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|223633991 | **Score:** | 21.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| | | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTTQLPAYVA | ILLFYVSRAS | CQDTFTAAVY | EHAAILPNAT | LTPVSREEAL | ALMNRNLDIL | EGAITSAADQ | GAHIIVTPED |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AIYGWNFNRD | SLYPYLEDIP | DPEVNWIPCN | NRNRFGQTPV | QERLSCLAKN | NSIYVVANIG | DKKPCDTSDP | QCPPDGRYQY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NTDVVFDSQG | KLVARYHKQN | LFMGENQFNV | PKEPEIVTFN | TTFGSFGIFT | CFDILFHDPA | VTLVKDFHVD | TIVFPTAWMN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VLPHLSAVEF | HSAWAMGMRV | NFLASNIHYP | SKKMTGSGIY | APNSSRAFHY | DMKTEEGKLL | LSQLDSHPSH | SAVVNWTSYA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SSIEALSSGN | KEFKGTVFFD | EFTFVKLTGV | AGNYTVCQKD | LCCHLSYKMS | ENIPNEVYAL | GAFDGLHTVE | GRYYLQICTL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LKCKTTNLNT | CGDSAETAST | RFEMFSLSGT | FGTQYVFPEV | LLSENQLAPG | EFQVSTDGRL | FSLKPTSGPV | LTVTLFGRLY |
| 490 | 500 | 510 | 520 | | | | |
| EKDWASNASS | GLTAQARIIM | LIVIAPIVCS | LSW | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2233 | 1 | 1043.7218 | 141.72 | 2 | 57.8 | 21.6 | 0 | 1-18 | -.MTTQLPAYVAILLFYVSR.A | |

# Detailed Protein Report

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## Protein 848: zinc finger protein 611 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|239787086 | **Score:** | 21.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 73.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMKEVLSTGQ | GNTEVIHTGT | LQRHESHHIG | DFCFQEIEKE | IHDIEFQCQE | DERNGLEAPM | TKIKKLTGST | DQHDHRHAGN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KPIKDQLGSS | FYSHLPELHI | FQIKGEIGNQ | LEKSTNDAPS | VSTFQRISCR | PQTQISNNYG | NNPLNSSLLP | QKQEVHMREK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SFQCNKSGKA | FNCSSLLRKH | QIPHLGDKQY | KCDVCGKLFN | HEQYLACHDR | CHTVEKPYKC | KECGKTFSQE | SSLTCHRRLH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TGVKRYNCNE | CGKIFGQNSA | LLIDKAIDTG | ENPYKCNECD | KAFNQQSQLS | HHRIHTGEKP | YKCEECDKVF | SRKSTIETHK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RIHTGEKPYR | CKVCDTAFTW | HSQLARHRRI | HTAKKTYKCN | ECGKTFSHKS | SLVCHHRLHG | GEKSYKCKVC | DKAFVWSSQL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AKHTRIDCGE | KPYKCNECGK | TFGQNSDLLI | HKSIHTGEQP | YKCDECEKVF | SRKSSLETHK | IGHTGEKPYK | CKVCDKAFAC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HSYLAKHTRI | HSGEKPYKCN | ECSKTFSHRS | YLVCHHRVHS | GEKPYKCNEC | SKTFSRRSSL | HCHRRLHSGE | KPYKCNECGN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TFRHCSSLIY | HRRLHTGEKS | YKCTICDKAF | VRNSLLSRHT | RIHTAEKPYK | CNECGKAFNQ | QSHLSRHHRI | HTGEKP |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1496 | 1 | 480.6916 | -110.23 | 2 | 48.9 | 10.2 | 0 | 54-62 | R.NGLEAPMTK.I | |

# Detailed Protein Report

## Protein 849: spindle and kinetochore-associated protein 3 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|260763912 | **Score:** | 21.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 43.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| | | **Sequence Coverage [%]:** | 8.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDPIRSFCGK | LRSLASTLDC | ETARLQRALD | GEESDFEDYP | MRILYDLHSE | VQTLKDDVNI | LLDKARLENQ | EGIDFIKATK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VLMEKNSMDI | MKIREYFQKY | GYSPRVKKNS | VHEQEAINSD | PELSNCENFQ | KTDVKDDLSD | PPVASSCISE | KSPRSPQLSD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FGLERYIVSQ | VLPNPPQAVN | NYKEEPVIVT | PPTKQSLVKV | LKTPKCALKM | DDFECVTPKL | EHFGISEYTM | CLNEDYTMGL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KNARNNKSEE | AIDTESRLND | NVFATPSPII | QQLEKSDAEY | TNSPLVPTFC | TPGLKIPSTK | NSIALVSTNY | PLSKTNSSSN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| DLEVEDRTSL | VLNSDTCFEN | LTDPSSPTIS | SYENLLRTPT | PPEVTKIPED | ILQKFQWIYP | TQKLNKMR | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1798 | 1 | 716.2952 | -131.52 | 3 | 52.3 | 11.4 | 1 | 367-383 | K.IPEDILQKFQWIYPTQK.L | |

BRUKER

# Detailed Protein Report

## Protein 850: PREDICTED: ubiquitin carboxyl-terminal hydrolase 37 isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530370695 | **Score:** | 21.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 83.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKITLRKMIH | HRLLPLQSSS | FYGSRAGSKE | HSSGGTNLDR | TNVSSQTPSA | KRSLGFLPQP | VPLSVKKLRC | NQDYTGWNKP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RVPLSSHQQQ | QLQGFSNLGN | TCYMNAILQS | LFSLQSFAND | LLKQGIPWKK | IPLNALIRRF | AHLLVKKDIC | NSETKKDLLK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KVKNAISATA | ERFSGYMQND | AHEFLSQCLD | QLKEDMEKLN | KTWKTEPVSG | EENSPDISAT | RAYTCPVITN | LEFEVQHSII |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CKACGEIIPK | REQFNDLSID | LPRRKKPLPP | RSIQDSLDLF | FRAEELEYSC | EKCGGKCALV | RHKFNRLPRV | LILHLKRYSF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NVALSLNNKI | GQQVIIPRYL | TLSSHCTENT | KPPFTLGWSA | HMAISRPLKA | SQMVNSCITS | PSTPSKKFTF | KSKSSLALCL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DSDSEDELKR | SVALSQRLCE | MLGNEQQQED | LEKDSKLCPI | EPDKSELENS | GFDRMSEEEL | LAAVLEISKR | DASPSLSHED |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DDKPTSSPDT | GFAEDDIQEM | PENPDTMETE | KPKTITELDP | ASFTEITKDC | DENKENKTPE | GSQGEVDWLQ | QYDMEREREE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QELQQALAQS | LQEQEAWEQK | EDDDLKRATE | LSLQEFNNSF | VDALGSDEDS | GNEDVFDMEY | TEAEAEELKR | NAEVITLVMY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| MTLRSKRGLL | TMTWRYQKSK | RLPCRVIEIG | VATSSFICTR | RSLMSCWKQK | RTLSHLARKW | GRLPVRPCEE | QTPGLAACTA |
| 730 | 740 | | | | | | |
| YLLLLPTSPF | LC | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 241 | 1 | 862.8312 | -77.86 | 2 | 31.8 | 10.8 | 0 | 394-409 | K.SSLALCLDSDSEDELK.R | |

# Detailed Protein Report

## Protein 851: aprataxin and PNK-like factor [Homo sapiens]

**Accession:** gi|27734905
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl, Oxidation

**Score:** 21.6
**MW [kDa]:** 56.9
**pI:** 4.8
**Sequence Coverage [%]:** 4.9
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSGGFELQPR | DGGPRVALAP | GETVIGRGPL | LGITDKRVSR | RHAILEVAGG | QLRIKPIHTN | PCFYQSSEKS | QLLPLKPNLW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CYLNPGDSFS | LLVDKYIFRI | LSIPSEVEMQ | CTLRNSQVLD | EDNILNETPK | SPVINLPHET | TGASQLEGST | EIAKTQMTPT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NSVSFLGENR | DCNKQQPILA | ERKRILPTWM | LAEHLSDQNL | SVPAISGGNV | IQGSGKEEIC | KDKSQLNTTQ | QGRRQLISSG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SSENTSAEQD | TGEECKNTDQ | EESTISSKEM | PQSFSAITLS | NTEMNNIKTN | AQRNKLPIEE | LGKVSKHKIA | TKRTPHKEDE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AMSCSENCSS | AQGDSLQDES | QGSHSESSSN | PSNPETLHAK | ATDSVLQGSE | GNKVKRTSCM | YGANCYRKNP | VHFQHFSHPG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DSDYGGVQIV | GQDETDDRPE | CPYGPSCYRK | NPQHKIEYRH | NTLPVRNVLD | EDNDNVGQPN | EYDLNDSFLD | DEEEDYEPTD |
| 490 | 500 | 510 | 520 | | | | |
| EDSDWEPGKE | DEEKEDVEEL | LKEAKRFMKR | K | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1865 | 1 | 813.2646 | -108.33 | 2 | 53.7 | 10.6 | 2 | 376-388 | K.RTSCMYGANCYRK.N | Carbamidomethyl: 10;<br>Oxidation: 5 |

# Detailed Protein Report

## Protein 852: protein kinase C-binding protein NELL2 isoform c precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|223029474 | **Score:** | 21.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 91.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| METGLGAPLF | KAWLLISVWG | LGVDPSLQID | VLTELELGES | TTGVRQVPGL | HNGTKAFLFQ | DTPRSIKAST | ATAEQFFQKL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RNKHEFTILV | TLKQTHLNSG | VILSIHHLDH | RYLELESSGH | RNEVRLHYRS | GSHRPHTEVF | PYILADDKWH | KLSLAISASH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LILHIDCNKI | YERVVEKPST | DLPLGTTFWL | GQRNNAHGYF | KGIMQDVQLL | VMPQGFIAQC | PDLNRTCPTC | NDFHGLVQKI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MELQDILAKT | SAKLSRAEQR | MNRLDQCYCE | RTCTMKGTTY | REFESWIDGC | KNCTCLNGTI | QCETLICPNP | DCPLKSALAY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VDGKCCKECK | SICQFQGRTY | FEGERNTVYS | SSGVCVLYEC | KDQTMKLVES | SGCPALDCPE | SHQITLSHSC | CKVCKGYDFC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SERHNCMENS | ICRNLNDRAV | CSCRDGFRAL | REDNAYCEDI | DECAEGRHYC | RENTMCVNTP | GSFMCICKTG | YIRIDDYSCT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EHDECITNQH | NCDENALCFN | TVGGHNCVCK | PGYTGNGTTC | KAFCKDGCRN | GGACIAANVC | ACPQGFTGPS | CETDIDECSD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GFVQCDSRAN | CINLPGWYHC | ECRDGYHDNG | MFSPSGESCE | DIDECGTGRH | SCANDTICFN | LDGGYDCRCP | HGKNCTGDCI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HDGKVKHNGQ | IWVLENDRCS | VCSCQNGFVM | CRRMVCDCEN | PTVDLFCCPE | CDPRLSSQCL | HQNGETLYNS | GDTWVQNCQQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CRCLQGEVDC | WPLPCPDVEC | EFSILPENEC | CPRCVTDPCQ | ADTIRNDITK | TCLDEMNVVR | FTGSSWIKHG | TECTLCQCKN |
| 810 | 820 | | | | | | |
| GHICCSVDPQ | CLQEL | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1555 | 1 | 932.3749 | -6.08 | 2 | 49.1 | 11.3 | 1 | 659-673 | R.CSVCSCQNGFVMCRR.M | Carbamidomethyl: 1, 4, 6 |

# Detailed Protein Report

## Protein 853: transcription factor SOX-6 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|224967050 | **Score:** | 21.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 88.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.9 |
| | | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 2 |

## Quantitation

***WUP:QUP*** **Median:** 2.39 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSKQATSPF | ACAADGEDAM | TQDLTSREKE | EGSDQHVASH | LPLHPIMHNK | PHSEELPTLV | STIQQDADWD | SVLSSQQRME |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SENNKLCSLY | SFRNTSTSPH | KPDEGSRDRE | IMTSVTFGTP | ERRKGSLADV | VDTLKQKKLE | EMTRTEQEDS | SCMEKLLSKD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WKEKMERLNT | SELLGEIKGT | PESLAEKERQ | LSTMITQLIS | LREQLLAAHD | EQKKLAASQI | EKQRQQMDLA | RQQQEQIARQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QQQLLQQQHK | INLLQQQIQV | QGHMPPLMIP | IFPHDQRTLA | AAAAAQQGFL | FPPGITYKPG | DNYPVQFIPS | TMAAAAASGL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SPLQLQQLYA | AQLASMQVSP | GAKMPSTPQP | PNTAGTVSPT | GIKNEKRGTS | PVTQVKDEAA | AQPLNLSSRP | KTAEPVKSPT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SPTQNLFPAS | KTSPVNLPNK | SSIPSPIGGS | LGRGSSLGKW | KSQHQEETYE | LDILSSLNSP | ALFGDQDTVM | KAIQEARKMR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EQIQREQQQQ | QPHGVDGKLS | SINNMGLNSC | RNEKERTRFE | NLGPQLTGKS | NEDGKLGPGV | IDLTRPEDAE | GSKAMNGSAA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KLQQYYCWPT | GGATVAEARV | YRDARGRASS | EPHIKRPMNA | FMVWAKDERR | KILQAFPDMH | NSNISKILGS | RWKSMSNQEK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QPYYEEQARL | SKIHLEKYPN | YKYKPRPKRT | CIVDGKKLRI | GEYKQLMRSR | RQEMRQFFTV | GQQPQIPITT | GTGVVYPGAI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TMATTTPSPQ | MTSDCSSTSA | SPEPSLPVIQ | STYGMKTDGG | SLAGNEMING | EDEMEMYDDY | EDDPKSDYSS | ENEAPEAVSA |
| 810 | | | | | | | |
| N | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 908 | 5 | 500.6509 | -222.19 | 2 | 40.9 | 11.4 | 0 | 232-239 | R.QQQEQIAR.Q | | |
| 1327 | 1 | 660.9680 | -58.76 | 3 | 46.7 | 10.1 | 0 | 344-363 | K.MPSTPQPPNTAGTVSPTGIK.N | | WUP:QUP 2.39 |

# Detailed Protein Report

**Protein 854:** **scavenger receptor cysteine-rich type 1 protein M130 isoform b precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|344179112 | **Score:** | 21.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 121.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSKLRMVLLE DSGSADFRRH FVNLSPFTIT VVLLLSACFV TSSLGGTDKE LRLVDGENKC SGRVEVKVQE EWGTVCNNGW
        90        100        110        120        130        140        150        160
SMEAVSVICN QLGCPTAIKA PGWANSSAGS GRIWMDHVSC RGNESALWDC KHDGWGKHSN CTHQQDAGVT CSDGSNLEMR
       170        180        190        200        210        220        230        240
LTRGGNMCSG RIEIKFQGRW GTVCDDNFNI DHASVICRQL ECGSAVSFSG SSNFGEGSGP IWFDDLICNG NESALWNCKH
       250        260        270        280        290        300        310        320
QGWGKHNCDH AEDAGVICSK GADLSLRLVD GVTECSGRLE VRFQGEWGTI CDDGWDSYDA AVACKQLGCP TAVTAIGRVN
       330        340        350        360        370        380        390        400
ASKGFGHIWL DSVSCQGHEP AIWQCKHHEW GKHYCNHNED AGVTCSDGSD LELRLRGGGS RCAGTVEVEI QRLLGKVCDR
       410        420        430        440        450        460        470        480
GWGLKEADVV CRQLGCGSAL KTSYQVYSKI QATNTWLFLS SCNGNETSLW DCKNWQWGGL TCDHYEEAKI TCSAHREPRL
       490        500        510        520        530        540        550        560
VGGDIPCSGR VEVKHGDTWG SICDSDFSLE AASVLCRELQ CGTVVSILGG AHFGEGNGQI WAEEFQCEGH ESHLSLCPVA
       570        580        590        600        610        620        630        640
PRPEGTCSHS RDVGVVCSRY TEIRLVNGKT PCEGRVELKT LGAWGSLCNS HWDIEDAHVL CQQLKCGVAL STPGGARFGK
       650        660        670        680        690        700        710        720
GNGQIWRHMF HCTGTEQHMG DCPVTALGAS LCPSEQVASV ICSGNQSQTL SSCNSSSLGP TRPTIPEESA VACIESGQLR
       730        740        750        760        770        780        790        800
LVNGGGRCAG RVEIYHEGSW GTICDDSWDL SDAHVVCRQL GCGEAINATG SAHFGEGTGP IWLDEMKCNG KESRIWQCHS
       810        820        830        840        850        860        870        880
HGWGQQNCRH KEDAGVICSE FMSLRLTSEA SREACAGRLE VFYNGAWGTV GKSSMSETTV GVVCRQLGCA DKGKINPASL
       890        900        910        920        930        940        950        960
DKAMSIPMWV DNVQCPKGPD TLWQCPSSPW EKRLASPSEE TWITCDNKIR LQEGPTSCSG RVEIWHGGSW GTVCDDSWDL
       970        980        990       1000       1010       1020       1030       1040
DDAQVVCQQL GCGPALKAFK EAEFGQGTGP IWLNEVKCKG NESSLWDCPA RRWGHSECGH KEDAAVNCTD ISVQKTPQKA
      1050       1060       1070       1080       1090       1100       1110       1120
TTGRSSRQSS FIAVGILGVV LLAIFVALFF LTKKRRQRQR LAVSSRGENL VHQIQYREMN SCLNADDLDL MNSSGGHSEP
      1130
H
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 276 | 1 | 636.2276 | -119.43 | 3 | 32.2 | 10.9 | 1 | 913-928 | K.RLASPSEETWITCDNK.I | Carbamidomethyl: 13 |

# Detailed Protein Report

## Protein 855: neuronal migration protein doublecortin isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|30181240 | **Score:** | 21.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 12.5 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|30181244 | refseq_human (refseq_human_20140103.fasta) | neuronal migration protein doublecortin isoform c [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MELDFGHFDE RDKTSRNMRG SRMNGLPSPT HSAHCSFYRT RTLQALSNEK KAKKVRFYRN GDRYFKGIVY AVSSDRFRSF
        90        100        110        120        130        140        150        160
DALLADLTRS LSDNINLPQG VRYIYTIDGS RKIGSMDELE EGESYVCSSD NFFKKVEYTK NVNPNWSVNV KTSANMKAPQ
       170        180        190        200        210        220        230        240
SLASSNSAQA RENKDFVRPK LVTIIRSGVK PRKAVRVLLN KKTAHSFEQV LTDITEAIKL ETGVVKKLYT LDGKQVTCLH
       250        260        270        280        290        300        310        320
DFFGDDDVFI ACGPEKFRYA QDDFSLDENE CRVMKGNPSA TAGPKASPTP QKTSAKSPGP MRRSKSPADS ANGTSSSQLS
       330        340        350        360        370
TPKSKQSPIS TPTSPGSLRK HKDLYLPLSL DDSDSLGDSM
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1753 | 1 | 626.2639 | 0.61 | 4 | 50.3 | 10.3 | 0 | 113-134 | K.IGSMDELEEGESYVCSSDNFFK.K | Oxidation: 4 |
| 1003 | 1 | 797.6785 | -61.53 | 3 | 42.6 | 11.1 | 2 | 152-174 | K.TSANMKAPQSLASSNSAQARENK.D | |

## Protein 856: RING finger and CHY zinc finger domain-containing protein 1 isoform 6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|512749778 | **Score:** | 21.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 11.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAPAVKSEAP | CCDKLYTCRL | CHDNNEDHQL | DRFKVKEVQC | INCEKIQHAQ | QTCEECSTLF | GEYYCDICHL | FDKDKKQYHC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ENCGICRIGP | KEDFFHCLKC | NLCLAMNLQG | RHKCIENVSR | QNCPICLEDI | HTSRVVAHVL | PCGHLLHRTC | YEEMLKEGYR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CPLCMHSALD | MTRYWRQLDD | EVAQTPMPSE | YQNMTVDILC | NDCNGRSTVQ | FHILGMKCKI | CESYNTAQAG | GRRISLDQQ |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 930 | 1 | 848.9319 | 71.43 | 2 | 41.7 | 10.7 | 2 | 74-87 | K.DKKQYHCENCGICR.I | |

# Detailed Protein Report

## Protein 857: myosin-10 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|367460087 | **Score:** | 21.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 228.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAQRTGLEDP | ERYLFVDRAV | IYNPATQADW | TAKKLVWIPS | ERHGFEAASI | KEERGDEVMV | ELAENGKKAM | VNKDDIQKMN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PPKFSKVEDM | AELTCLNEAS | VLHNLKDRYY | SGLIYTYSGL | FCVVINPYKN | LPIYSENIIE | MYRGKKRHEM | PPHIYAISES |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AYRCMLQDRE | DQSILCTGES | GAGKTENTKK | VIQYLAHVAS | SHKGRKDHNI | PGELERQLLQ | ANPILESFGN | AKTVKNDNSS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RFGKFIRINF | DVTGYIVGAN | IETYLLEKSR | AVRQAKDERT | FHIFYQLLSG | AGEHLKSDLL | LEGFNNYRFL | SNGYIPIPGQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QDKDNFQETM | EAMHIMGFSH | EEILSMLKVV | SSVLQFGNIS | FKKERNTDQA | SMPENTVAQK | LCHLLGMNVM | EFTRAILTPR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IKVGRDYVQK | AQTKEQADFA | VEALAKATYE | RLFRWLVHRI | NKALDRTKRQ | GASFIGILDI | AGFEIFELNS | FEQLCINYTN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EKLQQLFNHT | MFILEQEEYQ | REGIEWNFID | FGLDLQPCID | LIERPANPPG | VLALLDEECW | FPKATDKTFV | EKLVQEQGSH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SKFQKPRQLK | DKADFCIIHY | AGKVDYKADE | WLMKNMDPLN | DNVATLLHQS | SDRFVAELWK | DVDRIVGLDQ | VTGMTETAFG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SAYKTKKGMF | RTVGQLYKES | LTKLMATLRN | TNPNFVRCII | PNHEKRAGKL | DPHLVLDQLR | CNGVLEGIRI | CRQGFPNRIV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| FQEFRQRYEI | LTPNAIPKGF | MDGKQACERM | IRALELDPNL | YRIGQSKIFF | RAGVLAHLEE | ERDLKITDII | IFFQAVCRGY |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LARKAFAKKQ | QQLSALKVLQ | RNCAAYLKLR | HWQWWRVFTK | VKPLLQVTRQ | EEELQAKDEE | LLKVKEKQTK | VEGELEEMER |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KHQQLLEEKN | ILAEQLQAET | ELFAEAEEMR | ARLAAKKQEL | EEILHDLESR | VEEEEERNQI | LQNEKKKMQA | HIQDLEEQLD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| EEEGARQKLQ | LEKVTAEAKI | KKMEEEILLL | EDQNSKFIKE | KKLMEDRIAE | CSSQLAEEEE | KAKNLAKIRN | KQEVMISDLE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ERLKKEEKTR | QELEKAKRKL | DGETTDLQDQ | IAELQAQIDE | LKLQLAKKEE | ELQGALARGD | DETLHKNNAL | KVVRELQAQI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| AELQEDFESE | KASRNKAEKQ | KRDLSEELEA | LKTELEDTLD | TTAAQQELRT | KREQEVAELK | KALEEETKNH | EAQIQDMRQR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| HATALEELSE | QLEQAKRFKA | NLEKNKQGLE | TDNKELACEV | KVLQQVKAES | EHKRKKLDAQ | VQELHAKVSE | GDRLRVELAE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KASKLQNELD | NVSTLLEEAE | KKGIKFAKDA | ASLESQLQDT | QELLQEETRQ | KLNLSSRIRQ | LEEEKNSLQE | QQEEEEEARK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| NLEKQVLALQ | SQLADTKKKV | DDDLGTIESL | EEAKKKLLKD | AEALSQRLEE | KALAYDKLEK | TKNRLQQELD | DLTVDLDHQR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| QVASNLEKKQ | KKFDQLLAEE | KSISARYAEE | RDRAEAEARE | KETKALSLAR | ALEEALEAKE | EFERQNKQLR | ADMEDLMSSK |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| DDVGKNVHEL | EKSKRALEQQ | VEEMRTQLEE | LEDELQATED | AKLRLEVNMQ | AMKAQFERDL | QTRDEQNEEK | KRLLIKQVRE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LEAELEDERK | QRALAVASKK | KMEIDLKDLE | AQIEAANKAR | DEVIKQLRKL | QAQMKDYQRE | LEEARASRDE | IFAQSKESEK |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| KLKSLEAEIL | QLQEELASSE | RARRHAEQER | DELADEITNS | ASGKSALLDE | KRRLEARIAQ | LEEELEEEQS | NMELLNDRFR |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| KTTLQVDTLN | AELAAERSAA | QKSDNARQQL | ERQNKELKAK | LQELEGAVKS | KFKATISALE | AKIGQLEEQL | EQEAKERAAA |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| NKLVRRTEKK | LKEIFMQVED | ERRHADQYKE | QMEKANARMK | QLKRQLEEAE | EEATRANASR | RKLQRELDDA | TEANEGLSRE |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | | |
| VSTLKNRLRR | GGPISFSSSR | SGRRQLHLEG | ASLELSDDDT | ESKTSDVNET | QPPQSE | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2562 | 1 | 648.3620 | 94.94 | 2 | 62.7 | 10.9 | 0 | 1853-1862 | K.EIFMQVEDER.R | |

BRUKER

# Detailed Protein Report

## Protein 858: T-complex protein 10A homolog [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|105553088 | **Score:** | 21.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 35.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEKTPAAAEV | PREDSNAGEM | PSLQQQITSL | HQELGRQQSL | WADIHRKLQS | HMDALRKQNR | ELREELRGLQ | RQQWEAGKKP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AASPHAGRES | HTLALEPAFG | KISHLSADED | TTPKYAGRKS | QSATLLGQRW | SSNHLAPPKP | MSLKTERINS | GKTPPQEDRE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KSPPGRRQDR | SPAPTGRPTP | GAERRGVSED | GKIMHPSSRS | PQNSGGRKSP | VQASQATTLQ | EQTAAARGAD | RSSSVLGSSE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GGFLSRVQAD | EFASSAPDSA | ERQNLPVNPP | SSLEIAQAMD | TKMKKEEVQE | EKRHPKGKAD | DCRRSGFPSE | FPGALHAAPS |
| 330 | | | | | | | |
| RQDMGP | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 88 | 1 | 877.8653 | -84.40 | 2 | 31.0 | 21.3 | 2 | 193-208 | K.IMHPSSRSPQNSGGRK.S | Oxidation: 2 |

# Detailed Protein Report

## Protein 859: PREDICTED: C2 domain-containing protein 3 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530396574 | **Score:** | 21.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 186.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKQRKGQGSG | GSRGRKKRGL | SDISPSTSLP | PLVEGQLRCF | LKLTVNRVIW | KIAKPPTCVL | VRVRWWGETS | DGTLFCPRDA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LQTEPKAVRT | TTRYAIRCGP | KQFTSYLTDM | AVLVLEVITK | LDGLPIGRVQ | INGLAQLSPT | HQINGFFTIV | SSTSKKLGEL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QVSLALEPLS | ETYDSYHPLP | TTDMTENVLL | SKQGFRENTE | PSSTQFQVPS | RPRDIHTIKI | DGKELAANSS | RSTTPRGKDH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VCFAENPDTI | KDSSFGLQHS | LNSGQSLESV | TLKGRAPRKQ | MSLLNSSEFQ | PQIRTVAKSH | SDSCILSSNN | LPTKDLLSAL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LEQGNKLRNA | MVISAMKSSP | ETSMLLDQVH | PPINEDSLRA | STQIRAFSRN | RFKDHIEDHL | LPSTENTFWR | HDTKADTRAI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QLLLGSAELS | QGNFWDGLGS | PPDSPSPGSD | VYCISELNDP | QYDQSLLENL | FYTAPKSDTS | ISDFLSEEDD | IVPSKKISQS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TALARSSKVL | ESSDHKLKKR | SAGKRNRNLV | EQQMLSETPE | DAQTMTLSVD | RLALLGRTHS | VRIIIETMGV | PPDSPQMTPG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KKSYAGPPPK | VTTAKKRTFF | VEYHFPVGFS | ESGLGKTALI | TEVVRLASSK | ITDGKVKFQQ | RFVFPVQFGG | PMIEHWWNSN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LTFQIYVKKT | PQKKPEVIGS | VSLSLRAVIQ | SELLSFSDQL | PVQQENGQSP | FGPLKVTMEL | ITDNKDFTGI | NTKLSGNTHY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TPLCAPTSPN | KALPELNQDM | TCTKNPQNLN | QIHEETAKKA | QNLVLPNRKS | PSPVAPHPST | FVATPASHNL | VNQTNGTTKE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SALLLHVLLM | VPDGKDFISG | ESEKQSPCNV | YLNCKLFSTE | EVTRSVIAWG | TTQPVFNFSQ | VIPVSLSSKY | LERLKNNVMV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| IETWNKVRSP | GQDKLLGLVK | LPLHQFYMSF | KDAKISRLLL | DAQYPVVAVD | SYMPVIDVFS | GHQNGSLRVF | LAMGSSNQIM |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ALQRLKNEEG | TLPPFSPRPA | HFLDQPTAAS | VAMAEDRGNG | LMEHCFEIHI | EMVKGLAPLQ | ATVWGEADCY | VQYYFPVQHS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QSSVLKGPEF | LENGITLKPF | RTATTLCVPD | PIFNSEHHHS | LLLPAEVPVQ | RLLLSAFSAQ | GLVPGGGVQF | EIWCRYYYPN |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| VRDQKVAKGT | LPLSRICAMV | TTQHREDVGI | QTFNLPLTPR | IENRKELRNQ | SSGLLDVGLR | YRRSPRTAEG | VLAARTVSIS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VQIIRACGLQ | AAAKALAERE | PALQFSATVG | VNASVTTHLS | FLPQGEQRRT | HPVACSFCPE | FSHHVEFTCN | LVTQHCSGEA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| CFLAELLEFA | EVIFAVYHEN | TKSASDIISI | ESCKEYLLGV | VKVPTKELLI | KRSGITGWYP | IILPEDGGLP | HGLELMQKIV |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| GGLELSISFT | HRGDRERVLE | AAEHLGWSFE | NSLKDFVRMD | EGEPATVTIS | TPRLWLPIHC | VLLAGHNHIH | KNTYCYLRYK |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| FYDHEAFWTP | LKKPKESVNK | KQIMVTFKAS | KRAEVTRGPS | LLWYFREERL | EIQVWRAYGN | DSVERPHQTD | SWIGSAYVDL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ARLGERSART | LTVSGVYPLF | GRNASNLSGA | ALRVHVVLSS | LSSHLEPTHE | LDSMDCSSHS | ESEQLPRRND | EVQLSPPEVI |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| SCHQKSPAST | QVPCSSTTAE | VRLTQEGPAD | LDGTFAVSIL | VERAMHLSLK | GYQKSCFWTH | NKPWSSKFGI | KEMRRG |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1725 | 1 | 917.8011 | 39.11 | 3 | 51.9 | 10.3 | 0 | 508-531 | R.NLVEQQMLSETPEDAQTMTLSVDR.L | Oxidation: 7 |

# Detailed Protein Report

## Protein 860: PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform X6 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|530427511 | **Score:** | 21.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 60.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.5 |
|  |  | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 1.49 **CV:** 0.00 % **No. of Peptides:** 1

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEESMKKAAE | VLNKHSLSGR | PLKVKEDPDG | EHARRAMQKA | GRLGSTVFVA | NLDYKVGWKK | LKEVFSMAGV | VVRADILEDK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DGKSRGIGTV | TFEQSIEAVQ | AISMFNGQLL | FDRPMHVKMD | ERALPKGDFF | PPERPQQLPH | GLGGIGMGLG | PGGQPIDANH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LNKGIGMGNI | GPAGMGMEGI | GFGINKMGGM | EGPFGGGMEN | MGRFGSGMNM | GRINEILSNA | LKRGEIIAKQ | GGGGGGGSVP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GIERMGPGID | RLGGAGMERM | GAGLGHGMDR | VGSEIERMGL | VMDRMGSVER | MGSGIERMGP | LGLDHMASSI | ERMGQTMERI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GSGVERMGAG | MGFGLERMAA | PIDRVGQTIE | RMGSGVERMG | PAIERMGLSM | ERMVPAGMGA | GLERMGPVMD | RMATGLERMG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ANNLERMGLE | RMGANSLERM | GLERMGANSL | ERMGPAMGPA | LGAGIERMGL | AMGGGGGASF | DRAIEMERGN | FGGSFAGSFG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GAGGHAPGVA | RKACQIFVRN | LPFDFTWKML | KDKFNECGHV | LYADIKMENG | KSKGCGVVKF | ESPEVAERAC | RMMNGMKLSG |
| 570 | 580 |  |  |  |  |  |  |
| REIDVRIDRN | A |  |  |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 814 | 1 | 737.3793 | 37.51 | 3 | 40.2 | 10.9 | 0 | 164-186 | K.<br>GIGMGNIGPAGMGMEGIGFGINK.<br>M | Oxidation: 4, 12 | WUP:QUP 1.49 |

# Detailed Protein Report

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**Protein 861:** **PREDICTED: probable global transcription activator SNF2L1 isoform X5 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578838748 | **Score:** | 21.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 121.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEQDTAAVAA | TVAAADATAT | IVVIEDEQPG | PSTSQEEGAA | AAATEATAAT | EKGEKKKEKN | VSSFQLKLAA | KAPKSEKEMD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PEYEEKMKAD | RAKRFEFLLK | QTELFAHFIQ | PSAQKSPTSP | LNMKLGRPRI | KKDEKQSLIS | AGDYRHRRTE | QEEDEELLSE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SRKTSNVCIR | FEVSPSYVKG | GPLRDYQIRG | LNWLISLYEN | GVNGILADEM | GLGKTLQTIA | LLGYLKHYRN | IPGPHMVLVP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KSTLHNWMNE | FKRWVPSLRV | ICFVGDKDAR | AAFIRDEMMP | GEWDVCVTSY | EMVIKEKSVF | KKFHWRYLVI | DEAHRIKNEK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SKLSEIVREF | KSTNRLLLTG | TPLQNNLHEL | WALLNFLLPD | VFNSADDFDS | WFDTKNCLGD | QKLVERLHAV | LKPFLLRRIK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TDVEKSLPPK | KEIKIYLGLS | KMQREWYTKI | LMKDIDVLNS | SGKMDKMRLL | NILMQLRKCC | NHPYLFDGAE | PGPPYTTDEH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IVSNSGKMVV | LDKLLAKLKE | QGSRVLIFSQ | MTRLLDILED | YCMWRGYEYC | RLDGQTPHEE | REEAIEAFNA | PNSSKFIFML |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| STRAGGLGIN | LASADVVILY | DSDWNPQVDL | QAMDRAHRIG | QKKPVRVFRL | ITDNTVEERI | VERAEIKLRL | DSIVIQQGRL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IDQQSNKLAK | EEMLQMIRHG | ATHVFASKES | ELTDEDITTI | LERGEKKTAE | MNERLQKMGE | SSLRNFRMDI | EQSLYKFEGE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DYREKQKLGM | VEWIEPPKRE | RKANYAVDAY | FREALRVSEP | KIPKAPRPPK | QPNVQDFQFF | PPRLFELLEK | EILYYRKTIG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| YKVPRNPDIP | NPALAQREEQ | KKIDGAEPLT | PEETEEKEKL | LTQGFTNWTK | RDFNQFIKAN | EKYGRDDIDN | IAREVEGKSP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EEVMEYSAVF | WERCNELQDI | EKIMAQIERG | EARIQRRISI | KKALDAKIAR | YKAPFHQLRI | QYGTSKGKNY | TEEEDRFLIC |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| MLHKMGFDRE | NVYEELRQCV | RNAPQFRFDW | FIKSRTAMEF | QRRCNTLISL | IEKENMEIEE | RERAEKKKRA | TKTPMVKFSA |
| 1050 | | | | | | | |
| FS | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 966 | 1 | 711.3525 | 2.57 | 2 | 40.4 | 21.3 | 1 | 434-446 | K.DIDVLNSSGKMDK.M | |

# Detailed Protein Report

## Protein 862: zinc finger protein 425 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|48717241 | **Score:** | 21.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 87.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.6 |
| | | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MAEPASVTVT FDDVALYFSE QEWEILEKWQ KQMYKQEMKT NYETLDSLGY AFSKPDLITW MEQGRMLLIS EQGCLDKTRR
        90        100        110        120        130        140        150        160
TTSPPTDEQL NMKNTGKLLC FDDEGTPRTK EEDCRLNGPQ KQDLCAALRG KERKILLAQT ATFQSPSLRE TEILNKKVSI
       170        180        190        200        210        220        230        240
TAYDPDKKDL RHKPRETPGR LEIPTGPRCY SCYVCRKVFQ VRRDLLKHKR SHSKSQLCRY PKYKNSSRGK SELRRTQRLL
       250        260        270        280        290        300        310        320
CQKKRFQCSE CEKSYFLKGS LVTHQVVHTG QRPYPCPECD KTFRYRANLK KHLCLHRGER PFCCGECGRA FVQQCELTEH
       330        340        350        360        370        380        390        400
LRLHSGEKPF QCPQCDRCFR LKRGMKVHLT QHSGKRPFHC PECGRSFSRK AALKTHQRTH SEEKPFSCGE CGRKFIYKIK
       410        420        430        440        450        460        470        480
LDEHIRVHTG EKPFSCPECN KSFRLKRSLK AHGLQHIGKR PFQCPECSRG FFWRNAMRAH QRLHSEQKPF PCAECGKRFT
       490        500        510        520        530        540        550        560
RPSKLACHTR VHDRQKEFPC GECKKTFSQQ SRLTQHLKVH TTEKPFSCAE CGRSFRRRAH LTEHTRLHSG EEPFQCPECD
       570        580        590        600        610        620        630        640
KSFSWKASMK FHQRMHRDEK PFACGECDKT YTHQSQLTEH LRLHSGEKPY QCPECEKTFR LKGNLKSHLL QHSGQKPFSC
       650        660        670        680        690        700        710        720
VMCGKSFTQQ YRLTEHIRVH SGEKPFQCPE CDKSYCIRGS LKVHLYKHSG ERPFQCPECG KGFLQKRSLK AHLCLHSGER
       730        740        750        760
PFSCDECGRS FTYVGALKTH IAVHAKEKPS SL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1689 | 1 | 1043.8593 | -137.44 | 2 | 49.4 | 10.7 | 0 | 627-645 | K.SHLLQHSGQKPFSCVMCGK.S | |

# Detailed Protein Report

## Protein 863: thrombospondin type-1 domain-containing protein 7B [Homo sapiens]

**Accession:** gi|122937257

**Database:** refseq_human(refseq_human_20140103.fasta)

**Database Date:** 2015-11-30

**Modification(s):** Carbamidomethyl

**Score:** 21.2

**MW [kDa]:** 175.5

**pI:** 9.1

**Sequence Coverage [%]:** 1.5

**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MHNTADEVVL | YHKLAGPWGR | CTGDCGPGGV | QSRAVWCFHV | DGWTSHLSNC | GESNRPPKER | SCFRVCDWHS | DLFQWEVSDW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HHCVLVPYAR | GEVKPRTAEC | VTAQHGLQHR | MVRCIQKLNR | TVVANEICEH | FALQPPTEQA | CLIPCPRDCV | VSEFLPWSNC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SKGCGKKLQH | RTRAVIAPPL | FGGLQCPNLT | ESRACDAPIS | CPLGEEEYTF | SLKVGPWSKC | RLPHLKEINP | SGRTVLDFNS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DSNERVTFKH | QSYKAHHHSK | SWAIEIGYQT | RQVSCTRSDG | QNAMLSLCLQ | DSFPLTVQSC | IMPKDCETSQ | WSSWSPCSKT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CRSGSLLPGF | RSRSRNVKHM | AIGGGKECPE | LLEKEACIVE | GELLQQCPRY | SWRTSEWKEC | QVSLLLEQQD | PHWHVTGPVC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GGGIQTREVY | CAQSVPAAAA | LRAKEVSRPV | EKALCVGPAP | LPSQLCNIPC | STDCIVSSWS | AWGLCIHENC | HDPQGKKGFR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TRQRHVLMES | TGPAGHCPHL | VESVPCEDPM | CYRWLASEGI | CFPDHGKCGL | GHRILKAVCQ | NDRGEDVSGS | LCPVPPPPER |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KSCEIPCRMD | CVLSEWTEWS | SCSQSCSNKN | SDGKQTRSRT | ILALAGEGGK | PCPPSQALQE | HRLCNDHSCM | QLHWETSPWG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PCSEDTLVTA | LNATIGWNGE | ATCGVGIQTR | RVFCVKSHVG | QVMTKRCPDS | TRPETVRPCF | LPCKKDCIVT | AFSEWTPCPR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| MCQAGNATVK | QSRYRIIIQE | AANGGQECPD | TLYEERECED | VSLCPVYRWK | PQKWSPCILV | PESVWQGITG | SSEACGKGLQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TRAVSCISDD | NRSAEMMECL | KQTNGMPLLV | QECTVPCRED | CTFTAWSKFT | PCSTNCEATK | SRRRQLTGKS | RKKEKCQDSD |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LYPLVETELC | PCDEFISQPY | GNWSDCILPE | GRREPHRGLR | VQADSKECGE | GLRFRAVACS | DKNGRPVDPS | FCSSSGYIQE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KCVIPCPFDC | KLSDWSSWGS | CSSSCGIGVR | IRSKWLKEKP | YNGGRPCPKL | DLKNQAQVHE | AVPCYSECNQ | YSWVVEHWSS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| CKINNELRSL | RCGGGTQSRK | IRCVNTADGE | GGAVDSNLCN | QDEIPPETQS | CSLMCPNECV | MSEWGLWSKC | PQSCDPHTMQ |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RRTRHLLRPS | LNSRTCAEDS | QVQPCLLNEN | CFQFQYNLTE | WSTCQLSENA | PCGQGVRTRL | LSCVCSDGKP | VSMDQCEQHN |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LEKPQRMSIP | CLVECVVNCQ | LSGWTAWTEC | SQTCGHGGRM | SRTRFIIMPT | QGEGRPCPTE | LTQEKTCPVT | PCYSWVLGNW |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SACKLEGGDC | GEGVQIRSLS | CMVHSGSISH | AAGRVEDALC | GEMPFQDSIL | KQLCSVPCPG | DCHLTEWSEW | STCELTCIDG |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| RSFETVGRQS | RSRTFIIQSF | ENQDSCPQQV | LETRPCTGGK | CYHYTWKASL | WNNNERTVWC | QRSDGVNVTG | GCSPQARPAA |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| IRQCIPACRK | PFSYCTQGGV | CGCEKGYTEI | MKSNGFLDYC | MKVPGSEDKK | ADVKNLSGKN | RPVNSKIHDI | FKGWSLQPLD |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | | |
| PDGRVKIWVY | GVSGGAFLIM | IFLIFTSYLV | CKKPKPHQST | PPQQKPLTLA | YDGDLDM | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 417 | 1 | 475.6019 | -263.42 | 2 | 33.8 | 10.3 | 1 | 1052-1060 | R.CGGGTQSRK.I | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 864: zinc finger homeobox protein 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|306922394 | **Score:** | 21.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 274.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530404766 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger homeobox protein 2 isoform X1 [Homo sapiens] |

# Detailed Protein Report

```
        10          20          30          40          50          60          70          80
MATLNSASTT  GTTPSPGHNA  PSLPSDTFSS  STPSDPVTKD  PPAASSTSEN  MRSSEPGGQL  LESGCGLVPP  KEIGEPQEGP
        90         100         110         120         130         140         150         160
DCGHFPPNDP  GVEKDKEQEE  EEEGLPPMDL  SNHLFFTAGG  EAYLVAKLSL  PGGSELLLPK  GFPWGEAGIK  EEPSLPFLAY
       170         180         190         200         210         220         230         240
PPPSHLTALH  IQHGFDPIQG  FSSSDQILSH  DTSAPSPAAC  EERHGAFWSY  QLAPNPPGDP  KDGPMGNSGG  NHVAVFWLCL
       250         260         270         280         290         300         310         320
LCRLGFSKPQ  AFMDHTQSHG  VKLTPAQYQG  LSGSPAVLQE  GDEGCKALIS  FLEPKLPARP  SSDIPLDNSS  TVNMEANVAQ
       330         340         350         360         370         380         390         400
TEDGPPEAEV  QALILLDEEV  MALSPPSPPT  ATWDPSPTQA  KESPVAAGEA  GPDWFPEGQE  EDGGLCPPLN  QSSPTSKEGG
       410         420         430         440         450         460         470         480
TLPAPVGSPE  DPSDPPQPYR  LADDYTPAPA  AFQGLSLSSH  MSLLHSRNSC  KTLKCPKCNW  HYKYQQTLDV  HMREKHPESN
       490         500         510         520         530         540         550         560
SHCSYCSAGG  AHPRLARGES  YNCGYKPYRC  DVCNYSTTTK  GNLSIHMQSD  KHLANLQGFQ  AGPGGQGSPP  EASLPPSAGD
       570         580         590         600         610         620         630         640
KEPKTKSSWQ  CKVCSYETNI  SRNLRIHMTS  EKHMQNVLML  HQGLPLGLPP  GLMGPGPPPP  PGATPTSPPE  LFQYFGPQAL
       650         660         670         680         690         700         710         720
GQPQTPLAGP  GLRPDKPLEA  QLLLNGFHHV  GAPARKFPTS  APGSLSPDAH  LPPSQLLGSS  SDSLPTSPPP  DDSLSLKVFR
       730         740         750         760         770         780         790         800
CLVCQAFSTD  SLELLLYHCS  IGRSLPEAEW  KEVAGDTHRC  KLCCYGTQLK  ANFQLHLKTD  KHAQKYQLAA  HLREGGGAMG
       810         820         830         840         850         860         870         880
TPSPASLGDG  APYGSVSPLH  LRCNICDFES  NSKEKMQLHA  RGAAHEENSQ  IYKFLLDMEG  AEAGAELGLY  HCLLCAWETP
       890         900         910         920         930         940         950         960
SRLAVLQHLR  TPAHRDAQAQ  RRLQLLQNGP  TTEEGLAALQ  SILSFSHGQL  RTPGKAPVTP  LAEPPTPEKD  AQNKTEQLAS
       970         980         990        1000        1010        1020        1030        1040
EETENKTGPS  RDSANQTTVY  CCPYCSFLSP  ESSQVRAHTL  SQHAVQPKYR  CPLCQEQLVG  RPALHFHLSH  LHNVVPECVE
      1050        1060        1070        1080        1090        1100        1110        1120
KLLLVATTVE  MTFTTKVLSA  PTLSPLDNGQ  EPPTHGPEPT  PSRDQAAEGP  NLTPEASPDP  LPEPPLASVE  VPDKPSGSPG
      1130        1140        1150        1160        1170        1180        1190        1200
QPPSPAPSPV  PEPDAQAEDV  APPPTMAEEE  EGTTGELRSA  EPAPADSRHP  LTYRKTTNFA  LDKFLDPARP  YKCTVCKESF
      1210        1220        1230        1240        1250        1260        1270        1280
TQKNILLVHY  NSVSHLHKMK  KAAIDPSAPA  RGEAGAPPTT  TAATDKPFKC  TVCRVSYNQS  STLEIHMRSV  LHQTRSRGTK
      1290        1300        1310        1320        1330        1340        1350        1360
TDSKIEGPER  SQEEPKEGET  EGEVGTEKKG  PDTSGFISGL  PFLSPPPPPL  DLHRFPAPLF  TPPVLPPFPL  VPESLLKLQQ
      1370        1380        1390        1400        1410        1420        1430        1440
QQLLLPFYLH  DLKVGPKLTL  AGPAPVLSLP  AATPPPPPQP  PKAELAEREW  ERPPMAKEGN  EAGPSSPPDP  LPNEAARTAA
      1450        1460        1470        1480        1490        1500        1510        1520
KALLENFGFE  LVIQYNEGKQ  AVPPPPTPPP  PEALGGGDKL  ACGACGKLFS  NMLILKTHEE  HVHRRFLPFE  ALSRYAAQFR
      1530        1540        1550        1560        1570        1580        1590        1600
KSYDSLYPPL  AEPPKPPDGS  LDSPVPHLGP  PFLVPEPEAG  GTRAPEERSR  AGGHWPIEEE  ESSRGNLPPL  VPAGRRFSRT
      1610        1620        1630        1640        1650        1660        1670        1680
KFTEFQTQAL  QSFFETSAYP  KDGEVERLAS  LLGLASRVVV  VWFQNARQKA  RKNACEGGSM  PTGGGTGGAS  GCRRCHATFS
      1690        1700        1710        1720        1730        1740        1750        1760
CVFELVRHLK  KCYDDQTLEE  EEEEAERGEE  EEEVEEEEVE  EEQGLEPPAG  PEGPLPEPPD  GEELSQAEAT  KAGGKEPEEK
      1770        1780        1790        1800        1810        1820        1830        1840
ATPSPSPAHT  CDQCAISFSS  QDLLTSHRRL  HFLPSLQPSA  PPQLLDLPLL  VFGERNPLVA  ATSPMPGPPL  KRKHEDGSLS
      1850        1860        1870        1880        1890        1900        1910        1920
PTGSEAGGGG  EGEPPRDKRL  RTTILPEQLE  ILYRWYMQDS  NPTRKMLDCI  SEEVGLKKRV  VQVWFQNTRA  RERKGQFRST
      1930        1940        1950        1960        1970        1980        1990        2000
PGGVPSPAVK  PPATATPASL  PKFNLLLGKV  DDGTGREAPK  REAPAFPYPT  ATLASGPQPF  LPPGKEATTP  TPEPPLPLLP
      2010        2020        2030        2040        2050        2060        2070        2080
PPPPSEEEGP  EEPPKASPES  EACSLSAGDL  SDSSASSLAE  PESPGAGGTS  GGPGGGTGVP  DGMGQRRYRT  QMSSLQLKIM
      2090        2100        2110        2120        2130        2140        2150        2160
KACYEAYRTP  TMQECEVLGE  EIGLPKRVIQ  VWFQNARAKE  KKAKLQGTAA  GSTGGSSEGL  LAAQRTDCPY  CDVKYDFYVS
      2170        2180        2190        2200        2210        2220        2230        2240
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2846 | 1 | 806.4262 | 33.67 | 2 | 66.0 | 11.1 | 1 | 573-585 | K.VCSYETNISRNLR.I | Carbamidomethyl: 2 |
| 2841 | 1 | 945.5312 | -4.18 | 2 | 64.2 | 10.1 | 2 | 1816-1833 | R.NPLVAATSPMPGPPLKRK.H | Oxidation: 10 |

# Detailed Protein Report

## Protein 865: protein FAM78B [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|63003928 | **Score:** | 21.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 29.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 11.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGCIQSITCK | ARIRRENIVV | YDVCATIDQC | PTRIEETSPI | VLRYKTPYFK | ASARVVMPPI | PRHETWVVGW | IQACNQMEFF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NTYSDLGMSS | WELPDLREGR | VKAISDSDGV | SYPWYGNTTE | TVTLVGPTNK | ISRFSVSMND | NFYPSVTWAV | PVSDSNVPLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TRIKRDQSFT | TWLVAMNTTT | KEKIILQTIK | WRMRVDIEVD | PLQLLGQRAR | LVGRTQQEQP | RILSRMEPIP | PNALVKPNAN |
| 250 | 260 | 270 | | | | | |
| DAQVLMWRPK | RGPPLVVIPP | K | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1179 | 1 | 941.4167 | -103.81 | 2 | 44.9 | 10.9 | 1 | 193-208 | R.MRVDIEVDPLQLLGQR.A | |

# Detailed Protein Report

## Protein 866: splicing factor 3B subunit 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|54112121 | **Score:** | 21.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 135.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFLYNLTLQR | ATGISFAIHG | NFSGTKQQEI | VVSRGKILEL | LRPDPNTGKV | HTLLTVEVFG | VIRSLMAFRL | TGGTKDYIVV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GSDSGRIVIL | EYQPSKNMFE | KIHQETFGKS | GCRRIVPGQF | LAVDPKGRAV | MISAIEKQKL | VYILNRDAAA | RLTISSPLEA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HKANTLVYHV | VGVDVGFENP | MFACLEMDYE | EADNDPTGEA | AANTQQTLTF | YELDLGLNHV | VRKYSEPLEE | HGNFLITVPG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GSDGPSGVLI | CSENYITYKN | FGDQPDIRCP | IPRRRNDLDD | PERGMIFVCS | ATHKTKSMFF | FLAQTEQGDI | FKITLETDED |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MVTEIRLKYF | DTVPVAAAMC | VLKTGFLFVA | SEFGNHYLYQ | IAHLGDDDEE | PEFSSAMPLE | EGDTFFFQPR | PLKNLVLVDE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LDSLSPILFC | QIADLANEDT | PQLYVACGRG | PRSSLRVLRH | GLEVSEMAVS | ELPGNPNAVW | TVRRHIEDEF | DAYIIVSFVN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ATLVLSIGET | VEEVTDSGFL | GTTPTLSCSL | LGDDALVQVY | PDGIRHIRAD | KRVNEWKTPG | KKTIVKCAVN | QRQVVIALTG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GELVYFEMDP | SGQLNEYTER | KEMSADVVCM | SLANVPPGEQ | RSRFLAVGLV | DNTVRIISLD | PSDCLQPLSM | QALPAQPESL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CIVEMGGTEK | QDELGERGSI | GFLYLNIGLQ | NGVLLRTVLD | PVTGDLSDTR | TRYLGSRPVK | LFRVRMQGQE | AVLAMSSRSW |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LSYSYQSRFH | LTPLSYETLE | FASGFASEQC | PEGIVAISTN | TLRILALEKL | GAVFNQVAFP | LQYTPRKFVI | HPESNNLIII |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ETDHNAYTEA | TKAQRKQQMA | EEMVEAAGED | ERELAAEMAA | AFLNENLPES | IFGAPKAGNG | QWASVIRVMN | PIQGNTLDLV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QLEQNEAAFS | VAVCRFSNTG | EDWYVLVGVA | KDLILNPRSV | AGGFVYTYKL | VNNGEKLEFL | HKTPVEEVPA | AIAPFQGRVL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| IGVGKLLRVY | DLGKKKLLRK | CENKHIANYI | SGIQTIGHRV | IVSDVQESFI | WVRYKRNENQ | LIIFADDTYP | RWVTTASLLD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| YDTVAGADKF | GNICVVRLPP | NTNDEVDEDP | TGNKALWDRG | LLNGASQKAE | VIMNYHVGET | VLSLQKTTLI | PGGSESLVYT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TLSGGIGILV | PFTSHEDHDF | FQHVEMHLRS | EHPPLCGRDH | LSFRSYYFPV | KNVIDGDLCE | QFNSMEPNKQ | KNVSEELDRT |
| 1210 | 1220 | | | | | | |
| PPEVSKKLED | IRTRYAF | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2564 | 1 | 822.4530 | 49.65 | 2 | 62.7 | 10.1 | 0 | 329-343 | K.YFDTVPVAAAMCVLK.T | Oxidation: 11 |
| 2787 | 1 | 619.0056 | 136.85 | 3 | 66.0 | 11.0 | 0 | 817-832 | K.QQMAEEMVEAAGEDER.E | Oxidation: 3, 7 |

# Detailed Protein Report

## Protein 867: X-linked retinitis pigmentosa GTPase regulator-interacting protein 1 [Homo sapiens]

**Accession:** gi|112734867
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 21.1
**MW [kDa]:** 146.6
**pI:** 5.4
**Sequence Coverage [%]:** 2.2
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSHLVDPTSG | DLPVRDIDAI | PLVLPASKGK | NMKTQPPLSR | MNREELEDSF | FRLREDHMLV | KELSWKQQDE | IKRLRTTLLR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LTAAGRDLRV | AEEAAPLSET | ARRGQKAGWR | QRLSMHQRPQ | MHRLQGHFHC | VGPASPRRAQ | PRVQVGHRQL | HTAGAPVPEK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PKRGPRDRLS | YTAPPSFKEH | ATNENRGEVA | SKPSELVSGS | NSIISFSSVI | SMAKPIGLCM | PNSAHIMASN | TMQVEEPPKS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PEKMWPKDEN | FEQRSSLECA | QKAAELRASI | KEKVELIRLK | KLLHERNASL | VMTKAQLTEV | QEAYETLLQK | NQGILSAAHE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ALLKQVNELR | AELKEESKKA | VSLKSQLEDV | SILQMTLKEF | QERVEDLEKE | RKLLNDNYDK | LLESMLDSSD | SSSQPHWSNE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LIAEQLQQQV | SQLQDQLDAE | LEDKRKVLLE | LSREKAQNED | LKLEVTNILQ | KHKQEVELLQ | NAATISQPPD | RQSEPATHPA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VLQENTQIEP | SEPKNQEEKK | LSQVLNELQV | SHAETTLELE | KTRDMLILQR | KINVCYQEEL | EAMMTKADND | NRDHKEKLER |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LTRLLDLKNN | RIKQLEGILR | SHDLPTSEQL | KDVAYGTRPL | SLCLETLPAH | GDEDKVDISL | LHQGENLFEL | HIHQAFLTSA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ALAQAGDTQP | TTFCTYSFYD | FETHCTPLSV | GPQPLYDFTS | QYVMETDSLF | LHYLQEASAR | LDIHQAMASE | HSTLAAGWIC |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| FDRVLETVEK | VHGLATLIGA | GGEEFGVLEY | WMRLRFPIKP | SLQACNKRKK | AQVYLSTDVL | GGRKAQEEEF | RSESWEPQNE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LWIEITKCCG | LRSRWLGTQP | SPYAVYRFFT | FSDHDTAIIP | ASNNPYFRDQ | ARFPVLVTSD | LDHYLRREAL | SIHVFDDEDL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EPGSYLGRAR | VPLLPLAKNE | SIKGDFNLTD | PAEKPNGSIQ | VQLDWKFPYI | PPESFLKPEA | QTKGKDTKDS | SKISSEEEKA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SFPSQDQMAS | PEVPIEAGQY | RSKRKPPHGG | ERKEKEHQVV | SYSRRKHGKR | IGVQGKNRME | YLSLNILNGN | TPEQVNYTEW |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KFSETNSFIG | DGFKNQHEEE | EMTLSHSALK | QKEPLHPVND | KESSEQGSEV | SEAQTTDSDD | VIVPPMSQKY | PKADSEKMCI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EIVSLAFYPE | AEVMSDENIK | QVYVEYKFYD | LPLSETETPV | SLRKPRAGEE | IHFHFSKVID | LDPQEQQGRR | RFLFDMLNGQ |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DPDQGHLKFT | VVSDPLDEEK | KECEEVGYAY | LQLWQILESG | RDILEQELDI | VSPEDLATPI | GRLKVSLQAA | AVLHAIYKEM |
| 1290 | | | | | | | |
| TEDLFS | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1534 | 1 | 676.3317 | -93.91 | 2 | 49.4 | 10.1 | 0 | 16-28 | R.DIDAIPLVLPASK.G | |

# Detailed Protein Report

## Protein 868: late cornified envelope protein 3E [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|30410033 | **Score:** | 21.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 9.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 30.4 |
| | | **No. of unique Peptides:** | 2 |

```
         10         20         30         40         50         60         70         80
MSCQQNQKQC QPPPKCPSPK CPPKNPVQCL PPASSGCAPS SGGCGPSSEG GCFLNHHRRH HRCRRQRSNS CDRGSGQQGG
         90        100
GSGCCHGSGG CC
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1406 | 1 | 956.6395 | 178.07 | 1 | 47.2 | 10.6 | 1 | 16-24 | K.CPSPKCPPK.N | |
| 2462 | 1 | 885.2390 | -64.11 | 2 | 60.7 | 10.5 | 0 | 74-92 | R.GSGQQGGGSGCCHGSGGCC.- | Carbamidomethyl: 12, 18, 19 |

# Detailed Protein Report

**Protein 869:** **PREDICTED: probable cysteine--tRNA ligase, mitochondrial isoform X6 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578825266 | **Score:** | 21.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 50.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 7.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MVMGITDVDD | KIIKRANEMN | ISPASLASLY | EEDFKQDMAA | LKVLPPTVYL | RVTENIPQII | SFIEGIIARG | NAYSTAKGNV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YFDLKSRGDK | YGKLVGVVPG | PVGEPADSDK | RHASDFALWK | AAKPQEVFWA | SPWGPGRPGW | HIECSAIASM | VFGSQLDIHS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GGIDLAFPHH | ENEIAQCEVF | HQCEQWGNYF | LHSGHLHAKG | KEEKMSKSLK | NYITIKDFLK | TFSPDVFRFF | CLRSSYRSAI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DYSDSAMLQA | QQLLLGLGSF | LEDARAYMKG | QLACGSVREA | MLWERLSSTK | RAVKAALADD | FDTPRVVDAI | LGLAHHGNGQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LRASLKEPEG | PRSPAVFGAI | ISYFEQFFET | VGISLANQQY | VSGDGSEATL | HGVVDELVRF | RQKVRQFALA | MPEATGDARR |
| 410 | 420 | 430 | 440 | 450 | 460 | | |
| QQLLERQPLL | EACDTLRRGL | TAHGINIKDR | SSTTSTWELL | DQRTKDQKSA | G | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1538 | 1 | 720.8576 | -0.52 | 2 | 49.4 | 10.2 | 1 | 266-278 | R.AYMKGQLACGSVR.E | Carbamidomethyl: 9 |

# Detailed Protein Report

## Protein 870: calmodulin-binding transcription activator 1 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|54112401 | **Score:** | 21.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 183.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWRAEGKWLP | KTSRKSVSQS | VFCGTSTYCV | LNTVPPIEDD | HGNSNSSHVK | IFLPKKLLEC | LPKCSSLPKE | RHRWNTNEEI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AAYLITFEKH | EEWLTTSPKT | RPQNGSMILY | NRKKVKYRKD | GYCWKKRKDG | KTTREDHMKL | KVQGVECLYG | CYVHSSIIPT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FHRRCYWLLQ | NPDIVLVHYL | NVPAIEDCGK | PCGPILCSIN | TDKKEWAKWT | KEELIGQLKP | MFHGIKWTCS | NGNSSSGFSV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EQLVQQILDS | HQTKPQPRTH | NCLCTGSLGA | GGSVHHKCNS | AKHRIISPKV | EPRTGGYGSH | SEVQHNDVSE | GKHEHSHSKG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SSREKRNGKV | AKPVLLHQSS | TEVSSTNQVE | VPDTTQSSPV | SISSGLNSDP | DMVDSPVVTG | VSGMAVASVM | GSLSQSATVF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MSEVTNEAVY | TMSPTAGPNH | HLLSPDASQG | LVLAVSSDGH | KFAFPTTGSS | ESLSMLPTNV | SEELVLSTTL | DGGRKIPETT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| MNFDPDCFLN | NPKQGQTYGG | GGLKAEMVSS | NIRHSPPGER | SFSFTTVLTK | EIKTEDTSFE | QQMAKEAYSS | SAAAVAASSL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TLTAGSSLLP | SGGGLSPSTT | LEQMDFSAID | SNKDYTSSFS | QTGHSPHIHQ | TPSPSFFLQD | ASKPLPVEQN | THSSLSDSGG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TFVMPTVKTE | ASSQTSSCSG | HVETRIESTS | SLHLMQFQAN | FQAMTAEGEV | TMETSQAAEG | SEVLLKSGEL | QACSSEHYLQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PETNGVIRSA | GGVPILPGNV | VQGLYPVAQP | SLGNASNMEL | SLDHFDISFS | NQFSDLINDF | ISVEGGSSTI | YGHQLVSGDS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TALSQSEDGA | RAPFTQAEMC | LPCCSPQQGS | LQLSSSEGGA | STMAYMHVAE | VVSAASAQGT | LGMLQQSGRV | FMVTDYSPEW |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SYPEGGVKVL | ITGPWQEASN | NYSCLFDQIS | VPASLIQPGV | LRCYCPAHDT | GLVTLQVAFN | NQIISNSVVF | EYKARALPTL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PSSQHDWLSL | DDNQFRMSIL | ERLEQMERRM | AEMTGSQQHK | QASGGGSSGG | GSGSGNGGSQ | AQCASGTGAL | GSCFESRVVV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VCEKMMSRAC | WAKSKHLIHS | KTFRGMTLLH | LAAAQGYATL | IQTLIKWRTK | HADSIDLELE | VDPLNVDHFS | CTPLMWACAL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GHLEAAVVLY | KWDRRAISIP | DSLGRLPLGI | ARSRGHVKLA | ECLEHLQRDE | QAQLGQNPRI | HCPASEEPST | ESWMAQWHSE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| AISSPEIPKG | VTVIASTNPE | LRRPRSEPSN | YYSSESHKDY | PAPKKHKLNP | EYFQTRQEKL | LPTALSLEEP | NIRKQSPSSK |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| QSVPETLSPS | EGVRDFSREL | SPPTPETAAF | QASGSQPVGK | WNSKDLYIGV | STVQVTGNPK | GTSVGKEAAP | SQVRPREPMS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VLMMANREVV | NTELGSYRDS | AENEECGQPM | DDIQVNMMTL | AEHIIEATPD | RIKQENFVPM | ESSGLERTDP | ATISSTMSWL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ASYLADADCL | PSAAQIRSAY | NEPLTPSSNT | SLSPVGSPVS | EIAFEKPNLP | SAADWSEFLS | ASTSEKVENE | FAQLTLSDHE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| QRELYEAARL | VQTAFRKYKG | RPLREQQEVA | AAVIQRCYRK | YKQYALYKKM | TQAAILIQSK | FRSYYEQKKF | QQSRRAAVLI |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QKYYRSYKKC | GKRRQARRTA | VIVQQKLRSS | LLTKKQDQAA | RKIMRFLRRC | RHSPLVDHRL | YKRSERIEKG | QGT |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2758 | 1 | 1086.0280 | -55.01 | 2 | 65.6 | 10.5 | 1 | 209-226 | K.WTKEELIGQLKPMFHGIK.W | Oxidation: 13 |

# Detailed Protein Report

**Protein 871:** **PREDICTED: low-density lipoprotein receptor-related protein 2 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578804335 | **Score:** | 21.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 437.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.8 |
| | | **Sequence Coverage [%]:** | 0.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***WUP:QUP*** | **Median:** | 0.28 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MIFKQKIDGT | GREILAANRV | ENVESLAFDW | ISKNLYWTDS | HYKSISVMRL | ADKTRRTVVQ | YLNNPRSVVV | HPFAGYLFFT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DWFRPAKIMR | AWSDGSHLLP | VINTTLGWPN | GLAIDWAASR | LYWVDAYFDK | IEHSTFDGLD | RRRLGHIEQM | THPFGLAIFG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EHLFFTDWRL | GAIIRVRKAD | GGEMTVIRSG | IAYILHLKSY | DVNIQTGSNA | CNQPTHPNGD | CSHFCFPVPN | FQRVCGCPYG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MRLASNHLTC | EGDPTNEPPT | EQCGLFSFPC | KNGRCVPNYY | LCDGVDDCHD | NSDEQLCGTL | NNTCSSSAFT | CGHGECIPAH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WRCDKRNDCV | DGSDEHNCPT | HAPASCLDTQ | YTCDNHQCIS | KNWVCDTDND | CGDGSDEKNC | NSTETCQPSQ | FNCPNHRCID |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LSFVCDGDKD | CVDGSDEVGC | VLNCTASQFK | CASGDKCIGV | TNRCDGVFDC | SDNSDEAGCP | TRPPGMCHSD | EFQCQEDGIC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IPNFWECDGH | PDCLYGSDEH | NACVPKTCPS | SYFHCDNGNC | IHRAWLCDRD | NDCGDMSDEK | DCPTQPFRCP | SWQWQCLGHN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ICVNLSVVCD | GIFDCPNGTD | ESPLCNEPQP | DGNSCSDFNG | GCTHECVQEP | FGAKCLCPLG | FLLANDSKTC | EDIDECDILG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SCSQHCYNMR | GSFRCSCDTG | YMLESDGRTC | KVTASESLLL | LVASQNKIIA | DSVTSQVHNI | YSLVENGSYI | VAVDFDSISG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RIFWSDATQG | KTWSAFQNGT | DRRVVFDSSI | ILTETIAIDW | VGRNLYWTDY | ALETIEVSKI | DGSHRTVLIS | KNLTNPRGLA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LDPRMNEHLL | FWSDWGHHPR | IERASMDGSM | RTVIVQDKIF | WPCGLTIDYP | NRLLYFMDSY | LDYMDFCDYN | GHHRRQVIAS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DLIIRHPYAL | TLFEDSVYWT | DRATRRVMRA | NKWHGGNQSV | VMYNIQWPLG | IVAVHPSKQP | NSVNPCAFSR | CSHLCLLSSQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GPHFYSCVCP | SGWSLSPDLL | NCLRDDQPFL | ITVRQHIIFG | ISLNPEVKSN | DAMVPIAGIQ | NGLDVEFDDA | EQYIYWVENP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GEIHRVKTDG | TNRTVFASIS | MVGPSMNLAL | DWISRNLYST | NPRTQSIEVL | TLHGDIRYRK | TLIANDGTAL | GVGFPIGITV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DPARGKLYWS | DQGTDSGVPA | KIASANMDGT | SVKTLFTGNL | EHLECVTLDI | EEQKLYWAVT | GRGVIERGNV | DGTDRMILVH |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| QLSHPWGIAV | HDSFLYYTDE | QYEVIERVDK | ATGANKIVLR | DNVPNLRGLQ | VYHRRNAAES | SNGCSNNMNA | CQQICLPVPG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| GLFSCACATG | FKLNPDNRSC | SPYNSFIVVS | MLSAIRGFSL | ELSDHSETMV | PVAGQGRNAL | HVDVDVSSGF | IYWCDFSSSV |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ASDNAIRRIK | PDGSSLMNIV | THGIGENGVR | GIAVDWVAGN | LYFTNAFVSE | TLIEVLRINT | TYRRVLLKVT | VDMPRHIVVD |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| PKNRYLFWAD | YGQRPKIERS | FLDCTNRTVL | VSEGIVTPRG | LAVDRSDGYV | YWVDDSLDII | ARIRINGENS | EVIRYGSRYP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| TPYGITVFEN | SIIWVDRNLK | KIFQASKEPE | NTEPPTVIRD | NINWLRDVTI | FDKQVQPRSP | AEVNNNPCLE | NNGGCSHLCF |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| ALPGLHTPKC | DCAFGTLQSD | GKNCAISTEN | FLIFALSNSL | RSLHLDPENH | SPPFQTINVE | RTVMSLDYDS | VSDRIYFTQN |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LASGVGQISY | ATLSSGIHTP | TVIASGIGTA | DGIAFDWITR | RIYYSDYLNQ | MINSMAEDGS | NRTVIARVPK | PRAIVLDPCQ |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| GYLYWADWDT | HAKIERATLG | GNFRVPIVNS | SLVMPSGLTL | DYEEDLLYWV | DASLQRIERS | TLTGVDREVI | VNAAVHAFGL |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| TLYGGQYIYWT | DLYTQRIYRA | NKYDGSGQIA | MTTNLLSQPR | GINTVVKNQK | QQCNNPCEQF | NGGCSHICAP | GPNGAECQCP |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| HEGNWYLANN | RKHCIVDNGE | RCGASSFTCS | NGRCISEEWK | CDNDNDCGDG | SDEMESVCAL | HTCSPTAFTC | ANGRCVQYSY |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| RCDYYNDCGD | GSDEAGCLFR | DCNATTEFMC | NNRRCIPREF | ICNGVDNCHD | NNTSDEKNCP | DRTCQSGYTK | CHNSNICIPR |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| VYLCDGDNDC | GDNSDENPTY | CTTHTCSSSE | FQCASGRCIP | QHWYCDQETD | CFDASDEPAS | CGHSERTCLA | DEFKCDGGRC |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| IPSEWICDGD | NDCGDMSDED | KRHQCQNQNC | SDSEFLCVND | RPPDRRCIPQ | SWVCDGDVDC | TDGYDENQNC | TRRTCSENEF |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| TCGYGLCIPK | IFRCDRHNDC | GDYSDERGCL | YQTCQQNQFT | CQNGRCISKT | FVCDEDNDCG | DGSDELMHLC | HTPEPTCPPH |
| 2330 | 2340 | 2350 | 2360 | 2370 | 2380 | 2390 | 2400 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1208 | 1 | 441.6040 | -232.73 | 2 | 44.7 | 10.7 | 1 | 3501-3507 | K.YDGTDRR.V |  | WUP:QUP 0.28 |

# Detailed Protein Report

**Protein 872:** **PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform X3 [Homo sapiens]**

| | | | | |
|---|---|---|---|---|
| **Accession:** | gi\|578822281 | | **Score:** | 21.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | | **MW [kDa]:** | 83.2 |
| **Database Date:** | 2015-11-30 | | **pI:** | 5.4 |
| | | | **Sequence Coverage [%]:** | 2.9 |
| | | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNPCPCFFRL | GKGRRGSIRF | LSPPVFLSSD | LQLLQWGSEG | SLNHRDRNAA | PQLRLNQRGG | LRPYCLGAGR | GLGAGREAVT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SSRRRKNMAG | ASELGTGPGA | AGGDGDDSLY | PIAVLIDELR | NEDVQLRLNS | IKKLSTIALA | LGVERTRSEL | LPFLTDTIYD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EDEVLLALAE | QLGNFTGLVG | GPDFAHCLLP | PLENLATVEE | TVVRDKAVES | LRQISQEHTP | VALEAYFVPL | VKRLASGDWF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TSRTSACGLF | SVCYPRASNA | VKAEIRQQFR | SLCSDDTPMV | RRAAASKLGE | FAKVLELDSV | KSEIVPLFTS | LASDEQDSVR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LLAVEACVSI | AQLLSQDDLE | TLVMPTLRQA | AEDKSWRVRY | MVADRFSELQ | KAMGPKITLN | DLIPAFQNLL | KDCEAEVRAA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AAHKVKELGE | NLPIEDRETI | IMNQILPYIK | ELVSDTNQHV | KSALASVIMG | LSTILGKENT | IEHLLPLFLA | QLKDECPDVR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LNIISNLDCV | NEVIGIRQLS | QSLLPAIVEL | AEDAKWRVRL | AIIEYMPLLA | GQLGVEFFDE | KLNSLCMAWL | VDHVYAIREA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ATNNLMKLVQ | KFGTEWAQNT | IVPKVLVMAN | DPNYLHRMTT | LFCINALSEA | CGQEITTKQM | LPIVLKMAGD | QVANVRFNVA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KSLQKIGPIL | DTNALQGEVK | PVLQKLGQDE | DMDVKYFAQE | AISVVAQRLR | KLEFPVKDSG | EPSVPRADKN | HFPRPTVPGE |
| 730 | 740 | 750 | 760 | | | | |
| DMGKGPVYQL | RGDTRDTLAQ | LGIAELVHFS | QSTD | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 49 | 1 | 776.2880 | -178.77 | 2 | 30.5 | 10.1 | 2 | 46-58 | R.DRNAAPQLRLNQR.G | |

## Protein 873: WAP four-disulfide core domain protein 8 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|153946387 | **Score:** | 21.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 10.0 |
| | | **No. of unique Peptides:** | 2 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530418513 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: WAP four-disulfide core domain protein 8 isoform X1 [Homo sapiens] |
| gi\|153946389 | refseq_human (refseq_human_20140103.fasta) | WAP four-disulfide core domain protein 8 precursor [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MWTVRTEGGH FPLHSPTFSW RNVAFLLLLS LALEWTSAML TKKIKHKPGL CPKERLTCTT ELPDSCNTDF DCKEYQKCCF
        90        100        110        120        130        140        150        160
FACQKKCMDP FQEPCMLPVR HGNCNHEAQR WHFDFKNYRC TPFKYRGCEG NANNFLNEDA CRTACMLIVK DGQCPLFPFT
       170        180        190        200        210        220        230        240
ERKECPPSCH SDIDCPQTDK CCESRCGFVC ARAWTVKKGF CPRKPLLCTK IDKPKCLQDE ECPLVEKCCS HCGLKCMDPR
       250
R
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 391 | 1 | 862.7047 | -22.11 | 3 | 34.9 | 10.4 | 1 | 127-150 | R.GCEGNANNFLNEDACRTACMLIVK.D | |
| 288 | 1 | 881.8216 | 102.87 | 3 | 33.3 | 10.6 | 1 | 127-150 | R.GCEGNANNFLNEDACRTACMLIVK.D | Carbamidomethyl: 15 |

# Detailed Protein Report

## Protein 874: paraneoplastic antigen Ma2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|11464969 | **Score:** | 20.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MALALLEDWC | RIMSVDEQKS | LMVTGIPADF | EEAEIQEVLQ | ETLKSLGRYR | LLGKIFRKQE | NANAVLLELL | EDTDVSAIPS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EVQGKGGVWK | VIFKTPNQDT | EFLERLNLFL | EKEGQTVSGM | FRALGQEGVS | PATVPCISPE | LLAHLLGQAM | AHAPQPLLPM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RYRKLRVFSG | SAVPAPEEES | FEVWLEQATE | IVKEWPVTEA | EKKRWLAESL | RGPALDLMHI | VQADNPSISV | EECLEAFKQV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FGSLESRRTA | QVRYLKTYQE | EGEKVSAYVL | RLETLLRRAV | EKRAIPRRIA | DQVRLEQVMA | GATLNQMLWC | RLRELKDQGP |
| 330 | 340 | 350 | 360 | 370 | | | |
| PPSFLELMKV | IREEEEEEAS | FENESIEEPE | ERDGYGRWNH | EGDD | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1364 | 1 | 660.7454 | 137.08 | 3 | 47.2 | 20.9 | 0 | 295-311 | R.LEQVMAGATLNQMLWCR.L | Oxidation: 13 |

# Detailed Protein Report

## Protein 875: ubiquitin carboxyl-terminal hydrolase 34 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|110347427 | **Score:** | 20.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 404.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MCENCADLVE VLNEISDVEG GDGLQLRKEH TLKIFTYINS WTQRQCLCCF KEYKHLEIFN QVVCALINLV IAQVQVLRDQ

        90        100        110        120        130        140        150        160
LCKHCTTINI DSTWQDESNQ AEEPLNIDRE CNEGSTERQK SIEKKSNSTR ICNLTEEESS KSSDPFSLWS TDEKEKLLLC

       170        180        190        200        210        220        230        240
VAKIFQIQFP LYTAYKHNTH PTIEDISTQE SNILGAFCDM NDVEVPLHLL RYVCLFCGKN GLSLMKDCFE YGTPETLPFL

       250        260        270        280        290        300        310        320
IAHAFITVVS NIRIWLHIPA VMQHIIPFRT YVIRYLCKLS DQELRQSAAR NMADLMWSTV KEPLDTTLCF DKESLDLAFK

       330        340        350        360        370        380        390        400
YFMSPTLTMR LAGLSQITNQ LHTFNDVCNN ESLVSDTETS IAKELADWLI SNNVVEHIFG PNLHIEIIKQ CQVILNFLAA

       410        420        430        440        450        460        470        480
EGRLSTQHID CIWAAAQLKH CSRYIHDLFP SLIKNLDPVP LRHLLNLVSA LEPSVHTEQT LYLASMLIKA LWNNALAAKA

       490        500        510        520        530        540        550        560
QLSKQSSFAS LLNTNIPIGN KKEEEELRRT APSPWSPAAS PQSSDNSDTH QSGGSDIEMD EQLINRTKHV QQRLSDTEES

       570        580        590        600        610        620        630        640
MQGSSDETAN SGEDGSSGPG SSSGHSDGSS NEVNSSHASQ SAGSPGSEVQ SEDIADIEAL KEEDEDDDHG HNPPKSSCGT

       650        660        670        680        690        700        710        720
DLRNRKLESQ AGICLGDSQG MSERNGTSSG TGKDLVFNTE SLPSVDNRMR MLDACSHSED PEHDISGEMN ATHIAQGSQE

       730        740        750        760        770        780        790        800
SCITRTGDFL GETIGNELFN CRQFIGPQHH HHHHHHHHHH DGHMVDDMLS ADDVSCSSSQ VSAKSEKNMA DFDGEESGCE

       810        820        830        840        850        860        870        880
EELVQINSHA ELTSHLQQHL PNLASIYHEH LSQGPVVHKH QFNSNAVTDI NLDNVCKKGN TLLWDIVQDE DAVNLSEGLI

       890        900        910        920        930        940        950        960
NEAEKLLCSL VCWFTDRQIR MRFIEGCLEN LGNNRSVVIS LRLLPKLFGT FQQFGSSYDT HWITMWAEKE LNMMKLFFDN

       970        980        990       1000       1010       1020       1030       1040
LVYYIQTVRE GRQKHALYSH SAEVQVRLQF LTCVFSTLGS PDHFRLSLEQ VDILWHCLVE DSECYDDALH WFLNQVRSKD

      1050       1060       1070       1080       1090       1100       1110       1120
QHAMGMETYK HLFLEKMPQL KPETISMTGL NLFQHLCNLA RLATSAYDGC SNSELCGMDQ FWGIALRAQS GDVSRAAIQY

      1130       1140       1150       1160       1170       1180       1190       1200
INSYYINGKT GLEKEQEFIS KCMESLMIAS SSLEQESHSS LMVIERGLLM LKTHLEAFRR RFAYHLRQWQ IEGTGISSHL

      1210       1220       1230       1240       1250       1260       1270       1280
KALSDKQSLP LRVVCQPAGL PDKMTIEMYP SDQVADLRAE VTHWYENLQK EQINQQAQLQ EFGQSNRKGE FPGGLMGPVR

      1290       1300       1310       1320       1330       1340       1350       1360
MISSGHELTT DYDEKALHEL GFKDMQMVFV SLGAPRRERK GEGVQLPASC LPPPQKDNIP MLLLLQEPHL TTLFDLLEML

      1370       1380       1390       1400       1410       1420       1430       1440
ASFKPPSGKV AVDDSESLRC EELHLHAENL SRRVWELLML LPTCPNMLMA FQNISDEQSN DGFNWKELLK IKSAHKLLYA

      1450       1460       1470       1480       1490       1500       1510       1520
LEIIEALGKP NRRIRRESTG SYSDLYPDSD DSSEDQVENS KNSWSCKFVA AGGLQQLLEI FNSGILEPKE QESWTVWQLD

      1530       1540       1550       1560       1570       1580       1590       1600
CLACLLKLIC QFAVDPSDLD LAYHDVFAWS GIAESHRKRT WPGKSRKAAG DHAKGLHIPR LTEVFLVLVQ GTSLIQRLMS

      1610       1620       1630       1640       1650       1660       1670       1680
VAYTYDNLAP RVLKAQSDHR SRHEVSHYSM WLLVSWAHCC SLVKSSLADS DHLQDWLKKL TLLIPETAVR HESCSGLYKL

      1690       1700       1710       1720       1730       1740       1750       1760
SLSGLDGGDS INRSFLLLAA STLLKFLPDA QALKPIRIDD YEEEPILKPG CKEYFWLLCK LVDNIHIKDA SQTTLLDLDA

      1770       1780       1790       1800       1810       1820       1830       1840
LARHLADCIR SREILDHQDG NVEDDGLTGL LRLATSVVKH KPPFKFSREG QEFLRDIFNL LFLLPSLKDR QQPKCKSHSS

      1850       1860       1870       1880       1890       1900       1910       1920
RAAAYDLLVE MVKGSVENYR LIHNWVMAQH MQSHAPYKWD YWPHEDVRAE CRFVGLTNLG ATCYLASTIQ QLYMIPEARQ

      1930       1940       1950       1960       1970       1980       1990       2000
AVFTAKYSED MKHKTTLLEL QKMFTYLMES ECKAYNPRPF CKTYTMDKQP LNTGEQKDMT EFFTDLITKI EEMSPELKNT

      2010       2020       2030       2040       2050       2060       2070       2080
VKSLFGGVIT NNVVSLDCEH VSQTAEEFYT VRCQVADMKN IYESLDEVTI KDTLEGDNMY TCSHCGKKVR AEKRACFKKL

      2090       2100       2110       2120       2130       2140       2150       2160
PRILSFNTMR YTFNMVTMMK EKVNTHFSFP LRLDMTPYTE DFLMGKSERK EGFKEVSDHS KDSESYEYDL IGVTVHTGTA

      2170       2180       2190       2200       2210       2220       2230       2240
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2144 | 1 | 899.3487 | -134.27 | 2 | 56.7 | 10.7 | 0 | 404-419 | R.LSTQHIDCIWAAAQLK.H | |
| 1545 | 1 | 948.9999 | 79.00 | 2 | 47.6 | 10.2 | 0 | 647-664 | K.LESQAGICLGDSQGMSER.N | Oxidation: 15 |

# Detailed Protein Report

## Protein 876: regulator of G-protein signaling 11 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|557129067 | **Score:** | 20.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 51.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 7.0 |
| | | **No. of unique Peptides:** | 2 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAAGPAPPPG | RPRAQMPHLR | KMERVVVSMQ | DPDQGVKMRS | QRLLVTVIPH | AVTGSDVVQW | LAQKFCVSEE | EALHLGAVLV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QHGYIYPLRD | PRSLMLRPDE | TPYRFQVRLG | GAAIYLAKKN | IRKRGTLVDY | EKDCYDRLHK | KINHAWDLVL | MQAREQLRAA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KQRSKGDRLV | IACQEQTYWL | VNRPPPGAPD | VLEQGPGRGS | CAASRVLMTK | SADFHKREIE | YFRKALGRTR | VKSSVCLEAY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LSFCGQRGPH | DPLVSGCLPS | NPWISDNDAY | WVMNAPTVAA | PTKLRVERWG | FSFRELLEDP | VGRAHFMDFL | GKEFSGENLS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FWEACEELRY | GAQAQVPTLV | DAVYEQFLAP | GAAHWVNIDS | RTMEQTLEGL | RQPHRYVLDD | AQLHIYMLMK | KDSYPRFLKS |
| 410 | 420 | 430 | 440 | 450 | 460 | | |
| DMYKALLAEA | GIPLEMKRRV | FPFTWRPRHS | SPSPALLPTP | VEPTAACGPG | GGDGVA | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2135 | 1 | 754.0400 | 128.43 | 2 | 57.1 | 10.2 | 1 | 105-118 | R.FQVRLGGAAIYLAK.K | |
| 1806 | 1 | 697.3618 | 15.85 | 3 | 50.9 | 10.7 | 1 | 295-312 | R.ELLEDPVGRAHFMDFLGK.E | Oxidation: 13 |

# Detailed Protein Report

## Protein 877: zinc finger protein Helios isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|119220592 | **Score:** | 20.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| METEAIDGYI | TCDNELSPER | EHSNMAIDLT | SSTPNGQHAS | PSHMTSTNSV | KLEMQSDEEC | DRKPLSREDE | IRGHDEGSSL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EEPLIESSEV | ADNRKVQELQ | GEGGIRLPNG | ERPFHCNQCG | ASFTQKGNLL | RHIKLHSGEK | PFKCPFCSYA | CRRRDALTGH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LRTHSVGKPH | KCNYCGRSYK | QRSSLEEHKE | RCHNYLQNVS | MEAAGQVMSH | HVPPMEDCKE | QEPIMDNNIS | LVPFERPAVI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EKLTGNMGKR | KSSTPQKFVG | EKLMRFSYPD | IHFDMNLTYE | KEAELMQSHM | MDQAINNAIT | YLGAEALHPL | MQHPPSTIAE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VAPVISSAYS | QVYHPNRIER | PISRETADSH | ENNMDGPISL | IRPKSRPQER | EASPSNSCLD | STDSESSHDD | HQSYQGHPAL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NPKRKQSPAY | MKEDVKALDT | TKAPKGSLKD | IYKVFNGEGE | QIRAFKCEHC | RVLFLDHVMY | TIHMGCHGYR | DPLECNICGY |
| 490 | 500 | 510 | | | | | |
| RSQDRYEFSS | HIVRGEHTFH | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2120 | 1 | 1052.4607 | 1.63 | 3 | 56.9 | 20.8 | 0 | 192-219 | R.CHNYLQNVSMEAAGQVMSHHVPPMEDCK.E | |

# Detailed Protein Report

## Protein 878: PREDICTED: hedgehog-interacting protein isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530378067 | **Score:** | 20.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 76.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLKMLSFKLL | LLAVALGFFE | GDAKFGERNE | GSGARRRRCL | NGNPPKRLKR | RDRRMMSQLE | LLSGGEMLCG | GFYPRLSCCL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RSDSPGLGRL | ENKIFSVTNN | TECGKLLEEI | KCALCSPHSQ | SLFHSPEREV | LERDLVLPLL | CKDYCKEFFY | TCRGHIPGFL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QTTADEFCFY | YARKDGGLCF | PDFPRKQVRG | PASNYLDQME | EYDKVEEISR | KHKHNCFCIQ | EVVSGLRQPV | GALHSGDGSQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RLFILEKEGY | VKILTPEGEI | FKEPYLDIHK | LVQSGIKGGD | ERGLLSLAFH | PNYKKNGKLY | VSYTTNQERW | AIGPHDHILR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VVEYTVSRKN | PHQVDLRTAR | VFLEVAELHR | KHLGGQLLFG | PDGFLYIILG | DGMITLDDME | EMDGLSDFTG | SVLRLDVDTD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MCNVPYSIPR | SNPHFNSTNQ | PPEVFAHGLH | DPGRCAVDRH | PTDININLTI | LCSDSNGKNR | SSARILQIIK | GKDYESEPSL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LEFKPFSNGP | LVGGFVYRGC | QSERLYGSYV | FGDRNGNFLT | LQQSPVTKQW | QEKPLCLGTS | GSCRGYFSGH | ILGFGEDELG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EVYILSSSKS | MTQTHNGKLY | KIVDPKRPLM | PEECRATVQP | AQTLTSECSR | LCRNGYCTPT | GKCCCSPGWE | GDFCRTAKCE |
| 650 | 660 | 670 | 680 | 690 | | | |
| PACRHGGVCV | RPNKCLCKKG | YLGPQCEQVD | RNIRRVTRAD | IT | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1709 | 1 | 938.7505 | -122.25 | 2 | 49.7 | 10.2 | 1 | 623-638 | K.CCCSPGWEGDFCRTAK.C | Carbamidomethyl: 3, 12 |

# Detailed Protein Report

**Protein 879:** **PREDICTED: LOW QUALITY PROTEIN: Fanconi anemia group D2 protein-like [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530432405 | **Score:** | 20.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 99.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| | | **Sequence Coverage [%]:** | 3.4 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MEVGDWIEGH KAECGVGLQA HARIGALGHE EQRREDAAQI GSDHATELQE KLDLQHYVLP SRLQASXVNL KSKGRASSSG
        90        100        110        120        130        140        150        160
NQESSXQSCI SLLFDVIKSA IRYEKTISEA WIKAIENTAS VSEHEVFDLV MLFIIYSTNT QTKKYIDRVL RSKIRSGCIQ
       170        180        190        200        210        220        230        240
EQLLQSTFSV HYLVLKDMCS SILSLAQSLL HSLDQSIISF GSLLYKYAFK FFDTYCQQEV VGALVTHICS GNEAEVDTAL
       250        260        270        280        290        300        310        320
DVLLELVVLN PSAMMMNAVF VKGILDYLDN ISPQQIRKLF NVLSTLAFSK QNEASSHIQD DMHLVIRKQL SSTIFKYKLI
       330        340        350        360        370        380        390        400
GIFGAVTMAG IMVADRSGSS SLTQEVANLS DEQCTHVTSL LQLVHSCSEQ SPQASALYYD EFANLIQHEK LDPKALEWVG
       410        420        430        440        450        460        470        480
HTICNDFQDA FVVDSCVVPE GDFPFPVKAL YGLEEYDTQD GIAINLLPLL FSQDFAKDGG LVTSQESGQK LVSPLCLAPY
       490        500        510        520        530        540        550        560
FQLLRLYVER QHNGNLEEID SLLDCPIFLT DLEPGERLES MSAKERSFMC SLIFLILSWF REIVNAFCHE TSPEMKGKVL
       570        580        590        600        610        620        630        640
TRLKHIVELQ IILEKYLTDE GIAPDYVPPL GNFDVETLDI TLHTVTAISA KIRKRGKISK NQKTDGSKTS SSDTLSEEKN
       650        660        670        680        690        700        710        720
SECDPTPSHR GQMNKAWSPH LVEVLTGEAS AGPHVSSGFE AGVRRPTSLL SLGPALCPRR ELQPGVWTPL CLAVQLQRVN
       730        740        750        760        770        780        790        800
AVFFHCRLST RPEVASIESL GLDEQQCSQK AVVQAHLTQP ARLTSIIFAE DITTDQVLHC DATVDLIPGI QIVSTTRKLN
       810        820        830        840        850        860        870        880
LEDSPLELKI QALDSEGPLE GSFSQGGEGA AGGGAEEAEP TCEVGPKPWV ESSLALRGPC SRVCVLRAVA DPGARPCWSQ
       890        900        910
RWSLVQHILG KPTFSAMMRG
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1642 | 1 | 701.3735 | 1.06 | 3 | 50.3 | 10.4 | 0 | 882-899 | R.WSLVQHILGKPTFSAMMR.G | |

# Detailed Protein Report

## Protein 880: TBC1 domain family member 16 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|427918111 | **Score:** | 20.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | |
|---|---|---|---|
| ***WUP:QUP*** **Median:** 0.90 | **CV:** 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKQVAPDKTC | MQFSIRRPKL | PSSETHPEES | MYKRLGVSAW | LNHLNELGQV | EEEYKLRKVW | PFLLRYYSHE | STSEEREALR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LQKRKEYSEI | QQKRLSMTPE | EHRAFWRNVQ | FTVDKDVVRT | DRNNQFFRGE | DNPNVESMRR | ILLNYAVYNP | AVGYSQGMSD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LVAPILAEVL | DESDTFWCFV | GLMQNTIFVS | SPRDEDMEKQ | LLYLRELLRL | THVRFYQHLV | SLGEDGLQML | FCHRWLLLCF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KREFPEAEAL | RIWEACWAHY | QTDYFHLFIC | VAIVAIYGDD | VIEQQLATDQ | MLLHFGNLAM | HMNGELVLRK | ARSLLYQFRL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LPRIPCSLHD | LCKLCGSGMW | DSGSMPAVEC | TGHHPGSESC | PYGGTVEMPS | PKSLREGKKG | PKTPQDGFGF | RR |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 700 | 3 | 820.2521 | -180.55 | 2 | 37.2 | 20.7 | 1 | 3-16 | K.QVAPDKTCMQFSIR.R | Oxidation: 9 | WUP:QUP 0.90 |

# Detailed Protein Report

## Protein 881: PREDICTED: agrin isoform X7 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|578799100 | **Score:** | 20.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 154.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.8 |
|  |  | **No. of unique Peptides:** | 2 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLHVHACTHQ | ISLHVASAGP | CETCGDAVCA | FGAVCSAGQC | VCPRCEHPPP | GPVCGSDGVT | YGSACELREA | ACLQQTQIEE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ARAGPCEQAE | CGSGGSGSGE | DGDCEQELCR | QRGGIWDEDS | EDGPCVCDFS | CQSVPGSPVC | GSDGVTYSTE | CELKKARCES |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QRGLYVAAQG | ACRGPTFAPL | PPVAPLHCAQ | TPYGCCQDNI | TAARGVGLAG | CPSACQCNPH | GSYGGTCDPA | TGQCSCRPGV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GGLRCDRCEP | GFWNFRGIVT | DGRSGCTPCS | CDPQGAVRDD | CEQMTGLCSC | KPGVAGPKCG | QCPDGRALGP | AGCEADASAP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ATCAEMRCEF | GARCVEESGS | AHCVCPMLTC | PEANATKVCG | SDGVTYGNEC | QLKTIACRQG | LQISIQSLGP | CQEAVAPSTH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PTSASVTVTT | PGLLLSQALP | APPGALPLAP | SSTAHSQTTP | PPSSRPRTTA | SVPRTTVWPV | LTVPPTAPSP | APSLVASAFG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ESGSTDGSSD | EELSGDQEAS | GGGSGGLEPL | EGSSVATPGP | PVERASCYNS | ALGCCSDGKT | PSLDAEGSNC | PATKVFQGVL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ELEGVEGQEL | FYTPEMADPK | SELFGETARS | IESTLDDLFR | NSDVKKDFRS | VRLRDLGPGK | SVRAIVDVHF | DPTTAFRAPD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VARALLRQIQ | VSRRRSLGVR | RPLQEHVRFM | DFDWFPAFIT | GATSGAIAAG | ATARATTASR | LPSSAVTPRA | PHPSHTSQPV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AKTTAAPTTR | RPPTTAPSRV | PGRRPPAPQQ | PPKPCDSQPC | FHGGTCQDWA | LGGGFTCSCP | AGRGGAVCEK | VLGAPVPAFE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GRSFLAFPTL | RAYHTLRLAL | EFRALEPQGL | LLYNGNARGK | DFLALALLDG | RVQLRFDTGS | GPAVLTSAVP | VEPGQWHRLE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LSRHWRRGTL | SVDGETPVLG | ESPSGTDGLN | LDTDLFVGGV | PEDQAAVALE | RTFVGAGLRG | CIRLLDVNNQ | RLELGIGPGA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ATRGSGVGEC | GDHPCLPNPC | HGGAPCQNLE | AGRFHCQCPP | GRVGPTCADE | KSPCQPNPCH | GAAPCRVLPE | GGAQCECPLG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| REGTFCQTAS | GQDGSGPFLA | DFNGFSHLEL | RGLHTFARDL | GEKMALEVVF | LARGPSGLLL | YNGQKTDGKG | DFVSLALRDR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RLEFRYDLGK | GAAVIRSREP | VTLGAWTRVS | LERNGRKGAL | RVGDGPRVLG | ESPKSRKVPH | TVLNLKEPLY | VGGAPDFSKL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ARAAAVSSGF | DGAIQLVSLG | GRQLLTPEHV | LRQVDVTSFA | GHPCTRASGH | PCLNGASCVP | REAAYVCLCP | GGFSGPHCEK |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| GLVEKSAGDV | DTLAFDGRTF | VEYLNAVTES | ELANEIPVEK | ALQSNHFELS | LRTEATQGLV | LWSGKATERA | DYVALAIVDG |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| HLQLSYNLGS | QPVVLRSTVP | VNTNRWLRVV | AHREQREGSL | QVGNEAPVTG | SSPLGATQLD | TDGALWLGGL | PELPVGPALP |
| 1450 | 1460 | 1470 | 1480 |  |  |  |  |
| KAYGTGFVGC | LRDVVVGRHP | LHLLEDAVTK | PELRPCPTP |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1808 | 1 | 774.2788 | -97.08 | 2 | 52.4 | 10.1 | 0 | 540-554 | K.TPSLDAEGSNCPATK.V | Carbamidomethyl: 11 |
| 2489 | 1 | 981.1592 | 15.45 | 3 | 61.0 | 10.5 | 0 | 555-580 | K.VFQGVLELEGVEGQELFYTPEMADPK.S | Oxidation: 22 |

# Detailed Protein Report

## Protein 882: Fanconi anemia group J protein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|301897118 | **Score:** | 20.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 140.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSMWSEYTI | GGVKIYFPYK | AYPSQLAMMN | SILRGLNSKQ | HCLLESPTGS | GKSLALLCSA | LAWQQSLSGK | PADEGVSEKA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EVQLSCCCAC | HSKDFTNNDM | NQGTSRHFNY | PSTPPSERNG | TSSTCQDSPE | KTTLAAKLSA | KKQASIYRDE | NDDFQVEKKR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IRPLETTQQI | RKRHCFGTEV | HNLDAKVDSG | KTVKLNSPLE | KINSFSPQKP | PGHCSRCCCS | TKQGNSQESS | NTIKKDHTGK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SKIPKIYFGT | RTHKQIAQIT | RELRRTAYSG | VPMTILSSRD | HTCVHPEVVG | NFNRNEKCME | LLDGKNGKSC | YFYHGVHKIS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DQHTLQTFQG | MCKAWDIEEL | VSLGKKLKAC | PYYTARELIQ | DADIIFCPYN | YLLDAQIRES | MDLNLKEQVV | ILDEAHNIED |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CARESASYSV | TEVQLRFARD | ELDSMVNNNI | RKKDHEPLRA | VCCSLINWLE | ANAEYLVERD | YESACKIWSG | NEMLLTLHKM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GITTATFPIL | QGHFSAVLQK | EEKISPIYGK | EEAREVPVIS | ASTQIMLKGL | FMVLDYLFRQ | NSRFADDYKI | AIQQTYSWTN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QIDISDKNGL | LVLPKNKKRS | RQKTAVHVLN | FWCLNPAVAF | SDINGKVQTI | VLTSGTLSPM | KSFSSELGVT | FTIQLEANHI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IKNSQVWVGT | IGSGPKGRNL | CATFQNTETF | EFQDEVGALL | LSVCQTVSQG | ILCFLPSYKL | LEKLKERWLS | TGLWHNLELV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KTVIVEPQGG | EKTNFDELLQ | VYYDAIKYKG | EKDGALLVAV | CRGKVSEGLD | FSDDNARAVI | TIGIPFPNVK | DLQVELKRQY |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NDHHSKLRGL | LPGRQWYEIQ | AYRALNQALG | RCIRHRNDWG | ALILVDDRFR | NNPSRYISGL | SKWVRQQIQH | HSTFESALES |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LAEFSKKHQK | VLNVSIKDRT | NIQDNESTLE | VTSLKYSTSP | YLLEAASHLS | PENFVEDEAK | ICVQELQCPK | IITKNSPLPS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SIISRKEKND | PVFLEEAGKA | EKIVISRSTS | PTFNKQTKRV | SWSSFNSLGQ | YFTGKIPKAT | PELGSSENSA | SSPPRFKTEK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| MESKTVLPFT | DKCESSNLTV | NTSFGSCPQS | ETIISSLKID | ATLTRKNHSE | HPLCSEEALD | PDIELSLVSE | EDKQSTSNRD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| FETEAEDESI | YFTPELYDPE | DTDEEKNDLA | ETDRGNRLAN | NSDCILAKDL | FEIRTIKEVD | SAREVKAEDC | IDTKLNGILH |
| 1210 | 1220 | 1230 | 1240 | 1250 | | | |
| IEESKIDDID | GNVKTTWINE | LELGKTHEIE | IKNFKPSPSK | NKGMFPGFK | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2372 | 1 | 637.6653 | -235.01 | 2 | 60.1 | 10.2 | 0 | 941-950 | K.ICVQELQCPK.I | Carbamidomethyl: 2, 8 |

# Detailed Protein Report

## Protein 883: interleukin-4 receptor subunit alpha isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|384229037 | **Score:** | 20.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 88.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.7 |
| | | **No. of unique Peptides:** | 2 |

```
        10         20         30         40         50         60         70         80
MQKDARREGN MKVLQEPTCV SDYMSISTCE WKMNGPTNCS TELRLLYQLV FLLSEAHTCI PENNGGAGCV CHLLMDDVVS
        90        100        110        120        130        140        150        160
ADNYTLDLWA GQQLLWKGSF KPSEHVKPRA PGNLTVHTNV SDTLLLTWSN PYPPDNYLYN HLTYAVNIWS ENDPADFRIY
       170        180        190        200        210        220        230        240
NVTYLEPSLR IAASTLKSGI SYRARVRAWA QCYNTTWSEW SPSTKWHNSY REPFEQHLLL GVSVSCIVIL AVCLLCYVSI
       250        260        270        280        290        300        310        320
TKIKKEWWDQ IPNPARSRLV AIIIQDAQGS QWEKRSRGQE PAKCPHWKNC LTKLLPCFLE HNMKRDEDPH KAAKEMPFQG
       330        340        350        360        370        380        390        400
SGKSAWCPVE ISKTVLWPES ISVVRCVELF EAPVECEEEE EVEEEKGSFC ASPESSRDDF QEGREGIVAR LTESLFLDLL
       410        420        430        440        450        460        470        480
GEENGGFCQQ DMGESCLLPP SGSTSAHMPW DEFPSAGPKE APPWGKEQPL HLEPSPPASP TQSPDNLTCT ETPLVIAGNP
       490        500        510        520        530        540        550        560
AYRSFSNSLS QSPCPRELGP DPLLARHLEE VEPEMPCVPQ LSEPTTVPQP EPETWEQILR RNVLQHGAAA APVSAPTSGY
       570        580        590        600        610        620        630        640
QEFVHAVEQG GTQASAVVGL GPPGEAGYKA FSSLLASSAV SPEKCGFGAS SGEEGYKPFQ DLIPGCPGDP APVPVPLFTF
       650        660        670        680        690        700        710        720
GLDREPPRSP QSSHLPSSSP EHLGLEPGEK VEDMPKPPLP QEQATDPLVD SLGSGIVYSA LTCHLCGHLK QCHGQEDGGQ
       730        740        750        760        770        780        790        800
TPVMASPCCG CCCGDRSSPP TTPLRAPDPS PGGVPLEASL CPASLAPSGI SEKSKSSSSF HPAPGNAQSS SQTPKIVNFV
       810        820
SVGPTYMRVS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 710 | 1 | 661.8474 | 79.09 | 2 | 38.9 | 10.2 | 0 | 33-44 | K.MNGPTNCSTELR.L | |
| 1710 | 1 | 900.2977 | -32.09 | 3 | 49.7 | 10.4 | 0 | 711-736 | K.QCHGQEDGGQTPVMASPCCGCCCGDR.S | Carbamidomethyl: 19 |

# Detailed Protein Report

## Protein 884: PREDICTED: ankyrin repeat and protein kinase domain-containing protein 1 isoform X1 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|578822107 | **Score:** | 20.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 79.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
|  |  | **Sequence Coverage [%]:** | 1.7 |
|  |  | **No. of unique Peptides:** | 1 |

## Quantitation

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.89 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.16 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGHPLPYLAP | PLHSSDVNYL | IEEAAKMKKI | KFQHIVSIYG | VCKQPLGIVM | EFMANGSLEK | VLSTHSLCWK | LRFRIIHETS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LAMNFLHSIK | PPLLHLDLKP | GNILLDSNMH | VKISDFGLSK | WMEQSTRMQY | IERSALRGML | SYIPPEMFLE | SNKAPGPKYD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VYSFAIVIWE | LLTQKKPYSG | FNMMMIIIRV | AAGMRPSLQP | VSDQWPSEAQ | QMVDLMKRCW | DQDPKKRPCF | LDITIETDIL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LSLLQSRVAV | PESKALARKV | SCKLSLRQPG | EVNEDISQEL | MDSDSGNYLK | RALQLSDRKN | LVPRDEELCI | YENKVTPLHF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LVAQGSVEQV | RLLLAHEVDV | DCQTASGYTP | LLIAAQDQQP | DLCALLLAHG | ADANRVDEDG | WAPLHFAAQN | GDDGTARLLL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DHGACVDAQE | REGWTPLHLA | AQNNFENVAR | LLVSRQADPN | LHEAEGKTPL | HVAAYFGHVS | LVKLLTSQGA | ELDAQQRNLR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TPLHLAVERG | KVRAIQHLLK | SGAVPDALDQ | SGYGPLHTAA | ARGKYLICKM | LLRYGASLEL | PTHQGWTPLH | LAAYKGHLEI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IHLLAESHAN | MGALGAVNWT | PLHLAARHGE | EAVVSALLQC | GADPNAAEQS | GWTPLHLAVQ | RSTFLSVINL | LEHHANVHAR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NKVGWTPAHL | AALKGNTAIL | KVLVEAGAQL | DVQDGVSCTP | LQLALRSRKQ | GIMSFLEGKE | PSVATLGGSK | PGAEMEI |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2290 | 1 | 697.2835 | -121.83 | 2 | 58.5 | 20.5 | 0 | 32-43 | K.FQHIVSIYGVCK.Q |  | WUP:QUP 1.16<br>QU:MU 0.89 |

# Detailed Protein Report

**Protein 885:** **PREDICTED: receptor-type tyrosine-protein phosphatase U isoform X5 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578798179 | **Score:** | 20.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 132.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRSDLGVGAG | FEGDGQGQEP | PTPIAPPQLL | RAGPTYLIIQ | LNTNSIIGDG | PIVRKEIEYR | MARGPWAEVH | AVSLQTYKLW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HLDPDTEYEI | SVLLTRPGDG | GTGRPGPPLI | SRTKCAEPMR | APKGLAFAEI | QARQLTLQWE | PLGYNVTRCH | TYTVSLCYHY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TLGSSHNQTI | RECVKTEQGV | SRYTIKNLLP | YRNVHVRLVL | TNPEGRKEGK | EVTFQTDEDV | PSGIAAESLT | FTPLEDMIFL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KWEEPQEPNG | LITQYEISYQ | SIESSDPAVN | VPGPRRTISK | LRNETYHVFS | NLHPGTTYLF | SVRARTGKGF | GQAALTEITT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NISAPSFDYA | DMPSPLGESE | NTITVLLRPA | QGRGAPISVY | QVIVEEERAR | RLRREPGGQD | CFPVPLTFEA | ALARGLVHYF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GAELAASSLP | EAMPFTVGDN | QTYRGFWNPP | LEPRKAYLIY | FQAASHLKGE | TRLNCIRIAR | KAACKESKRP | LEVSQRSEEM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GLILGICAGG | LAVLILLLGA | IIVIIRKGKP | VNMTKATVNY | RQEKTHMMSA | VDRSFTDQST | LQEDERLGLS | FMDTHGYSTR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GDQRSGGVTE | ASSLLGGSPR | RPCGRKGSPY | HTGQLHPAVR | VADLLQHINQ | MKTAEGYGFK | QEYESFFEGW | DATKKKDKVK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GSRQEPMPAY | DRHRVKLHPM | LGDPNADYIN | ANYIDIRINR | EGYHRSNHFI | ATQGPKPEMV | YDFWRMVWQE | HCSSIVMITK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LVEVGRVKCS | RYWPEDSDTY | GDIKIMLVKT | ETLAEYVVRT | FALERRGYSA | RHEVRQFHFT | AWPEHGVPYH | ATGLLAFIRR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VKASTPPDAG | PIVIHCSAGT | GRTGCYIVLD | VMLDMAECEG | VVDIYNCVKT | LCSRRVNMIQ | TEEQYIFIHD | AILEACLCGE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TTIPVSEFKA | TYKEMIRIDP | QSNSSQLREE | FQTLNSVTPP | LDVEECSIAL | LPRNRDKNRS | MDVLPPDRCL | PFLISTDGDS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NNYINAALTD | SYTRSAAFIV | TLHPLQSTTP | DFWRLVYDYG | CTSIVMLNQL | NQSNSAWPCL | QYWPEPGRQQ | YGLMEVEFMS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GTADEDLVAR | VFRVQNISRL | QEGHLLVRHF | QFLRWSAYRD | TPDSKKAFLH | LLAEVDKWQA | ESGDGRTIVH | CLNGGGRSGT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | | |
| FCACATVLEM | IRCHNLVDVF | FAAKTLRNYK | PNMVETMDQY | HFCYDVALEY | LEGLESR | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1388 | 1 | 844.8990 | -55.98 | 2 | 47.0 | 10.3 | 0 | 354-368 | R.GAPISVYQVIVEEER.A | |

# Detailed Protein Report

## Protein 886: notch homolog 2 N-terminal-like protein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|46397353 | **Score:** | 20.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 25.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 11.0 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MCVTYHNGTG | YCKCPEGFLG | EYCQHRDPCE | KNRCQNGGTC | VAQAMLGKAT | CRCASGFTGE | DCQYSTSHPC | FVSRPCLNGG |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| TCHMLSRDTY | ECTCQVGFTG | KECQWTDACL | SHPCANGSTC | TTVANQFSCK | CLTGFTGQKC | ETDVNECDIP | GHCQHGGTCL |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| NLPGSYQCQC | LQGFTGQYCD | SLYVPCAPSP | CVNGGTCRQT | GDFTFECNCL | PETVRRGTEL | WERDREVWNG | KEHDEN |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1871 | 2 | 1037.3636 | -66.59 | 3 | 53.2 | 20.4 | 1 | 1-26 | -.MCVTYHNGTGYCKCPEGFLGEYCQHR.D | Carbamidomethyl: 2, 23 |

# Detailed Protein Report

## Protein 887: PDZ domain-containing RING finger protein 4 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|142976783 | **Score:** | 20.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 89.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.75 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.30 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGCNLCTFQK | REEHYKLLYE | VSQVNGKDLS | KATHEEAVEA | FRNAKEPIVV | QVLRRTPLSR | PAYGMASEVQ | LMNASTQTDI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TFEHIMALAK | LRPPTPPVPD | ICPFLLSDSC | HSLHPMEHEF | YEDNEYISSL | PADADRTEDF | EYEEVELCRV | SSQEKLGLTV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CYRTDDEEDT | GIYVSEVDPN | SIAAKDGRIR | EGDRILQING | EDVQNREEAV | ALLSNDECKR | IVLLVARPEI | QLDEGWLEDE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RNEFLEELNL | EMLEEEHNEA | MQPTANEVEQ | PKKQEEEEGT | TDTATSSSNN | HEKDSGVGRT | DESLRNDESS | EQENAAEDPN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| STSLKSKRDL | GQSQDTLGSV | ELQYNESLVS | GEYIDSDCIG | NPDEDCERFR | QLLELKCKIR | NHGEYDLYYS | SSTIECNQGE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QEGVEHELQL | LNEELRNIEL | ECQNIMQAHR | LQKVTDQYGD | IWTLHDGGFR | NYNTSIDMQR | GKLDDIMEHP | EKSDKDSSSA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YNTAESCRST | PLTVDRSPDS | SLPRVINLTN | KKNLRSTMAA | TQSSSGQSSK | ESTSTKAKTT | EQGCSAESKE | KVLEGSKLPD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QEKAVSEHIP | YLSPYHSSSY | RYANIPAHAR | HYQSYMQLIQ | QKSAVEYAQS | QLSLVSMCKE | SQKCSEPKME | WKVKIRSDGT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RYITKRPVRD | RILKERALKI | KEERSGMTTD | DDTMSEMKMG | RYWSKEERKQ | HLVRAKEQRR | RREFMMRSRL | ECLKESPQSG |
| 730 | 740 | 750 | 760 | 770 | 780 | | |
| SEGKKEINII | ELSHKKMMKK | RNKKILDNWM | TIQELMTHGA | KSPDGTRVHN | AFLSVTTV | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 546 | 1 | 639.3340 | -61.92 | 2 | 35.3 | 10.2 | 2 | 369-378 | R.FRQLLELKCK.I | | QU:MU 2.75<br>WUP:QUP 0.30 |

# Detailed Protein Report

## Protein 888: nuclear factor of activated T-cells, cytoplasmic 2 isoform D [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|209862843 | **Score:** | 20.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 97.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQREAAFRLG | HCHPLRIMGS | VDQEEPNAHK | VASPPSGPAY | PDDVLDYGLK | PYSPLASLSG | EPPGRFGEPD | RVGPQKFLSA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AKPAGASGLS | PRIEITPSHE | LIQAVGPLRM | RDAGLLVEQP | PLAGVAASPR | FTLPVPGFEG | YREPLCLSPA | SSGSSASFIS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DTFSPYTSPC | VSPNNGGPDD | LCPQFQNIPA | HYSPRTSPIM | SPRTSLAEDS | CLGRHSPVPR | PASRSSSPGA | KRRHSCAEAL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VALPPGASPQ | RSRSPSPQPS | SHVAPQDHGS | PAGYPPVAGS | AVIMDALNSL | ATDSPCGIPP | KMWKTSPDPS | PVSAAPSKAG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LPRHIYPAVE | FLGPCEQGER | RNSAPESILL | VPPTWPKPLV | PAIPICSIPV | TASLPPLEWP | LSSQSGSYEL | RIEVQPKPHH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RAHYETEGSR | GAVKAPTGGH | PVVQLHGYME | NKPLGLQIFI | GTADERILKP | HAFYQVHRIT | GKTVTTTSYE | KIVGNTKVLE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IPLEPKNNMR | ATIDCAGILK | LRNADIELRK | GETDIGRKNT | RVRLVFRVHI | PESSGRIVSL | QTASNPIECS | QRSAHELPMV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ERQDTDSCLV | YGGQQMILTG | QNFTSESKVV | FTEKTTDGQQ | IWEMEATVDK | DKSQPNMLFV | EIPEYRNKHI | RTPVKVNFYV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| INGKRKRSQP | QHFTYHPVPA | IKTEPTDEYD | PTLICSPTHG | GLGSQPYYPQ | HPMVAESPSC | LVATMAPCQQ | FRTGLSSPDA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RYQQQNPAAV | LYQRSKSLSP | SLLGYQQPAL | MAAPLSLADA | HRSVLVHAGS | QGQSSALLHP | SPTNQQASPV | IHYSPTNQQL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RCGSHQEFQH | IMYCENFAPG | TTRPGPPPVS | QGQRLSPGSY | PTVIQQQNAT | SQRAAKNGPP | VSDQKEVLPA | GVTIKQEQNL |
| 890 | 900 | 910 | | | | | |
| DQTYLDDELI | DTHLSWIQNI | L | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 644 | 1 | 852.1620 | 38.48 | 3 | 38.0 | 10.0 | 2 | 478-500 | K.VLEIPLEPKNNMRATIDCAGILK.L | Oxidation: 12 |

# Detailed Protein Report

## Protein 889: PREDICTED: sodium channel and clathrin linker 1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530377155 | **Score:** | 20.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.8 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.55 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MQLLEEANLQ | KSQALLEEKQ | KEEDIEKMKE | TVSRFVQDAT | IRTKKEVANT | KKQCNIQISR | LTEELSALQM | ECAEKQGQIE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RVIKEKKAVE | EELEKIYREG | RGNESDYRKL | EEMHQRFLVS | ERSKDDLQLR | LTRAENRIKQ | LETDSSEEIS | RYQEMIQKLQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NVLESERENC | GLVSEQRLKL | QQENKQLRKE | TESLRKIALE | AQKKAKVKIS | TMEHEFSIKE | RGFEVQLREM | EDSNRNSIVE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LRHLLATQQK | AANRWKEETK | KLTESAEIRI | NNLKSELSRQ | KLHTQELLSQ | LEMANEKVAE | NEKLILEHQE | KANRLQRRLS |
| 330 | 340 | 350 | 360 | | | | |
| QAEERAASAS | QQLSVITVQR | RKAASLMNLE | NI | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 629 | 1 | 509.6880 | -216.14 | 2 | 37.4 | 20.2 | 2 | 43-51 | R.TKKEVANTK.K | | WUP:QUP 0.55 |

# Detailed Protein Report

**Protein 890:** **PREDICTED: Down syndrome cell adhesion molecule isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578836469 | **Score:** | 20.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 210.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| | | **Sequence Coverage [%]:** | 0.7 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MIIYILPLCS NLFYQPIKIE QRKISLKVTF SKGKKHFCPL KLTLIFDLNV GPFCSTEALP VKIRGSRFLI TSTGALYIKD
        90        100        110        120        130        140        150        160
VQNEDGLYNY RCITRHRYTG ETRQSNSARL FVSDPANSAP SILDGFDHRK AMAGQRVELP CKALGHPEPD YRWLKDNMPL
       170        180        190        200        210        220        230        240
ELSGRFQKTV TGLLIENIRP SDSGSYVCEV SNRYGTAKVI GRLYVKQPLK ATISPRKVKS SVGSQVSLSC SVTGTEDQEL
       250        260        270        280        290        300        310        320
SWYRNGEILN PGKNVRITGI NHENLIMDHM VKSDGGAYQC FVRKDKLSAQ DYVQVVLEDG TPKIISAFSE KVVSPAEPVS
       330        340        350        360        370        380        390        400
LMCNVKGTPL PTITWTLDDD PILKGGSHRI SQMITSEGNV VSYLNISSSQ VRDGGVYRCT ANNSAGVVLY QARINVRGPA
       410        420        430        440        450        460        470        480
SIRPMKNITA IAGRDTYIHC RVIGYPYYSI KWYKNSNLLP FNHRQVAFEN NGTLKLSDVQ KEVDEGEYTC NVLVQPQLST
       490        500        510        520        530        540        550        560
SQSVHVTVKV PPFIQPFEFP RFSIGQRVFI PCVVVSGDLP ITITWQKDGR PIPGSLGVTI DNIDFTSSLR ISNLSLMHNG
       570        580        590        600        610        620        630        640
NYTCIARNEA AAVEHQSQLI VRVPPKFVVQ PRDQDGIYGK AVILNCSAEG YPVPTIVWKF SKGAGVPQFQ PIALNGRIQV
       650        660        670        680        690        700        710        720
LSNGSLLIKH VVEEDSGYYL CKVSNDVGAD VSKSMYLTVK IPAMITSYPN TTLATQGQKK EMSCTAHGEK PIIVRWEKED
       730        740        750        760        770        780        790        800
RIINPEMARY LVSTKEVGEE VISTLQILPT VREDSGFFSC HAINSYGEDR GIIQLTVQEP PDPPEIEIKD VKARTITLRW
       810        820        830        840        850        860        870        880
TMGFDGNSPI TGYDIECKNK SDSWDSAQRT KDVSPQLNSA TIIDIHPSST YSIRMYAKNR IGKSEPSNEL TITADEAAPD
       890        900        910        920        930        940        950        960
GPPQEVHLEP ISSQSIRVTW KAPKKHLQNG IIRGYQIGYR EYSTGGNFQF NIISVDTSGD SEVYTLDNLN KFTQYGLVVQ
       970        980        990       1000       1010       1020       1030       1040
ACNRAGTGPS SQEIITTTLE DVPSYPPENV QAIATSPESI SISWSTLSKE ALNGILQGFR VIYWANLMDG ELGEIKNITT
      1050       1060       1070       1080       1090       1100       1110       1120
TQPSLELDGL EKYTNYSIQV LAFTRAGDGV RSEQIFTRTK EDVPGPPAGV KAAAASASMV FVSWLPPLKL NGIIRKYTVF
      1130       1140       1150       1160       1170       1180       1190       1200
CSHPYPTVIS EFEASPDSFS YRIPNLSRNR QYSVWVVAVT SAGRGNSSEI ITVEPLAKAP ARILTFSGTV TTPWMKDIVL
      1210       1220       1230       1240       1250       1260       1270       1280
PCKAVGDPSP AVKWMKDSNG TPSLVTIDGR RSIFSNGSFI IRTVKAEDSG YYSCIANNNW GSDEIILNLQ VQVPPDQPRL
      1290       1300       1310       1320       1330       1340       1350       1360
TVSKTTSSSI TLSWLPGDNG GSSIRGYILQ YSEDNSEQWG SFPISPSERS YRLENLKCGT WYKFTLTAQN GVGPGRISEI
      1370       1380       1390       1400       1410       1420       1430       1440
IEAKTLGKEP QFSKEQELFA SINTTRVRLN LIGWNDGGCP ITSFTLEYRP FGTTVWTTAQ RTSLSKSYIL YDLQEATWYE
      1450       1460       1470       1480       1490       1500       1510       1520
LQMRVCNSAG CAEKQANFAT LNYDGSTIPP LIKSVVQNEE GLTTNEGLKM LVTISCILVG VLLLFVLLLV VRRRRREQRL
      1530       1540       1550       1560       1570       1580       1590       1600
KRLRDAKSLA EMLMSKNTRT SDTLSKQQQT LRMHIDIPRA QLLIEERDTM ETIDDRSTVL LTDADFGEAA KQKSLTVTHT
      1610       1620       1630       1640       1650       1660       1670       1680
VHYQSVSQAT GPLVDVSDAR PGTNPTTRRN AKAGPTARNR YASQWTLNRP HPTISAHTLT TDWRLPTPRA AGSVDKESDS
      1690       1700       1710       1720       1730       1740       1750       1760
YSVSPSQDTD RARSSMVSTE SASSTYEELA RAYEHAKMEE QLRHAKFTIT ECFISDTSSE QLTAGTNEYT DSLTSSTPSE
      1770       1780       1790       1800       1810       1820       1830       1840
SGICRFTASP PKPQDGGRVM NMAVPKAHRP GDLIHLPPYL RMDFLLNRGG PGTSRDLSLG QACLEPQKSR TLKRPTVLEP
      1850       1860       1870       1880       1890       1900       1910
IPMEAASSAS STREGQSWQP GAVATLPQRE GAELGQAAKM SSSQESLLDS RGHLKGNNPY AKSYTLV
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 432 | 1 | 719.8247 | -131.20 | 2 | 35.4 | 20.1 | 1 | 394-406 | R.INVRGPASIRPMK.N | |

# Detailed Protein Report

## Protein 891: induced myeloid leukemia cell differentiation protein Mcl-1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|33519458 | **Score:** | 20.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 28.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MFGLKRNAVI | GLNLYCGGAG | LGAGSGGATR | PGGRLLATEK | EASARREIGG | GEAGAVIGGS | AGASPPSTLT | PDSRRVARPP |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| PIGAEVPDVT | ATPARLLFFA | PTRRAAPLEE | MEAPAADAIM | SPEEELDGYE | PEPLGKRPAV | LPLLELVGES | GNNTSTDGSL |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| PSTPPPAEEE | EDELYRQSLE | IISRYLREQA | TGAKDTKPMG | RSGATSRKAL | ETLRRVGDGV | QRNHETAFQG | WVCGVLPCRG |
| **250** | **260** | **270** | **280** | | | | |
| PRRWHQECAA | GFCRCCWSRS | WFGISNKIAL | L | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1897 | 1 | 568.7721 | -60.60 | 2 | 52.1 | 20.1 | 1 | 185-194 | R.YLREQATGAK.D | |

# Detailed Protein Report

**Protein 892:** **uromodulin-like 1 isoform 4 [Homo sapiens]**

**Accession:** gi|338753361
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl, Oxidation

**Score:** 20.0
**MW [kDa]:** 136.4
**pI:** 5.4
**Sequence Coverage [%]:** 1.6
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVYRTQYLVV | EVPESRNVTD | CCEGYEQLGL | YCVLPLNQSG | QFTSRPGACP | AEGPEPSTSP | CSLDIDCPGL | EKCCPWSGGR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YCMAPAPQAP | ERDPVGSWYN | VTILVKMDFK | ELQQVDPRLL | NHMRLLHSLV | TSALQPMAST | VHHLHSAPGN | ASTTVSRLLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GLPRPLPVAD | VSTLLGDIAK | RVYEVISVQV | QDVNECFYEE | LNACSGRELC | ANLEGSYWCV | CHQEAPATSP | RKLNLEWEDC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PPVSDYVVLN | VTSDSFQVSW | RLNSTQNHTF | HVRVYRGMEL | LRSARTQSQA | LAVAGLEAGV | LYRVKTSYQG | CGADVSTTLT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IKTNAQVFEV | TIKIVNHNLT | EKLLNRSSVE | YQDFSRQLLH | EVESSFPPVV | SDLYRSGKLR | MQIVSLQAGS | VVVRLKLTVQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DPGFPMGIST | LAPILQPLLA | STVFQIDRQG | TRVQDWDECV | DSAEHDCSPA | AWCINLEGSY | TCQCRTTRDA | TPSRAGRACE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GDLVSPTGGG | LSAATGVTVP | GLGTGTAALG | LENFTLSPSP | GYPQGTPAAG | QAWTPEPSPR | RGGSNVVGYD | RNNTGKGVEQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ELQGNSIMEP | PSWPSPTEDP | TGHFLWHATR | STRETLLNPT | WLRNEDSGPS | GSVDLPLTST | LTALKTPACV | PVSIGRIMVS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NVTSTGFHLA | WEADLAMDST | FQLTLTSMWS | PAVVLETWNT | SVTLSGLEPG | VLHLVEIMAK | ACGKEGARAH | LKVRTAARKL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| IGKVRIKNVR | YSESFRNASS | QEYRDFLELF | FRMVRGSLPA | TMCQHMDAGG | VRMEVVSVTN | GSIVVEFHLL | IIADVDVQEV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SAAFLTAFQT | VPLLEVIRGD | TFIQDYDECE | RKEDDCVPGT | SCRNTLGSFT | CSCEGGAPDF | PVEYSERPCE | GDSPGNETWA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TSPERPLTTA | GTKAAFVQGT | SPTPQGLPQR | LNLTGAVRVL | CEIEKVVVAI | QKRFLQQESI | PESSLYLSHP | SCNVSHSNGT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| HVLLEAGWSE | CGTLMQSNMT | NTVVRTTLRN | DLSQEGIIHH | LKILSPIYCA | FQNDLLTSSG | FTLEWGVYTI | IEDLHGAGNF |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VTEMQLFIGD | SPIPQNYSVS | ASDDVRIEVG | LYRQKSNLKV | VLTECWATPS | SNARDPITFS | FINNSCPVPN | TYTNVIENGN |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SNKAQFKLRI | FSFINDSIVY | LHCKLRVCME | SPGATCKINC | NNFRLLQNSE | TSATHQMSWG | PLIRSEGEPP | HAEAGLGAGY |
| 1210 | 1220 | 1230 | 1240 | 1250 | | | |
| VVLIVVAIFV | LVAGTATLLI | VRYQRMNGRY | NFKIQSNNFS | YQVFYE | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 24 | 1 | 1103.5077 | 4.39 | 2 | 30.0 | 20.0 | 1 | 753-772 | R.MVRGSLPATMCQHMDAGGVR.M | Carbamidomethyl: 11;<br>Oxidation: 10, 14 |

# Detailed Protein Report

**Protein 893:** **uncharacterized protein KIAA0226-like isoform f [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|557947998 | **Score:** | 20.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 50.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.6 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MIISAMEKMK CNILSQQQTE SWSKEVSGLL GSDQPDSEMT FDTNIKQESG SSTSSYSGYE GCAVLQVSPV TETRTYHDVK
        90        100        110        120        130        140        150        160
EICKCDVDEF VILELGDFND ITETCSCSCS SSKSVTYEPD FNSAELLAKE LYRVFQKCWI LSVVNSQLAG SLSAAGSIVV
       170        180        190        200        210        220        230        240
NEECVRKDFE SSMNVVQEIK FKSRIRGTED WAPPRFQIIF NIHPPLKRDL VVAAQNFFCA GCGTPVEPKF VKRLRYCEYL
       250        260        270        280        290        300        310        320
GKYFCDCCHS YAESCIPARI LMMWDFKKYY VSNFSKQLLD SIWHQPIFNL LSIGQSLYAK AKELDRVKEI QEQLFHIKKL
       330        340        350        360        370        380        390        400
LKTCRFANSA LKEFEQVPGH LTDELHLFSL EDLVRIKKGL LAPLLKDILK ASLAHVAGCE LCQGKGFICE FCQNTTVIFP
       410        420        430        440        450
FQTATCRRCS ACRACFHKQC FQSSECPRCA RITARRKLLE SVASAAT
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2445 | 1 | 597.3363 | -141.46 | 2 | 58.8 | 20.0 | 2 | 356-366 | R.IKKGLLAPLLK.D | |

# Detailed Protein Report

## Protein 894: PREDICTED: angiopoietin-1 receptor isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530390111 | **Score:** | 20.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 120.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDSLASLVLC | GVSLLLSGTV | EGAMDLILIN | SLPLVSDAET | SLTCIASGWR | PHEPITIGRD | FEALMNQHQD | PLEVTQDVTR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EWAKKVVWKR | EKASKINGAY | FCEGRVRGEA | IRIRTMKMRQ | QASFLPATLT | MTVDKGDNVN | ISFKKVLIKE | EDAVIYKNGS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FIHSVPRHEV | PDILEVHLPH | AQPQDAGVYS | ARYIGGNLFT | SAFTRLIVRR | CEAQKWGPEC | NHLCTACMNN | GVCHEDTGEC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ICPPGFMGRT | CEKACELHTF | GRTCKERCSG | QEGCKSYVFC | LPDPYGCSCA | TGWKGLQCNE | GIQRMTPKIV | DLPDHIEVNS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GKFNPICKAS | GWPLPTNEEM | TLVKPDGTVL | HPKDFNHTDH | FSVAIFTIHR | ILPPDSGVWV | CSVNTVAGMV | EKPFNISVKV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LPKPLNAPNV | IDTGHNFAVI | NISSEPYFGD | GPIKSKKLLY | KPVNHYEAWQ | HIQVTNEIVT | LNYLEPRTEY | ELCVQLVRRG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EGGEGHPGPV | RRFTTASIGL | PPPRGLNLLP | KSQTTLNLTW | QPIFPSSEDD | FYVEVERRSV | QKSDQQNIKV | PGNLTSVLLN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NLHPREQYVV | RARVNTKAQG | EWSEDLTAWT | LSDILPPQPE | NIKISNITHS | SAVISWTILD | GYSISSITIR | YKVQGKNEDQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HVDVKIKNAT | ITQYQLKGLE | PETAYQVDIF | AENNIGSSNP | AFSHELVTLP | ESQAPADLGG | GKMLLIAILG | SAGMTCLTVL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LAFLIILQLK | RANVQRRMAQ | AFQNREEPAV | QFNSGTLALN | RKVKNNPDPT | IYPVLDWNDI | KFQDVIGEGN | FGQVLKARIK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KDGLRMDAAI | KRMKEYASKD | DHRDFAGELE | VLCKLGHHPN | IINLLGACEH | RGYLYLAIEY | APHGNLLDFL | RKSRVLETDP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| AFAIANSTAS | TLSSQQLLHF | AADVARGMDY | LSQKQFIHRD | LAARNILVGE | NYVAKIADFG | LSRGQEVYVK | KTMGRLPVRW |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| MAIESLNYSV | YTTNSDVWSY | GVLLWEIVSL | GGTPYCGMTC | AELYEKLPQG | YRLEKPLNCD | DEVYDLMRQC | WREKPYERPS |
| 1050 | 1060 | 1070 | 1080 | 1090 | | | |
| FAQILVSLNR | MLEERKTYVN | TTLYEKFTYA | GIDCSAEEAA | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2675 | 1 | 841.3883 | -72.13 | 2 | 63.6 | 20.0 | 1 | 936-950 | K.IADFGLSRGQEVYVK.K | |

# Detailed Protein Report

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**Protein 895:** **ovochymase-2 precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|373838920 | **Score:** | 19.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 62.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLISRNKLIL | LLGIVFFERG | KSATLSLPKA | PSCGQSLVKV | QPWNYFNIFS | RILGGSQVEK | GSYPWQVSLK | QRQKHICGGS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IVSPQWVITA | AHCIANRNIV | STLNVTAGEY | DLSQTDPGEQ | TLTIETVIIH | PHFSTKKPMD | YDIALLKMAG | AFQFGHFVGP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ICLPELREQF | EAGFICTTAG | WGRLTEGGVL | SQVLQEVNLP | ILTWEECVAA | LLTLKRPISG | KTFLCTGFPD | GGRDACQGDS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GGSLMCRNKK | GAWTLAGVTS | WGLGCGRGWR | NNVRKSDQGS | PGIFTDISKV | LPWIHEHIQT | GNRRKSSRAW | CSEQDVIVSG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AEGKLHFPES | LHLYYESKQR | CVWTLLVPEE | MHVLLSFSHL | DVESCHHSYL | SMYSLEDRPI | GKFCGESLPS | SILIGSNSLR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LKFVSDATDN | AAGFNLTYKA | LKPNYIPDSG | CSYLTVLFEE | GLIQSLNYPE | NYSDKANCDW | IFQASKHHLI | KLSFQSLEIE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ESGDCTSDYV | TVHSDVERKK | EIARLCGYDV | PTPVLSPSSI | MLISFQSDEN | GTCRGFQATV | SFIPKAVYPD | LNISISEDES |
| 570 | | | | | | | |
| MFLET | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1535 | 3 | 850.5690 | 134.04 | 2 | 47.5 | 19.9 | 0 | 290-303 | K.VLPWIHEHIQTGNR.R | |

# Detailed Protein Report

## Protein 896: thymopoietin isoform alpha [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4507555 | **Score:** | 19.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 75.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.5 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPEFLEDPSV | LTKDKLKSEL | VANNVTLPAG | EQRKDVYVQL | YLQHLTARNR | PPLPAGTNSK | GPPDFSSDEE | REPTPVLGSG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AAAAGRSRAA | VGRKATKKTD | KPRQEDKDDL | DVTELTNEDL | LDQLVKYGVN | PGPIVGTTRK | LYEKKLLKLR | EQGTESRSST |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PLPTISSSAE | NTRQNGSNDS | DRYSDNEEGK | KKEHKKVKST | RDIVPFSELG | TTPSGGGFFQ | GISFPEISTR | PPLGSTELQA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AKKVHTSKGD | LPREPLVATN | LPGRGQLQKL | ASERNLFISC | KSSHDRCLEK | SSSSSSQPEH | SAMLVSTAAS | PSLIKETTTG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YYKDIVENIC | GREKSGIQPL | CPERSHISDQ | SPLSSKRKAL | EESESSQLIS | PPLAQAIRDY | VNSLLVQGGV | GSLPGTSNSM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PPLDVENIQK | RIDQSKFQET | EFLSPPRKVP | RLSEKSVEER | DSGSFVAFQN | IPGSELMSSF | AKTVVSHSLT | TLGLEVAKQS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QHDKIDASEL | SFPFHESILK | VIEEEWQQVD | RQLPSLACKY | PVSSREATQI | LSVPKVDDEI | LGFISEATPL | GGIQAASTES |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| CNQQLDLALC | RAYEAAASAL | QIATHTAFVA | KAMQADISQA | AQILSSDPSR | THQALGILSK | TYDAASYICE | AAFDEVKMAA |
| 650 | 660 | 670 | 680 | 690 | 700 | | |
| HTMGNATVGR | RYLWLKDCKI | NLASKNKLAS | TPFKGGTLFG | GEVCKVIKKR | GNKH | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1398 | 2 | 991.6129 | 89.59 | 1 | 47.6 | 19.9 | 1 | 657-665 | K.DCKINLASK.N | |

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# Detailed Protein Report

## Protein 897: retinol dehydrogenase 10 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|25282469 | **Score:** | 19.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.9 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNIVVEFFVV | TFKVLWAFVL | AAARWLVRPK | EKSVAGQVCL | ITGAGSGLGR | LFALEFARRR | ALLVLWDINT | QSNEETAGMV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RHIYRDLEAA | DAAALQAGNG | EEEILPHCNL | QVFTYTCDVG | KRENVYLTAE | RVRKEVGEVS | VLVNNAGVVS | GHHLLECPDE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LIERTMMVNC | HAHFWTTKAF | LPTMLEINHG | HIVTVASSLG | LFSTAGVEDY | CASKFGVVGF | HESLSHELKA | AEKDGIKTTL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VCPYLVDTGM | FRGCRIRKEI | EPFLPPLKPD | YCVKQAMKAI | LTDQPMICTP | RLMYIVTFMK | SILPFEAVVC | MYRFLGADKC |
| 330 | 340 | 350 | | | | | |
| MYPFIAQRKQ | ATNNNEAKNG | I | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 365 | 1 | 639.8907 | 24.31 | 2 | 33.2 | 19.8 | 2 | 51-60 | R.LFALEFARRR.A | |

# Detailed Protein Report

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## Protein 898: PREDICTED: DNA topoisomerase 2-binding protein 1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530373836 | **Score:** | 19.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 170.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| | | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSRNDKEPFF | VKFLKSSDNS | KCFFKALESI | KEFQSEEYLQ | IITEEEALKI | KENDRSLYIC | DPFSGVVFDH | LKKLGCRIVG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PQVVIFCMHH | QRCVPRAEHP | VYNMVMSDVT | ISCTSLEKEK | REEVHKYVQM | MGGRVYRDLN | VSVTHLIAGE | VGSKKYLVAA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NLKKPILLPS | WIKTLWEKSQ | EKKITRYTDI | NMEDFKCPIF | LGCIICVTGL | CGLDRKEVQQ | LTVKHGGQYM | GQLKMNECTH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LIVQEPKGQK | YECAKRWNVH | CVTTQWFFDS | IEKGFCQDES | IYKTEPRPEA | KTMPNSSTPT | SQINTIDNVS | NISNINASCV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SESICNSLNS | KLEPTLENLE | NLDVSAFQAP | EDLLDGCRIY | LCGFSGRKLD | KLRRLINSGG | GVRFNQLNED | VTHVIVGDYD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DELKQFWNKS | AHRPHVVGAK | WLLECFSKGY | MLSEEPYIHA | NYQPVEIPVS | HKPESKAALL | KKKNSSFSKK | DFAPSEKHEQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ADEDLLSQYE | NGSSTVVEAK | TSEARPFNDS | THAEPLNDST | HISLQEENQS | SVSHCVPDVS | TITEEGLFSQ | KSFLVLGFSN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ENESNIANII | KENAGKIMSL | LSRTVADYAV | VPLLGCEVEA | TVGEVVTNTW | LVTCIDYQTL | FDPKSNPLFT | PVPVMTGMTP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LEDCVISFSQ | CAGAEKESLT | FLANLLGASV | QEYFVRKSNA | KKGMFASTHL | ILKERGGSKY | EAAKKWNLPA | VTIAWLLETA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RTGKRADESH | FLIENSTKEE | RSLETEITNG | INLNSDTAEH | PGTRLQTHRK | TVVTPLDMNR | FQSKAFRAVV | SQHARQVAAS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PAVGQPLQKE | PSLHLDTPSK | FLSKDKLFKP | SFDVKDALAA | LETPGRPSQQ | KRKPSTPLSE | VIVKNLQLAL | ANSSRNAVAL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SASPQLKEAQ | SEKEEAPKPL | HKVVVCVSKK | LSKKQSELNG | IAASLGADYR | WSFDETVTHF | IYQGRPNDTN | REYKSVKERG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VHIVSEHWLL | DCAQECKHLP | ESLYPHTYNP | KMSLDISAVQ | DGRLCNSRLL | SAVSSTKDDE | PDPLILEEND | VDNMATNNKE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SAPSNGSGKN | DSKGVLTQTL | EMRENFQKQL | QEIMSATSIV | KPQGQRTSLS | RSGCNSASST | PDSTRSARSG | RSRVLEALRQ |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SRQTVPDVNT | EPSQNEQIIW | DDPTAREERA | RLASNLQWPS | CPTQYSELQV | DIQNLEDSPF | QKPLHDSEIA | KQAVCDPGNI |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| RVTEAPKHPI | SEELETPIKD | SHLIPTPQAP | SIAFPLANPP | VAPHPREKII | TIEETHEELK | KQYIFQLSSL | NPQERIDYCH |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LIEKLGGLVI | EKQCFDPTCT | HIVVGHPLRN | EKYLASVAAG | KWVLHRSYLE | ACRTAGHFVQ | EEDYEWGSSS | ILDVLTGINV |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| QQRRLALAAM | RWRKKIQQRQ | ESGIVEGAFS | GWKVILHVDQ | SREAGFKRLL | QSGGAKVLPG | HSVPLFKEAT | HLFSDLNKLK |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| PDDSGVNIAE | AAAQNVYCLR | TEYIADYLMQ | ESPPHVENYC | LPEAISFIQN | NKELGTGLSQ | KRKAPTEKNK | IKRPVH |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1880 | 1 | 697.5427 | 213.85 | 2 | 51.8 | 19.8 | 0 | 796-809 | R.QVAASPAVGQPLQK.E | |

# Detailed Protein Report

## Protein 899: alpha-2-HS-glycoprotein preproprotein [Homo sapiens]

**Accession:** gi|156523970

**Database:** refseq_human(refseq_human_20140103.fasta)

**Database Date:** 2015-11-30

**Modification(s):** Carbamidomethyl

**Score:** 19.8

**MW [kDa]:** 39.3

**pI:** 5.4

**Sequence Coverage [%]:** 6.5

**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKSLVLLLCL | AQLWGCHSAP | HGPGLIYRQP | NCDDPETEEA | ALVAIDYINQ | NLPWGYKHTL | NQIDEVKVWP | QQPSGELFEI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EIDTLETTCH | VLDPTPVARC | SVRQLKEHAV | EGDCDFQLLK | LDGKFSVVYA | KCDSSPDSAE | DVRKVCQDCP | LLAPLNDTRV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VHAAKAALAA | FNAQNNGSNF | QLEEISRAQL | VPLPPSTYVE | FTVSGTDCVA | KEATEAAKCN | LLAEKQYGFC | KATLSEKLGG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AEVAVTCMVF | QTQPVSSQPQ | PEGANEAVPT | PVVDPDAPPS | PPLGAPGLPP | AGSPPDSHVL | LAAPPGHQLH | RAHYDLRHTF |
| 330 | 340 | 350 | 360 | 370 | | | |
| MGVVSLGSPS | GEVSHPRKTR | TVVQPSVGAA | AGPVVPPCPG | RIRHFKV | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2906 | 1 | 860.4973 | 66.36 | 3 | 65.1 | 19.8 | 0 | 188-211 | R.AQLVPLPPSTYVEFTVSGTDCVAK.E | Carbamidomethyl: 21 |

# Detailed Protein Report

## Protein 900: fructose-bisphosphate aldolase A isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4557305 | **Score:** | 19.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| | | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|193794814 | refseq_huma (refseq_human_20140103.fasta) | fructose-bisphosphate aldolase A isoform 1 [Homo sapiens] |
| gi\|34577112 | refseq_huma (refseq_human_20140103.fasta) | fructose-bisphosphate aldolase A isoform 1 [Homo sapiens] |
| gi\|34577110 | refseq_huma (refseq_human_20140103.fasta) | fructose-bisphosphate aldolase A isoform 1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPYQYPALTP | EQKKELSDIA | HRIVAPGKGI | LAADESTGSI | AKRLQSIGTE | NTEENRRFYR | QLLLTADDRV | NPCIGGVILF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HETLYQKADD | GRPFPQVIKS | KGGVVGIKVD | KGVVPLAGTN | GETTTQGLDG | LSERCAQYKK | DGADFAKWRC | VLKIGEHTPS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ALAIMENANV | LARYASICQQ | NGIVPIVEPE | ILPDGDHDLK | RCQYVTEKVL | AAVYKALSDH | HIYLEGTLLK | PNMVTPGHAC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TQKFSHEEIA | MATVTALRRT | VPPAVTGITF | LSGGQSEEEA | SINLNAINKC | PLLKPWALTF | SYGRALQASA | LKAWGGKKEN |
| 330 | 340 | 350 | 360 | 370 | | | |
| LKAAQEEYVK | RALANSLACQ | GKYTPSGQAG | AAASESLFVS | NHAY | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 476 | 1 | 717.8845 | 24.70 | 2 | 35.9 | 19.8 | 0 | 2-13 | M.PYQYPALTPEQK.K | |

# Detailed Protein Report

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**Protein 901:** **choline-phosphate cytidylyltransferase B isoform 2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|253795514 | **Score:** | 19.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVGHQECIME | EDNRAPQLWR | KTLTAPAPFA | DETNCQCQAP | HEKLTIAQAR | LGTPADRPVR | VYADGIFDLF | HSGHARALMQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AKTLFPNSYL | LVGVCSDDLT | HKFKGFTVMN | EAERYEALRH | CRYVDEVIRD | APWTLTPEFL | EKHKIDFVAH | DDIPYSSAGS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DDVYKHIKEA | GMFVPTQRTE | GISTSDIITR | IVRDYDVYAR | RNLQRGYTAK | ELNVSFINEK | RYRFQNQVDK | MKEKVKNVEE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RSKEFVNRVE | EKSHDLIQKW | EEKSREFIGN | FLELFGPDGA | WKQMFQERSS | RMLQALSPKQ | SPVSSPTRSR | SPSRSPSPTF |
| 330 | 340 | 350 | 360 | | | | |
| SWLPLKTSPP | SSPKAASASI | SSMSEGDEDE | K | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 125 | 1 | 1301.5081 | -71.85 | 2 | 31.5 | 19.7 | 2 | 1-21 | -.MVGHQECIMEEDNRAPQLWRK.T | Oxidation: 1, 9 |

# Detailed Protein Report

**Protein 902:** **CMP-N-acetylneuraminate-beta-1,4-galactoside alpha-2,3-sialyltransferase isoform n [Homo sapiens]**

| | | | | |
|---|---|---|---|---|
| **Accession:** | gi\|394953753 | | **Score:** | 19.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | | **MW [kDa]:** | 26.7 |
| **Database Date:** | 2015-11-30 | | **pI:** | 10.2 |
| | | | **Sequence Coverage [%]:** | 4.8 |
| | | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGLLVFVRNL | LLALCLFLVL | GFLYYSAWKL | HLLQWEEDSK | YDRLGFLLNL | DSKLFSKPAP | MFLDDSFRKW | ARIREFVPPF |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| GIKGQDNLIK | AILSVTKEYR | LTPALDSLRC | RRCIIVGNGG | VLANKSLGSR | IDDYDIVVRL | NSAPVKGFEK | DVGSKTTLRI |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| TYPEGAMQRP | EQYERDSLFV | LAGFKWQDFK | WLKYIVYKER | VSWTHNIQRE | KEFLRKLVKA | RVITDLSSGI | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2153 | 1 | 1131.4149 | -196.06 | 1 | 56.8 | 19.7 | 1 | 220-230 | K.ARVITDLSSGI.- | |

# Detailed Protein Report

## Protein 903: PREDICTED: exostosin-like 1 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578798624 | **Score:** | 19.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 53.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.70 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQSWRRRKSL | WLALSASWLL | LVLLGGFSLL | RLALPPRPRP | GASQGWPRWL | DAELLQSFSQ | PGELPEDAVS | PPQAPHGGSC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NWESCFDTSK | CRGDGLKVFV | YPAVGTISET | HRRILASIEG | SRFYTFSPAG | ACLLLLLSLD | AQTGECSSMP | LQWNRGRNHL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VLRLHPAPCP | RTFQLGQAMV | AEASPTVDSF | RPGFDVALPF | LPEAHPLRGG | APGQLRQHSP | QPGVALLALE | EERGGWRTAD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TGSSACPWDG | RCEQDPGPGQ | TQRQETLPNA | TFCLISGHRP | EAASRFLQAL | QAGCIPVLLS | PRWELPFSEV | IDWTKAAIVA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DERLPLQVLA | ALQEMSPARV | LALRQQTQFL | WDAYFSSVEK | VIHTTLEVIQ | DRIFGTSAHP | SLLWNSPPGA | LLALSTFSTS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PQDFPFYYLQ | QGSRPEGRFS | ALIWVGPPGQ | PPLKLIQAVA | GSQHCAQFTK | LTSQTSSTLR | KITPAPRNPP | SAPDPRLQEQ |
| 490 | | | | | | | |
| PPIL | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 933 | 1 | 712.4616 | 88.10 | 2 | 40.0 | 19.7 | 0 | 361-372 | K.VIHTTLEVIQDR.I | | QU:MU 0.70 |

# Detailed Protein Report

## Protein 904: interferon regulatory factor 2-binding protein-like [Homo sapiens]

**Accession:** gi|33457336
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 19.6
**MW [kDa]:** 82.6
**pI:** 9.6
**Sequence Coverage [%]:** 1.5
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSAAQVSSSR | RQSCYLCDLP | RMPWAMIWDF | SEPVCRGCVN | YEGADRIEFV | IETARQLKRA | HGCFQDGRSP | GPPPPVGVKT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VALSAKEAAA | AAAAAAAAAA | AAQQQQQQQQ | QQQQQQQQQQ | QQQQQQQLNH | VDGSSKPAVL | AAPSGLERYG | LSAAAAAAAA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AAAAVEQRSR | FEYPPPPVSL | GSSSHTARLP | NGLGGPNGFP | KPTPEEGPPE | LNRQSPNSSS | AAASVASRRG | THGGLVTGLP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NPGGGGGPQL | TVPPNLLPQT | LLNGPASAAV | LPPPPPHALG | SRGPPTPAPP | GAPGGPACLG | GTPGVSATSS | SASSSTSSSV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AEVGVGAGGK | RPGSVSSTDQ | ERELKEKQRN | AEALAELSES | LRNRAEEWAS | KPKMVRDTLL | TLAGCTPYEV | RFKKDHSLLG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RVFAFDAVSK | PGMDYELKLF | IEYPTGSGNV | YSSASGVAKQ | MYQDCMKDFG | RGLSSGFKYL | EYEKKHGSGD | WRLLGDLLPE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AVRFFKEGVP | GADMLPQPYL | DASCPMLPTA | LVSLSRAPSA | PPGTGALPPA | APSGRGAAAS | LRKRKASPEP | PDSAEGALKL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GEEQQRQQWM | ANQSEALKLT | MSAGGFAAPG | HAAGGPPPPP | PPLGPHSNRT | TPPESAPQNG | PSPMAALMSV | ADTLGTAHSP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KDGSSVHSTT | ASARRNSSSP | VSPASVPGQR | RLASRNGDLN | LQVAPPPPSA | HPGMDQVHPQ | NIPDSPMANS | GPLCCTICHE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RLEDTHFVQC | PSVPSHKFCF | PCSRESIKAQ | GATGEVYCPS | GEKCPLVGSN | VPWAFMQGEI | ATILAGDVKV | KKERDP |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2766 | 1 | 659.8617 | 61.81 | 2 | 63.1 | 19.6 | 0 | 331-342 | K.RPGSVSSTDQER.E | |

# Detailed Protein Report

## Protein 905: integrin beta-like protein 1 isoform 3 [Homo sapiens]

**Accession:** gi|418203907
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 19.5
**MW [kDa]:** 43.9
**pI:** 5.0
**Sequence Coverage [%]:** 3.0
**No. of unique Peptides:** 1

## Quantitation

***QU:MU*** **Median:** 2.42 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNLVAVMGAF | NKGHGKCDCG | KCKCDQGWYG | DACQYPTNCD | LTKKKSNQMC | KNSQDIICSN | AGTCHCGRCK | CDNSDGSGLV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YGKFCECDDR | ECIDDETEEI | CGGHGKCYCG | NCYCKAGWHG | DKCEFQCDIT | PWESKRRCTS | PDGKICSNRG | TCVCGECTCH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DVDPTGDWGD | IHGDTCECDE | RDCRAVYDRY | SDDFCSGHGQ | CNCGRCDCKA | GWYGKKCEHP | QSCTLSAEES | IRKCQGSSDL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PCSGRGKCEC | GKCTCYPPGD | RRVYGKTCEC | DDRRCEDLDG | VVCGGHGTCS | CGRCVCERGW | FGKLCQHPRK | CNMTEEQSKN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LCESADGILC | SGKGSCHCGK | CICSAEEWYI | SGEFCDCDDR | DCDKHDGLIC | TGNGICSCGN | CECWDGWNGN | ACEIWLGSEY |
| 410 | | | | | | | |
| P | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 864 | 1 | 647.7154 | -186.04 | 2 | 40.9 | 19.5 | 0 | 1-12 | -.MNLVAVMGAFNK.G | | QU:MU 2.42 |

# Detailed Protein Report

**Protein 906:** **rho GTPase-activating protein 19 isoform 3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|374093192 | **Score:** | 19.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPHQKLSALI | DAICSFVICN | DSSLRGQPII | FNPDFFVEKL | RHEKPEIFTE | LVVSNITRLI | DLPGTELAQL | MGEVDLKLPG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GAGPASGFFR | SLMSLKRKEK | GVIFGSPLTE | EGIAQIYQLI | EYLHKNLRVE | GLFRVPGNSV | RQQILRDALN | NGTDIDLESG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EFHSNDVATL | LKMFLGELPE | PLLTHKHFNA | HLKIADLMQF | DDKGNKTNIP | DKDRQIEALQ | LLFLILPPPN | RNLLKLLLDL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LYQTAKKQDK | NKMSAYNLAL | MFAPHVLWPK | NVTANDLQEN | ITKLNSGMAF | MIKHSQKLFK | APAYIRECAR | LHYLGSRTQA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SKDDLDLIAS | CHTKSFQLAK | SQKRNRVDSC | PHQEETQHHT | EEALRELFQH | VHDMPESAKK | KQLIRQFNKQ | SLTQTPGREP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| STSQVQKRAR | SRSFSGLIKR | KVLGNQMMSE | KKKKNPTPES | VAIGELKGTS | KENRNLLFSG | SPAVTMTPTR | LKWSEGKKEG |
| 490 | | | | | | | |
| KKGFL | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 693 | 1 | 556.2788 | -12.08 | 2 | 37.1 | 19.5 | 0 | 284-293 | K.LNSGMAFMIK.H | |

# Detailed Protein Report

## Protein 907: protein S100-A9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4506773 | **Score:** | 19.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 13.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 11.4 |
| | | **No. of unique Peptides:** | 1 |

```
         10         20         30         40         50         60         70         80
MTCKMSQLER NIETIINTFH QYSVKLGHPD TLNQGEFKEL VRKDLQNFLK KENKNEKVIE HIMEDLDTNA DKQLSFEEFI
         90        100        110        120
MLMARLTWAS HEKMHEGDEG PGHHHKPGLG EGTP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 217 | 1 | 728.3427 | -30.59 | 2 | 32.7 | 19.4 | 0 | 26-38 | K.LGHPDTLNQGEFK.E | |

# Detailed Protein Report

## Protein 908: PREDICTED: NT-3 growth factor receptor isoform X9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578827025 | **Score:** | 19.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 55.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDVSLCPAKC | SFWRIFLLGS | VWLDYVGSVL | ACPANCVCSK | TEINCRRPDD | GNLFPLLEGQ | DSGNSNGNAS | INITDISRNI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TSIHIENWRS | LHTLNAVDME | LYTGLQKLTI | KNSGLRSIQP | RAFAKNPHLR | YINLSSNRLT | TLSWQLFQTL | SLRELQLEQN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FFNCSCDIRW | MQLWQEQGEA | KLNSQNLYCI | NADGSQLPLF | RMNISQCDLP | EISVSHVNLT | VREGDNAVIT | CNGSGSPLPD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VDWIVTGLQS | INTHQTNLNW | TNVHAINLTL | VNVTSEDNGF | TLTCIAENVV | GMSNASVALT | VYYPPRVVSL | EEPELRLEHC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IEFVVRGNPP | PTLHWLHNGQ | PLRESKIIHV | EYYQEGEISE | GCLLFNKPTH | YNNGNYTLIA | KNPLGTANQT | INGHFLKEPF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PVDEVSPTPP | ITVTHKPEED | TFGVSIAVGL | AAFACVLLVV | LFVMINKYGR | RSKFGMKDGL | ELLAVLLKCD | SKQLKNKEGN |
| 490 | 500 | | | | | | |
| KMKNNNGKKK | RATSA | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 342 | 1 | 699.2835 | -131.98 | 3 | 32.9 | 19.3 | 2 | 454-472 | K.FGMKDGLELLAVLLKCDSK.Q | Oxidation: 3 |

# Detailed Protein Report

## Protein 909: PREDICTED: cleavage and polyadenylation specificity factor subunit 7 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530397403 | **Score:** | 19.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.38 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.48 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530397405 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: cleavage and polyadenylation specificity factor subunit 7 isoform X6 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MWTTDQQLIQ VIRSIGVYDV VELKFAENRA NGQSKGYAEV VVASENSVHK LLELLPGKVL NGEKVDVRPA TRQNLSQFEA
        90        100        110        120        130        140        150        160
QARKRECVRV PRGGIPPRAH SRDSSDSADG RATPSENLVP SSARVDKPPS VLPYFNRPPS ALPLMGLPPP PIPPPPPLSS
       170        180        190        200        210        220        230        240
SFGVPPPPPG IHYQHLMPPP PRLPPHLAVP PPGAIPPALH LNPAFFPPPN ATVGPPPDTY MKASAPYNHH GSRDSGPPPS
       250        260        270        280        290        300        310        320
TVSEAEFEDI MKRNRAISSS AISKAVSGAS AGDYSDAIET LLTAIAVIKQ SRVANDERCR VLISSLKDCL HGIEAKSYSV
       330        340        350        360        370        380        390
GASGSSSRKR HRSRERSPSR SRESSRRHRD LLHNEDRHDD YFQERNREHE RHRDRERDRH H
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2002 | 3 | 794.7799 | -153.57 | 2 | 54.9 | 19.3 | 0 | 36-50 | K.GYAEVVVASENSVHK.L | | WUP:QUP 0.48<br>QU:MU 1.38 |

# Detailed Protein Report

## Protein 910: PREDICTED: CD300c molecule-like isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530356604 | **Score:** | 19.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 18.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 7.6 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578846497 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: CD300c molecule-like isoform X4 [Homo sapiens] |
| gi\|578831945 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: CD300c molecule-like isoform X3 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MGAVGESLSV QCRYEEKYKT FNKYWCRQPC LPIWHEMVET GGSEGVVRSD QVIITDHPGD LTFTVTLENL TADDAGKYRC
        90        100        110        120        130        140        150        160
GIATILQEDG LSGFLPDPFF QVQVLVSSAS STENSVKTPA SPTRPSQCQG SLPSSTCFLL LPLLKVPLLL SILGAILWVN
       170        180
RPWRTPWTES
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2788 | 2 | 676.8636 | 66.68 | 2 | 63.4 | 19.2 | 0 | 1-13 | -.MGAVGESLSVQCR.Y | Oxidation: 1 |

# Detailed Protein Report

## Protein 911: pigment epithelium-derived factor precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|39725934 | **Score:** | 19.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 4.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MQALVLLLCI | GALLGHSSCQ | NPASPPEEGS | PDPDSTGALV | EEEDPFFKVP | VNKLAAAVSN | FGYDLYRVRS | STSPTTNVLL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SPLSVATALS | ALSLGAEQRT | ESIIHRALYY | DLISSPDIHG | TYKELLDTVT | APQKNLKSAS | RIVFEKKLRI | KSSFVAPLEK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SYGTRPRVLT | GNPRLDLQEI | NNWVQAQMKG | KLARSTKEIP | DEISILLLGV | AHFKGQWVTK | FDSRKTSLED | FYLDEERTVR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VPMMSDPKAV | LRYGLDSDLS | CKIAQLPLTG | SMSIIFFLPL | KVTQNLTLIE | ESLTSEFIHD | IDRELKTVQA | VLTVPKLKLS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YEGEVTKSLQ | EMKLQSLFDS | PDFSKITGKP | IKLTQVEHRA | GFEWNEDGAG | TTPSPGLQPA | HLTFPLDYHL | NQPFIFVLRD |
| 410 | 420 | | | | | | |
| TDTGALLFIG | KILDPRGP | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1722 | 1 | 1044.9651 | -138.77 | 2 | 51.3 | 19.2 | 0 | 263-281 | K.IAQLPLTGSMSIIFFLPLK.V | |

# Detailed Protein Report

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## Protein 912: PREDICTED: clusterin isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578815184 | **Score:** | 19.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 4.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQVCSQPQRG | CVREQSAINT | APPSAHNAAS | PGGARGHRVP | LTEACKDSRI | GGMMKTLLLF | VGLLLTWESG | QVLGDQTVSD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NELQEMSNQG | SKYVNKEIQN | AVNGVKQIKT | LIEKTNEERK | TLLSNLEEAK | KKKEDALNET | RESETKLKEL | PGVCNETMMA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LWEECKPCLK | QTCMKFYARV | CRSGSGLVGR | QLEEFLNQSS | PFYFWMNGDR | IDSLLENDRQ | QTHMLDVMQD | HFSRASSIID |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ELFQDRFFTR | EPQDTYHYLP | FSLPHRRPHF | FFPKSRIVRS | LMPFSPYEPL | NFHAMFQPFL | EMIHEAQQAM | DIHFHSPAFQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HPPTEFIREG | DDDRTVCREI | RHNSTGCLRM | KDQCDKCREI | LSVDCSTNNP | SQAKLRRELD | ESLQVAERLT | RKYNELLKSY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QWKMLNTSSL | LEQLNEQFNW | VSRLANLTQG | EDQYYLRVTT | VASHTSDSDV | PSGVTEVVVK | LFDSDPITVT | VPVEVSRKNP |
| 490 | 500 | 510 | | | | | |
| KFMETVAEKA | LQEYRKKHRE | E | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1641 | 1 | 1052.5617 | 47.24 | 2 | 50.3 | 19.2 | 0 | 14-35 | R.EQSAINTAPPSAHNAASPGGAR.G | |

# Detailed Protein Report

## Protein 913: protein FAM83G [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|115392150 | **Score:** | 19.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 90.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.30 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.66 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAFSQVQCLD | DNHVNWRSSE | SKPEFFYSEE | QRLALEALVA | RGRDAFYEVL | KRENIRDFLS | ELELKRILET | IEVYDPGSED |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PRGTGPSQGP | EDNGVGDGEE | ASGADGVPIE | AEPLPSLEYW | PQKSDRSIPQ | LDLGWPDTIA | YRGVTRASVY | MQPPIDGQAH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IKEVVRKMIS | QAQKVIAVVM | DMFTDVDIFK | DLLDAGFKRK | VAVYIIVDES | NVKYFLHMCE | RACMHLGHLK | NLRVRSSGGT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EFFTRSATKF | KGALAQKFMF | VDGDRAVCGS | YSFTWSAART | DRNVISVLSG | QVVEMFDRQF | QELYLMSHSV | SLKGIPMEKE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PEPEPIVLPS | VVPLVPAGTV | AKKLVNPKYA | LVKAKSVDEI | AKISSEKQEA | KKPLGLKGPA | LAEHPGELPE | LLPPIHPGLL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HLERANMFEY | LPTWVEPDPE | PGSDILGYIN | IIDPNIWNPQ | PSQMNRIKIR | DTSQASAQHQ | LWKQSQDSRP | RPEPCPPPEP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SAPQDGVPAE | NGLPQGDPEP | LPPVPKPRTV | PVADVLARDS | SDIGWVLELP | KEEAPQNGTD | HRLPRMAGPG | HAPLQRQLSV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TQDDPESLGV | GLPNGLDGVE | EEDDDDYVTL | SDQDSHSGSS | GRGPGPRRPS | VASSVSEEYF | EVREHSVPLR | RRHSEQVANG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PTPPPRRQLS | APHITRGTFV | GPQGGSPWAQ | SRGREEADAL | KRMQAQRSTD | KEAQGQQFHH | HRVPASGTRD | KDGFPGPPRY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RSAADSVQSS | TRNAGPAMAG | PHHWQAKGGQ | VPRLLPDPGS | PRLAQNARPM | TDGRATEEHP | SPFGIPYSKL | SQSKHLKART |
| 810 | 820 | 830 | | | | | |
| GGSQWASSDS | KRRAQAPRDR | KDP | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 546 | 5 | 492.6414 | -231.48 | 2 | 36.4 | 19.0 | 0 | 44-51 | R.DAFYEVLK.R | | WUP:QUP 0.66<br>QU:MU 2.30 |

# Detailed Protein Report

## Protein 914: piezo-type mechanosensitive ion channel component 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|257900451 | **Score:** | 19.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 317.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 0.5 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASEVVCGLI | FRLLLPICLA | VACAFRYNGL | SFVYLIYLLL | IPLFSEPTKT | TMQGHTGRLL | KSLCFISLSF | LLLHIIFHIT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LVSLEAQHRI | APGYNCSTWE | KTFRQIGFES | LKGADAGNGI | RVFVPDIGMF | IASLTIWLLC | RNIVQKPVTD | EAAQSNPEFE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NEELAEGEKI | DSEEALIYEE | DFNGGDGVEG | ELEESTKLKM | FRRLASVASK | LKEFIGNMIT | TAGKVVVTIL | LGSSGMMLPS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LTSSVYFFVF | LGLCTWWSWC | RTFDPLLFSC | LCVLLAIFTA | GHLIGLYLYQ | FQFFQEAVPP | NDYYARLFGI | KSVIQTDCSS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TWKIIVNPDL | SWYHHANPIL | LLVMYYTLAT | LIRIWLQEPL | VQDEGTKEED | KALACSPIQI | TAGRRRSLWY | ATHYPTDERK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LLSMTQDDYK | PSDGLLVTVN | GNPVDYHTIH | PSLPMENGPG | KADLYSTPQY | RWEPSDESSE | KREEEEEEKE | EFEEERSREE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KRSIKVHAMV | SVFQFIMKQS | YICALIAMMA | WSITYHSWLT | FVLLIWSCTL | WMIRNRRKYA | MISSPFMVVY | GNLLLILQYI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| WSFELPEIKK | VPGFLEKKEP | GELASKILFT | ITFWLLLRQH | LTEQKALQEK | EALLSEVKIG | SQENEEKDEE | LQDIQVEGEP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KEEEEEEAKE | EKQERKKVEQ | EEAEEEDEQD | IMKVLGNLVV | AMFIKYWIYV | CGGMFFFVSF | EGKIVMYKII | YMVLFLFCVA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LYQVHYEWWR | KILKYFWMSV | VIYTMLVLIF | IYTYQFENFP | GLWQNMTGLK | KEKLEDLGLK | QFTVAELFTR | IFIPTSFLLV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| CILHLHYFHD | RFLELTDLKS | IPSKEDNTIY | RLAHPEGSLP | DLTMMHLTAS | LEKPEVRKLA | EPGEEKLEGY | SEKAQKGDLG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KDSEESEEDG | EEEEESEEEE | ETSDLRNKWH | LVIDRLTVLF | LKFLEYFHKL | QVFMWWILEL | HIIKIVSSYI | IWVSVKEVSL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FNYVFLISWA | FALPYAKLRR | LASSVCTVWT | CVIIVCKMLY | QLQTIKPENF | SVNCSLPNEN | QTNIPFNELN | KSLLYSAPID |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PTEWVGLRKS | SPLLVYLRNN | LLMLAILAFE | VTIYRHQEYY | RGRNNLTAPV | SRTIFHDITR | LHLDDGLINC | AKYFINYFFY |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KFGLETCFLM | SVNVIGQRMD | FYAMIHACWL | IAVLYRRRRK | AIAEIWPKYC | CFLACIITFQ | YFICIGIPPA | PCRDYPWRFK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| GASFNDNIIK | WLYFPDFIVR | PNPVFLVYDF | MLLLCASLQR | QIFEDENKAA | VRIMAGDNVE | ICMNLDAASF | SQHNPVPDFI |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| HCRSYLDMSK | VIIFSYLFWF | VLTIIFITGT | TRISIFCMGY | LVACFYFLLF | GGDLLLKPIK | SILRYWDWLI | AYNVFVITMK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| NILSIGACGY | IGTLVHNSCW | LIQAFSLACT | VKGYQMPAAN | SPCTLPSGEA | GIIWDSICFA | FLLLQRRVFM | SYYFLHVVAD |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| IKASQILASR | GAELFQATIV | KAVKARIEEE | KKSMDQLKRQ | MDRIKARQQK | YKKGKERMLS | LTQEPGEGQD | MQKLSEEDDE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| READKQKAKG | KKKQWWRPWV | DHASMVRSGD | YYLFETDSEE | EEEEELKKED | EEPPRRSAFQ | FVYQAWITDP | KTALRQRHKE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KKRSAREERK | RRRKGSKEGP | VEWEDREDEP | IKKKSDGPDN | IIKRIFNILK | FTWVLFLATV | DSFTTWLNSI | SREHIDISTV |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LRIERCMLTR | EIKKGNVPTR | ESIHMYYQNH | IMNLSRESGL | DTIDEHPGAA | SGAQTAHRMD | SLDSHDSISS | EPTQCTMLYS |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| RQGTTETIEE | VEAEQEEEAG | STAPEPREAK | EYEATGYDVG | AMGAEEASLT | PEEELTQFST | LDGDVEAPPS | YSKAVSFEHL |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| SFGSQDDSAG | KNRMAVSPDD | SRTDKLGSSI | LPPLTHELTA | SELLLKKMFH | DDELEESEKF | YVGQPRFLLL | FYAMYNTLVA |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| RSEMVCYFVI | ILNHMVSASM | ITLLLPILIF | LWAMLSVPRP | SRRFWMMAIV | YTEVAIVVKY | FFQFGFFPWN | KNVEVNKDKP |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| YHPPNIIGVE | KKEGYVLYDL | IQLLALFFHR | SILKCHGLWD | EDDMTESGMA | REESDDELSL | GHGRRDSSDS | LKSINLAASV |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| ESVHVTFPEQ | QTAVRRKRSG | SSSEPSQRSS | FSSNRSQRGS | TSTRNSSQKG | SSVLSIKQKG | KRELYMEKLQ | EHLIKAKAFT |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 48 | 1 | 518.2542 | -34.31 | 3 | 29.5 | 19.0 | 0 | 486-498 | K.VHAMVSVFQFIMK.Q | Oxidation: 12 |

# Detailed Protein Report

## Protein 915: PREDICTED: rho GTPase-activating protein 18 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530384204 | **Score:** | 18.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 66.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 3.99 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSWLSSSQGV | VLTAYHPSGK | DQTVGNSHAK | AGEEATSSRR | YGQYTMNQES | TTIKVMEKPP | FDRSISQDSL | DELSMEDYWI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ELENIKKSSE | NSQEDQEVVV | VKEPDEGELE | EEWLKEAGLS | NLFGESAGDP | QESIVFLSTL | TRTQAAAVQK | RVETVSQTLR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KKNKQYQIPD | VRDIFAQQRE | SKETAPGGTE | SQSLRTNENK | YQGRDDEASN | LVGEEKLIPP | EETPAPETDI | NLEVSFAEQA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LNQKESSKEK | IQKSKGDDAT | LPSFRLPKDK | TGTTRIGDLA | PQDMKKVCHL | ALIELTALYD | VLGIELKQQK | AVKIKTKDSG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LFCVPLTALL | EQDQRKVPGM | RIPLIFQKLI | SRIEERGLET | EGLLRIPGAA | IRIKNLCQEL | EAKFYEGTFN | WESVKQHDAA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SLLKLFIREL | PQPLLSVEYL | KAFQAVQNLP | TKKQQLQALN | LLVILLPDAN | RDTLKALLEF | LQRVIDNKEK | NKMTVMNVAM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VMAPNLFMCH | ALGLKSSEQR | EFVMAAGTAN | TMHLLIKYQK | LLWTIPKFIV | NQVRKQNTEN | HKKDKRAMKK | LLKKMAYDRE |
| 570 | 580 | 590 | | | | | |
| KYEKQDKSTN | DWGCPDSQER | RSFFV | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 875 | 1 | 491.6668 | -208.81 | 2 | 40.5 | 18.8 | 0 | 396-404 | K.QHDAASLLK.L | | QU:MU 3.99 |

# Detailed Protein Report

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**Protein 916:** **protein dispatched homolog 2 [Homo sapiens]**

**Accession:** gi|25121980
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 18.7
**MW [kDa]:** 151.9
**pI:** 9.3
**Sequence Coverage [%]:** 0.6
**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MDGDSSSSSG GSGPAPGPGP EGEQRPEGEP LAPDGGSPDS TQTKAVPPEA SPERSCSLHS CPLEDPSSSS GPPPTTSTLQ

        90        100        110        120        130        140        150        160
PVGPSSPLAP AHFTYPRALQ EYQGGSSLPG LGDRAALCSH GSSLSPSPAP SQRDGTWKPP AVQHHVVSVR QERAFQMPKS

       170        180        190        200        210        220        230        240
YSQLIAEWPV AVLMLCLAVI FLCTLAGLLG ARLPDFSKPL LGFEPRDTDI GSKLVVWRAL QALTGPRKLL FLSPDLELNS

       250        260        270        280        290        300        310        320
SSSHNTLRPA PRGSAQESAV RPRRMVEPLE DRRQENFFCG PPEKSYAKLV FMSTSSGSLW NLHAIHSMCR MEQDQIRSHT

       330        340        350        360        370        380        390        400
SFGALCQRTA ANQCCPSWSL GNYLAVLSNR SSCLDTTQAD AARTLALLRT CALYYHSGAL VPSCLGPGQN KSPRCAQVPT

       410        420        430        440        450        460        470        480
KCSQSSAIYQ LLHFLLDRDF LSPQTTDYQV PSLKYSLLFL PTPKGASLMD IYLDRLATPW GLADNYTSVT GMDLGLKQEL

       490        500        510        520        530        540        550        560
LRHFLVQDTV YPLLALVAIF FGMALYLRSL FLTLMVLLGV LGSLLVAFFL YQVAFRMAYF PFVNLAALLL LSSVCANHTL

       570        580        590        600        610        620        630        640
IFFDLWRLSK SQLPSGGLAQ RVGRTMHHFG YLLLVSGLTT SAAFYASYLS RLPAVRCLAL FMGTAVLVHL ALTLVWLPAS

       650        660        670        680        690        700        710        720
AVLHERYLAR GCARRARGRW EGSAPRRLLL ALHRRLRGLR RAAAGTSRLL FQRLLPCGVI KFRYIWICWF AALAAGGAYI

       730        740        750        760        770        780        790        800
AGVSPRLRLP TLPPPGGQVF RPSHPFERFD AEYRQLFLFE QLPQGEGGHM PVVLVWGVLP VDTGDPLDPR SNSSLVRDPA

       810        820        830        840        850        860        870        880
FSASGPEAQR WLLALCHRAR NQSFFDTLQE GWPTLCFVET LQRWMESPSC ARLGPDLCCG HSDFPWAPQF FLHCLKMMAL

       890        900        910        920        930        940        950        960
EQGPDGTQDL GLRFDAHGSL AALVLQFQTN FRNSPDYNQT QLFYNEVSHW LAAELGMAPP GLRRGWFTSR LELYSLQHSL

       970        980        990       1000       1010       1020       1030       1040
STEPAVVLGL ALALAFATLL LGTWNVPLSL FSVAAVAGTV LLTVGLLVLL EWQLNTAEAL FLSASVGLSV DFTVNYCISY

      1050       1060       1070       1080       1090       1100       1110       1120
HLCPHPDRLS RVAFSLRQTS CATAVGAAAL FAAGVLMLPA TVLLYRKLGI ILMMVKCVSC GFASFFFQSL CCFFGPEKNC

      1130       1140       1150       1160       1170       1180       1190       1200
GQILWPCAHL PWDAGTGDPG GEKAGRPRPG SVGGMPGSCS EQYELQPLAR RRSPSFDTST ATSKLSHRPS VLSEDLQLHD

      1210       1220       1230       1240       1250       1260       1270       1280
GPCCSRPPPA PASPRELLLD HQAVFSQCPA LQTSSPYKQA GPSPKTRARQ DSQGEEAEPL PASPEAPAHS PKAKAADPPD

      1290       1300       1310       1320       1330       1340       1350       1360
GFCSSASTLE GLSVSDETCL STSEPSARVP DSVGVSPDDL DDTGQPVLER GQLNGKRDTL WLALRETVYD PSLPASHHSS

      1370       1380       1390       1400       1410
LSWKGRGGPG DGSPVVLPNS QPDLPDVWLR RPSTHTSGYS S
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1767 | 2 | 1011.7857 | 227.39 | 1 | 51.9 | 18.7 | 0 | 811-818 | R.WLLALCHR.A | |

# Detailed Protein Report

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## Protein 917: zinc finger protein 2 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|62865883 | **Score:** | 18.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 43.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 2.85 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLENYNSIVS | LGLPVPQPDV | IFQLKRGDKP | WMVDLHGSEE | REWPESVSLD | WETKPEIHDA | SDKKSEGSLR | ECLGRQSPLC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PKFEVHTPNG | RMGTEKQSPS | GETRKKSLSR | DKGLRRRSAL | SREILTKERH | QECSDCGKTF | FDHSSLTRHQ | RTHTGEKPYD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CRECGKAFSH | RSSLSRHLMS | HTGESPYECS | VCSKAFFDRS | SLTVHQRIHT | GEKPFQCNEC | GKAFFDRSSL | TRHQRIHTGE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SPYECHQCGK | AFSQKSILTR | HQLIHTGRKP | YECNECGKAF | YGVSSLNRHQ | KAHAGDPRYQ | CNECGKAFFD | RSSLTQHQKI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| HTGDKPYECS | ECGKAFSQRC | RLTRHQRVHT | GEKPFECTVC | GKVFSSKSSV | IQHQRRYAKQ | GID | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1080 | 1 | 795.3895 | 26.37 | 3 | 43.6 | 18.6 | 1 | 208-227 | R.IHTGEKPFQCNECGKAFFDR.S | Carbamidomethyl: 10 | WUP:QUP 2.85 |

# Detailed Protein Report

## Protein 918: glycogenin-1 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|296040507 | **Score:** | 18.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 5.4 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MTDQAFVTLT TNDAYAKGAL VLGSSLKQHR TTRRLVVLAT PQVSDSMRKV LETVFDEVIM VDVLDSGDSA HLTLMKRPEL
        90        100        110        120        130        140        150        160
GVTLTKLHCW SLTQYSKCVF MDADTLVLAN IDDLFDREEL SAAPDPGWPD CFNSGVFVYQ PSVETYNQLL HLASEQGSFD
       170        180        190        200        210        220        230        240
GGDQGILNTF FSSWATTDIR KHLPFIYNLS SISIYSYLPA FKVKMSQEPY HICPLGRSQL WHSRLYPRKN GRNDGNRARL
       250        260        270        280
IIWEQIPLTT SRGNLTLTSS RNTAFFCEHI HFTSLVSDT
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2695 | 1 | 822.4608 | -0.36 | 2 | 64.8 | 18.6 | 1 | 35-49 | R.LVVLATPQVSDSMRK.V | |

# Detailed Protein Report

## Protein 919: PREDICTED: dyslexia-associated protein KIAA0319-like protein isoform X6 [Homo sapiens]

**Accession:** gi|578799795
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 18.5
**MW [kDa]:** 76.2
**pI:** 5.4
**Sequence Coverage [%]:** 2.2
**No. of unique Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578799797 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: dyslexia-associated protein KIAA0319-like protein isoform X7 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEGKHSQILK | LSKLTPGLYE | FKVIVEGQNA | HGEGYVNVTV | KPEPRKNRPP | IAIVSPQFQE | ISLPTTSTVI | DGSQSTDDDK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IVQYHWEELK | GPLREEKISE | DTAILKLSKL | VPGNYTFSLT | VVDSDGATNS | TTANLTVNKA | VDYPPVANAG | PNQVITLPQN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SITLFGNQST | DDHGITSYEW | SLSPSSKGKV | VEMQGVRTPT | LQLSAMQEGD | YTYQLTVTDT | IGQQATAQVT | VIVQPENNKP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PQADAGPDKE | LTLPVDSTTL | DGSKSSDDQK | IISYLWEKTQ | GPDGVQLENA | NSSVATVTGL | QVGTYVFTLT | VKDERNLQSQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SSVNVIVKEE | INKPPIAKIT | GNVVITLPTS | TAELDGSKSS | DDKGIVSYLW | TRDEGSPAAG | EVLNHSDHHP | ILFLSNLVEG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TYTFHLKVTD | AKGESDTDRT | TVEVKPDPRK | NNLVEIILDI | NVSQLTERLK | GMFIRQIGVL | LGVLDSDIIV | QKIQPYTEQS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TKMVFFVQNE | PPHQIFKGHE | VAAMLKSELR | KQKADFLIFR | ALEVNTVTCQ | LNCSDHGHCD | SFTKRCICDP | FWMENFIKVQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LRDGDSNCEW | SVLYVIIATF | VIVVALGILS | WTVICCCKRQ | KGKPKRKSKY | KILDATDQES | LELKPTSRAG | IKQKGLLLSS |
| 650 | 660 | 670 | 680 | 690 | 700 | | |
| SLMHSESELD | SDDAIFTWPD | REKGKLLHGQ | NGSVPNGQTP | LKARSPREEI | L | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2117 | 1 | 788.3020 | -135.99 | 2 | 56.3 | 18.5 | 0 | 250-264 | K.ELTLPVDSTTLDGSK.S | |

# Detailed Protein Report

**Protein 920:** **PREDICTED: E3 ubiquitin-protein ligase pellino homolog 3 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578821247 | **Score:** | 18.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| | | **Sequence Coverage [%]:** | 11.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MADPRWPDGW | TDHQWSPGDA | PGRRLLRGLS | PGCLAGDLGL | WECVHIAGQP | LSPAAGQAVR | PFYCLWQVEN | ESNVLQDGSL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IDLCGATLLW | RTPAGLLRAP | TLKQLEAQRQ | EANAARPQCP | VGLSTLAFPS | PARGRTAPDK | QQPWVYVRCG | HVHGYHGWGC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RRERGPQERE | CPLCRLVGPY | VPLWLGQEAG | LCLDPGPPSH | AFAPCGHVCS | EKTARYWAQT | PLPHGTHAFH | AACPFCGAWL |
| 250 | 260 | | | | | | |
| TGEHGCVRLI | FQGPLD | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 36 | 2 | 1069.4752 | -74.05 | 3 | 30.1 | 18.5 | 1 | 104-133 | K.QLEAQRQEANAARPQCPVGLSTLAFPSPAR.G | |

# Detailed Protein Report

## Protein 921: PREDICTED: arginine/serine-rich protein PNISR isoform X7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578812668 | **Score:** | 18.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 82.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.7 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578812672 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: arginine/serine-rich protein PNISR isoform X9 [Homo sapiens] |
| gi\|578812670 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: arginine/serine-rich protein PNISR isoform X8 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MHQQPPHPPP | DQPWMPPTPG | PMDIVPPSED | SNSQDSGEFA | PDNRHIFNQN | NHNFGGPPDN | FAVGPVNQFD | YQHGAAFGPP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QGGFHPPYWQ | PGPPGPPAPP | QNRRERPSSF | RDRQRSPIAL | PVKQEPPQID | AVKRRTLPAW | IREGLEKMER | EKQKKLEKER |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MEQQRSQLSK | KEKKATEDAE | GGDGPRLPQR | SKFDSDEEEE | DTENVEAASS | GKVTRSPSPV | PQEEHSDPEM | TEEEKEYQMM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LLTKMLLTEI | LLDVTDEEIY | YVAKDAHRKA | TKAPAKQLAQ | SSALASLTGL | GGLGGYGSGD | SEDERSDRGS | ESSDTDDEEL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RHRIRQKQEA | FWRKEKEQQL | LHDKQMEEEK | QQTERVTKEM | NEFIHKEQNS | LSLLEAREAD | GDVVNEKKRT | PNETTSVLEP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KKEHKEKEKQ | GRSRSGSSSS | GSSSSNSRTS | STSSTVSSSS | YSSSSGSSRT | SSRSSSPKRK | KRHSRSRSPT | IKARRSRSRS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YSRRIKIESN | RARVKIRDRR | RSNRNSIERE | RRRNRSPSRE | RRRSRSRSRD | RRTNRASRSR | SRDRRKIDDQ | RGNLSGNSHK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HKGEAKEQER | KKERSRSIDK | DRKKKDKERE | REQDKRKEKQ | KREEKDFKFS | SQDDRLKRKR | ESERTFSRSG | SISVKIIRHD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SRQDSKKSTT | KDSKKHSGSD | SSGRSSSESP | GSSKEKKAKK | PKHSRSRSVE | KSQRSGKKAS | RKHKSKSRSR | STTPPRRKR |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2313 | 2 | 599.8930 | -40.29 | 3 | 59.4 | 18.5 | 1 | 306-321 | R.SDRGSESSDTDDEELR.H | |

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# Detailed Protein Report

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**Protein 922:** **PREDICTED: SH3-containing GRB2-like protein 3-interacting protein 1 isoform X9 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530363468 | **Score:** | 18.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 68.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MMEGLKKRTR KAFGIRKKEK DTDSTGSPDR DGIKKSNGAP NGFYAEIDWE RYNSPELDEE GYSIRPEEPG STKGKHFYSS

        90        100        110        120        130        140        150        160
SESEEEEESH KKFNIKIKPL QSKDILKNAA TVDELKASIG NIALSPSPVG AIKRNLSSEE VARPRRSTPT PELISKKPPD

       170        180        190        200        210        220        230        240
DTTALAPLFG PPLESAFDEQ KTEVLLDQPE IWGSGQPINP SMESPKLTRP FPTGTPPPLP PKNVPATPPR TGSPLTIGPG

       250        260        270        280        290        300        310        320
ASSPARPATP LVPCRSTTPP PPPPRPPSRP KLPPGKPGVG DVSRPFSPPI HSSSPPPIAP LARAESTSSI SSTNSLSAAT

       330        340        350        360        370        380        390        400
TPTVENEQPS LVWFDRGKFY LTFEGSSRGP SPLTMGAQDT LPVAAAFTET VNAYFKGADP SKCIVKITGE MVLSFPAGIT

       410        420        430        440        450        460        470        480
RHFANNPSPA ALTFRVINFS RLEHVLPNPQ LLCCDNTQND ANTKEFWVNM PNLMTHLKKV SEQKPQATYY NVDMLKYQVS

       490        500        510        520        530        540        550        560
AQGIQSTPLN LAVNWRCEPS STDLRIDYKY NTDAMTTAVA LNNVQFLVPI DGGVTKLQAV LPPAVWNAEQ QRILWKIPDI

       570        580        590        600        610        620        630
SQKSENGGVG SLLARFQLSE GPSKPSPLVV QFTSEGSTLS GCDIELVGAG YRFSLIKKRF AAGKYLADN
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 363 | 1 | 629.3611 | 47.90 | 2 | 33.2 | 18.5 | 0 | 135-145 | R.NLSSEEVARPR.R | |

# Detailed Protein Report

## Protein 923: alpha-tocopherol transfer protein-like isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|85861243 | **Score:** | 18.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | |
|---|---|---|---|
| ***WUP:QUP*** | **Median:** 2.06 | **CV:** 0.00 % | **No. of Peptides:** 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530418391 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: alpha-tocopherol transfer protein-like isoform X1 [Homo sapiens] |
| gi\|85861250 | refseq_human (refseq_human_20140103.fasta) | alpha-tocopherol transfer protein-like isoform 1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSEESDSLRT | SPSVASLSEN | ELPPPPEPPG | YVCSLTEDLV | TKAREELQEK | PEWRLRDVQA | LRDMVRKEYP | NLSTSLDDAF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LLRFLRARKF | DYDRALQLLV | NYHSCRRSWP | EVFNNLKPSA | LKDVLASGFL | TVLPHTDPRG | CHVVCIRPDR | WIPSNYPITE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NIRAIYLTLE | KLIQSEETQV | NGIVILADYK | GVSLSKASHF | GPFIAKKVIG | ILQDGFPIRI | KAVHVVNEPR | IFKGIFAIIK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PFLKEKIANR | FFLHGSDLNS | LHTNLPRSIL | PKEYGGTAGE | LDTATWNAVL | LASEDDFVKE | FCQPVPACDS | ILGQTLLPEG |
| 330 | 340 | 350 | | | | | |
| LTSDAQCDDS | LRAVKSQLYS | CY | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 22 | 1 | 537.7431 | -87.57 | 2 | 29.9 | 18.5 | 0 | 197-206 | K.ASHFGPFIAK.K | | WUP:QUP 2.06 |

# Detailed Protein Report

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## Protein 924: PREDICTED: sodium-dependent phosphate transporter 1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530369350 | **Score:** | 18.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 47.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | |
|---|---|---|---|
| ***WUP:QUP*** | **Median:** 3.80 | **CV:** 0.00 % | **No. of Peptides:** 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578804806 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: sodium-dependent phosphate transporter 1 isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKRKIEREIK | CSPSESPLME | KKNSLKEDHE | ETKLSVGDIE | NKHPVSEVGP | ATVPLQAVVE | ERTVSFKLGD | LEEAPERERL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PSVDLKEETS | IDSTVNGAVQ | LPNGNLVQFS | QAVSNQINSS | GHYQYHTVHK | DSGLYKELLH | KLHLAKVGDC | MGDSGDKPLR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RNNSYTSYTM | AICGMPLDSF | RAKEGEQKGE | EMEKLTWPNA | DSKKRIRMDS | YTSYCNAVSD | LHSASEIDMS | VKAEMGLGDR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KGSNGSLEEW | YDQDKPEVSL | LFQFLQILTA | CFGSFAHGGN | DVSNAIGPLV | ALYLVYDTGD | VSSKVATPIW | LLLYGGVGIC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VGLWVWGRRV | IQTMGKDLTP | ITPSSGFSIE | LASALTVVIA | SNIGLPISTT | HCKVGSVVSV | GWLRSKKAVD | WRLFRNIFMA |
| 410 | 420 | 430 | | | | | |
| WFVTVPISGV | ISAAIMAIFR | YVILRM | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2008 | 1 | 687.3490 | -72.18 | 2 | 55.5 | 18.4 | 1 | 374-386 | K.VGSVVSVGWLRSK.K | | WUP:QUP 3.80 |

# Detailed Protein Report

## Protein 925: homeobox protein Nkx-2.4 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|157426823 | **Score:** | 18.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 36.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.8 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSLSPKHTTP | FSVSDILSPI | EETYKKFSGA | MDGAPPGLGA | PLGAAAAYRA | PPPGPSSQAA | TVAGMQPSHA | MAGHNAAAAA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AAAAAAAAAA | ATYHMPPGVS | QFPHGAMGSY | CNGGLGNMGE | LPAYTDGMRG | GAATGWYGAN | PDPRYSSISR | FMGPSAGVNV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AGMGSLTGIA | DAAKSLGPLH | AAAAAAAPRR | KRRVLFSQAQ | VYELERRFKQ | QKYLSAPERE | HLASMIHLTP | TQVKIWFQNH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RYKMKRQAKD | KAAQQLQQEG | GLGPPPPPPP | SPRRVAVPVL | VKDGKPCQNG | ASTPTPGQAG | PQPPAPTPAP | ELEELSPSPP |
| 330 | 340 | 350 | 360 |  |  |  |  |
| ALHGPGGGLA | ALDAAAGEYS | GGVLGANLLY | GRTW |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2128 | 1 | 1131.4206 | -132.38 | 2 | 56.5 | 18.4 | 1 | 26-49 | K.KFSGAMDGAPPGLGAPLGAAAAYR.A | Oxidation: 6 |

# Detailed Protein Report

## Protein 926: tripartite motif-containing protein 6 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|310772221 | **Score:** | 18.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 36.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 8.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|310772223 | refseq_huma (refseq_human_20140103.fasta) | tripartite motif-containing protein 6 isoform 3 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEPERCRIQT | EFNQLRNILD | RVEQRELKKL | EQEEKKGLRI | IEEAENDLVH | QTQSLRELIS | DLERRCQGST | MELLQDVSDV |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| TERSEFWTLR | KPEALPTKLR | SMFRAPDLKR | MLRVCRELTD | VQSYWVDVTL | NPHTANLNLV | LAKNRRQVRF | VGAKVSGPSC |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| LEKHYDCSVL | GSQHFSSGKH | YWEVDVAKKT | AWILGVCSNS | LGPTFSFNHF | AQNHSAYSRY | QPQSGYWVIG | LQHNHEYRAY |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| EDSSPSLLLS | MTVPPRRVGV | FLDYEAGTVS | FYNVTNHGFP | IYTFSKYYFP | TTLCPYFNPC | NCVIPMTLRR | PSS |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1236 | 1 | 903.7473 | -4.54 | 3 | 45.6 | 18.4 | 1 | 155-179 | K.VSGPSCLEKHYDCSVLGSQHFSSGK.H | Carbamidomethyl: 13 |

# Detailed Protein Report

## Protein 927: PREDICTED: NHS-like protein 2 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578838353 | **Score:** | 18.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 144.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.49 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.96 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAMGTLVLGY | GLKGAGIVLP | NNSFLDADTV | EIKEIGFAGI | CSLLAEVTAA | EREVSPLRGS | DSGLWLRTLP | RERQAQLTVN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FPRLSAVTGP | TGPGWLWVEC | SGVEKERGNS | LLNPQLLSLG | WAAQEQLQWA | KEYVIDGTKV | LGNGVQESPW | APTEEPRDRV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WDSVEPVGSL | PPVWAQHTLF | SCGFLVIHTA | GMERTDSVTL | FWIRGAAANS | GRENATATAH | SRSSWRQPVN | VFLSSGRPPS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VEELLREAQL | NLQSLLQEEY | EEQYSEARLV | GQTFRSSDEA | TKPTPNPRPQ | SARRLEFILM | PTKRQLSEDE | TTTQGVRAPE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ASLSLSTTAD | KQTAWNSLFP | LPILEEKRWP | QLCSTQSDIV | PINISGQQFD | KHASLRHSLF | NTETAVNPKS | TLRRRRTIIG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FSNFSQRDQG | HSNSPAGSVA | HSTTSDIRPS | HSVPEGVHGR | VAVGQDARFP | SLTSPVLRTP | SSEPDEPHQA | RSGPNPPGME |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SMGMVYSVPS | SCNGPTESTF | STSWKGDAFT | YMTPSATSQS | NQVNENGKNP | SCGNSWVSLN | KVPPLVPKEA | ATLLVARDNP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AGCSGSAGYP | ERLIQQRHMP | ERPSKIGLLT | SGTSRLETGP | GGASRFRERS | LSVPTDSGTT | DVDYDEEQKA | NEACALPFAS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TSSEGSNSAD | NIASLSAQQE | AQHRRQRSKS | ISLRKAKKKP | SPPTRSVSLV | KDEPGLLPEG | GSALPKDQRP | KSLCLSLEHQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GHHSSHPDAQ | GHPAIPNHKD | PESTQFSHHW | YLTDWKSGDT | YQSLSSSSTA | TGTTVIECTQ | VQGSSESLAS | PSTSRATTPS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QLSIEVEARE | ISSPGRPPGL | MSPSSGYSSQ | SETPTPTVSM | SLTLGHLPPP | SSSVRVRPVV | PERKSSLPPT | SPMEKFPKSR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LSFDLPLTSS | PNLDLSGMSI | SIRSKTKVSR | HHSETNFGVK | LAQKTNPNQP | IMPMVTQSDL | RSVRLRSVSK | SEPEDDIESP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| EYAEEPRAEE | VFTLPERKTK | PPVAEKPPVA | RRPPSLVHKP | PSVPEEYALT | SPTLAMPPRS | SIQHARPLPQ | DSYTVVRKPK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PSSFPDGRSP | GESTAPSSLV | FTPFASSSDA | FFSGTQQPPQ | GSVEDEGPKV | RVLPERISLQ | SQEEAEKKKG | KIPPPVPKKP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SVLYLPLTSP | TAQMEAYVAE | PRLPLSPIIT | LEEDTKCPAT | GDDLQSLGQR | VTSTPQADSE | REASPLGSSV | EPGTEEKSLI |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SDKTAEWIAE | DDDDVFVASR | TTEDLFTVIH | RSKRKLLGWK | EPGEAFVGGR | TSSHSPIKNT | AESPISESTA | TAGSGSSANL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | | |
| DAGRNDDFKA | LLQKKGSKAT | PRSRPSAAEL | LKTTNPLARR | IIAQFSKDYE | TTDNPST | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1160 | 1 | 713.6536 | -103.02 | 3 | 44.1 | 18.4 | 2 | 53-71 | R.EVSPLRGSDSGLWLRTLPR.E | | QU:MU 0.49<br>WUP:QUP 1.96 |

# Detailed Protein Report

## Protein 928: PREDICTED: retinoid isomerohydrolase isoform X1 [Homo sapiens]

**Accession:** gi|578799557
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 18.1
**MW [kDa]:** 65.6
**pI:** 8.4
**Sequence Coverage [%]:** 1.9
**No. of unique Peptides:** 1

## Quantitation

***QU:MU*** **Median:** 0.29 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQKVLKPVAV | LKQCGYSPRT | PKAAQGYLRK | ALGADTGTSK | TGFSSPRRVE | HPAGGYKKLF | ETVEELSSPL | TAHVTGRIPL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| WLTGSLLRCG | PGLFEVGSEP | FYHLFDGQAL | LHKFDFKEGH | VTYHRRFIRT | DAYVRAMTEK | RIVITEFGTC | AFPDPCKNIF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SRFFSYFRGV | EVTDNALVNV | YPVGEDYYAC | TETNFITKIN | PETLETIKQV | DLCNYVSVNG | ATAHPHIEND | GTVYNIGNCF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GKNFSIAYNI | VKIPPLQADK | EDPISKSEIV | VQFPCSDRFK | PSYVHSFGLT | PNYIVFVETP | VKINLFKFLS | SWSLWGANYM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DCFESNETMG | VWLHIADKKR | KKYLNNKYRT | SPFNLFHHIN | TYEDNGFLIV | DLCCWKGFEF | VYNYLYLANL | RENWEEVKKN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ARKAPQPEVR | RYVLPLNIDK | ADTGKNLVTL | PNTTATAILC | SDETIWLEPE | VLFSGPRQAF | EFPQINYQKY | CGKPYTYAYG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LGLNHFVPDR | LCKLNVKTKE | TWVWQEPDSY | PSEPIFVSHP | DALEEDDGVV | LSVVVSPGAG | QKPAYLLILN | AKDLSEVARA |
| 570 | 580 | | | | | | |
| EVEINIPVTF | HGLFKKS | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1724 | 1 | 524.7781 | -13.64 | 2 | 51.3 | 18.1 | 1 | 30-40 | R.KALGADTGTSK.T | | QU:MU | 0.29 |

# Detailed Protein Report

## Protein 929: RING finger and transmembrane domain-containing protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|109134327 | **Score:** | 18.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPLFLLSLPT | PPSASGHERR | QRPEAKTSGS | EKKYLRAMQA | NRSQLHSPPG | TGSSEDASTP | QCVHTRLTGE | GSCPHSGDVH |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| IQINSIPKEC | AENASSRNIR | SGVHSCAHGC | VHSRLRGHSH | SEARLTDDTA | AESGDHGSSS | FSEFRYLFKW | LQKSLPYILI |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| LSVKLVMQHI | TGISLGIGLL | TTFMYANKSI | VNQVFLRERS | SKIQCAWLLV | FLAGSSVLLY | YTFHSQSLYY | SLIFLNPTLD |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| HLSFWEVFWI | VGITDFILKF | FFMGLKCLIL | LVPSFIMPFK | SKGYWYMLLE | ELCQYYRTFV | PIPVWFRYLI | SYGEFGNVTR |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| WSLGILLALL | YLILKLLEFF | GHLRTFRQVL | RIFFTQPSYG | VAASKRQCSD | VDDICSICQA | EFQKPILLIC | QHIFCEECMT |
| **410** | **420** | **430** | **440** | | | | |
| LWFNREKTCP | LCRTVISDHI | NKWKDGATSS | HLQIY | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 241 | 1 | 879.7331 | -87.01 | 3 | 33.0 | 18.0 | 0 | 165-188 | K.LVMQHITGISLGIGLLTTFMYANK.S | Oxidation: 20 |

# Detailed Protein Report

## Protein 930: PREDICTED: RING finger protein 10 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530401582 | **Score:** | 18.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 85.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.0 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MPLSSPNAAA TASDMDKNSG SNSSSASSGS SKGQQPPRSA SAGPAGESKP KSDGKNSSGS KRYNRKRELS YPKNESFNNQ
        90        100        110        120        130        140        150        160
SRRSSSQKSK TFNKMPPQRG GGSSKLFSSS FNGGRRDEVA EAQRAEFSPA QFSGPKKINL NHLLNFTFEP RGQTGHFEGS
       170        180        190        200        210        220        230        240
GHGSWGKRNK WGHKPFNKEL FLQANCQFVV SEDQDYTAHF ADPDTLVNWD FVEQVRICSH EVPSCPICLY PPTAAKITRC
       250        260        270        280        290        300        310        320
GHIFCWACIL HYLSLSEKTW SKCPICYSSV HKKDLKSVVA TESHQYVVGD TITMQLMKRE KGVLVALPKS KWMNVDHPIH
       330        340        350        360        370        380        390        400
LGDEQHSQYS KLLLASKEQV LHRVVLEEKV ALEQQLAEEK HTPESCFIEA AIQELKTREE ALSGLAGSRR EVTGVVAALE
       410        420        430        440        450        460        470        480
QLVLMAPLAK ESVFQPRKSL LQQGVLEYLS AFDEETTEVC SLDTPSRPLA LPLVEEEEAV SEPEPEGLPE ACDDLELADD
       490        500        510        520        530        540        550        560
NLKEGTICTE SSQQEPITKS GFTRLSSSPC YYFYQAEDGQ HMFLHPVNVR CLVREYGSLE RSPEKISATV VEIAGYSMSE
       570        580        590        600        610        620        630        640
DVRQRHRYLS HLPLTCEFSI CELALQPPVV SKETLEMFSD DIEKRKRQRQ KKAREERRRE RRIEIEENKK QGKYFLLTPL
       650        660        670        680        690        700        710        720
SPTASQGSPS FCVGSLEEDS PFPSFAQMLR VGKAKADVWP KTAPKKDENS LVPPAPVDSD GESDNSDRVP VPSFQNSFSQ
       730        740        750        760        770
AIEAAFMKLD TPATSDPLSE EKGGKKRKKQ KQKLLFSTSV VHTK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2030 | 1 | 788.2772 | -117.15 | 2 | 55.3 | 18.0 | 0 | 2-17 | M.PLSSPNAAATASDMDK.N | |

# Detailed Protein Report

## Protein 931: dysferlin isoform 9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|195976754 | **Score:** | 17.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 235.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLRVFILYAE | NVHTPDTDIS | DAYCSAVFAG | VKKRTKVIKN | SVNPVWNEGF | EWDLKGIPLD | QGSELHVVVK | DHETMGRNRF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LGEAKVPLRE | VLATPSLSAS | FNAPLLDTKK | QPTGASLVLQ | VSYTPLPGAV | PLFPPPTPLE | PSPTLPDLDV | VADTGGEEDT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EDQGLTGDEA | EPFLDQSGGP | GAPTTPRKLP | SRPPPHYPGI | KRKRSAPTSR | KLLSDKPQDF | QIRVQVIEGR | QLPGVNIKPV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VKVTAAGQTK | RTRIHKGNSP | LFNETLFFNL | FDSPGELFDE | PIFITVVDSR | SLRTDALLGE | FRMDVGTIYR | EPRHAYLRKW |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LLLSDPDDFS | AGARGYLKTS | LCVLGPGDEA | PLERKDPSED | KEDIESNLLR | PTGVALRGAH | FCLKVFRAED | LPQMDDAVMD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NVKQIFGFES | NKKNLVDPFV | EVSFAGKMLC | SKILEKTANP | QWNQNITLPA | MFPSMCEKMR | IRIIDWDRLT | HNDIVATTYL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SMSKISAPGG | EIEVDDYLGF | LPTFGPCYIN | LYGSPREFTG | FPDPYTELNT | GKGEGVAYRG | RLLLSLETKL | VEHSEQKVED |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LPADDILRVE | KYLRRRKYSL | FAAFYSATML | QDVDDAIQFE | VSIGNYGNKF | DMTCLPLAST | TQYSRAVFDG | CHYYYLPWGN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VKPVVVLSSY | WEDISHRIET | QNQLLGIADR | LEAGLEQVHL | ALKAQCSTED | VDSLVAQLTD | ELIAGCSQPL | GDIHETPSAT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HLDQYLYQLR | THHLSQITEA | ALALKLGHSE | LPAALEQAED | WLLRLRALAE | EPQNSLPDIV | IWMLQGDKRV | AYQRVPAHQV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LFSRRGANYC | GKNCGKLQTI | FLKYPMEKVP | GARMPVQIRV | KLWFGLSVDE | KEFNQFAEGK | LSVFAETYEN | ETKLALVGNW |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GTTGLTYPKF | SDVTGKIKLP | KDSFRPSAGW | TWAGDWFVCP | EKTLLHDMDA | GHLSFVEEVF | ENQTRLPGGQ | WIYMSDNYTD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VNGEKVLPKD | DIECPLGWKW | EDEEWSTDLN | RAVDEQGWEY | SITIPPERKP | KHWVPAEKMY | YTHRRRRWVR | LRRRDLSQME |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ALKRHRQAEA | EGEGWEYASL | FGWKFHLEYR | KTDAFRRRRW | RRRMEPLEKT | GPAAVFALEG | ALGGVMDDKS | EDSMSVSTLS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| FGVNRPTISC | IFDYGNRYHL | RCYMYQARDL | AAMDKDSFSD | PYAIVSFLHQ | SQKTVVVKNT | LNPTWDQTLI | FYEIEIFGEP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ATVAEQPPSI | VVELYDHDTY | GADEFMGRCI | CQPSLERMPR | LAWFPLTRGS | QPSGELLASF | ELIQREKPAI | HHIPGFEVQE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TSRILDESED | TDLPYPPPQR | EANIYMVPQN | IKPALQRTAI | EILAWGLRNM | KSYQLANISS | PSLVVECGGQ | TVQSCVIRNL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| RKNPNFDICT | LFMEVMLPRE | ELYCPPITVK | VIDNRQFGRR | PVVGQCTIRS | LESFLCDPYS | AESPSPQGGP | DDVSLLSPGE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DVLIDIDDKE | PLIPIQEEEF | IDWWSKFFAS | IGEREKCGSY | LEKDFDTLKV | YDTQLENVEA | FEGLSDFCNT | FKLYRGKTQE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ETEDPSVIGE | FKGLFKIYPL | PEDPAIPMPP | RQFHQLAAQG | PQECLVRIYI | VRAFGLQPKD | PNGKCDPYIK | ISIGKKSVSD |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QDNYIPCTLE | PVFGKMFELT | CTLPLEKDLK | ITLYDYDLLS | KDEKIGETVV | DLENRLLSKF | GARCGLPQTY | CVSGPNQWRD |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| QLRPSQLLHL | FCQQHRVKAP | VYRTDRVMFQ | DKEYSIEEIE | AGRIPNPHLG | PVEERLALHV | LQQQGLVPEH | VESRPLYSPL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| QPDIEQGKLQ | MWVDLFPKAL | GRPGPPFNIT | PRRARRFFLR | CIIWNTRDVI | LDDLSLTGEK | MSDIYVKGWM | IGFEEHKQKT |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| DVHYRSLGGE | GNFNWRFIFP | FDYLPAEQVC | TIAKKDAFWR | LDKTESKIPA | RVVFQIWDND | KFSFDDFLGS | LQLDLNRMPK |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| PAKTAKKCSL | DQLDDAFHPE | WFVSLFEQKT | VKGWWPCVAE | EGEKKILAGK | LEMTLEIVAE | SEHEERPAGQ | GRDEPNMNPK |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | |
| LEDPRRPDTS | FLWFTSPYKT | MKFILWRRFR | WAIILFIILF | ILLLFLAIFI | YAFPNYAAMK | LVKPFS | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2537 | 1 | 941.5642 | 96.79 | 2 | 62.3 | 17.9 | 0 | 1552-1567 | R.QFHQLAAQGPQECLVR.I | Carbamidomethyl: 13 |

# Detailed Protein Report

## Protein 932: probable G-protein coupled receptor 27 [Homo sapiens]

**Accession:** gi|9506747
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 17.9
**MW [kDa]:** 39.8
**pI:** 10.7
**Sequence Coverage [%]:** 6.7
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MANASEPGGS | GGGEAAALGL | KLATLSLLLC | VSLAGNVLFA | LLIVRERSLH | RAPYYLLLDL | CLADGLRALA | CLPAVMLAAR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RAAAAAGAPP | GALGCKLLAF | LAALFCFHAA | FLLLGVGVTR | YLAIAHHRFY | AERLAGWPCA | AMLVCAAWAL | ALAAAFPPVL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DGGGDDEDAP | CALEQRPDGA | PGALGFLLLL | AVVVGATHLV | YLRLLFFIHD | RRKMRPARLV | PAVSHDWTFH | GPGATGQAAA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NWTAGFGRGP | TPPALVGIRP | AGPGRGARRL | LVLEEFKTEK | RLCKMFYAVT | LLFLLLWGPY | VVASYLRVLV | RPGAVPQAYL |
| 330 | 340 | 350 | 360 | 370 | 380 | | |
| TASVWLTFAQ | AGINPVVCFL | FNRELRDCFR | AQFPCCQSPR | TTQATHPCDL | KGIGL | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 250 | 1 | 910.4923 | 61.03 | 3 | 32.8 | 17.9 | 2 | 351-375 | R.AQFPCCQSPRTTQATHPCDLKGIGL.- | Carbamidomethyl: 6 |

# Detailed Protein Report

**Protein 933:** **immunoglobulin-like domain-containing receptor 1 isoform 3 precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|315259080 | **Score:** | 17.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 52.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.8 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAWPKLPAPW | LLLCTWLPAG | CLSLLVTVQH | TERYVTLFAS | IILKCDYTTS | AQLQDVVVTW | RFKSFCKDPI | FDYYSASYQA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ALSLGQDPSN | DCNDNQREVR | IVAQRRGQNE | PVLGVDYRQR | KITIQNPLAR | HRYMKQAQAL | GPQMMGKPLY | WGADRSSQVS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SYPMHPLLQR | DLSLPSSLPQ | MPMTQTTNQP | PIANGVLEYL | EKELRNLNLA | QPLPPDLKGR | FGHPCSMLSS | LGSEVVERRI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IHLPPLIRDL | SSSRRTSDSL | HQQWLTPIPS | RPWDLREGRS | HHHYPDFHQE | LQDRGPKSWA | LERRELDPSW | SGRHRSSRLN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GSPIHWSDRD | SLSDVPSSSE | ARWRPSHPPF | RSRCQERPRR | PSPRESTQRH | GRRRRHRSYS | PPLPSGLSSW | SSEEDKERQP |
| 410 | 420 | 430 | 440 | 450 | 460 | | |
| QSWRAHRRGS | HSPHWPEEKP | PSYRSLDITP | GKNSRKKGSV | ERRSEKDSSH | SGRSVVI | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2765 | 1 | 673.8074 | -46.32 | 2 | 65.0 | 17.9 | 0 | 107-118 | R.GQNEPVLGVDYR.Q | |

# Detailed Protein Report

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## Protein 934: NUT family member 1 isoform 3 [Homo sapiens]

**Accession:** gi|50233787
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 17.8
**MW [kDa]:** 120.3
**pI:** 5.2
**Sequence Coverage [%]:** 1.6
**No. of unique Peptides:** 1

## Quantitation

***WUP:QUP*** **Median:** 0.10 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASDGASALP | GPDMSMKPSA | ALSPSPALPF | LPPTSDPPDH | PPREPPPQPI | MPSVFSPDNP | LMLSAFPSSL | LVTGDGGPCL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SGAGAGKVIV | KVKTEGGSAE | PSQTQNFILT | QTALNSTAPG | TPCGGLEGPA | PPFVTASNVK | TILPSKAVGV | SQEGPPGLPP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QPPPPVAQLV | PIVPLEKAWP | GPHGTTGEGG | PVATLSKPSL | GDRSKISKDV | YENFRQWQRY | KALARRHLSQ | SPDTEALSCF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LIPVLRSLAR | LKPTMTLEEG | LPLAVQEWEH | TSNFDRMIFY | EMAERFMEFE | AEEMQIQNTQ | LMNGSQGLSP | ATPLKLDPLG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PLASEVCQQP | VYIPKKAASK | TRAPRRRQRK | AQRPPAPEAP | KEIPPEAVKE | YVDIMEWLVG | THLATGESDG | KQEEEGQQQE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EEGMYPDPGL | LSYINELCSQ | KVFVSKVEAV | IHPQFLADLL | SPEKQRDPLA | LIEELEQEEG | LTLAQLVQKR | LMALEEEEDA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EAPPSFSGAQ | LDSSPSGSVE | DEDGDGRLRP | SPGLQGAGGA | ACLGKVSSSG | KRAREVHGGQ | EQALDSPRGM | HRDGNTLPSP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SSWDLQPELA | APQGTPGPLG | VERRGSGKVI | NQVSLHQDGH | LGGAGPPGHC | LVADRTSEAL | PLCWQGGFQP | ESTPSLDAGL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AELAPLQGQG | LEKQVLGLQK | GQQTGGRGVL | PQGKEPLAVP | WEGSSGAMWG | DDRGTPMAQS | YDQNPSPRAA | GERDDVCLSP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GVWLSSEMDA | VGLELPVQIE | EVIESFQVEK | CVTEYQEGCQ | GLGSRGNISL | GPGETLVPGD | TESSVIPCGG | TVAAAALEKR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NYCSLPGPLR | ANSPPLRSKE | NQEQSCETVG | HPSDLWAEGC | FPLLESGDST | LGSSKETLPP | TCQGNLLIMG | TEDASSLPEA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SQEAGSRGNS | FSPLLETIEP | VNILDVKDDC | GLQLRVSEDT | CPLNVHSYDP | QGEGRVDPDL | SKPKNLAPLQ | ESQESYTTGT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PKATSSHQGL | GSTLPRRGTR | NAIVPRETSV | SKTHRSADRA | KGKEKKKKEA | EEEDEELSNF | AYLLASKLSL | SPREHPLSPH |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| HASGGQGSQR | ASHLLPAGAK | GPSKLPYPVA | KSGKRALAGG | PAPTEKTPHS | GAQLGVPREK | PLALGVVRPS | QPRKRRCDSF |
| 1130 | 1140 | | | | | | |
| VTGRRKKRRR | SQ | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1503 | 1 | 671.1069 | 119.58 | 3 | 47.1 | 17.8 | 2 | 800-817 | K.RNYCSLPGPLRANSPPLR.S | | WUP:QUP 0.10 |

# Detailed Protein Report

## Protein 935: PREDICTED: vitamin D-binding protein isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578809023 | **Score:** | 17.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 47.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| | | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKRVLVLLLA | VAFGHALERG | RDYEKNKVCK | EFSHLGKEDF | TSLSLVLYSR | KFPSGTFEQV | SQLVKEVVSL | TEACCAEGAD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PDCYDTRTSA | LSAKSCESNS | PFPVHPGTAE | CCTKEGLERK | LCMAALKHQP | QEFPTYVEPT | NDEICEAFRK | DPKEYANQFM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WEYSTNYGQA | PLSLLVSYTK | SYLSMVGSCC | TSASPTVCFL | KERLQLKHLS | LLTTLSNRVC | SQYAAYGEKK | SRLSNLIKLA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QKVPTADLED | VLPLAEDITN | ILSKCCESAS | EDCMAKELPE | HTVKLCDNLS | TKNSKFEDCC | QEKTAMDVFV | CTYFMPAAQL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PELPDVELPT | NKDVCDPGNT | KVMDKYTFEL | SRRTHLPEVF | LSKVLEPTLK | SLGECCDVED | STTCFNAKGP | LLKKELSSFI |
| 410 | 420 | 430 | | | | | |
| DKGQELCADY | SENTFTEYKK | KLMLN | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1937 | 1 | 847.8487 | -130.42 | 2 | 52.6 | 17.8 | 1 | 51-65 | R.KFPSGTFEQVSQLVK.E | |

# Detailed Protein Report

## Protein 936: nicotinate phosphoribosyltransferase isoform 2 [Homo sapiens]

**Accession:** gi|558472750
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 17.8
**MW [kDa]:** 56.1
**pI:** 5.4
**Sequence Coverage [%]:** 1.9
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAEQDPEAR | AAARPLLTDL | YQATMALGYW | RAGRARDAAE | FELFFRRCPF | GGAFALAAGL | RDCVRFLRAF | RLRDADVQFL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ASVLPPDTDP | AFFEHLRALD | CSEVTVRALP | EGSLAFPGVP | LLQVSGPLLV | VQLLETPLLC | LVSYASLVAT | NAARLRLIAG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PEKRLLEMGL | RRAQGPDGGL | TASTYSYLGG | FDSSSNVLAG | QLRGVPVAGT | LAHSFVTSFS | GSEVPPDPML | APAAGEGPGV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DLAAKAQVWL | EQVCAHLGLG | VQEPHPGERA | AFVAYALAFP | RAFQGLLDTY | SVWRSGLPNF | LAVALALGEL | GYRAVGVRLD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SGDLLQQAQE | IRKVFRAAAA | QFQVPWLESV | LIVVSNNIDE | EALARLAQEG | SEVNVIGIGT | SVVTCPQQPS | LGGVYKLVAV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GGQPRMKLTE | DPEKQTLPGS | KAAFRLLGSD | GSPLMDMLQL | AEEPVPQAGQ | ELRVWPPGAQ | EPCTVRPAQL | CEPLPSLAES |
| 490 | 500 | 510 | 520 | 530 | | | |
| RALAQLSLSR | LSPEHRRLRS | PAQYQVVLSE | RLQALVNSLC | AGQSP | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1733 | 1 | 576.7624 | -176.53 | 2 | 52.0 | 17.8 | 2 | 155-164 | R.LRLIAGPEKR.L | |

# Detailed Protein Report

**Protein 937:** **PREDICTED: uncharacterized protein LOC101930405 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530356052 | **Score:** | 17.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 8.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTHSRRQGRS | EPPWGTQDTR | GTQETRGTSG | PSGLQGALRT | LGNTQNHQEA | LRTTRGPSGH | QSVLRTSGGA | QDLQRVIRTP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EGAQNTRSCL | RNFWMKTSPP | LTLLLWERSP | SLGIPKCLHS | VIRTEHTGLT | REFVLSWVFL | VAILKCVQCE | DQLVESGGGL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VQPGGSLRPS | CAASGFAFSS | YVLHWVRRAP | GKGPEWVSAI | GTGGDTYYAD | SVMGRFTISR | DNAKKSLYLQ | MNSLIAEDMA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | |
| VYYCARDTVR | GSQSPSSVLC | GDYLGTNVDN | RSEGDELAWT | KWDVDVKFIL | CCTNNHRFNF | LTSSIRKRV | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2764 | 1 | 920.1235 | 28.38 | 3 | 65.7 | 17.7 | 1 | 189-215 | R.APGKGPEWVSAIGTGGDTYYADSVMGR.F | Oxidation: 25 |

# Detailed Protein Report

## Protein 938: PREDICTED: transcription regulator protein BACH1 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578836626 | **Score:** | 17.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSLSENSVFA | YESSVHSTNV | LLSLNDQRKK | DVLCDVTIFV | EGQRFRAHRS | VLAACSSYFH | SRIVGQADGE | LNITLPEEVT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VKGFEPLIQF | AYTAKLILSK | ENVDEVCKCV | EFLSVHNIEE | SCFQFLKFKF | LDSTADQQEC | PRKKCFSSHC | QKTDLKLSLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DQRDLETDEV | EEFLENKNVQ | TPQCKLRRYQ | GNAKASPPLQ | DSASQTYESM | CLEKDAALAL | PSLCPKYRKF | QKAFGTDRVR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TGESSVKDIH | ASVQPNERSE | NECLGGVPEC | RDLQVMLKCD | ESKLAMEPEE | TKKDPASQCP | TEKSEVTPFP | HNSSIDPHGL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YSLSLLHTYD | QYGDLNFAGM | QNTTVLTEKP | LSGTDVQEKT | FGESQDLPLK | SDLGTREDSS | VASSDRSSVE | REVAEHLAKG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FWSDICSTDT | PCQMQLSPAV | AKDGSEQISQ | KRSECPWLGI | RISESPEPGQ | RTFTTLSSVN | CPFISTLSTE | GCSSNLEIGN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DDYVSEPQQE | PCPYACVISL | GDDSETDTEG | DSESCSAREQ | ECEVKLPFNA | QRIISLSRND | FQSLLKMHKL | TPEQLDCIHD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| IRRRSKNRIA | AQRCRKRKLD | CIQNLESEIE | KLGSVENLMC | QEVFHTILRT | LDTCSDSSVS | AKQ | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1691 | 1 | 1011.6416 | 141.51 | 2 | 51.4 | 17.7 | 1 | 547-562 | K.MHKLTPEQLDCIHDIR.R | Carbamidomethyl: 11;<br>Oxidation: 1 |

# Detailed Protein Report

## Protein 939: PREDICTED: kin of IRRE-like protein 3 isoform X1 [Homo sapiens]

**Accession:** gi|530398440
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 17.6
**MW [kDa]:** 84.1
**pI:** 6.6
**Sequence Coverage [%]:** 2.1
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKPFQLDLLF | VCFFLFSQEL | GLQKRGCCLV | LGYMAKDKFR | RMNEGQVYSF | SQQPQDQVVV | SGQPVTLLCA | IPEYDGFVLW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IKDGLALGVG | RDLSSYPQYL | VVGNHLSGEH | HLKILRAELQ | DDAVYECQAI | QAAIRSRPAR | LTVLVPPDDP | VILGGPVISL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RAGDPLNLTC | HADNAKPAAS | IIWLRKGEVI | NGATYSKTLL | RDGKRESIVS | TLFISPGDVE | NGQSIVCRAT | NKAIPGGKET |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SVTIDIQHPP | LVNLSVEPQP | VLEDNVVTFH | CSAKANPAVT | QYRWAKRGQI | IKEASGEVYR | TTVDYTYFSE | PVSCEVTNAL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GSTNLSRTVD | VYFGPRMTTE | PQSLLVDLGS | DAIFSCAWTG | NPSLTIVWMK | RGSGVVLSNE | KTLTLKSVRQ | EDAGKYVCRA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VVPRVGAGER | EVTLTVNGPP | IISSTQTQHA | LHGEKGQIKC | FIRSTPPPDR | IAWSWKENVL | ESGTSGRYTV | ETISTEEGVI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| STLTISNIVR | ADFQTIYNCT | AWNSFGSDTE | IIRLKEQESV | PMAVIIGVAV | GAGVAFLVLM | ATIVAFCCAR | SQRNLKGVVS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AKNDIRVEIV | HKEPASGREG | EEHSTIKQLM | MDRGEFQQDS | VLKQLEVLKE | EEKEFQNLKD | PTNGYYSVNT | FKEHHSTPTI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SLSSCQPDLR | PAGKQRVPTG | MSFTNIYSTL | SGQGRLYDYG | QRFVLGMGSS | SIELCEREFQ | RGSLSDSSSF | LDTQCDSSVS |
| 730 | 740 | 750 | 760 | 770 | | | |
| SSGKQDGYVQ | FDKASKASAS | SSHHSQSSSQ | NSDPSRPLQR | RMQTHV | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1604 | 1 | 910.4351 | -62.80 | 2 | 49.8 | 17.6 | 2 | 563-578 | K.NDIRVEIVHKEPASGR.E | |

# Detailed Protein Report

## Protein 940: PREDICTED: zinc finger protein 33B isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578819760 | **Score:** | 17.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 92.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.65 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.44 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPHPLATSAF | LRFRLSFCLS | HVLRGRRSRD | FRGLPALLWR | MQPEERVSCI | FRVVSVFPRT | EQNEQGYCAH | KPEVIFRLEQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GEEPWRLEEE | FPSQSFPVWT | ADHLKERSQE | NQSKHLWEVV | FINNEMLTKE | QGNVIGIPFN | MDVSSFPSRK | MFCQYDSRGM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SFNTVSELVI | SKINYLGKKS | DEFNACGKLL | LNIKHDETHT | REKNEVLKNR | NTLSHRENTL | QHEKIQTLDH | NFEYSICQET |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LLEKAVFNTR | KRENAEENNC | DYNEFGRTFC | DSSSLLFHQI | PPSKDSHYEF | SDCEKFLCVK | STLSKHDGVP | VKHYDCGESG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NNFRRKLCLS | QLQKGDKGEK | HFECNECGKA | FWEKSHLTRH | QRVHTGEKHF | QCNQCGKTFW | EKSNLTKHQR | SHTGEKPFEC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NECGKAFSHK | SALTLHQRTH | TGEKPYQCNA | CGKTFYQKSD | LTKHQRTHTG | QKPYECYECG | KSFCMNSHLT | VHQRTHTGEK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PFECLECGKS | FCQKSHLTQH | QRTHIGDKPY | ECNACGKTFY | HKSVLTRHQI | IHTGLKPYEC | YECGKTFCLK | SDLTIHQRTH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TGEKPFACPE | CGKFFSHKST | LSQHYRTHTG | EKPYECHECG | KIFYNKSYLT | KHNRTHTGEK | PYECNECGKT | FCQKSQLTQH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QRIHIGEKPY | ECNECGKAFC | HKSALIVHQR | THTQEKPYKC | NECGKSFCVK | SGLILHERKH | TGEKPYECNE | CGKSFSHKSS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LTVHHRAHTG | EKSCQCNECG | KIFYRKSDLA | KHQRSHTGEK | PYECNTCRKT | FSQKSNLIVH | QRTHIGEKPY | E |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 24 | 1 | 1103.4962 | -22.42 | 2 | 29.2 | 17.6 | 0 | 60-77 | R.TEQNEQGYCAHKPEVIFR.L | Carbamidomethyl: 9 | WUP:QUP 0.44<br>QU:MU 1.65 |

# Detailed Protein Report

## Protein 941: E-selectin precursor [Homo sapiens]

**Accession:** gi|187960042
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl, Oxidation

**Score:** 17.6
**MW [kDa]:** 66.6
**pI:** 5.1
**Sequence Coverage [%]:** 2.6
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MIASQFLSAL | TLVLLIKESG | AWSYNTSTEA | MTYDEASAYC | QQRYTHLVAI | QNKEEIEYLN | SILSYSPSYY | WIGIRKVNNV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| WVWVGTQKPL | TEEAKNWAPG | EPNNRQKDED | CVEIYIKREK | DVGMWNDERC | SKKKLALCYT | AACTNTSCSG | HGECVETINN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YTCKCDPGFS | GLKCEQIVNC | TALESPEHGS | LVCSHPLGNF | SYNSSCSISC | DRGYLPSSME | TMQCMSSGEW | SAPIPACNVV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ECDAVTNPAN | GFVECFQNPG | SFPWNTTCTF | DCEEGFELMG | AQSLQCTSSG | NWDNEKPTCK | AVTCRAVRQP | QNGSVRCSHS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PAGEFTFKSS | CNFTCEEGFM | LQGPAQVECT | TQGQWTQQIP | VCEAFQCTAL | SNPERGYMNC | LPSASGSFRY | GSSCEFSCEQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GFVLKGSKRL | QCGPTGEWDN | EKPTCEAVRC | DAVHQPPKGL | VRCAHSPIGE | FTYKSSCAFS | CEEGFELHGS | TQLECTSQGQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| WTEEVPSCQV | VKCSSLAVPG | KINMSCSGEP | VFGTVCKFAC | PEGWTLNGSA | ARTCGATGHW | SGLLPTCEAP | TESNIPLVAG |
| 570 | 580 | 590 | 600 | 610 | 620 | | |
| LSAAGLSLLT | LAPFLLWLRK | CLRKAKKFVP | ASSCQSLESD | GSYQKPSYIL | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2878 | 1 | 872.9387 | 57.19 | 2 | 64.7 | 17.6 | 0 | 502-517 | K.INMSCSGEPVFGTVCK.F | Carbamidomethyl: 15;<br>Oxidation: 3 |

# Detailed Protein Report

## Protein 942: amiloride-sensitive sodium channel subunit alpha isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4506815 | **Score:** | 17.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 75.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.5 |
| | | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEGNKLEEQD | SSPPQSTPGL | MKGNKREEQG | LGPEPAAPQQ | PTAEEEALIE | FHRSYRELFE | FFCNNTTIHG | AIRLVCSQHN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RMKTAFWAVL | WLCTFGMMYW | QFGLLFGEYF | SYPVSLNINL | NSDKLVFPAV | TICTLNPYRY | PEIKEELEEL | DRITEQTLFD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LYKYSSFTTL | VAGSRSRRDL | RGTLPHPLQR | LRVPPPPHGA | RRARSVASSL | RDNNPQVDWK | DWKIGFQLCN | QNKSDCFYQT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YSSGVDAVRE | WYRFHYINIL | SRLPETLPSL | EEDTLGNFIF | ACRFNQVSCN | QANYSHFHHP | MYGNCYTFND | KNNSNLWMSS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MPGINNGLSL | MLRAEQNDFI | PLLSTVTGAR | VMVHGQDEPA | FMDDGGFNLR | PGVETSISMR | KETLDRLGGD | YGDCTKNGSD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VPVENLYPSK | YTQQVCIHSC | FQESMIKECG | CAYIFYPRPQ | NVEYCDYRKH | SSWGYCYYKL | QVDFSSDHLG | CFTKCRKPCS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VTSYQLSAGY | SRWPSVTSQE | WVFQMLSRQN | NYTVNNKRNG | VAKVNIFFKE | LNYKTNSESP | SVTMVTLLSN | LGSQWSLWFG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SSVLSVVEMA | ELVFDLLVIM | FLMLLRRFRS | RYWSPGRGGR | GAQEVASTLA | SSPPSHFCPH | PMSLSLSQPG | PAPSPALTAP |
| 650 | 660 | 670 | | | | | |
| PPAYATLGPR | PSPGGSAGAS | SSTCPLGGP | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2868 | 1 | 873.7778 | -171.39 | 2 | 64.6 | 17.6 | 0 | 477-492 | R.KPCSVTSYQLSAGYSR.W | |

# Detailed Protein Report

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## Protein 943: GS homeobox 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|33457326 | **Score:** | 17.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 9.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 4.95 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.49 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MPRSFLVDSL VLREAGEKKA PEGSPPPLFP YAVPPPHALH GLSPGACHAR KAGLLCVCPL CVTASQLHGP PGPPALPLLK
        90        100        110        120        130        140        150        160
ASFPPFGSQY CHAPLGRQHS AVSPGVAHGP AAAAAAAALY QTSYPLPDPR QFHCISVDSS SNQLPSSKRM RTAFTSTQLL
       170        180        190        200        210        220        230        240
ELEREFASNM YLSRLRRIEI ATYLNLSEKQ VKIWFQNRRV KHKKEGKGSN HRGGGGGGAG GGGSAPQGCK CASLSSAKCS
       250        260        270
EDDDELPMSP SSSGKDDRDL TVTP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 42 | 1 | 1096.9830 | -8.41 | 2 | 30.2 | 17.6 | 1 | 213-238 | R.<br>GGGGGGAGGGGSAPQGCKCASI<br>C | Carbamidomethyl: 17, 19 | WUP:QUP<br>QU:MU | 0.49<br>4.95 |

# Detailed Protein Report

**Protein 944:** **PREDICTED: leucine-rich repeat and IQ domain-containing protein 1 isoform X6 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578824314 | **Score:** | 17.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 191.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDDDDAKLKA | EIEAELDKLS | ISSLEKEDIE | SDAKSETQSD | DSDTDSVELP | ESVLHCINII | KNRSKAVEEL | ILQDLEDTDI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LSCSYGAVSN | NHMHLRTGLS | TEYEESSEQL | IKILSEIEKE | EFMRSKTDCA | TPDFVPEPSP | HDLPMDEHVL | PDDADINFGY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CEVEEKCRQS | FEAWQEKQKE | LEDKEKQTLK | AQRDREEKQF | QEEEEKRHCW | MKQFKVEKKK | LENIQKQEQD | KMNDELYKEE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KIWKEKFKQH | EEYIRNLHLQ | MEEERTRFKD | QQEKEKNSLL | KQQNNAAVKI | QAKYKAFVAY | QKYGPIIKEQ | IESKKRKAQE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WKEKEAKIRQ | KEEENRKRLE | EEQRIKEERK | KQKEEERKRR | EKEYEEKKNI | VKQEREQLIS | KEKIILREDA | SQQLIISSAL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KKSGYNNKHL | SLEDISNDKG | DIAKNLVDEN | SKKQEDVLLW | LVEESNMKEN | VDRQTILKES | IQVKLKESIS | SQTILADFKM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EEKNENLAKK | RCSEELVKQE | RKYENTDNKT | ELGNSDLKGN | LKEQFPLQEL | KSDAQKEEKI | MKHVINENTG | QKTQIILGHN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QEISEVKTNE | EQKIIKDNQQ | KKIQKVEKEE | IQEQNGLLYK | DKDTLVISVK | QRSLSLTSEN | SKDVRENVIL | QEKEIYSKSK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EIEENPKDNA | WNSGIVIFNT | TDTMINIEGK | RNDQDYVLGR | HAPCEGLSNY | NAESSMVSKE | VNSLKSEIRN | ISEKCHENAP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EPDSMTCCVS | ESTLLYSIEE | RRLAWIKSFK | PWLEIFKQNQ | QKKIVRRKRP | VKCPANMTPA | LDKLEILRCG | PWDTLQQVTT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VTFQDLPGCV | LSTLAECTNL | QFLSLRRCGL | TSLHSLSNCK | KLKYIDAQEN | HIEAIECENL | ENLCVVLLNK | NQLTSLHGLD |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GCTNIQCLEL | SYNKITRIGG | LESLKNLQQL | ILDHNQLINT | KGLCDTPTIV | YLDCSHNHLT | DVEGVENCGL | LQILKLQGNY |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LSELPSLENL | VLLRELHLDD | NSISTVEAFS | SYWLPLLQNI | TISQNSLTKI | VPLFHFVSLE | KLDVSHNCLS | DLKSAIKWFD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ACYSLHELSL | TGNPLLQETN | WRDSLLKVLP | ALRILNGNIL | NSNSESRTEE | HNQLGSAGFL | ALCQSQIREF | NLLIENYITG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KGDVFTLDTA | ENLCHYFKKL | MILSTEYRHA | HERGDVTITK | KDESEAQKNH | LAPTNSDSTL | QNGVFYSCAR | EGEPDSPDIP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EKWMDSVSSH | SPLSKSATCE | NMEGRHQEIL | VCQKREDSKA | SSIPTIRIPF | KEVVMTNSLL | RNHQNIEPSE | KIMAAVVIQS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| YWRGYLMRRQ | THFSTRLHTA | ATEGLPNSSI | KNQTILKKGK | RENIVNIRKQ | REKAAILIQA | VWKGFILRKK | LTTALEAIKN |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| EESDEEYREI | DLEDFIFDEA | ALEEEWLALD | STRFPSQTLL | LSNQLHWPKI | PGNLKWDDTS | FNLPSNPAQA | WLCNDKENLS |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SSEHTQFNSR | SENKTSSWTP | ESKTSRKSLL | KSEKEKKISE | EWGFKDISTA | QQMLKRAQKM | KSKKLKKKID | STVRLALFKN |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| NENKVSLPKS | PKMVQPRRDG | YFEGIEEDPI | HKDTTANEKL | ERNREYTYQW | LHTQVGVHET | TSSRNMKCNH | FLPELDPDVL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | | |
| NGGRVQLVAR | LVSREDTDLD | LFSMTNGSAL | SVNREKKNQA | HRHSAGSSSK | LWFPSKLI | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 862 | 1 | 1198.5391 | -67.11 | 2 | 39.2 | 17.6 | 1 | 1290-1311 | R.QTHFSTRLHTAATEGLPNSSIK.N | |

# Detailed Protein Report

## Protein 945: PREDICTED: unconventional myosin-VI isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530383156 | **Score:** | 17.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 144.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEDGKPVWAP | HPTDGFQMGN | IVDIGPDSLT | IEPLNQKGKT | FLALINQVFP | AEEDSKKDVE | DNCSLMYLNE | ATLLHNIKVR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YSKDRIYTYV | ANILIAVNPY | FDIPKIYSSE | AIKSYQGKSL | GTRPPHVFAI | ADKAFRDMKV | LKMSQSIIVS | GESGAGKTEN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TKFVLRYLTE | SYGTGQDIDD | RIVEANPLLE | AFGNAKTVRN | NNSSRFGKFV | EIHFNEKSSV | VGGFVSHYLL | EKSRICVQGK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EERNYHIFYR | LCAGASEDIR | EKLHLSSPDN | FRYLNRGCTR | YFANKETDKQ | ILQNRKSPEY | LKAGSMKDPL | LDDHGDFIRM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CTAMKKIGLD | DEEKLDLFRV | VAGVLHLGNI | DFEEAGSTSG | GCNLKNKSAQ | SLEYCAELLG | LDQDDLRVSL | TTRVMLTTAG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GTKGTVIKVP | LKVEQANNAR | DALAKTVYSH | LFDHVVNRVN | QCFPFETSSY | FIGVLDIAGF | EYFEHNSFEQ | FCINYCNEKL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QQFFNERILK | EEQELYQKEG | LGVNEVHYVD | NQDCIDLIEA | KLVGILDILD | EENRLPQPSD | QHFTSAVHQK | HKDHFRLTIP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RKSKLAVHRN | IRDDEGFIIR | HFAGAVCYET | TQFVEKNNDA | LHMSLESLIC | ESRDKFIREL | FESSTNNNKD | TKQKAGKLSF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ISVGNKFKTQ | LNLLLDKLRS | TGASFIRCIK | PNLKMTSHHF | EGAQILSQLQ | CSGMVSVLDL | MQGGYPSRAS | FHELYNMYKK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YMPDKLARLD | PRLFCKALFK | ALGLNENDYK | FGLTKVFFRP | GKFAEFDQIM | KSDPDHLAEL | VKRVNHWLTC | SRWKKVQWCS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LSVIKLKNKI | KYRAEACIKM | QKTIRMWLCK | RRHKPRIDGL | VKVGTLKKRL | DKFNEVVSVL | KDGKPEMNKQ | IKNLEISIDT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LMAKIKSTMM | TQEQIQKEYD | ALVKSSEELL | SALQKKKQQE | EEAERLRRIQ | EEMEKERKRR | EEDEKRRRKE | EEERRMKLEM |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| EAKRKQEEEE | RKKREDDEKR | IQAEVEAQLA | RQKEEESQQQ | AVLEQERRDR | ELALRIAQSE | AELISDEAQA | DLALRRGPAV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LATKAAAGTK | KYDLSKWKYA | ELRDTINTSC | DIELLAACRE | EFHRRLKVYH | AWKSKNKKRN | TETEQRAPKS | VTDYAQQNPA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| AQIPARQREI | EMNRQQRFFR | IPFIRPADQY | KDPQSKKKGW | WYAHFDGPWI | ARQMELHPDK | PPILLVAGKD | DMEMCELNLE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | | |
| ETGLTRKRGA | EILPRQFEEI | WERCGGIQYL | QNAIESRQAR | PTYATAMLQS | LLK | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1221 | 1 | 985.1783 | 21.41 | 3 | 44.9 | 17.5 | 1 | 368-393 | K.SAQSLEYCAELLGLDQDDLRVSLTTR.V | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 946: histone deacetylase complex subunit SAP25 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|284004891 | **Score:** | 17.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 20.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| | | **Sequence Coverage [%]:** | 8.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTPLAPWDPK | YEAKAGPRPV | WGANCSSGAS | FSGRTLCHPS | FWPLYEAASG | RGLRPVAPAT | GHWNGQQAPP | DAGFPVVCCE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DVFLSDPLLP | RGQRVPLYLS | KAPQQMMGSL | KLLPPPPIMS | ARVLPRPSPS | RGPSTAWLSG | PELIALTGLL | QMSQGEPRPS |
| 170 | 180 | 190 | 200 | | | | |
| SSAVGPPDHT | SDPPSPCGSP | SSSQGADLSL | PQTPDTHCP | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2810 | 2 | 945.9828 | -31.58 | 2 | 63.7 | 17.5 | 1 | 95-111 | R.VPLYLSKAPQQMMGSLK.L | |

# Detailed Protein Report

## Protein 947: differential display clone 8 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|343780900 | **Score:** | 17.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 63.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530411299 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: differential display clone 8 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDGAMWLSLC | PDNEDLLWRK | KHKLLQARGK | GDLALQRRAD | AKLWKNYQLQ | RLAEELRRGY | QEAQHLHVGG | LDRLQSARLL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GWGGGRAREN | EPDSQGPIQR | RSARPPRAKE | KHRAALSEER | SCREELGQQH | PRHSRPRKTA | ASPEKPQTTK | ATGRMNSHLA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PPEKRKGRPE | PSTKSGGGRC | AIHPRRSKGA | DLERSNPLVA | AVGEIGLVEE | KEKGTARAGR | RQLGKGAVCF | VPALTSRSQG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QSLEGKLRDL | GQLWPADSSC | RREAVSPASQ | CTLREKNKWQ | KELELAFEEL | FNINRKLKKH | LCLYLALKPR | MDQRPGEGHA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FSEMQECGAG | TPRGKKMADP | EMLPAGEPRS | PAEEEAQQAA | SKTDLKTFMG | KAQNQKYQGT | VKPTFRNGSQ | TLSPEAGIFI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NKEDSLLYST | ESGQETPKLG | TLAEGSLQLH | LQDQADRVGS | TASRQRQKAE | MEQRRQKQLE | SLEQMEHPDM | SLEIHYKAEL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EKERREQRRA | RLAHLKSSST | RAQERERGSE | LSTTSPSGTS | LADDDRHSQM | IRDQQQQILQ | QNRLHKQFLE | EARKCLREFQ |
| 570 | | | | | | | |
| NIC | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2733 | 1 | 848.4051 | -142.97 | 2 | 65.3 | 17.4 | 2 | 297-310 | K.LKKHLCLYLALKPR.M | |

# Detailed Protein Report

## Protein 948: solute carrier organic anion transporter family member 1B1 [Homo sapiens]

**Accession:** gi|225543525
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 17.4
**MW [kDa]:** 76.4
**pI:** 9.7
**Sequence Coverage [%]:** 1.9
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDQNQHLNKT | AEAQPSENKK | TRYCNGLKMF | LAALSLSFIA | KTLGAIIMKS | SIIHIERRFE | ISSSLVGFID | GSFEIGNLLV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IVFVSYFGSK | LHRPKLIGIG | CFIMGIGGVL | TALPHFFMGY | YRYSKETNIN | SSENSTSTLS | TCLINQILSL | NRASPEIVGK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GCLKESGSYM | WIYVFMGNML | RGIGETPIVP | LGLSYIDDFA | KEGHSSLYLG | ILNAIAMIGP | IIGFTLGSLF | SKMYVDIGYV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DLSTIRITPT | DSRWVGAWWL | NFLVSGLFSI | ISSIPFFFLP | QTPNKPQKER | KASLSLHVLE | TNDEKDQTAN | LTNQGKNITK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NVTGFFQSFK | SILTNPLYVM | FVLLTLLQVS | SYIGAFTYVF | KYVEQQYGQP | SSKANILLGV | ITIPIFASGM | FLGGYIIKKF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KLNTVGIAKF | SCFTAVMSLS | FYLLYFFILC | ENKSVAGLTM | TYDGNNPVTS | HRDVPLSYCN | SDCNCDESQW | EPVCGNNGIT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YISPCLAGCK | SSSGNKKPIV | FYNCSCLEVT | GLQNRNYSAH | LGECPRDDAC | TRKFYFFVAI | QVLNLFFSAL | GGTSHVMLIV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KIVQPELKSL | ALGFHSMVIR | ALGGILAPIY | FGALIDTTCI | KWSTNNCGTR | GSCRTYNSTS | FSRVYLGLSS | MLRVSSLVLY |
| 650 | 660 | 670 | 680 | 690 | 700 | | |
| IILIYAMKKK | YQEKDINASE | NGSVMDEANL | ESLNKNKHFV | PSAGADSETH | C | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 216 | 1 | 487.1727 | -168.54 | 3 | 32.4 | 17.4 | 2 | 10-22 | K.TAEAQPSENKKTR.Y | |

# Detailed Protein Report

**Protein 949:** **t-SNARE domain-containing protein 1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|223972648 | **Score:** | 17.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 55.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.95 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.50 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSYGSIARGG GLGSRGPFGG PSRQGCQPLE CARCWTEYGI RHFPCPSPES KLQNRCVGKD GEGDLGPAGT PIVPRARKRG
        90        100        110        120        130        140        150        160
PGVAPEGSRM PEPTSSPTIG PRKDSAAGPH GRMAGPSTTR AKKRKPNFCP QETEVLVSKV SKHHQLLFGT GLLKAEPTRR
       170        180        190        200        210        220        230        240
YRVWSRILQA VNALGYCRRD VVDLKHKWRD LRAVVRRKLG DLRKAAHGPS PGSGKPQALA LTPVEQVVAK TFSCQALPSE
       250        260        270        280        290        300        310        320
GFSLEPPRAT QVDPCNLQEL FQEMSANVFR INSSVTSLER SLQSLGTPSD TQELRDSLHT AQQETNKTIA ASASSVKQMA
       330        340        350        360        370        380        390        400
ELLRSSCPQE RLQQERPQLD RLKTQLSDAI QCYGVVQKKI AEKSRALLPM AQRGSKQSPQ APFAELADDE KVFNGSDNMW
       410        420        430        440        450        460        470        480
QGQEQALLPD ITEEDLEAIR LREEAILQME SNLLDVNQII KDLASMVSEQ GEAVDSIEAS LEAASSHAEA ARQLLAGASR
       490        500        510        520
HQLQRHKIKC CFLSAGVTAL LVIIIIIATS VRK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 258 | 1 | 442.7344 | 36.28 | 2 | 32.0 | 17.4 | 0 | 1-8 | -.MSYGSIAR.G | | WUP:QUP 0.50<br>QU:MU 0.95 |

# Detailed Protein Report

## Protein 950: PREDICTED: ubiquitin thioesterase ZRANB1 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530393888 | **Score:** | 17.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 44.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.04 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLAILLTEVS | QQAAKCIPAM | VCPELTEQIR | REIAASLHQR | KGDFACYFLT | DLVTFTLPAD | IEDLPPTVQE | KLFDEVLDRD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VQKELEEESP | IINWSLELAT | RLDSRLYALW | NRTAGDCLLD | SVLQATWGIY | DKDSVLRKAL | HDSLHDCSHW | FYTRWKDWES |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WYSQSFGLHF | SLREEQWQED | WAFILSLASQ | PGASLEQTHI | FVLAHILRRP | IIVYGVKYYK | SFRGETLGYT | RFQGVYLPLL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| WEQSFCWKSP | IALGYTRGHF | SALVAMENDG | YGNRGAGANL | NTDDDVTITF | LPLVDSERKL | LHVHFLSAQE | LGNEEQQEKL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| LREWLDCCVT | EGGVLVAMQK | SSRRRNHPLV | TQMVEKWLDR | YRQIRPCTSL | SDGEEDEDDE | DE | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2848 | 3 | 648.3529 | 16.16 | 2 | 64.3 | 17.3 | 0 | 346-356 | R.NHPLVTQMVEK.W | | WUP:QUP 0.04 |

# Detailed Protein Report

**Protein 951:** **arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 isoform d [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|206597515 | **Score:** | 17.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 127.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTKKEEPPPS | RVPRAVRVAS | LLSEGEELSG | DDQGDEEEDD | HAYEGVPNGG | WHTSSLSLSL | PSTIAAPHPM | DGPPGGSTPV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TPVIKAGWLD | KNPPQGSYIY | QKRWVRLDTD | HLRYFDSNKD | AYSKRFISVA | CISHVAAIGD | QKFEVITNNR | TFAFRAESDV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ERKEWMQALQ | QAMAEQRARA | RLSSAYLLGV | PGSEQPDRAG | SLELRGFKNK | LYVAVVGDKV | QLYKNLEEYH | LGIGITFIDM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SVGNVKEVDR | RSFDLTTPYR | IFSFSADSEL | EKEQWLEAMQ | GAIAEALSTS | EVAERIWAAA | PNRFCADCGA | PQPDWASINL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CVVICKRCAG | EHRGLGAGVS | KVRSLKMDRK | VWTETLIEAL | CAAVTTTDLA | ETQALLGCGA | GINCFSGDPE | APTPLALAEQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AGQTLQMEFL | RNNRTTEVPR | LDSMKPLEKH | YSVVLPTVSH | SGFLYKTASA | GKLLQDRRAR | EEFSRRWCVL | GDGVLSYFEN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ERAVTPNGEI | RASEIVCLAV | PPPDTHGFEH | TFEVYTEGER | LYLFGLESAE | QAHEWVKCIA | KAFVPPLAED | LLARDFERLG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RLPYKAGLSL | QRAQEGWFSL | SGSELRAVFP | EGPCEEPLQL | RKLQELSIQG | DSENQVLVLV | ERRRTLYIQG | ERRLDFMGWL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GAIQKAAASM | GDTLSEQQLG | DSDIPVIVYR | CVDYITQCGL | TSEGIYRKCG | QTSKTQRLLE | SLRQDARSVH | LKEGEQHVDD |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VSSALKRFLR | DLPDGLFTRA | QRLTWLEASE | IEDEEEKVSR | YRELLVRLPP | VNRATVKALI | SHLYCVQCFS | DTNQMNVHNL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AIVFGPTLFQ | TDGQDYKAGR | VVEDLINHYV | VVFSVDEEEL | RKQREEITAI | VKMRVAGTAS | GTQHAGDFIC | TVYLEEKKAE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TEQHIKVPAS | MTAEELTLEI | LDRRNVGIRE | KDYWTCFEVN | EREEAERPLH | FAEKVLPILH | GLGTDSHLVV | KKHQAMEAML |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LYLASRVGDT | KHGMMKFRED | RSLLGLGLPS | GGFHDRYFIL | NSSCLRLYKE | VRSHRPEKEW | PIKSLKVYLG | VKKKLRPPTC |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| WGFTVVHETE | KHEKQQWYLC | CDTQMELREW | FATFLFVQHD | GLVWPSEPSR | VSRAVPEVRL | GSVSLIPLRG | SENEMRRSVA |
| 1130 | 1140 | | | | | | |
| AFTADPLSLL | RNV | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2177 | 1 | 937.2849 | -128.31 | 2 | 57.1 | 17.3 | 0 | 1055-1068 | K.QQWYLCCDTQMELR.E | Carbamidomethyl: 7 |

# Detailed Protein Report

## Protein 952: PREDICTED: nef-associated protein 1 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530391237 | **Score:** | 17.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 32.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 4.7 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530391241 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: nef-associated protein 1 isoform X4 [Homo sapiens] |
| gi\|530391239 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: nef-associated protein 1 isoform X3 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MIHGTPVLDI KPYIAEYDSP QNVMEPLADF NLQNNQHTPN TVSQSDSKTD SCDQRQLSGC DEPQPHHSTK RKPKCPEDRT
        90        100        110        120        130        140        150        160
SEENYLTHSD TARIQQAFPM HREIAVDFGL ESRRDQSSSV AEEQIGPYCP EKSFSEKGTD KKLERVEGAA VLQGSRAETQ
       170        180        190        200        210        220        230        240
PMAPHCPAGR ADGAPRSVVP AWVTEAPVAT LEVRFTPHAE MDLGQLSSQD VGQASFKYFQ SAEEAKRAIE AVLSADPRSV
       250        260        270        280        290        300
YRRKLCQDRL FYFTVDIAHV TCWFGDGFAE VLRIKPASEP VHMTGPVGSL VSLGS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2863 | 1 | 812.4116 | 56.30 | 2 | 66.2 | 17.2 | 0 | 80-93 | R.TSEENYLTHSDTAR.I | |

# Detailed Protein Report

**Protein 953:** **PREDICTED: dephospho-CoA kinase domain-containing protein isoform X4 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530412893 | **Score:** | 17.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 14.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 9.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578831425 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: dephospho-CoA kinase domain-containing protein isoform X7 [Homo sapiens] |
| gi\|578831423 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: dephospho-CoA kinase domain-containing protein isoform X6 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MFLVGLTGGI ASGKSSVIQV FQQLGCAVID VDVMARHVVQ PGYPAHRRIV EVFGTEVLLE NGDINRKVLG DLIFNQPDRR
        90        100        110        120        130        140
QLLNAITHPE IRKEMMKETF KYFLREPRTS PRGKKHVPSA LKEADSLMRR DT
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 1 | 819.8504 | -66.08 | 2 | 29.4 | 17.2 | 2 | 94-105 | K.EMMKETFKYFLR.E | Oxidation: 2 |

# Detailed Protein Report

## Protein 954: vacuolar protein sorting-associated protein 26A isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|17978519 | **Score:** | 17.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSFLGGFFGP | ICEIDIVLND | GETRKMAEMK | TEDGKVEKHY | LFYDGESVSG | KVNLAFKQPG | KRLEHQGIRI | EFVGQIELFN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DKSNTHEFVN | LVKELALPGE | LTQSRSYDFE | FMQVEKPYES | YIGANVRLRY | FLKVTIVRRL | TDLVKEYDLI | VHQLATYPDV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NNSIKMEVGI | EDCLHIEFEY | NKSKYHLKDV | IVGKIYFLLV | RIKIQHMELQ | LIKKEITGIG | PSTTTETETI | AKYEIMDGAP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VKGESIPIRL | FLAGYDPTPT | MRDVNKKFSV | RYFLNLVLVD | EEDRRYFKQQ | EIILWRKAPE | KLRKQRTNFH | QRFESPESQA |
| 330 | | | | | | | |
| SAEQPEM | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2850 | 1 | 826.4426 | -32.68 | 2 | 66.0 | 17.2 | 2 | 286-297 | R.YFKQQEIILWRK.A | |

# Detailed Protein Report

## Protein 955: trichohyalin [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|148746195 | **Score:** | 17.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 253.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSPLLRSICD | ITEIFNQYVS | HDCDGAALTK | KDLKNLLERE | FGAVLRRPHD | PKTVDLILEL | LDLDSNGRVD | FNEFLLFIFK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VAQACYYALG | QATGLDEEKR | ARCDGKESLL | QDRRQEEDQR | RFEPRDRQLE | EEPGQRRRQK | RQEQERELAE | GEEQSEKQER |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LEQRDRQRRD | EELWRQRQEW | QEREERRAEE | EQLQSCKGHE | TEEFPDEEQL | RRRELLELRR | KGREEKQQQR | RERQDRVFQE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EEEKEWRKRE | TVLRKEEEKL | QEEEPQRQRE | LQEEEEQLRK | LERQELRRER | QEEEQQQQRL | RREQQLRRKQ | EEERREQQEE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RREQQERREQ | QEERREQQLR | REQEERREQQ | LRREQEEERR | EQQLRREQEE | ERREQQLRRE | QQLRREQQLR | REQQLRREQQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LRREQQLRRE | QQLRREQQLR | REQQLRREQE | EERHEQKHEQ | ERREQRLKRE | QEERRDWLKR | EEETERHEQE | RRKQQLKRDQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EEERRERWLK | LEEEERREQQ | ERREQQLRRE | QEERREQRLK | RQEEEERLQQ | RLRSEQQLRR | EQEERREQLL | KREEEKRLEQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ERREQRLKRE | QEERRDQLLK | REEERRQQRL | KREQEERLEQ | RLKREEVERL | EQEERREQRL | KREEPEEERR | QQLLKSEEQE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ERRQQQLRRE | QQERREQRLK | REEEEERLEQ | RLKREHEEER | REQELAEEEQ | EQARERIKSR | IPKWQWQLES | EADARQSKVY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SRPRKQEGQR | RRQEQEEKRR | RRESELQWQE | EERAHRQQQE | EEQRRDFTWQ | WQAEEKSERG | RQRLSARPPL | REQRERQLRA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EERQQREQRF | LPEEEEKEQR | RRQRREREKE | LQFLEEEEQL | QRRERAQQLQ | EEEDGLQEDQ | ERRRSQEQRR | DQKWRWQLEE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ERKRRRHTLY | AKPALQEQLR | KEQQLLQEEE | EELQREEREK | RRRQEQERQY | REEEQLQQEE | EQLLREEREK | RRRQERERQY |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RKDKKLQQKE | EQLLGEEPEK | RRRQEREKKY | REEEELQQEE | EQLLREEREK | RRRQEWERQY | RKKDELQQEE | EQLLREEREK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RRLQERERQY | REEEELQQEE | EQLLGEERET | RRRQELERQY | RKEEELQQEE | EQLLREEPEK | RRRQERERQC | REEEELQQEE |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EQLLREEREK | RRRQELERQY | REEEEVQQEE | EQLLREEPEK | RRRQELERQY | REEEELQQEE | EQLLREEQEK | RRQERERQYR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EEEELQRQKR | KQRYRDEDQR | SDLKWQWEPE | KENAVRDNKV | YCKGRENEQF | RQLEDSQLRD | RQSQQDLQHL | LGEQQERDRE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| QERRRWQQRD | RHFPEEEQLE | REEQKEAKRR | DRKSQEEKQL | LREEREEKRR | RQETDRKFRE | EEQLLQEREE | QPLRRQERDR |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KFREEELRHQ | EQGRKFLEEE | QRLRRQERER | KFLKEEQQLR | CQEREQQLRQ | DRDRKFREEE | QQLSRQERDR | KFREEEQQVR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| RQERERKFLE | EEQQLRQERH | RKFREEEQLL | QEREEQQLHR | QERDRKFLEE | EQQLRRQERD | RKFREQELRS | QEPERKFLEE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| EQQLHRQQRQ | RKFLQEEQQL | RRQERGQQRR | QDRDRKFREE | EQLRQEREEQ | QLSRQERDRK | FRLEEQKVRR | QEQERKFMED |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| EQQLRRQEGQ | QQLRQERDRK | FREDEQLLQE | REEQQLHRQE | RDRKFLEEEP | QLRRQEREQQ | LRHDRDRKFR | EEEQLLQEGE |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| EQQLRRQERD | RKFREEEQQL | RRQERERKFL | QEEQQLRRQE | LERKFREEEQ | LRQETEQEQL | RRQERYRKIL | EEEQLRPERE |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| EQQLRRQERD | RKFREEEQLR | QEREEQQLRS | QESDRKFREE | EQLRQEREEQ | QLRPQQRDGK | YRWEEEQLQL | EEQEQRLRQE |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| RDRQYRAEEQ | FATQEKSRRE | EQELWQEEEQ | KRRQERERKL | REEHIRRQQK | EEQRHRQVGE | IKSQEGKGHG | RLLEPGTHQF |
| 1930 | 1940 | 1950 | | | | | |
| ASVPVRSSPL | YEYIQEQRSQ | YRP | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2093 | 2 | 974.3559 | -134.06 | 2 | 54.5 | 17.2 | 1 | 828-842 | R.EKELQFLEEEEQLQR.R | |

# Detailed Protein Report

## Protein 956: gamma-tubulin complex component 4 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|38454194 | **Score:** | 17.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 76.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MIHELLLALS | GYPGSIFTWN | KRSGLQVSQD | FPFLHPSETS | VLNRLCRLGT | DYIRFTEFIE | QYTGHVQQQD | HHPSQQGQGG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LHGIYLRAFC | TGLDSVLQPY | RQALLDLEQE | FLGDPHLSIS | HVNYFLDQFQ | LLFPSVMVVV | EQIKSQKIHG | CQILETVYKH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SCGGLPPVRS | ALEKILAVCH | GVMYKQLSAW | MLHGLLLDQH | EEFFIKQGPS | SGNVSAQPEE | DEEDLGIGGL | TGKQLRELQD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LRLIEEENML | APSLKQFSLR | VEILPSYIPV | RVAEKILFVG | ESVQMFENQN | VNLTRKGSIL | KNQEDTFAAE | LHRLKQQPLF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SLVDFEQVVD | RIRSTVAEHL | WKLMVEESDL | LGQLKIIKDF | YLLGRGELFQ | AFIDTAQHML | KTPPTAVTEH | DVNVAFQQSA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HKVLLDDDNL | LPLLHLTIEY | HGKEHKDATQ | AREGPSRETS | PREAPASGWA | ALGLSYKVQW | PLHILFTPAV | LEKYNVVFKY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LLSVRRVQAE | LQHCWALQMQ | RKHLKSNQTD | AIKWRLRNHM | AFLVDNLQYY | LQVDVLESQF | SQLLHQINST | RDFESIRLAH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DHFLSNLLAQ | SFILLKPVFH | CLNEILDLCH | SFCSLVSQNL | GPLDERGAAQ | LSILVKGFSR | QSSLLFKILS | SVRNHQINSD |
| 650 | 660 | 670 | | | | | |
| LAQLLLRLDY | NKYYTQAGGT | LGSFGM | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1982 | 4 | 726.7832 | -60.06 | 2 | 54.7 | 17.2 | 0 | 653-666 | K.YYTQAGGTLGSFGM.- | |

# Detailed Protein Report

**Protein 957:** **PREDICTED: uncharacterized protein KIAA1211 isoform X7 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578808650 | **Score:** | 17.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 124.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEEKVAPVKP | SRPKRHFSSA | GTIESVNLDA | IPLAIARLDN | SAAKHKLAVK | PKKQRVSKKH | RRLAQDPQHE | QGGLESRPCL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DQNGHPGEDK | PTWHEEEPNP | LDSEEERRRQ | EDYWRELEAK | CKRQKAEAAE | KRRLEEQRLQ | ALERRLWEEN | RRQELLEEEG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EGQEPPLEAE | RAPREEQQRS | LEAPGWEDAE | RREREEERRL | EAEEERRRLQ | AQAQAEERRR | LEEDARLEER | RRQEEEEGRC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AEELKRQEEE | EAEGWEELEQ | QEAEVQGPPE | ALEETGEGRR | GAEEEDLGEE | EEEGQAHLED | WRGQLSELLN | DFEERLEDQE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RLKPEGQREH | SEEPGICEEQ | NPEAERRREQ | QGRSGDFQGA | DRPGPEEKRE | EGDTEPLLKQ | EGPVEAAQPP | VERKEAAALE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QGRKVEELRW | QEVDERQTMP | RPYTFQVSSG | GKQILFPKVN | LSPVTPAKDT | GLTAAPQEPK | APKASPVQHA | LPSSLSVPHT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AILVTGAQLC | GPAVNLSQIK | DTACKSLLGL | EEKKHAEAPA | GENPPRGPGD | ARAGSGKAKP | RQESPSSASA | LAEWASIRSR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ILKNAESDPR | SSERDQLRPG | DESTPRGRCD | SRGNQRKTPP | VNAKFSIMPA | WQKFSDGGTE | TSKQSTEAES | IRKRPMLGPS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EETAPQPPPA | GVRELGKGPE | KSEMHREPAD | TTEGCKFAKD | LPSFLVPSLP | YPPQKVVAHT | EFTTSSDSET | ANGIAKPDPV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| MPGGEEKASP | FGIKLRRTNY | SLRFNCDQQA | EQKKKKRHSS | TGDSADAGPP | AAGSARGEKE | MEGVALKHGP | SLPQERKQAP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| STRRDSAEPS | SSRSVPVAHP | GPPPASSQTP | APEHDKAANK | MPLAQKPALA | PKPTSQTPPA | SPLSKLSRPY | LVELLSRRAG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RPDPEPSEPS | KEDQESSDRR | PPSPPGPEER | KGQKRDEEEE | ATERKPASPP | LPATQQEKPS | QTPEAGRKEK | PMLQSRHSLD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GSKLTEKVET | AQPLWITLAL | QKQKGFREQQ | ATREERKQAR | EAKQAEKLSK | ENVSVSVQPG | SSSVSRAGSL | HKSTALPEEK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RPETAVSRLE | RREQLKKANT | LPTSVTVEIS | DSAPPAPLVK | EVTKRFSTPD | AAPVSTEPAW | LALAKRKAKA | WSDCPQIIK |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1846 | 3 | 734.2644 | -176.08 | 2 | 51.4 | 17.1 | 1 | 1027-1040 | R.AGSLHKSTALPEEK.R | |

# Detailed Protein Report

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**Protein 958:** **PREDICTED: SLIT-ROBO Rho GTPase-activating protein 2 isoform X7 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578800751 | **Score:** | 17.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 110.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTSPAKFKKD | KEIIAEYDTQ | VKEIRAQLTE | QMKCLDQQCE | LRVQLLQDLQ | DFFRKKAEIE | MDYSRNLEKL | AERFLAKTRS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TKDQQFKKDQ | NVLSPVNCWN | LLLNQVKRES | RDHTTLSDIY | LNNIIPRFVQ | VSEDSGRLFK | KSKEVGQQLQ | DDLMKVLNEL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YSVMKTYHMY | NADSISAQSK | LKEAEKQEEK | QIGKSVKQED | RQTPRSPDST | ANVRIEEKHV | RRSSVKKIEK | MKEKRQAKYT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ENKLKAIKAR | NEYLLALEAT | NASVFKYYIH | DLSDLIDQCC | DLGYHASLNR | ALRTFLSAEL | NLEQSKHEGL | DAIENAVENL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DATSDKQRLM | EMYNNVFCPP | MKFEFQPHMG | DMASQLCAQQ | PVQSELVQRC | QQLQSRLSTL | KIENEEVKKT | MEATLQTIQD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IVTVEDFDVS | DCFQYSNSME | SVKSTVSETF | MSKPSIAKRR | ANQQETEQFY | FTKMKEYLEG | RNLITKLQAK | HDLLQKTLGE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SQRTDCSLAR | RSSTVRKQDS | SQAIPLVVES | CIRFISRHGL | QHEGIFRVSG | SQVEVNDIKN | AFERGEDPLA | GDQNDHDMDS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IAGVLKLYFR | GLEHPLFPKD | IFHDLMACVT | MDNLQERALH | IRKVLLVLPK | TTLIIMRYLF | AFLNHLSQFS | EENMMDPYNL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AICFGPSLMS | VPEGHDQVSC | QAHVNELIKT | IIIQHENIFP | SPRELEGPVY | SRGGSMEDYC | DSPHGETTSV | EDSTQDVTAE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HHTSDDECEP | IEAIAKFDYV | GRTARELSFK | KGASLLLYQR | ASDDWWEGRH | NGIDGLIPHQ | YIVVQDTEDG | VVERSSPKSE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IEVISEPPEE | KVTARAGASC | PSGGHVADIY | LANINKQRKR | PESGSIRKTF | RSDSHGLSSS | LTDSSSPGVG | ASCRPSSQPI |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| MSQSLPKEGP | DKCSISGHGS | LNSISRHSSL | KNRLDSPQIR | KTATAGRSKS | FNNHRPMDPE | VIAQRSNPTS | KNPTTGATPS |
| 970 | 980 | | | | | | |
| SSLRRLSQLY | NFH | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2584 | 2 | 914.0716 | -57.66 | 3 | 62.3 | 17.1 | 2 | 928-951 | R.SKSFNNHRPMDPEVIAQRSNPTSK.N | |

# Detailed Protein Report

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## **Protein 959:** protein cramped-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|223972612 | **Score:** | 17.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 134.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.55 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTVKLGDGGS | GEDGLKKLGK | RAADEESLEG | EGAGGADAAE | ESSGTKRDEK | TPRAGADGPP | APPGAPQAPS | PPQGSPQDQH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HFLRSSVRPQ | SKRPRKDPPS | AVGSGNAGGS | GPRGKGAEGG | GSSSGNVSGV | APAAPAGGSR | SSSRNLGSSG | GEKEEGKKVR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RQWESWSTED | KNTFFEGLYE | HGKDFEAIQN | NIALKYKKKG | KPASMVKNKE | QVRHFYYRTW | HKITKYIDFD | HVFSRGLKKS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SQELYGLICY | GELRKKIGGC | MDDKNATKLN | ELIQVGATTV | RYKGRNLRIK | APMCRALKKL | CDPDGLSDEE | DQKPVRLPLK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VPIELQPRNN | HAWARVQSLA | QNPRLRMIVE | LHRKVSSLIE | FLKQKWALHE | VRVRKTLEER | QLQDSCSAPM | QEKVTLHLFP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GENCTLTPLP | GVARVVHSKA | FCTVHWQEGG | RCKQSAKDAH | VLPPAQILGI | QSGQGTARGQ | VKCPRSGAEG | KGVGRPPPAA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DALQSSGESS | PESAPGEGAA | LSLSSPDAPD | RPPPRHQDTG | PCLEKTPAEG | RDSPTREPGA | LPCACGQLPD | LEDELSLLDP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LPRYLKSCQD | LIVPEQCRCA | DTRPGSEQPP | LGGAASPEVL | APVSKEAADL | APTGPSPRPG | PGLLLDVCTK | DLADAPAEEL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QEKGSPAGPP | PSQGQPAARP | PKEVPASRLA | QQLREEGWNL | QTSESLTLAE | VYLMMGKPSK | LQLEYDWLGP | GRQDPRPGSL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PTALHKQRLL | SCLLKLISTE | VNPKLALEAN | TISTASVRPA | QEEQSMTPPG | KVVTVSSRSP | RCPRNQASLR | SSKTFPPSSA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PCSSGLRNPP | RPLLVPGPSS | TGSNDSDGGL | FAVPTTLPPN | SRHGKLFSPS | KEAELTFRQH | LNSISMQSDF | FLPKPRKLRN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RHLRKPLVVQ | RTLLPRPSEN | QSHNVCSFSI | LSNSSVTGRG | SFRPIQSSLT | KAALSRPIVP | KVLPPQATSH | LASAIDLAAT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SAGILSGNPL | PALDTEGLSG | ISPLSSDEVT | GAISGQDSTG | THQDGDTLPT | VGGSDPFVSI | PSRPEQEPVA | DSFQGSSVLS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LSELPKAPLQ | NGLSIPLSSS | ESSSTRLSPP | DVSALLDISL | PGPPEDALSQ | GEPATHISDS | IIEIAISSGQ | YGEGVPLSPA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KLNGSDSSKS | LPSPSSSPQP | HWIASPTHDP | QWYPSDSTDS | SLSSLFASFI | SPEKSRKMLP | TPIGTNSGTS | LLGPSLLDGN |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | |
| SRDSFVSRSL | ADVAEVVDSQ | LVCMMNENSI | DYISRFNDLA | QELSIAEPGR | REALFDGGGG | GPAVSDLSQ | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2985 | 1 | 846.4337 | -1.84 | 2 | 66.1 | 17.1 | 2 | 1-17 | -.MTVKLGDGGSGEDGLKK.L | | WUP:QUP 0.55 |

# Detailed Protein Report

## Protein 960: PREDICTED: mucin-3A [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578844260 | **Score:** | 17.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.4 |
| | | **Sequence Coverage [%]:** | 9.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.40 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MLCADVVETE VGMEVSVDQQ FSPDLNDNTS QAYRDFNKTF WNQMQKIFAD MQGFTFKGVE ILSLRNGSIV VDYLVLLEMP
         90        100        110        120        130        140        150        160
FSPQLESEYE QVKTTLKEGL QNASQDANSC QDSQTLCFKP DSIKVNNNSK TELTPEAICR RAAPTGYEEF YFPLVEATRL
        170        180        190        200
RCVTKCTSGV DNAIDCHQGQ CVLETSGPAC R
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1444 | 1 | 1086.6084 | 26.40 | 2 | 46.4 | 17.1 | 1 | 47-65 | K.IFADMQGFTFKGVEILSLR.N | | QU:MU 0.40 |

# Detailed Protein Report

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## Protein 961: alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|167857778 | **Score:** | 17.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 50.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | |
|---|---|---|---|
| ***WUP:QUP*** | **Median:** 0.44 | **CV:** 0.00 % | **No. of Peptides:** 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578811120 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase isoform X4 [Homo sapiens] |
| gi\|578811118 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase isoform X3 [Homo sapiens] |
| gi\|530381058 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase isoform X2 [Homo sapiens] |
| gi\|530381056 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase isoform X1 [Homo sapiens] |
| gi\|167857786 | refseq_human (refseq_human_20140103.fasta) | alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase [Homo sapiens] |
| gi\|167857784 | refseq_human (refseq_human_20140103.fasta) | alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase [Homo sapiens] |
| gi\|167857782 | refseq_human (refseq_human_20140103.fasta) | alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase [Homo sapiens] |
| gi\|167857780 | refseq_human (refseq_human_20140103.fasta) | alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLKKQSAGLV | LWGAILFVAW | NALLLLFFWT | RPAPGRPPSV | SALDGDPASL | TREVIRLAQD | AEVELERQRG | LLQQIGDALS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SQRGRVPTAA | PPAQPRVPVT | PAPAVIPILV | IACDRSTVRR | CLDKLLHYRP | SAELFPIIVS | QDCGHEETAQ | AIASYGSAVT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HIRQPDLSSI | AVPPDHRKFQ | GYYKIARHYR | WALGQVFRQF | RFPAAVVVED | DLEVAPDFFE | YFRATYPLLK | ADPSLWCVSA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| WNDNGKEQMV | DASRPELLYR | TDFFPGLGWL | LLAELWAELE | PKWPKAFWDD | WMRRPEQRQG | RACIRPEISR | TMTFGRKGVS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HGQFFDQHLK | FIKLNQQFVH | FTQLDLSYLQ | REAYDRDFLA | RVYGAPQLQV | EKVRTNDRKE | LGEVRVQYTG | RDSFKAFAKA |
| 410 | 420 | 430 | 440 | 450 | | | |
| LGVMDDLKSG | VPRAGYRGIV | TFQFRGRRVH | LAPPLTWEGY | DPSWN | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1777 | 1 | 881.9118 | 17.60 | 2 | 50.6 | 17.1 | 0 | 231-246 | K.ADPSLWCVSAWNDNGK.E | | WUP:QUP 0.44 |

# Detailed Protein Report

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## Protein 962: structural maintenance of chromosomes protein 4 isoform 2 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|570700827 | **Score:** | 17.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 144.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
|  |  | **Sequence Coverage [%]:** | 1.2 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPRKGTQPST | ARRREEGPPP | PSPDGASSDA | EPEPPSGRTE | SPATAAAMTN | EAGAPRLMIT | HIVNQNFKSY | AGEKILGPFH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KRFSCIIGPN | GSGKSNVIDS | MLFVFGYRAQ | KIRSKKLSVL | IHNSDEHKDI | QSCTVEVHFQ | KIIDKEGDDY | EVIPNSNFYV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SRTACRDNTS | VYHISGKKKT | FKDVGNLLRS | HGIDLDHNRF | LILQGEVEQI | AMMKPKGQTE | HDEGMLEYLE | DIIGCGRLNE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PIKVLCRRVE | ILNEHRGEKL | NRVKMVEKEK | DALEGEKNIA | IEFLTLENEI | FRKKNHVCQY | YIYELQKRIA | EMETQKEKIH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EDTKEINEKS | NILSNEMKAK | NKDVKDTEKK | LNKITKFIEE | NKEKFTQLDL | EDVQVREKLK | HATSKAKKLE | KQLQKDKEKV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EEFKSIPAKS | NNIINETTTR | NNALEKEKEK | EEKKLKEVMD | SLKQETQGLQ | KEKESREKEL | MGFSKSVNEA | RSKMDVAQSE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LDIYLSRHNT | AVSQLTKAKE | ALIAASETLK | ERKAAIRDIE | GKLPQTEQEL | KEKEKELQKL | TQEETNFKSL | VHDLFQKVEE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AKSSLAMNRS | RGKVLDAIIQ | EKKSGRIPGI | YGRLGDLGAI | DEKYDVAISS | CCHALDYIVV | DSIDIAQECV | NFLKRQNIGV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ATFIGLDKMA | VWAKKMTEIQ | TPENTPRLFD | LVKVKDEKIR | QAFYFALRDT | LVADNLDQAT | RVAYQKDRRW | RVVTLQGQII |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EQSGTMTGGG | SKVMKGRMGS | SLVIEISEEE | VNKMESQLQN | DSKKAMQIQE | QKVQLEERVV | KLRHSEREMR | NTLEKFTASI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QRLIEQEEYL | NVQVKELEAN | VLATAPDKKK | QKLLEENVSA | FKTEYDAVAE | KAGKVEAEVK | RLHNTIVEIN | NHKLKAQQDK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LDKINKQLDE | CASAITKAQV | AIKTADRNLQ | KAQDSVLRTE | KEIKDTEKEV | DDLTAELKSL | EDKAAEVVKN | TNAAEESLPE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| IQKEHRNLLQ | ELKVIQENEH | ALQKDALSIK | LKLEQIDGHI | AEHNSKIKYW | HKEISKISLH | PIEDNPIEEI | SVLSPEDLEA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| IKNPDSITNQ | IALLEARCHE | MKPNLGAIAE | YKKKEELYLQ | RVAELDKITY | ERDSFRQAYE | DLRKQRLNEF | MAGFYIITNK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LKENYQMLTL | GGDAELELVD | SLDPFSEGIM | FSVRPPKKSW | KKIFNLSGGE | KTLSSLALVF | ALHHYKPTPL | YFMDEIDAAL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 |  |
| DFKNVSIVAF | YIYEQTKNAQ | FIIISLRNNM | FEISDRLIGI | YKTYNITKSV | AVNPKEIASK | GLC |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 305 | 4 | 862.8209 | -132.71 | 2 | 33.5 | 17.0 | 2 | 457-471 | R.EKELMGFSKSVNEAR.S |  |

# Detailed Protein Report

## Protein 963: single-minded homolog 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21614542 | **Score:** | 17.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 85.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530383967 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: single-minded homolog 1 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKEKSKNAAR | TRREKENSEF | YELAKLLPLP | SAITSQLDKA | SIIRLTTSYL | KMRVVFPEGL | GEAWGHSSRT | SPLDNVGREL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GSHLLQTLDG | FIFVVAPDGK | IMYISETASV | HLGLSQVELT | GNSIYEYIHP | ADHDEMTAVL | TAHQPYHSHF | VQEYEIERSF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FLRMKCVLAK | RNAGLTCGGY | KVIHCSGYLK | IRQYSLDMSP | FDGCYQNVGL | VAVGHSLPPS | AVTEIKLHSN | MFMFRASLDM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KLIFLDSRVA | ELTGYEPQDL | IEKTLYHHVH | GCDTFHLRCA | HHLLLVKGQV | TTKYYRFLAK | HGGWVWVQSY | ATIVHNSRSS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RPHCIVSVNY | VLTDTEYKGL | QLSLDQISAS | KPAFSYTSSS | TPTMTDNRKG | AKSRLSSSKS | KSRTSPYPQY | SGFHTERSES |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DHDSQWGGSP | LTDTASPQLL | DPADRPGSQH | DASCAYRQFS | DRSSLCYGFA | LDHSRLVEER | HFHTQACEGG | RCEAGRYFLG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TPQAGREPWW | GSRAALPLTK | ASPESREAYE | NSMPHIASVH | RIHGRGHWDE | DSVVSSPDPG | SASESGDRYR | TEQYQSSPHE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PSKIETLIRA | TQQMIKEEEN | RLQLRKAPSD | QLASINGAGK | KHSLCFANYQ | QPPPTGEVCH | GSALANTSPC | DHIQQREGKM |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LSPHENDYDN | SPTALSRISS | PNSDRISKSS | LILAKDYLHS | DISPHQTAGD | HPTVSPNCFG | SHRQYFDKHA | YTLTGYALEH |
| 730 | 740 | 750 | 760 | 770 | | | |
| LYDSETIRNY | SLGCNGSHFD | VTSHLRMQPD | PAQGHKGTSV | IITNGS | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2165 | 1 | 938.2937 | -146.48 | 2 | 56.9 | 17.0 | 1 | 227-241 | K.LHSNMFMFRASLDMK.L | Oxidation: 5, 7, 14 |

# Detailed Protein Report

## Protein 964: neugrin precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|75677385 | **Score:** | 17.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 32.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 5.2 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAVTLSLLLG | GRVCAAVTRC | GFATRGVAGP | GPIGREPDPD | SDWEPEEREL | QEVESTLKRQ | KQAIRFQKIR | RQMEAPGAPP |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| RTLTWEAMEQ | IRYLHEEFPE | SWSVPRLAEG | FDVSTDVIRR | VLKSKFLPTL | EQKLKQDQKV | LKKAGLAHSL | QHLRGSGNTS |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| KLLPAGHSVS | GSLLMPGHEA | SSKDPNHSTA | LKVIESDTHR | TNTPRRRKGR | NKEIQDLEES | FVPVAAPLGH | PRELQKYSSD |
| **250** | **260** | **270** | **280** | **290** | **300** | | |
| SESPRGTGSG | ALPSGQKLEE | LKAEEPDNFS | SKVVQRGREF | FDSNGNFLYR | I | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 912 | 1 | 836.1322 | 143.24 | 2 | 41.0 | 17.0 | 2 | 140-154 | K.VLKKAGLAHSLQHLR.G | |

# Detailed Protein Report

## Protein 965: leucine-rich repeat-containing protein 69 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|193788651 | **Score:** | 16.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.40 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTERLLIKAL | SGGKNTKIIT | LNGKKMTKMP | SALGKLPGLK | TLVLQNNLIP | KVCPELCNLT | QLTTLNLGNN | LLEEVPEEMK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YLTSLKNLHL | SGNRICRFAP | GACDGLQNLI | LLNLNNNHLT | QLPQEVSRLK | SLTYMSINYN | QLASIPRELC | FLENLVELQL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NYNQLICIPE | EIKFLKKLQK | LLLARNNIGV | LPEELCDLKK | LRILDIAGNI | IQIFPSGFQD | LKLREFYCEG | NPLFLQQPVI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| STQQENVWSL | QEITSRFVMN | QLAENNPFLM | DDIERYPQVR | SMISQGKTCA | ICGQYFITVW | LECVRFVPPP | KDWKISKNLK |
| 330 | 340 | 350 | | | | | |
| LVPLQVLICS | YKCFTQRDPN | LFGIAQV | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2170 | 1 | 682.3011 | -106.73 | 3 | 57.5 | 16.9 | 2 | 81-97 | K.YLTSLKNLHLSGNRICR.F | Carbamidomethyl: 16 | QU:MU | 0.40 |

# Detailed Protein Report

**Protein 966:** **PREDICTED: histone-lysine N-methyltransferase SUV420H2 isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578835047 | **Score:** | 16.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 33.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTSASCTQPA | SGVLSCGWAQ | PPSSTMAPDC | KPNCKFVPAD | GNAACVKVLR | DIEPGDEVTC | FYGEGFFGEK | NEHCECHTCE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RKGEGAFRTR | PREPALPPRP | LDKYQLRETK | RRLQQGLDSG | SRQGLLGPRA | CVHPSPLRRD | PFCAACQPLR | LPACSARPDT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SPLWLQWLPQ | PQPRVRPRKR | RRPRPRRAPV | LSTHHAARVS | LHRWGGCGPH | CRLRGEALVA | LGQPPHARWA | PQQDWHWARR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | |
| YGLPYVVRVD | LRRLAPAPPA | TPAPAGTPGP | ILIPKQALAF | APFSPPKRLR | LVVSHGSIDL | DVGGEEL | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2733 | 1 | 639.3478 | 87.44 | 2 | 62.6 | 16.9 | 0 | 140-150 | R.DPFCAACQPLR.L | Carbamidomethyl: 4 |

# Detailed Protein Report

## Protein 967: proto-oncogene tyrosine-protein kinase Src [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4885609 | **Score:** | 16.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.7 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|38202217 | refseq_human (refseq_human_20140103.fasta) | proto-oncogene tyrosine-protein kinase Src [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGSNKSKPKD | ASQRRRSLEP | AENVHGAGGG | AFPASQTPSK | PASADGHRGP | SAAFAPAAAE | PKLFGGFNSS | DTVTSPQRAG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PLAGGVTTFV | ALYDYESRTE | TDLSFKKGER | LQIVNNTEGD | WWLAHSLSTG | QTGYIPSNYV | APSDSIQAEE | WYFGKITRRE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SERLLLNAEN | PRGTFLVRES | ETTKGAYCLS | VSDFDNAKGL | NVKHYKIRKL | DSGGFYITSR | TQFNSLQQLV | AYYSKHADGL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CHRLTTVCPT | SKPQTQGLAK | DAWEIPRESL | RLEVKLGQGC | FGEVWMGTWN | GTTRVAIKTL | KPGTMSPEAF | LQEAQVMKKL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RHEKLVQLYA | VVSEEPIYIV | TEYMSKGSLL | DFLKGETGKY | LRLPQLVDMA | AQIASGMAYV | ERMNYVHRDL | RAANILVGEN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LVCKVADFGL | ARLIEDNEYT | ARQGAKFPIK | WTAPEAALYG | RFTIKSDVWS | FGILLTELTT | KGRVPYPGMV | NREVLDQVER |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| GYRMPCPPEC | PESLHDLMCQ | CWRKEPEERP | TFEYLQAFLE | DYFTSTEPQY | QPGENL | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1597 | 1 | 1018.4971 | -18.56 | 3 | 49.7 | 16.9 | 2 | 272-298 | R.LEVKLGQGCFGEVWMGTWNGTTRVAIK.T | Carbamidomethyl: 9; Oxidation: 15 |

# Detailed Protein Report

## Protein 968: protein GNAS isoform GNASS [Homo sapiens]

**Accession:** gi|18426900
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 16.9
**MW [kDa]:** 44.2
**pI:** 5.9
**Sequence Coverage [%]:** 4.2
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGCLGNSKTE | DQRNEEKAQR | EANKKIEKQL | QKDKQVYRAT | HRLLLLGAGE | SGKSTIVKQM | RILHVNGFNG | DSEKATKVQD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IKNNLKEAIE | TIVAAMSNLV | PPVELANPEN | QFRVDYILSV | MNVPDFDFPP | EFYEHAKALW | EDEGVRACYE | RSNEYQLIDC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AQYFLDKIDV | IKQADYVPSD | QDLLRCRVLT | SGIFETKFQV | DKVNFHMFDV | GGQRDERRKW | IQCFNDVTAI | IFVVASSSYN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MVIREDNQTN | RLQEALNLFK | SIWNNRWLRT | ISVILFLNKQ | DLLAEKVLAG | KSKIEDYFPE | FARYTTPEDA | TPEPGEDPRV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| TRAKYFIRDE | FLRISTASGD | GRHYCYPHFT | CAVDTENIRR | VFNDCRDIIQ | RMHLRQYELL | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 50 | 1 | 930.9411 | -14.59 | 2 | 30.5 | 16.9 | 1 | 59-74 | K.QMRILHVNGFNGDSEK.A | Oxidation: 2 |

# Detailed Protein Report

## Protein 969: zinc finger protein 383 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|23097321 | **Score:** | 16.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| | | **Sequence Coverage [%]:** | 5.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530415862 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 383 isoform X4 [Homo sapiens] |
| gi\|530415860 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 383 isoform X3 [Homo sapiens] |
| gi\|530415856 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 383 isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAEGSVMFSD | VSIDFSQEEW | DCLDPVQRDL | YRDVMLENYG | NLVSMGLYTP | KPQVISLLEQ | GKEPWMVGRE | LTRGLCSDLE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SMCETKLLSL | KKEVYEIELC | QREIMGLTKH | GLEYSSFGDV | LEYRSHLAKQ | LGYPNGHFSQ | EIFTPEYMPT | FIQQTFLTLH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QIINNEDRPY | ECKKCGKAFS | QNSQFIQHQR | IHIGEKSYEC | KECGKFFSCG | SHVTRHLKIH | TGEKPFECKE | CGKAFSCSSY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LSQHQRIHTG | KKPYECKECG | KAFSYCSNLI | DHQRIHTGEK | PYECKVCGKA | FTKSSQLFQH | ARIHTGEKPY | ECKECGKAFT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QSSKLVQHQR | IHTGEKPYEC | KECGKAFSSG | SALTNHQRIH | TGEKPYDCKE | CGKAFTQSSQ | LRQHQRIHAG | EKPFECLECG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KAFTQNSQLF | QHQRIHTDEK | PYECNECGKA | FNKCSNLTRH | LRIHTGEKPY | NCKECGKAFS | SGSDLIRHQG | IHTNK |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 156 | 1 | 930.1966 | 69.57 | 3 | 31.9 | 16.8 | 2 | 206-229 | K.FFSCGSHVTRHLKIHTGEKPFECK.E | |

# Detailed Protein Report

## Protein 970: PREDICTED: N-acetylgalactosamine-6-sulfatase isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530424709 | **Score:** | 16.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| | | **Sequence Coverage [%]:** | 3.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQMLVSGWEE | ADGHIPHLKT | KQKWRRKTAW | ADRGAAPSCT | HAGDAEMGWG | DLGVYGEPSR | ETPNLDRMAA | EGLLFPNFYS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ANPLCSPSRA | ALLTGRLPIR | NGFYTTNAHA | RNAYTPQEIV | GGIPDSEQLL | PELLKKAGYV | SKIVGKWHLG | HRPQFHPLKH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GFDEWFGSPN | CHFGPYDNKA | RPNIPVYRDW | EMVGRYYEEF | PINLKTGEAN | LTQIYLQEAL | DFIKRQARHH | PFFLYWAVDA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| THAPVYASKP | FLGTSQRGRY | GDAVREIDDS | IGKILELLQD | LHVADNTFVF | FTSDNGAALI | SAPEQGGSNG | PFLCGKQTTF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EGGMREPALA | WWPGHVTAGQ | VSHQLGSIMD | LFTTSLALAG | LTPPSDRAID | GLNLLPTLLQ | GRLMDRPIFY | YRGDTLMAAT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LGQHKAHFWT | WTNSWENFRQ | GIDFCPGQNV | SGVTTHNLED | HTKLPLIFHL | GRDPGERFPL | SFASAEYQEA | LSRITSVVQQ |
| 490 | 500 | 510 | 520 | 530 | | | |
| HQEALVPAQP | QLNVCNWAVM | NWAPPGCEKL | GKCLTPPESI | PKKCLWSH | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2101 | 1 | 1023.8833 | -120.72 | 2 | 56.7 | 16.8 | 0 | 2-19 | M.QMLVSGWEEADGHIPHLK.T | |

# Detailed Protein Report

**Protein 971:** **PREDICTED: probable tubulin polyglutamylase TTLL2 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578812991 | **Score:** | 16.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAEDEPSGAL | LKPLVFRVDE | TTPAVVQSVL | LERGWNKFDK | QEQNAEDWNL | YWRTSSFRMT | EHNSVKPWQQ | LNHHPGTTKL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TRKDCLAKHL | KHMRRMYGTS | LYQFIPLTFV | MPNDYTKFVA | EYFQERQMLG | TKHSYWICKP | AELSRGRGIL | IFSDFKDFIF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DDMYIVQKYI | SNPLLIGRYK | CDLRIYVCVT | GFKPLTIYVY | QEGLVRFATE | KFDLSNLQNN | YAHLTNSSIN | KSGASYEKIK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EVIGHGCKWT | LSRFFSYLRS | WDVDDLLLWK | KIHRMVILTI | LAIAPSVPFA | ANCFELFGFD | ILIDDNLKPW | LLEVNYSPAL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TLDCSTDVLV | KRKLVHDIID | LIYLNGLRNE | GREASNATHG | NSNIDAAKSD | RGGLDAPDCL | PYDSLSFTSR | MYNEDDSVVE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KAVSVRPEAA | PASQLEGEMS | GQDFHLSTRE | MPQSKPKLRS | RHTPHKTLMP | YASLFQSHSC | KTKTSPCVLS | DRGKAPDPQA |
| 490 | 500 | 510 | 520 | | | | |
| GNFVLVFPFN | EATLGASRNG | LNVKRIIQEL | QKLMNKQHS | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 429 | 1 | 542.2853 | -31.85 | 2 | 35.0 | 16.8 | 1 | 239-248 | K.IKEVIGHGCK.W | |

# Detailed Protein Report

## Protein 972: SH2 domain-containing protein 4A isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|292658785 | **Score:** | 16.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWRVIEPPCP | GAPSTENGKS | VHWKLGADKE | VWVWVMGEHH | LDKPYDVLCN | EIIAERARLK | AEQEAEEPRK | THSEEFTNSL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KTKSQYHDLQ | APDNQQTKDI | WKKVAEKEEL | EQGSRPAPTL | EEEKIRSLSS | SSRNIQQMLA | DSINRMKAYA | FHQKKESMKK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KQDEEINQIE | EERTKQICKS | WKEDSEWQAS | LRKSKAADEK | RRSLAKQARE | DYKRLSLGAQ | KGRGGERLQS | PLRVPQKPER |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PPLPPKPQFL | NSGAYPQKPL | RNQGVVRTLS | SSAQEDIIRW | FKEEQLPLRA | GYQKTSDTIA | PWFHGILTLK | KANELLLSTG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MPGSFLIRVS | ERIKGYALSY | LSEDGCKHFL | IDASADAYSF | LGVDQLQHAT | LADLVEYHKE | EPITSLGKEL | LLYPCGQQDQ |
| 410 | | | | | | | |
| LPDYLELFE | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1206 | 1 | 798.1046 | 26.39 | 3 | 45.2 | 16.8 | 2 | 125-145 | K.IRSLSSSSRNIQQMLADSINR.M | Oxidation: 14 |

# Detailed Protein Report

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**Protein 973:** **PREDICTED: uncharacterized protein C11orf63 isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530398394 | **Score:** | 16.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 81.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSKRKLIPKL | SIQSPVLHTN | LNVQSTHPPL | KKEDLHRISK | DSLESDSESL | TQEIMCHSEF | DDRIRGNGME | PDSLDEEESP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RWGSLHEMEE | EASGKAAQMA | REQNHHTWDQ | GANNRQQPIE | DKYSDLRYDP | NWKSKKEEGQ | LLSVEALPES | TDSSLENLPL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| APLYPSQETS | MELSGGKGEQ | KESPQSAASL | LGSEFLSPNY | EHGARRSKPF | SELSDSDLEE | KSSSLSPYVK | SSSSHNEVFL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PGSRGPRRRK | SKQHFVEKNK | LTLGLPTPKT | DSYLQLHNKK | RGESHPEQIS | YPVRVTDKTS | IQNAKEMENA | AIDPEDKWHQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RAQQLKNYQE | HWSQYESTKS | SNVPRGQPSD | MVNDHQPSRR | PAKLKIRKQC | KHQNGLKSST | TEEVTASQGN | QNNPPRQQQN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QNKPLDTSTK | PESIVIMHAS | NNDVQASRAL | RSHNLKETSN | TFAPPKQAFD | KVLSKNSTGC | DSGLNVNKER | GHKDQEEKRF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SYQQLHTLSD | MDLNNLNELS | KRHVLLSQKG | SQFVYHINTH | GSTKNKKQLK | QPYTETKYRN | LEMLWKFHSS | SDSQTVRASP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DSWLTQIMEQ | HQQALVQLTD | VQPSEGALSS | VTLPPILSRV | ESESQLSSER | SQRNQVKISR | SNSEGYLFQL | EKGKKHKKRS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SSKNTKLKGY | QKRDVKLGGL | GPDFESIRDK | TQKLIQQKEY | AKQVKEYNMK | TLSILSKPQT | EKTQKKSAIP | RQKN |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2757 | 1 | 840.9032 | -14.10 | 2 | 64.8 | 16.8 | 1 | 437-451 | K.ETSNTFAPPKQAFDK.V | |

# Detailed Protein Report

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## **Protein 974:** DNA repair and recombination protein RAD54-like [Homo sapiens]

**Accession:** gi|216548186

**Database:** refseq_human(refseq_human_20140103.fasta)

**Database Date:** 2015-11-30

**Score:** 16.7

**MW [kDa]:** 84.3

**pI:** 9.8

**Sequence Coverage [%]:** 2.4

**No. of unique Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|216548193 | refseq_human (refseq_human_20140103.fasta) | DNA repair and recombination protein RAD54-like [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRRSLAPSQL | AKRKPEGRSC | DDEDWQPGLV | TPRKRKSSSE | TQIQECFLSP | FRKPLSQLTN | QPPCLDSSQH | EAFIRSILSK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PFKVPIPNYQ | GPLGSRALGL | KRAGVRRALH | DPLEKDALVL | YEPPPLSAHD | QLKLDKEKLP | VHVVVDPILS | KVLRPHQREG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VKFLWECVTS | RRIPGSHGCI | MADEMGLGKT | LQCITLMWTL | LRQSPECKPE | IDKAVVVSPS | SLVKNWYNEV | GKWLGGRIQP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LAIDGGSKDE | IDQKLEGFMN | QRGARVSSPI | LIISYETFRL | HVGVLQKGSV | GLVICDEGHR | LKNSENQTYQ | ALDSLNTSRR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VLISGTPIQN | DLLEYFSLVH | FVNSGILGTA | HEFKKHFELP | ILKGRDAAAS | EADRQLGEER | LRELTSIVNR | CLIRRTSDIL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SKYLPVKIEQ | VVCCRLTPLQ | TELYKRFLRQ | AKPAEELLEG | KMSVSSLSSI | TSLKKLCNHP | ALIYDKCVEE | EDGFVGALDL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FPPGYSSKAL | EPQLSGKMLV | LDYILAVTRS | RSSDKVVLVS | NYTQTLDLFE | KLCRARRYLY | VRLDGTMSIK | KRAKVVERFN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SPSSPDFVFM | LSSKAGGCGL | NLIGANRLVM | FDPDWNPAND | EQAMARVWRD | GQKKTCYIYR | LLSAGTIEEK | IFQRQSHKKA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LSSCVVDEEQ | DVERHFSLGE | LKELFILDEA | SLSDTHDRLH | CRRCVNSRQI | RPPPDGSDCT | SDLAGWNHCT | DKWGLRDEVL |
| 730 | 740 | 750 | | | | | |
| QAAWDAASTA | ITFVFHQRSH | EEQRGLR | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 656 | 1 | 677.1638 | 133.53 | 3 | 37.8 | 16.7 | 2 | 134-151 | K.LDKEKLPVHVVVDPILSK.V | |

# Detailed Protein Report

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**Protein 975:** **PREDICTED: vesicle-associated membrane protein 1 isoform X4 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578822686 | **Score:** | 16.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 12.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 15.5 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSAPAQPPAE GTEGTAPGGG PPGPPPNMTS NRRLQQTQAQ VEEVVDIIRV NVDKVLERDQ KLSELDDRAD ALQAGASQFE
        90        100        110        120
SSAAKLKRKY WWKNCKMMIM LGAICAIIVV VIVRRG
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2520 | 1 | 973.1016 | 37.36 | 2 | 62.1 | 16.7 | 0 | 97-114 | K.MMIMLGAICAIIVVVIVR.R | |

# Detailed Protein Report

## Protein 976: POC1 centriolar protein homolog A isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|239787760 | **Score:** | 16.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAPCAEDPS | LERHFKGHRD | AVTCVDFSIN | TKQLASGSMD | SCLMVWHMKP | QSRAYRFTGH | KDAVTCVNFS | PSGHLLASGS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RDKTVRIWVP | NVKGESTVFR | AHTATVRSVH | FCSDGQSFVT | ASDDKTVKVW | ATHRQKFLFS | LSQHINWVRC | AKFSPDGRLI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VSASDDKTVK | LWDKSSRECV | HSYCEHGGFV | TYVDFHPSGT | CIAAAGMDNT | VKVWDVRTHR | LLQHYQLHSA | AVNGLSFHPS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GNYLITASSD | STLKILDLME | GRLLYTLHGH | QGPATTVAFS | RTGEYFASGG | SDEQVMVWKS | NFDIVDHGEV | TKVPRPPATL |
| 330 | 340 | 350 | 360 | | | | |
| ASSMGNLTVS | ILEQRLTLTE | DKLKQCLENQ | QLIMQRATP | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2441 | 1 | 638.3753 | 21.87 | 2 | 58.8 | 16.6 | 1 | 159-170 | R.LIVSASDDKTVK.L | |

# Detailed Protein Report

## Protein 977: BPI fold-containing family B member 6 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|28372525 | **Score:** | 16.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 6.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLRILCLALC | SLLTGTRADP | GALLRLGMDI | MNQVQSAMDE | SHILEKMAAE | AGKKQPGMKP | IKGITNLKVK | DVQLPVITLN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FVPGVGIFQC | VSTGMTVTGK | SFMGGNMEII | VALNITATNR | LLRDEETGLP | VFKSEGCEVI | LVNVKTNLPS | NMLPKMVNKF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LDSTLHKVLP | GLMCPAIDAV | LVYVNRKWTN | LSDPMPVGQM | GTVKYVLMSA | PATTASYIQL | DFSPVVQQQK | GKTIKLADAG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EALTFPEGYA | KGSSQLLLPA | TFLSAELALL | QKSFHVNIQD | TMIGELPPQT | TKTLARFIPE | VAVAYPKSKP | LTTQIKIKKP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PKVTMKTGKS | LLHLHSTLEM | FAARWRSKAP | MSLFLLEVHF | NLKVQYSVHE | NQLQMATSLD | RLLSLSRKSS | SIGNFNEREL |
| 410 | 420 | 430 | 440 | 450 | 460 | | |
| TGFITSYLEE | AYIPVVNDVL | QVGLPLPDFL | AMNYNLAELD | IVENALMLDL | KLG | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1632 | 1 | 1061.4621 | -60.44 | 3 | 50.1 | 16.5 | 1 | 18-46 | R.ADPGALLRLGMDIMNQVQSAMDESHILEK.M | |

# Detailed Protein Report

## Protein 978: eukaryotic translation initiation factor 6 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|31563374 | **Score:** | 16.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 23.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| | | **Sequence Coverage [%]:** | 10.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAVRASFENN | CEIGCFAKLT | NTYCLVAIGG | SENFYRCGGS | PGAYGGGEAC | AGVKSSGSGR | VPAPLPRHHR | VHVPTVCSRA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SSPIPSPWCT | RLSPAAASSG | ACVWETEEIL | ADVLKVEVFR | QTVADQVLVG | SYCVFSNQGG | LVHPKTSIED | QDELSSLLQV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | |
| PLVAGTVNRG | SEVIAAGMVV | NDWCAFCGLD | TTSTELSVVE | SVFKLNEAQP | STIATSMRDS | LIDSLT | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2446 | 1 | 862.1749 | 63.34 | 3 | 61.1 | 16.5 | 0 | 146-169 | K.TSIEDQDELSSLLQVPLVAGTVNR.G | |

# Detailed Protein Report

**Protein 979:** **trefoil factor 3 precursor [Homo sapiens]**

**Accession:** gi|281485608
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 16.5
**MW [kDa]:** 10.2
**pI:** 7.6
**Sequence Coverage [%]:** 19.1
**No. of unique Peptides:** 1

```
         10         20         30         40         50         60         70         80
MKRVLSCVPE PTVVMAARAL CMLGLVLALL SSSSAEEYVG LSANQCAVPA KDRVDCGYPH VTPKECNNRG CCFDSRIPGV
         90        100
PWCFKPLQEA ECTF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2651 | 1 | 993.9806 | -55.80 | 2 | 64.1 | 16.5 | 2 | 1-18 | -.MKRVLSCVPEPTVVMAAR.A | |

# Detailed Protein Report

## Protein 980: ribosomal RNA-processing protein 8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|12758125 | **Score:** | 16.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 50.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.36 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.91 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MFEEPEWAEA APVAAGLGPV ISRPPPAASS QNKGSKRRQL LATLRALEAA SLSQHPPSLC ISDSEEEEEE RKKKCPKKAS
        90        100        110        120        130        140        150        160
FASASAEVGK KGKKKCQKQG PPCSDSEEEV ERKKKCHKQA LVGSDSAEDE KRKRKCQKHA PINSAQHLDN VDQTGPKAWK
       170        180        190        200        210        220        230        240
GSTTNDPPKQ SPGSTSPKPP HTLSRKQWRN RQKNKRRCKN KFQPPQVPDQ APAEAPTEKT EVSPVPRTDS HEARAGALRA
       250        260        270        280        290        300        310        320
RMAQRLDGAR FRYLNEQLYS GPSSAAQRLF QEDPEAFLLY HRGFQSQVKK WPLQPVDRIA RDLRQRPASL VVADFGCGDC
       330        340        350        360        370        380        390        400
RLASSIRNPV HCFDLASLDP RVTVCDMAQV PLEDESVDVA VFCLSLMGTN IRDFLEEANR VLKPGGLLKV AEVSSRFEDV
       410        420        430        440        450        460
RTFLRAVTKL GFKIVSKDLT NSHFFLFDFQ KTGPPLVGPK AQLSGLQLQP CLYKRR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 719 | 1 | 690.8999 | -31.62 | 2 | 39.0 | 16.5 | 2 | 402-413 | R.TFLRAVTKLGFK.I | | QU:MU 1.36<br>WUP:QUP 0.91 |

# Detailed Protein Report

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## Protein 981: unconventional myosin-Ia [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4885503 | **Score:** | 16.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 118.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|365733629 | refseq_huma (refseq_human_20140103.fasta) | unconventional myosin-Ia [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPLLEGSVGV | EDLVLLEPLV | EESLLKNLQL | RYENKEIYTY | IGNVVISVNP | YQQLPIYGPE | FIAKYQDYTF | YELKPHIYAL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ANVAYQSLRD | RDRDQCILIT | GESGSGKTEA | SKLVMSYVAA | VCGKGEQVNS | VKEQLLQSNP | VLEAFGNAKT | IRNNNSSRFG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KYMDIEFDFK | GSPLGGVITN | YLLEKSRLVK | QLKGERNFHI | FYQLLAGADE | QLLKALKLER | DTTGYAYLNH | EVSRVDGMDD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ASSFRAVQSA | MAVIGFSEEE | IRQVLEVTSM | VLKLGNVLVA | DEFQASGIPA | SGIRDGRGVR | EIGEMVGLNS | EEVERALCSR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TMETAKEKVV | TALNVMQAQY | ARDALAKNIY | SRLFDWIVNR | INESIKVGIG | EKKKVMGVLD | IYGFEILEDN | SFEQFVINYC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NEKLQQVFIE | MTLKEEQEEY | KREGIPWTKV | DYFDNGIICK | LIEHNQRGIL | AMLDEECLRP | GVVSDSTFLA | KLNQLFSKHG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HYESKVTQNA | QRQYDHTMGL | SCFRICHYAG | KVTYNVTSFI | DKNNDLLFRD | LLQAMWKAQH | PLLRSLFPEG | NPKQASLKRP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PTAGAQFKSS | VAILMKNLYS | KSPNYIRCIK | PNEHQQRGQF | SSDLVATQAR | YLGLLENVRV | RRAGYAHRQG | YGPFLERYRL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LSRSTWPHWN | GGDREGVEKV | LGELSMSSGE | LAFGKTKIFI | RSPKTLFYLE | EQRRLRLQQL | ATLIQKIYRG | WRCRTHYQLM |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RKSQILISSW | FRGNMQKKCY | GKIKASVLLI | QAFVRGWKAR | KNYRKYFRSE | AALTLADFIY | KSMVQKFLLG | LKNNLPSTNV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LDKTWPAAPY | KCLSTANQEL | QQLFYQWKCK | RFRDQLSPKQ | VEILREKLCA | SELFKGKKAS | YPQSVPIPFC | GDYIGLQGNP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KLQKLKGGEE | GPVLMAEAVK | KVNRGNGKTS | SRILLLTKGH | VILTDTKKSQ | AKIVIGLDNV | AGVSVTSLKD | GLFSLHLSEM |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SSVGSKGDFL | LVSEHVIELL | TKMYRAVLDA | TQRQLTVTVT | EKFSVRFKEN | SVAVKVVQGP | AGGDNSKLRY | KKKGSHCLEV |
| 1050 | | | | | | | |
| TVQ | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 717 | 1 | 1100.6526 | 53.81 | 2 | 38.9 | 16.4 | 2 | 569-587 | K.SSVAILMKNLYSKSPNYIR.C | Oxidation: 7 |

# Detailed Protein Report

## Protein 982: AN1-type zinc finger protein 5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5174755 | **Score:** | 16.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 23.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 16.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|503774511 | refseq_human (refseq_human_20140103.fasta) | AN1-type zinc finger protein 5 [Homo sapiens] |
| gi\|503774491 | refseq_human (refseq_human_20140103.fasta) | AN1-type zinc finger protein 5 [Homo sapiens] |
| gi\|503774489 | refseq_human (refseq_human_20140103.fasta) | AN1-type zinc finger protein 5 [Homo sapiens] |
| gi\|156231049 | refseq_human (refseq_human_20140103.fasta) | AN1-type zinc finger protein 5 [Homo sapiens] |
| gi\|156231047 | refseq_human (refseq_human_20140103.fasta) | AN1-type zinc finger protein 5 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MAQETNQTPG PMLCSTGCGF YGNPRTNGMC SVCYKEHLQR QQNSGRMSPM GTASGSNSPT SDSASVQRAD TSLNNCEGAA
        90        100        110        120        130        140        150        160
GSTSEKSRNV PVAALPVTQQ MTEMSISRED KITTPKTEVS EPVVTQPSPS VSQPSTSQSE EKAPELPKPK KNRCFMCRKK
       170        180        190        200        210        220
VGLTGFDCRC GNLFCGLHRY SDKHNCPYDY KAEAAAKIRK ENPVVVAEKI QRI
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1730 | 1 | 1273.8446 | -16.45 | 3 | 51.9 | 16.4 | 1 | 1-35 | -.MAQETNQTPGPMLCSTGCGFYGNPRTNGMCSVCYK.E | Carbamidomethyl: 30;<br>Oxidation: 29 |

# Detailed Protein Report

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## Protein 983: round spermatid basic protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|38683851 | **Score:** | 16.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 90.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 5.34 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFISGRRTAD | KWRAEERLQC | PAGSARAALA | RCADGGAVGP | FKCVFVGEMA | AQVGAVRVVR | AVAAQEEPDK | EGKEKPHAGV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SPRGVKRQRR | SSSGGSQEKR | GRPSQEPPLA | PPHRRRRSRQ | HPGPLPPTNA | APTVPGPVEP | LLLPPPPPPS | LAPAGPAVAA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PLPAPSTSAL | FTFSPLTVSA | AGPKHKGHKE | RHKHHHHRGP | DGDPSSCGTD | LKHKDKQENG | ERTGGVPLIK | APKRETPDEN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GKTQRADDFV | LKKIKKKKKK | KHREDMRGRR | LKMYNKEVQT | VCAGLTRISK | EILTQGQINS | TSGLNKESFR | YLKDEQLCRL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NLGMQEYRVP | QGVQTPFMTH | QEHSIRRNFL | KTGTKFSNFI | HEEHQSNGGA | LVLHAYMDEL | SFLSPMEMER | FSEEFLALTF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SENEKNAAYY | ALAIVHGAAA | YLPDFLDYFA | FNFPNTPVKM | EILGKKDIET | TTISNFHTQV | NRTYCCGTYR | AGPMRQISLV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GAVDEEVGDY | FPEFLDMLEE | SPFLKMTLPW | GTLSSLRLQC | RSQSDDGPIM | WVRPGEQMIP | TADMPKSPFK | RRRSMNEIKN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LQYLPRTSEP | REVLFEDRTR | AHADHVGQGF | DWQSTAAVGV | LKAVQFGEWS | DQPRITKDVI | CFHAEDFTDV | VQRLQLDLHE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PPVSQCVQWV | DEAKLNQMRR | EGIRYARIQL | CDNDIYFIPR | NVIHQFKTVS | AVCSLAWHIR | LKQYHPVVEA | TQNTESNSNM |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DCGLTGKREL | EVDSQCVRIK | TESEEACTEI | QLLTTASSSF | PPASELNLQQ | DQKTQPIPVL | KVESRLDSDQ | QHNLQEHSTT |
| 810 | | | | | | | |
| SV | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1924 | 1 | 768.8264 | -78.40 | 2 | 54.4 | 16.4 | 0 | 43-57 | K.CVFVGEMAAQVGAVR.V | | WUP:QUP 5.34 |

# Detailed Protein Report

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**Protein 984:** **PREDICTED: NACHT, LRR and PYD domains-containing protein 8 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530415693 | **Score:** | 16.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 117.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 2.39 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSDVNPPSDT | PIPFSSSSTH | SSHIPPWTFS | CYPGSPCENG | VMLYMRNVSH | EELQRFKQLL | LTELSTGTMP | ITWDQVETAS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| WAEVVHLLIE | RFPGRRAWDV | TSNIFAIMNC | DKMCVVVRRE | INAILPTLEP | EDLNVGETQV | NLEEGESGKI | RRYKSNVMEK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FFPIWDITTW | PGNQRDFFYQ | GVHRHEEYLP | CLLLPKRPQG | RQPKTVAIQG | APGIGKTILA | KKVMFEWARN | KFYAHKRWCA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FYFHCQEVNQ | TTDQSFSELI | EQKWPGSQDL | VSKIMSKPDQ | LLLLLDGFEE | LTSTLIDRLE | DLSEDWRQKL | PGSVLLSSLL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SKTMLPEATL | LIMIRFTSWQ | TCKPLLKCPS | LVTLPGFNTM | EKIKYFQMYF | GHTEEGDQVL | SFAMENTILF | SMCRVPVVCW |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MVCSGLKQQM | ERGNNLTQSC | PNATSVFVRY | ISSLFPTRAE | NFSRKIHQAQ | LEGLCHLAAD | SMWHRKWVLG | KEDLEEAKLD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QTGVTAFLGM | SILRRIAGEE | DHYVFTLVTF | QEFFAALFYV | LCFPQRLKNF | HVLSHVNIQR | LIASPRGSKS | YLSHMGLFLF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GFLNEACASA | VEQSFQCKVS | FGNKRKLLKV | IPLLHKCDPP | SPGSGVPQLF | YCLHEIREEA | FVSQALNDYH | KVVLRIGNNK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EVQVSAFCLK | RCQYLHEVEL | TVTLNFMNVW | KLSSSSHPGS | EAPESNGLHR | WWQDLCSVFA | TNDKLEVLTM | TNSVLGPPFL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KALAAALRHP | QCKLQKLLLR | RVNSTMLNQD | LIGVLTGNQH | LRYLEIQHVE | VESKAVKLLC | RVLRSPRCRL | QCLRLEDCLA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TPRIWTDLGN | NLQGNGHLKT | LILRKNSLEN | CGAYYLSVAQ | LERLSQSKML | THLSLAENAL | KDEGAKHIWN | ALPHLRCPLQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RLVLRKCDLT | FNCCQDMISA | LCKNKTLKSL | DLSFNSLKDD | GVILLCEALK | NPDCTLQILE | LENCLFTSIC | CQAMASMLRK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | |
| NQHLRHLDLS | KNAIGVYGIL | TLCEAFSSQK | KREEVIFCIP | AWTRITSFSP | TPHPPDFTGK | SDCLSQINP | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1190 | 1 | 660.9872 | 74.48 | 3 | 43.1 | 16.4 | 0 | 887-903 | K.CDLTFNCCQDMISALCK.N | Carbamidomethyl: 16;<br>Oxidation: 11 | WUP:QUP 2.39 |

# Detailed Protein Report

## Protein 985: caytaxin [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|29336043 | **Score:** | 16.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 42.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.4 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGTTEATLRM | ENVDVKEEWQ | DEDLPRPLPE | ETGVELLGSP | VEDTSSPPNT | LNFNGAHRKR | KTLVAPEINI | SLDQSEGSLL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SDDFLDTPDD | LDINVDDIET | PDETDSLEFL | GNGNELEWED | DTPVATAKNM | PGDSADLFGD | GTTEDGSAAN | GRLWRTVIIG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EQEHRIDLHM | IRPYMKVVTH | GGYYGEGLNA | IIVFAACFLP | DSSLPDYHYI | MENLFLYVIS | SLELLVAEDY | MIVYLNGATP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RRRMPGIGWL | KKCYQMIDRR | LRKNLKSLII | VHPSWFIRTV | LAISRPFISV | KFINKIQYVH | SLEDLEQLIP | MEHVQIPDCV |
| 330 | 340 | 350 | 360 | 370 | 380 | | |
| LQYEEERLKA | RRESARPQPE | FVLPRSEEKP | EVAPVENRSA | LVSEDQETSM | S | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 518 | 1 | 593.2066 | -241.45 | 2 | 36.1 | 16.4 | 2 | 243-252 | R.RMPGIGWLKK.C | |

# Detailed Protein Report

## Protein 986: glycine N-methyltransferase [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|9506741 | **Score:** | 16.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 32.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 8.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MVDSVYRTRS | LGVAAEGLPD | QYADGEAARV | WQLYIGDTRS | RTAEYKAWLL | GLLRQHGCQR | VLDVACGTGV | DSIMLVEEGF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SVTSVDASDK | MLKYALKERW | NRRHEPAFDK | WVIEEANWMT | LDKDVPQSAE | GGFDAVICLG | NSFAHLPDCK | GDQSEHRLAL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KNIASMVRAG | GLLVIDHRNY | DHILSTGCAP | PGKNIYYKSD | LTKDVTTSVL | IVNNKAHMVT | LDYTVQVPGA | GQDGSPGLSK |
| 250 | 260 | 270 | 280 | 290 | 300 | | |
| FRLSYYPHCL | ASFTELLQAA | FGGKCQHSVL | GDFKPYKPGQ | TYIPCYFIHV | LKRTD | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1352 | 1 | 926.2202 | 91.62 | 3 | 46.5 | 16.4 | 1 | 241-264 | K.FRLSYYPHCLASFTELLQAAFGGK.C | Carbamidomethyl: 9 |

# Detailed Protein Report

## Protein 987: PREDICTED: 5-hydroxytryptamine receptor 2B isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530370281 | **Score:** | 16.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| | | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWPLPLVLCP | AWLFLDVLFS | TASIMHLCAI | SVDRYIAIKK | PIQANQYNSR | ATAFIKITVV | WLISIGIAIP | VPIKGIETDV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DNPNNITCVL | TKERFGDFML | FGSLAAFFTP | LAIMIVTYFL | TIHALQKKAY | LVKNKPPQRL | TWLTVSTVFQ | RDETPCSSPE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KVAMLDGSRK | DKALPNSGDE | TLMRRTSTIG | KKSVQTISNE | QRASKVLGIV | FFLFLLMWCP | FFITNITLVL | CDSCNQTTLQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MLLEIFVWIG | YVSSGVNPLV | YTLFNKTFRD | AFGRYITCNY | RATKSVKTLR | KRSSKIYFRN | PMAENSKFFK | KHGIRNGINP |
| 330 | 340 | 350 | 360 | 370 | | | |
| AMYQSPMRLR | SSTIQSSSII | LLDTLLLTEN | EGDKTEEQVS | YV | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2778 | 3 | 973.5049 | 25.18 | 2 | 65.9 | 16.4 | 0 | 75-92 | K.GIETDVDNPNNITCVLTK.E | |

# Detailed Protein Report

## Protein 988: netrin receptor UNC5B isoform 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|349585210 | **Score:** | 16.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 102.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGARSGARGA | LLLALLLCWD | PRLSQAGTDS | GSEVLPDSFP | SAPAEPLPYF | LQEPQDAYIV | KNKPVELRCR | AFPATQIYFK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CNGEWVSQND | HVTQEGLDEA | TGLRVREVQI | EVSRQQVEEL | FGLEDYWCQC | VAWSSAGTTK | SRRAYVRIAY | LRKNFDQEPL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GKEVPLDHEV | LLQCRPPEGV | PVAEVEWLKN | EDVIDPTQDT | NFLLTIDHNL | IIRQARLSDT | ANYTCVAKNI | VAKRRSTTAT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VIVYVNGGWS | SWAEWSPCSN | RCGRGWQKRT | RTCTNPAPLN | GGAFCEGQAF | QKTACTTICP | VDGAWTEWSK | WSACSTECAH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WRSRECMAPP | PQNGGRDCSG | TLLDSKNCTD | GLCMQMLEAS | GDAALYAGLV | VAIFVVVAIL | MAVGVVVYRR | NCRDFDTDIT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DSSAALTGGF | HPVNFKTARP | SNPQLLHPSV | PPDLTASAGI | YRGPVYALQD | STDKIPMTNS | PLLDPLPSLK | VKVYSSSTTG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SGPGLADGAD | LLGVLPPGTY | PSDFARDTHF | LHLRSASLGS | QQLLGLPRDP | GSSVSGTFGC | LGGRLSIPGT | GVSLLVPNGA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IPQGKFYEMY | LLINKAESTL | PLSEGTQTVL | SPSVTCGPTG | LLLCRPVILT | MPHCAEVSAR | DWIFQLKTQA | HQGHWEEVVT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LDEETLNTPC | YCQLEPRACH | ILLDQLGTYV | FTGESYSRSA | VKRLQLAVFA | PALCTSLEYS | LRVYCLEDTP | VALKEVLELE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RTLGGYLVEE | PKPLMFKDSY | HNLRLSLHDL | PHAHWRSKLL | AKYQEIPFYH | IWSGSQKALH | CTFTLERHSL | ASTELTCKIC |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VRQVEGEGQI | FQLHTTLAET | PAGSLDTLCS | APGSTVTTQL | GPYAFKIPLS | IRQKICNSLD | APNSRGNDWR | MLAQKLSMDR |
| 890 | 900 | 910 | 920 | 930 | 940 | | |
| YLNYFATKAS | PTGVILDLWE | ALQQDDGDLN | SLASALEEMG | KSEMLVAVAT | DGDC | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2113 | 1 | 937.8434 | -94.24 | 2 | 56.3 | 16.4 | 1 | 855-870 | K.ICNSLDAPNSRGNDWR.M | Carbamidomethyl: 2 |

# Detailed Protein Report

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**Protein 989:** **PREDICTED: leukocyte immunoglobulin-like receptor subfamily B member 3-like isoform X4 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578841261 | **Score:** | 16.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| | | **Sequence Coverage [%]:** | 10.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578842247 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: leukocyte immunoglobulin-like receptor subfamily B member 3-like isoform X4 [Homo sapiens] |
| gi\|578842007 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: leukocyte immunoglobulin-like receptor subfamily B member 3-like isoform X4 [Homo sapiens] |
| gi\|578841795 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: leukocyte immunoglobulin-like receptor subfamily B member 3-like isoform X4 [Homo sapiens] |
| gi\|578841561 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: leukocyte immunoglobulin-like receptor subfamily B member 3-like isoform X4 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSPVTSAHAG | TYRCYGSYSS | NPHLLSHPSE | PLELVVSGHS | GGSSLPPTGP | PSTPGLGRYL | EVLIGVSVAF | VLLLFLLLFL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LLRRQRHSKH | RTSDQRKTDF | QRPAGAAETE | PKDRGLLRRS | SPAADVQEEN | LYAAVKDTQS | EDRVELDSQS | PHDEDPQAVT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YAPVKHSSPR | REMASPPSSL | SGEFLDTKDR | QVEEDRQMDT | EAAASEASQD | VTYAQLHSLT | LRRKATEPPP | SQEGEPPAEP |
| 250 | | | | | | | |
| SIYATLAIH | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1409 | 1 | 927.1324 | 25.05 | 3 | 47.2 | 16.3 | 2 | 119-143 | R.RSSPAADVQEENLYAAVKDTQSEDR.V | |

# Detailed Protein Report

## Protein 990: nucleolar complex protein 2 homolog [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|157694511 | **Score:** | 16.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 84.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAAAGSRKRR | LAELTVDEFL | ASGFDSESES | ESENSPQAET | REAREAARSP | DKPGGSPSAS | RRKGRASEHK | DQLSRLKDRD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PEFYKFLQEN | DQSLLNFSDS | DSSEEEEGPF | HSLPDVLEEA | SEEEDGAEEG | EDGDRVPRGL | KGKKNSVPVT | VAMVERWKQA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AKQRLTPKLF | HEVVQAFRAA | VATTRGDQES | AEANKFQVTD | SAAFNALVTF | CIRDLIGCLQ | KLLFGKVAKD | SSRMLQPSSS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PLWGKLRVDI | KAYLGSAIQL | VSCLSETTVL | AAVLRHISVL | VPCFLTFPKQ | CRMLLKRMVV | VWSTGEESLR | VLAFLVLSRV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CRHKKDTFLG | PVLKQMYITY | VRNCKFTSPG | ALPFISFMQW | TLTELLALEP | GVAYQHAFLY | IRQLAIHLRN | AMTTRKKETY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QSVYNWQYVH | CLFLWCRVLS | TAGPSEALQP | LVYPLAQVII | GCIKLIPTAR | FYPLRMHCIR | ALTLLSGSSG | AFIPVLPFIL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EMFQQVDFNR | KPGRMSSKPI | NFSVILKLSN | VNLQEKAYRD | GLVEQLYDLT | LEYLHSQAHC | IGFPELVLPV | VLQLKSFLRE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| CKVANYCRQV | QQLLGKVQEN | SAYICSRRQR | VSFGVSEQQA | VEAWEKLTRE | EGTPLTLYYS | HWRKLRDREI | QLEISGKERL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EDLNFPEIKR | RKMADRKDED | RKQFKDLFDL | NSSEEDDTEG | FSERGILRPL | STRHGVEDDE | EDEEEGEEDS | SNSEDGDPDA |
| 730 | 740 | 750 | | | | | |
| EAGLAPGELQ | QLAQGPEDEL | EDLQLSEDD | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1281 | 1 | 1023.0326 | -11.94 | 2 | 46.1 | 16.3 | 1 | 276-292 | R.HISVLVPCFLTFPKQCR.M | Carbamidomethyl: 16 |

# Detailed Protein Report

## Protein 991: PREDICTED: myotubularin-related protein 10 isoform X3 [Homo sapiens]

**Accession:** gi|530406111
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 16.3
**MW [kDa]:** 60.5
**pI:** 9.4
**Sequence Coverage [%]:** 4.5
**No. of unique Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578840992 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: myotubularin-related protein 10 isoform X3 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MISTCLPEYI | VVPSSLADQD | LKIFSHSFVG | RRMPLWCWSH | SNGSALVRMA | LIKDVLQQRK | IDQRICNAIT | KSHPQRSDVY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KSDLDKTLPN | IQEVQAAFVK | LKQLCVNEPF | EETEEKWLSS | LENTRWLEYV | RAFLKHSAEL | VYMLESKHLS | VVLQEEEGRD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LSCCVASLVQ | VMLDPYFRTI | TGFQSLIQKE | WVMAGYQFLD | RCNHLKRSEK | ESPLFLLFLD | ATWQLLEQYP | AAFEFSETYL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AVLYDSTRIS | LFGTFLFNSP | HQRVKQSTEF | AISKNIQLGD | EKGLKFPSVW | DWSLQFTAKD | RTLFHNPFYI | GKSTPCIQNG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SVKSFKRTKK | SYSSTLRGMP | SALKNGIISD | QELLPRRNSL | ILKPKPDPAQ | QTDSQNSDTE | QYFREWFSKP | ANLHGVILPR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VSGTHIKLWK | LCYFRWVPEA | QISLGGSITA | FHKLSLLADE | VDVLSRMLRQ | QRSGPLEACY | GELGQSRMYF | NASGPHHTDT |
| 490 | 500 | 510 | 520 | 530 | | | |
| SGTPEFLSSS | FPFSPVGNLC | RRSILGTPLS | KFLSGAKIWL | STETLANED | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1260 | 1 | 903.4372 | -43.14 | 3 | 45.9 | 16.3 | 2 | 77-100 | R.SDVYKSDLDKTLPNIQEVQAAFVK.L | |

# Detailed Protein Report

## Protein 992: inositol hexakisphosphate kinase 1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|55769518 | **Score:** | 16.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 8.7 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MLDGNSGLSS EKISHNPWSL RCHKQQLSRM RSESKDRKLY KFLLLENVVH HFKYPCVLDL KMGTRQHGDD ASAEKAARQM
        90        100        110        120        130        140        150        160
RKCEQSTSAT LGVRVCGMQV YQLDTGHYLC RNKYYGRGLS IEGFRNALYQ YLHNGLDLRR DLFEPILSKL RGLKAVLERQ
       170        180        190        200        210        220        230        240
ASYRFYSSSL LVIYDGKECR AESCLDRRSE MRLKHLDMVL PEVASSCGPS TSPSNTSPEA GPSSQPKVDV RMIDFAHSTF
       250        260        270        280
KGFRDDPTVH DGPDRGYVFG LENLISIMEQ MRDENQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1510 | 1 | 982.5936 | 72.36 | 3 | 48.6 | 16.3 | 2 | 42-65 | K.FLLLENVVHHFKYPCVLDLKMGTR.Q | Carbamidomethyl: 15;<br>Oxidation: 21 |

# Detailed Protein Report

## Protein 993: VWFA and cache domain-containing protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|110578649 | **Score:** | 16.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 136.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRRLAAEELG | VVTMQRIFNS | FVYTEKISNG | ESEVQQLAKK | IREKFNRYLD | VVNRNKQVVE | ASYTAHLTSP | LTAIQDCCTI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PPSMMEFDGN | FNTNVSRTIS | CDRLSTTVNS | RAFNPGRDLN | SVLADNLKSN | PGIKWQYFSS | EEGIFTVFPA | HKFRCKGSYE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HRSRPIYVST | VRPQSKHIVV | ILDHGASVTD | TQLQIAKDAA | QVILSAIDEH | DKISVLTVAD | TVRTCSLDQC | YKTFLSPATS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ETKRKMSTFV | SSVKSSDSPT | QHAVGFQKAF | QLIRSTNNNT | KFQANTDMVI | IYLSAGITSK | DSSEEDKKAT | LQVINEENSF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LNNSVMILTY | ALMNDGVTGL | KELAFLRDLA | EQNSGKYGVP | DRMALPVIKG | SMMVLNQLSN | LETTVGRFYT | NLPNRMIDEA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VFSLPFSDEM | GDGLIMTVSK | PCYFGNLLLG | IVGVDVNLAY | ILEDVTYYQD | SLASYTFLID | DKGYTLMHPS | LTRPYLLSEP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PLHTDIIHYE | NIPKFELVRQ | NILSLPLGSQ | IIAVPVNSSL | SWHINKLRET | GKEAYNVSYA | WKMVQDTSFI | LCIVVIQPEI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PVKQLKNLNT | VPSSKLLYHR | LDLLGQPSAC | LHFKQLATLE | SPTIMLSAGS | FSSPYEHLSQ | PETKRMVEHY | TAYLSDNTRL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IANPGLKFSV | RNEVMATSHV | TDEWMTQMEM | SSLNTYIVRR | YIATPNGVLR | IYPGSLMDKA | FDPTRRQWYL | HAVANPGLIS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LTGPYLDVGG | AGYVVTISHT | IHSSSTQLSS | GHTVAVMGID | FTLRYFYKVL | MDLLPVCNQD | GGNKIRCFIM | EDRGYLVAHP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TLIDPKGHAP | VEQQHITHKE | PLVANDILNH | PNFVKKNLCN | SFSDRTVQRF | YKFNTSLAGD | LTNLVHGSHC | SKYRLARIPG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TNAFVGIVNE | TCDSLAFCAC | SMVDRLCLNC | HRMEQNECEC | PCECPLEVNE | CTGNLTNAEN | RNPSCEVHQE | PVTYTAIDPG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LQDALHQCVN | SRCSQRLESG | DCFGVLDCEW | CMVDSDGKTH | LDKPYCAPQK | ECFGGIVGAK | SPYVDDMGAI | GDEVITLNMI |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KSAPVGPVAG | GIMGCIMVLV | LAVYAYRHQI | HRRSHQHMSP | LAAQEMSVRM | SNLENDRDER | DDDSHEDRGI | ISNTRFIAAV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| IERHAHSPER | RRRYWGRSGT | ESDHGYSTMS | PQEDSENPPC | NNDPLSAGVD | VGNHDEDLDL | DTPPQTAALL | SHKFHHYRSH |
| 1210 | 1220 | 1230 | | | | | |
| HPTLHHSHHL | QAAVTVHTVD | AEC | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1955 | 3 | 899.3551 | -148.74 | 2 | 54.3 | 16.3 | 1 | 118-134 | R.DLNSVLADNLKSNPGIK.W | |

# Detailed Protein Report

## Protein 994: ankyrin repeat domain-containing protein 40 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|16418357 | **Score:** | 16.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.80 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNALLEQKEQ | QERLREAAAL | GDIREVQKLV | ESGVDVNSQN | EVNGWTCLHW | ACKRNHGQVV | SYLLKSGADK | EILTTKGEMP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VQLTSRREIR | KIMGVEEEDD | DDDDDDNLPQ | LKKESELPFV | PNYLANPAFP | FIYTPTAEDS | AQMQNGGPST | PPASPPADGS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PPLLPPGEPP | LLGTFPRDHT | SLALVQNGDV | SAPSAILRTP | ESTKPGPVCQ | PPVSQSRSLF | SSVPSKPPMS | LEPQNGTYAG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PAPAFQPFFF | TGAFPFNMQE | LVLKVRIQNP | SLRENDFIEI | ELDRQELTYQ | ELLRVCCCEL | GVNPDQVEKI | RKLPNTLLRK |
| 330 | 340 | 350 | 360 | 370 | | | |
| DKDVARLQDF | QELELVLMIS | ENNFLFRNAA | STLTERPCYN | RRASKLTY | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 866 | 1 | 567.1365 | -261.08 | 2 | 39.3 | 16.3 | 0 | 77-86 | K.GEMPVQLTSR.R | Oxidation: 3 | QU:MU 0.80 |

# Detailed Protein Report

## Protein 995: soluble lamin-associated protein of 75 kDa [Homo sapiens]

**Accession:** gi|153792633
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 16.3
**MW [kDa]:** 74.9
**pI:** 4.4
**Sequence Coverage [%]:** 2.7
**No. of unique Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530379249 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: soluble lamin-associated protein of 75 kDa isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAFPVDMLEN | CSHEELENSA | EDYMSDLRCG | DPENPECFSL | LNITIPISLS | NVGFVPLYGG | DQTQKILALF | APEDSLTAVA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LYLADQWWAI | DDIVKTSVPS | REGLKQVSTL | GERVVLYVLN | RIIYRKQEME | RNEIPFLCHS | STDYAKILWK | KGEAIGFYSV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KPTGSICASF | LTQSYQLPVL | DTMFLRKKYR | GKDFGLHMLE | DFVDSFTEDA | LGLRYPLSSL | MYTACKQYFE | KYPGDHELLW |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EVEGVGHWYQ | RIPVTRALQR | EALKILALSQ | NEPKRPMSGE | YGPASVPEYE | ARTEDNQSSE | MQLTIDSLKD | AFASTSEGHD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KTSVSTHTRS | GNLKRPKIGK | RFQDSEFSSS | QGEDEKTSQT | SLTASINKLE | STARPSESSE | EFLEEEPEQR | GIEFEDESSD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RDARPALETQ | PQQEKQDGEK | ESELEPMNGE | IMDDSLKTSL | ITEEEDSTSE | VLDEELKLQP | FNSSEDSTNL | VPLVVESSKP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PEVDAPDKTP | RIPDSEMLMD | EGTSDEKGHM | EEKLSLLPRK | KAHLGSSDNV | ATMSNEERSD | GGFPNSVIAE | FSEEPVSENL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SPNTTSSLED | QGEEGVSEPQ | ETSTALPQSS | LIEVELEDVP | FSQNAGQKNQ | SEEQSEASSE | QLDQFTQSAE | KAVDSSSEEI |
| 650 | 660 | 670 | 680 | | | | |
| EVEVPVVDRR | NLRRKAKGHK | GPAKKKAKLT | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2565 | 1 | 973.4946 | 40.45 | 2 | 62.7 | 16.3 | 1 | 521-538 | K.KAHLGSSDNVATMSNEER.S | |

# Detailed Protein Report

## Protein 996: apoptosis regulatory protein Siva isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|11277470 | **Score:** | 16.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 11.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| | | **Sequence Coverage [%]:** | 14.5 |
| | | **No. of unique Peptides:** | 1 |

```
         10         20         30         40         50         60         70         80
MPKRSCPFAD VAPLQLKVRV SQRELSRGVC AERYSQEVFD PSGVASIACS SCVRAVDGKA VCGQCERALC GQCVRTCWGC
         90        100        110        120
GSVACTLCGL VDCSDMYEKV LCTSCAMFET
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2602 | 1 | 885.4491 | -46.37 | 2 | 62.6 | 16.2 | 2 | 2-17 | M.PKRSCPFADVAPLQLK.V | |

# Detailed Protein Report

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**Protein 997:** **nutritionally-regulated adipose and cardiac enriched protein homolog isoform b [Homo sapiens]**

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|56605684 | **Score:** | 16.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 18.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.3 |
|  |  | **Sequence Coverage [%]:** | 8.8 |
|  |  | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|556695443 | refseq_huma (refseq_human_20140103.fasta) | nutritionally-regulated adipose and cardiac enriched protein homolog isoform b [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MRTAAGAVSP | DSRPETRRQT | RKNEEAAWGP | RVCRAEREDN | RKCPPSILKR | SRPEHHRPEA | KPQRTSRRVW | FREPPAVTVH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YIADKNATAT | VRVPGRPRPH | GGSLLLQLCV | CVLLVLALGL | YCGRAKPVAT | ALEDLRARLL | GLVLHLRHVA | LTCWRGLLRL |
| 170 |  |  |  |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2183 | 1 | 862.9063 | -57.86 | 2 | 57.7 | 16.2 | 0 | 51-64 | R.SRPEHHRPEAKPQR.T |  |

# Detailed Protein Report

## Protein 998: cyclin-dependent kinase 4 [Homo sapiens]

**Accession:** gi|4502735
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 16.2
**MW [kDa]:** 33.7
**pI:** 6.6
**Sequence Coverage [%]:** 4.3
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MATSRYEPVA | EIGVGAYGTV | YKARDPHSGH | FVALKSVRVP | NGGGGGGGLP | ISTVREVALL | RRLEAFEHPN | VVRLMDVCAT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SRTDREIKVT | LVFEHVDQDL | RTYLDKAPPP | GLPAETIKDL | MRQFLRGLDF | LHANCIVHRD | LKPENILVTS | GGTVKLADFG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LARIYSYQMA | LTPVVVTLWY | RAPEVLLQST | YATPVDMWSV | GCIFAEMFRR | KPLFCGNSEA | DQLGKIFDLI | GLPPEDDWPR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | |
| DVSLPRGAFP | PRGPRPVQSV | VPEMEESGAQ | LLLEMLTFNP | HKRISAFRAL | QHSYLHKDEG | NPE | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 463 | 1 | 717.8711 | -17.46 | 2 | 35.8 | 16.2 | 1 | 23-35 | K.ARDPHSGHFVALK.S | |

# Detailed Protein Report

**Protein 999:** **PREDICTED: spermidine/spermine N(1)-acetyltransferase-like protein 1 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578838360 | **Score:** | 16.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 75.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNQSGTNQSS | LSDSNQAGIN | QPSTNSLGMN | QMDMNQGSAS | LYEMNQVDMK | QPSMSQAGMR | QSGTNLPDIN | QPDMKQPDTW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QLGRSQPGML | QQELSQLVLS | KAGISQPDPS | QPGPSQSGPS | QSRMRQIGTN | QSGMSQPVMQ | QLDSQSGGSQ | PSMRQVGTSQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LGTSQIGMSQ | PGTWQTGLSQ | PVLRQPNMSP | PGMWQPGVQQ | PGISQQVPSH | PDMSQPGMSQ | QVPSQPGIRQ | PDTSQSCKNQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TDMSQPDANQ | SSLSDSNQTG | IIQPSPSLLG | MNQMDMNQWS | ASLYEMNQVD | MKQPSMSQAG | MRQSGTNLPD | INQPGMKQPG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TWQLGRSQPG | MWPQSLSELV | LSEASISQPG | PPQRAPSQSG | PRQSSTSQAG | TNQSGISQPV | MWQLDMRQSG | GSQPSMRQVG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TSQSGTSQIG | MSQPGTWQTG | LSQPVPRQPN | KSPPGMWQRG | MWQPGMSQQV | PSQLGMRQPG | TSQSSKNQTG | MSHPGRGQPG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IWEPGPSQPG | LSQQDLNQLV | LSQPGLSQPG | RSQPSVSQMG | MRQTSMDYFQ | IRHAEAGDCP | EILRLIKELA | ACENMLDAME |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LTAADLLRDG | FGDNPLFYCL | IAEVNDQQKP | SGKLTVGFAM | YYFTYDSWTG | KVLYLEDFYV | TQAYQGLGIG | AEMLKRLSQI |
| 650 | 660 | 670 | 680 | 690 | 700 | | |
| AITTQCNCMH | FLVVIWNQAS | INYYTSRGAL | DLSSEEGWHL | FRFNREELLD | MAWEE | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2493 | 1 | 841.3809 | 1.11 | 2 | 61.7 | 16.2 | 1 | 683-695 | R.FNREELLDMAWEE.- | |

# Detailed Protein Report

## Protein 1000: pre-mRNA-splicing factor CWC22 homolog [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|55749769 | **Score:** | 16.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 105.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530370697 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: pre-mRNA-splicing factor CWC22 homolog isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKSSVAQIKP | SSGHDRRENL | NSYQRNSSPE | DRYEEQERSP | RDRDYFDYSR | SDYEHSRRGR | SYDSSMESRN | RDREKRRERE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RDTDRKRSRK | SPSPGRRNPE | TSVTQSSSAQ | DEPATKKKKD | ELDPLLTRTG | GAYIPPAKLR | MMQEQITDKN | SLAYQRMSWE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ALKKSINGLI | NKVNISNISI | IIQELLQENI | VRGRGLLSRS | VLQAQSASPI | FTHVYAALVA | IINSKFPQIG | ELILKRLILN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FRKGYRRNDK | QLCLTASKFV | AHLINQNVAH | EVLCLEMLTL | LLERPTDDSV | EVAIGFLKEC | GLKLTQVSPR | GINAIFERLR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NILHESEIDK | RVQYMIEVMF | AVRKDGFKDH | PIILEGLDLV | EEDDQFTHML | PLEDDYNPED | VLNVFKMDPN | FMENEEKYKA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IKKEILDEGD | TDSNTDQDAG | SSEEDEEEEE | EEGEEDEEGQ | KVTIHDKTEI | NLVSFRRTIY | LAIQSSLDFE | ECAHKLLKME |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FPESQTKELC | NMILDCCAQQ | RTYEKFFGLL | AGRFCMLKKE | YMESFEGIFK | EQYDTIHRLE | TNKLRNVAKM | FAHLLYTDSL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PWSVLECIKL | SEETTTSSSR | IFVKIFFQEL | CEYMGLPKLN | ARLKDETLQP | FFEGLLPRDN | PRNTRFAINF | FTSIGLGGLT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DELREHLKNT | PKVIVAQKPD | VEQNKSSPSS | SSSASSSSES | DSSDSDSDSS | DSSSESSSEE | SDSSSISSHS | SASANDVRKK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GHGKTRSKEV | DKLIRNQQTN | DRKQKERRQE | HGHQETRTER | ERRSEKHRDQ | NSSGSNWRDP | ITKYTSDKDV | PSERNNYSRV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ANDRDQEMHI | DLENKHGDPK | KKRGERRNSF | SENEKHTHRI | KDSENFRRKD | RSKSKEMNRK | HSGSRSDEDR | YQNGAERRWE |
| 890 | 900 | 910 | | | | | |
| KSSRYSEQSR | ESKKNQDRRR | EKSPAKQK | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 844 | 2 | 820.2213 | -164.89 | 2 | 40.1 | 16.2 | 0 | 488-501 | K.ELCNMILDCCAQQR.T | |

# Detailed Protein Report

## Protein 1001: neuroplastin isoform a precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|9257240 | **Score:** | 16.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | |
|---|---|---|---|---|
| ***QU:MU*** | **Median:** 0.62 | **CV:** 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** 2.43 | **CV:** 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSGSSLPSAL | ALSLLLVSGS | LLPGPGAAQN | EPRIVTSEEV | IIRDSPVLPV | TLQCNLTSSS | HTLTYSYWTK | NGVELSATRK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NASNMEYRIN | KPRAEDSGEY | HCVYHFVSAP | KANATIEVKA | APDITGHKRS | ENKNEGQDAT | MYCKSVGYPH | PDWIWRKKEN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GMPMDIVNTS | GRFFIINKEN | YTELNIVNLQ | ITEDPGEYEC | NATNAIGSAS | VVTVLRVRSH | LAPLWPFLGI | LAEIIILVVI |
| 250 | 260 | 270 | 280 | 290 | | | |
| IVVYEKRKRP | DEVPDDDEPA | GPMKTNSTNN | HKDKNLRQRN | TN | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1720 | 1 | 892.3075 | -96.70 | 2 | 51.8 | 16.1 | 0 | 249-264 | K.RPDEVPDDDEPAGPMK.T | Oxidation: 15 | WUP:QUP 2.43<br>QU:MU 0.62 |

BRUKER

# Detailed Protein Report

## Protein 1002: PREDICTED: exonuclease 3'-5' domain-containing protein 2 isoform X4 [Homo sapiens]

**Accession:** gi|530404104
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 16.1
**MW [kDa]:** 42.3
**pI:** 9.7
**Sequence Coverage [%]:** 1.9
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLRLSQRTRN | SPGEKNDDHS | SWRKVLEKCQ | GVVDIPFRSK | GMSRLGEEVN | GEATESQQKP | RNKKSKMDGM | VPGNHQGRDP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RKHKRKPLGV | GYSARKSPLY | DNCFLHAPDG | QPLCTCDRRK | AQWYLDKGIG | ELVSEEPFVV | KLRFEPAGRP | ESPGDYYLMV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KENLCVVCGK | RDSYIRKNVI | PHEYRKHFPI | EMKDHNSHDV | LLLCTSCHAI | SNYYDNHLKQ | QLAKEFQAPI | GSEEGLRLLE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DPERRQVRSG | ARALLNAESL | PTQRKEELLQ | ALREFYNTDV | VTEEMLQEAA | SLETRISNEN | YVPHGLKVVQ | CHSQGGLRSL |
| 330 | 340 | 350 | 360 | 370 | | | |
| MQLESRWRQH | FLDSMQPKHL | PQQWSVDHNH | QKLLRKFGED | LPIQLS | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1568 | 1 | 917.7517 | 323.46 | 1 | 49.3 | 16.1 | 0 | 187-193 | K.HFPIEMK.D | Oxidation: 6 |

# Detailed Protein Report

## Protein 1003: E3 ubiquitin-protein ligase RNF128 isoform 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|37588871 | **Score:** | 16.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 44.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNQENRSSFF | WLLVIFTFLL | KITASFSMSA | YVTVTYYNET | SNYTAIETCE | CGVYGLASPV | ANAMGVVGIP | KNNNYQACDH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NTEFSNTKKP | WIALIERGNC | TFSEKIQTAG | RRNADAVVIY | NAPETGNQTI | QMANFGAVDI | VAIMIGNLKG | TKILQSIQRG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IQVTMVIEVG | KKHGPWVNHY | SIFFVSVSFF | IITAATVGYF | IFYSARRLRN | ARAQSRKQRQ | LKADAKKAIG | RLQLRTLKQG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DKEIGPDGDS | CAVCIELYKP | NDLVRILTCN | HIFHKTCVDP | WLLEHRTCPM | CKCDILKALG | IEVDVEDGSV | SLQVPVSNEI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SNSASSHEED | NRSETASSGY | ASVQGTDEPP | LEEHVQSTNE | SLQLVNHEAN | SVAVDVIPHV | DNPTFEEDET | PNQETAVREI |
| 410 | | | | | | | |
| KS | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1192 | 1 | 1207.8125 | 98.47 | 2 | 45.1 | 16.1 | 2 | 150-171 | K.GTKILQSIQRGIQVTMVIEVGK.K | Oxidation: 16 |

# Detailed Protein Report

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## Protein 1004: PREDICTED: UHRF1-binding protein 1-like isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578823458 | **Score:** | 16.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 113.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSSSVVVRLA | DFNIYQVSTA | EQCRSSPKSM | ICCNKKSLYL | PQEMSAVYIE | FTEYYYPDGK | DFPIPSPNLY | SQLNALQFTV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DERSILWLNQ | FLLDLKQSLN | QFMAVYKLND | NSKSDEHVDV | RVDGLMLKFV | IPSEVKSECH | QDQPRAISIQ | SSEMIATNTR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HCPNCRHSDL | EALFQDFKDC | DFFSKTYTSF | PKSCDNFNLL | HPIFQRHAHE | QDTKMHEIYK | GNITPQLNKN | TLKTSAATDV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| WAVYFSQFWI | DYEGMKSGKG | RPISFVDSFP | LSIWICQPTR | YAESQKEPQT | CNQVSLNTSQ | SESSDLAGRL | KRKKLLKEYY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| STESEPLTNG | GQKPSSSDTF | FRFSPSSSEA | DIHLLVHVHK | HVSMQINHYQ | YLLLLFLHES | LILLSENLRK | DVEAVTGSPA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SQTSICIGIL | LRSAELALLL | HPVDQANTLK | SPVSESVSPV | VPDYLPTENG | DFLSSKRKQI | SRDINRIRSV | TVNHMSDNRS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| MSVDLSHIPL | KDPLLFKSAS | DTNLQKGISF | MDYLSDKHLG | KISEDESSGL | VYKSGSGEIG | SETSDKKDSF | YTDSSSILNY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| REDSNILSFD | SDGNQNILSS | TLTSKGNETI | ESIFKAEDLL | PEAASLSENL | DISKEETPPV | RTLKSQSSLS | GKPKERCPPN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LAPLCVSYKN | MKRSSSQMSL | DTISLDSMIL | EEQLLESDGS | DSHMFLEKGN | KKNSTTNYRG | TAESVNAGAN | LQNYGETSPD |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AISTNSEGAQ | ENHDDLMSVV | VFKITGVNGE | IDIRGEDTEI | CLQVNQVTPD | QLGNISLRHY | LCNRPVGSDQ | KAVIHSKSSP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EISLRFESGP | GAVIHSLLAE | KNGFLQCHIE | NFSTEFLTSS | LMNIQHFLED | ETVATVMPMK | IQVSNTKINL | KDDSPRSSTV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SLEPAPVTVH | IDHLVVERSD | DGSFHIRDSH | MLNTGNDLKE | NVKSDSVLLT | SGKYDLKKQR | SVTQATQTSP | GVPWPSQSAN |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | | |
| FPEFSFDFTR | EQLMEENESL | KQELAKAKMA | LAEAHLEKDA | LLHHIKKMTV | E | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2057 | 1 | 731.3545 | -14.44 | 2 | 56.1 | 16.1 | 0 | 637-649 | R.CPPNLAPLCVSYK.N | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 1005: PREDICTED: WD repeat-containing protein 70 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578809933 | **Score:** | 16.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 43.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.8 |
| | | **Sequence Coverage [%]:** | 6.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MERSGPSEVT | GSDASGPDPQ | LAVTMGFTGF | GKKARTFDLE | AMFEQTRRTA | VERSRKTLEA | REKEEEMNRE | KELRRQNEDI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EPTSSRSNVV | RDCSKSSSRD | TSSSESEQSS | DSSDDELIGP | PLPPKMVGKP | VNFMEEDILG | PLPPPLNEEE | EEAEEEEEEE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EEEENPVHKI | PDSHEITLKH | GTKTVSALGL | DPSGARLVTG | GYDYDVKFWD | FAGMDASFKA | FRSLQPCECH | QIKSLQYSNT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GDMILVVSGS | SQAKVIDRDG | FEVMECIKGD | QYIVDMANTK | GHTAMLHTGS | WHPKIKGEFM | TCSNDATVRT | WEVENPKKQK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| SVFKPRTMQG | KKVIPTTCTY | SRDGNLIAAA | CQNGSIQIWD | RNLTSNKLRL | SYGTVCMLWA | HTEVCVM | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1703 | 1 | 901.3942 | -60.47 | 3 | 51.1 | 16.1 | 1 | 343-367 | R.DGNLIAAACQNGSIQIWDRNLTSNK.L | |

# Detailed Protein Report

## Protein 1006: PREDICTED: putative zinc finger protein 66-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578846704 | **Score:** | 16.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 32.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.2 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSRNPKNVKN VAKPLSTPVP LLHTTHKIIH TGEKSHKCEE CGKAFNWSSQ LAIHKITHTG EQPYKRKECS KAFNHPTTPS
        90        100        110        120        130        140        150        160
SHKKTHTGEK PCKCDKCGKA FIFSSTLSKH EKIHTGEKPY KCEECGKAFR WSSHLTTHKI THTGEKPYKC EECGNGFKYS
       170        180        190        200        210        220        230        240
STLTEHKIIH TGEKSYKCEE CGKAFNWPSQ LAIHKVTHTG EQPYKCKECG KAFKHPATLS SHNKTHTGEK PYKCDKCGKA
       250        260        270        280        290
FISSSTLSKH EKIHTGEKPY KCEECGKAFN WSSDFNKHKR IHSGQKPIL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2133 | 1 | 1045.4499 | -1.32 | 2 | 56.6 | 16.1 | 1 | 150-167 | K.CEECGNGFKYSSTLTEHK.I | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 1007: PREDICTED: alpha-(1,3)-fucosyltransferase 11 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578819000 | **Score:** | 16.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 51.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.68 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.33 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MAAGPIRVVL VLLGVLSVCA ASGHGSVAER EAGGEAEWAE PWDGAVFRPP SALGAVGVTR SSGTPRPGRE EAGDLPVLLW
        90        100        110        120        130        140        150        160
WSPGLFPHFP GDSERIECAR GACVASRNRR ALRDSRTRAL LFYGTDFRAS AAPLPRLAHQ SWALLHEESP LNNFLLSHGP
       170        180        190        200        210        220        230        240
GIRLFNLTST FSRHSDYPLS LQWLPGTAYL RRPVPPPMER AEWRRRGYAP LLYLQSHCDV PADRDRYVRE LMRHIPVDSY
       250        260        270        280        290        300        310        320
GKCLQNRELP TARLQDTATA TTEDPELLAF LSRYKFHLAL ENAICNDYMT EKLWRPMHLG AVPVYRGSPS VRDWMPNNHS
       330        340        350        360        370        380        390        400
VILIDDFESP QKLAEFIDFL DKNDEEYMKY LAYKQPGGIT NQFLLDSLKH REWGVNDPLL PNYLNGFECF VCDYELARLD
       410        420        430        440        450        460
AEKAHAASPG DSPVFEPHIA QPSHMDCPVP TPGFGNVEEI PENDRYWMLL HFDAPSF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 310 | 1 | 464.6377 | -111.51 | 2 | 32.6 | 16.1 | 0 | 343-349 | K.NDEEYMK.Y | | QU:MU 0.68<br>WUP:QUP 1.33 |

# Detailed Protein Report

## Protein 1008: bleomycin hydrolase [Homo sapiens]

**Accession:** gi|4557367
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 16.1
**MW [kDa]:** 52.5
**pI:** 5.8
**Sequence Coverage [%]:** 1.3
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSSGLNSEK | VAALIQKLNS | DPQFVLAQNV | GTTHDLLDIC | LKRATVQRAQ | HVFQHAVPQE | GKPITNQKSS | GRCWIFSCLN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VMRLPFMKKL | NIEEFEFSQS | YLFFWDKVER | CYFFLSAFVD | TAQRKEPEDG | RLVQFLLMNP | ANDGGQWDML | VNIVEKYGVI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PKKCFPESYT | TEATRRMNDI | LNHKMREFCI | RLRNLVHSGA | TKGEISATQD | VMMEEIFRVV | CICLGNPPET | FTWEYRDKDK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NYQKIGPITP | LEFYREHVKP | LFNMEDKICL | VNDPRPQHKY | NKLYTVEYLS | NMVGGRKTLY | NNQPIDFLKK | MVAASIKDGE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AVWFGCDVGK | HFNSKLGLSD | MNLYDHELVF | GVSLKNMNKA | ERLTFGESLM | THAMTFTAVS | EKDDQDGAFT | KWRVENSWGE |
| 410 | 420 | 430 | 440 | 450 | 460 | | |
| DHGHKGYLCM | TDEWFSEYVY | EVVVDRKHVP | EEVLAVLEQE | PIILPAWDPM | GALAE | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2854 | 2 | 702.3710 | 93.58 | 1 | 66.1 | 16.1 | 0 | 126-131 | K.EPEDGR.L | |

# Detailed Protein Report

## Protein 1009: cation channel sperm-associated protein 2 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|26051223 | **Score:** | 16.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 62.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAAYQQEEQM | QLPRADAIRS | RLIDTFSLIE | HLQGLSQAVP | RHTIRELLDP | SRQKKLVLGD | QHQLVRFSIK | PQRIEQISHA |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| QRLLSRLHVR | CSQRPPLSLW | AGWVLECPLF | KNFIIFLVFL | NTIILMVEIE | LLESTNTKLW | PLKLTLEVAA | WFILLIFILE |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| ILLKWLSNFS | VFWKSAWNVF | DFVVTMLSLL | PEVVVLVGVT | GQSVWLQLLR | ICRVLRSLKL | LAQFRQIQII | ILVLVRALKS |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| MTFLLMLLLI | FFYIFAVTGV | YVFSEYTRSP | RQDLEYHVFF | SDLPNSLVTV | FILFTLDHWY | ALLQDVWKVP | EVSRIFSSIY |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| FILWLLLGSI | IFRSIIVAMM | VTNFQNIRKE | LNEEMARREV | QLKADMFKRQ | IIQRRKNMSH | EALTSSHSKI | EDSSRGASQQ |
| **410** | **420** | **430** | **440** | **450** | **460** | **470** | **480** |
| RESLDLSEVS | EVESNYGATE | EDLITSASKT | EETLSKKREY | QSSSCVSSTS | SSYSSSSESR | FSESIGRLDW | ETLVHENLPG |
| **490** | **500** | **510** | **520** | **530** | **540** | | |
| LMEMDQDDRV | WPRDSLFRYF | ELLEKLQYNL | EERKKLQEFA | VQALMNLEDK | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2773 | 1 | 711.3671 | 55.94 | 3 | 65.8 | 16.0 | 1 | 377-395 | K.NMSHEALTSSHSKIEDSSR.G | Oxidation: 2 |

# Detailed Protein Report

## Protein 1010: PREDICTED: cGMP-inhibited 3',5'-cyclic phosphodiesterase B isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530395463 | **Score:** | 16.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 115.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRRDERDAKA | MRSLQPPDGA | GSPPESLRNG | YVKSCVSPLR | QDPPRGFFFH | LCRFCNVELR | PPPASPQQPR | RCSPFCRARL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SLGALAAFVL | ALLLGAEPES | WAAGAAWLRT | LLSVCSHSLS | PLFSIACAFF | FLTCFLTRTK | RGPGPGRSCG | SWWLLALPAC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CYLGDFLVWQ | WWSWPWGDGD | AGSAAPHTPP | EAAAGRLLLV | LSCVGLLLTL | AHPLRLRHCV | LVLLLASFVW | WVSFTSLGSL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PSALRPLLSG | LVGGAGCLLA | LGLDHFFQIR | EAPLHPRLSS | AAEEKVPVIR | PRRRSSCVSL | GETAASYYGS | CKIFRRPSLP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CISREQMILW | DWDLKQWYKP | HYQGLNRNSL | PTPQLRRSSG | TSGLLPVEQS | SRWDRNNGKR | PHQEFGISSQ | GCYLNGPFNS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NLLTIPKQRS | SSVSLTHHVG | LRRAGVLSSL | SPVNSSNHGP | VSTGSLTNRS | PIEFPDTADF | LNKPSVILQR | SLGNAPNTPD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FYQQLRNSDS | NLCNSCGHQM | LKYVSTSESD | GTDCCSGKSG | EEENIFSKES | FKLMETQQEE | ETEKKDSRKL | FQEGDKWLTE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EAQSEQQTNI | EQEVSLDLIL | VEEYDSLIEK | MSNWNFPIFE | LVEKMGEKSG | RILSQVMYTL | FQDTGLLEIF | KIPTQQFMNY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FRALENGYRD | IPYHNRIHAT | DVLHAVWYLT | TRPVPGLQQI | HNGCGTGNET | DSDGRINHGR | IAYISSKSCS | NPDESYGCLS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SNIPALELMA | LYVAAAMHDY | DHPGRTNAFL | VATNAPQAVL | YNDRSVLENH | HAASAWNLYL | SRPEYNFLLH | LDHVEFKRFR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FLVIEAILAT | DLKKHFDFLA | EFNAKANDVN | SNGIEWSNEN | DRLLVCQVCI | KLADINGPAK | VRDLHLKWTE | GIVNEFYEQG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DEEANLGLPI | SPFMDRSSPQ | LAKLQESFIT | HIVGPLCNSY | DAAGLLPGQW | LEAEEDNDTE | SGDDEDGEEL | DTEDEEMENN |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | |
| LNPKPPRRKS | RRRIFCQLMH | HLTENHKIWK | EIVEEEEKCK | ADGNKLQVEN | SSLPQADEIQ | VIEEADEEE | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1602 | 1 | 978.1827 | 141.31 | 2 | 50.3 | 16.0 | 1 | 843-860 | R.LLVCQVCIKLADINGPAK.V | Carbamidomethyl: 4 |

# Detailed Protein Report

## Protein 1011: PREDICTED: E3 ubiquitin-protein ligase RNF126 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530425318 | **Score:** | 15.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 30.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 7.4 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAEASPHPGR | YFCHCCSVEI | VPRLPDYICP | RCESGFIEEL | PEETRSTENG | SAPSTAPTDQ | SRPPLEHVDQ | HLFTLPQGYG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QFAFGIFDDS | FEIPTFPPGA | QADDGRDPES | RRERDHPSRH | RIIQQLVNGI | ITPATIPSLG | PWGVLHSNPM | DYAWGANGLD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AIITQLLNQF | ENTGPPPADK | EKIQALPTVP | VTEEHVGSGL | ECPVCKDDYA | LGERVRQLPC | NHLFHDGCIV | PWLEQHDSCP |
| 250 | 260 | 270 | 280 | 290 | | | |
| VCRKSLTGQN | TATNPPGLTG | VSFSSSSSSS | SSSSPSNENA | TSNS | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2345 | 1 | 857.4373 | 45.18 | 3 | 59.8 | 15.9 | 1 | 11-31 | R.YFCHCCSVEIVPRLPDYICPR.C | Carbamidomethyl: 6 |

# Detailed Protein Report

## Protein 1012: protein diaphanous homolog 2 isoform 12C [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|6382071 | **Score:** | 15.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 124.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 2.12 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEQPGAAASG | AGGGSEEPGG | GRSNKRSAGN | RAANEEETKN | KPKLNIQIKT | LADDVRDRIT | SFRKSTVKKE | KPLIQHPIDS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QVAMSEFPAA | QPLYDERSLN | LSEKEVLDLF | EKMMEDMNLN | EEKKAPLRNK | DFTTKREMVV | QYISATAKSG | GLKNSKHECT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LSSQEYVHEL | RSGISDEKLL | NCLESLRVSL | TSNPVSWVNN | FGHEGLGLLL | DELEKLLDKK | QQENIDKKNQ | YKLIQCLKAF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MNNKFGLQRI | LGDERSLLLL | ARAIDPKQPN | MMTEIVKILS | AICIVGEENI | LDKLLGAITT | AAERNNRERF | SPIVEGLENQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EALQLQVACM | QFINALVTSP | YELDFRIHLR | NEFLRSGLKT | MLPDLKEKEN | DELDIQLKVF | DENKEDDLTE | LSHRLNDIRA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EMDDMNEVYH | LLYNMLKDTA | AENYFLSILQ | HFLLIRNDYY | IRPQYYKIIE | ECVSQIVLHC | SGMDPDFKYR | QRLDIDLTHL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IDSCVNKAKV | EESEQKAAEF | SKKFDEEFTA | RQEAQAELQK | RDEKIKELEA | EIQQLRTQAQ | VLSSSSGIPG | PPAAPPLPGV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GPPPPPPAPP | LPGGAPLPPP | PPPLPGMMGI | PPPPPPPLLF | GGPPPPPPLG | GVPPPPGISL | NLPYGMKQKK | MYKPEVSMKR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| INWSKIEPTE | LSENCFWLRV | KEDKFENPDL | FAKLALNFAT | QIKVQKNAEA | LEEKKTGPTK | KKVKELRILD | PKTAQNLSIF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LGSYRMPYED | IRNVILEVNE | DMLSEALIQN | LVKHLPEQKI | LNELAELKNE | YDDLCEPEQF | GVVMSSVKML | QPRLSSILFK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LTFEEHINNI | KPSIIAVTLA | CEELKKSESF | NRLLELVLLV | GNYMNSGSRN | AQSLGFKINF | LCKIRDTKSA | DQKTTLLHFI |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ADICEEKYRD | ILKFPEELEH | VESASKVSAQ | ILKSNLASME | QQIVHLERDI | KKFPQAENQH | DKFVEKMTSF | TKTAREQYEK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LSTMHNNMMK | LYENLGEYFI | FDSKTVSIEE | FFGDLNNFRT | LFLEAVRENN | KRREMEEKTR | RAKLAKEKAE | QEKLERQKKK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | | |
| KQLIDINKEG | DETGVMDNLL | EALQSGAAFR | DRRKRIPRNP | VVNHPCATRA | NPRSAT | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2360 | 1 | 1151.7502 | 128.51 | 2 | 57.8 | 15.9 | 2 | 469-487 | K.YRQRLDIDLTHLIDSCVNK.A | | WUP:QUP 2.12 |

# Detailed Protein Report

## Protein 1013: PREDICTED: zinc finger protein ZnFP12-like isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578833784 | **Score:** | 15.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 58.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578846680 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: zinc finger protein ZnFP12-like isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWETFRNLAT | IGTKQKEWNI | EEQYKNQGRN | LRNHMVERLC | ESKEGSHGGE | GFSQIANLSL | NKKTPSGGKL | WESSVCGKVL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SHHSSLNRHI | RSYTRHKLYK | CQEYGEKPYK | CKKCGKPFSY | LQSFKKHKRT | HSAGIVYKCK | ACGKAFSCQR | SFQIHGRTHT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GDKPFKCKEC | GKAFRYHQSA | QKHEKAHTGE | KPYKCKECGK | PFIYRHSARA | HERNHTVQKR | YECKQCGKTY | ISSVGFQAHE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RTHTGEKPYE | CKKCGKVFVY | HNSAQRHEKT | HTGEKPYKCK | ECGKAFSYHC | TAQKHERNHT | AQKHYECKLC | GKTYLSPLGF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QAHESTHTGD | KPFECKKCGK | AFRYYYSAQR | HERTHTGEKP | YKCKECGKAF | YCCSSARRHE | RMHTAKKQYE | CKKCGKTYIT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LAGFQIHERT | HTGEKPYECK | QCGKAFSSSS | YIHIHERIHT | GEKPYECKEC | GKPFSFLTGF | RVHMRMHTGE | KPYKCKDCGN |
| 490 | 500 | | | | | | |
| AFIWRASLQY | HVKKVHAE | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2755 | 1 | 821.9192 | 59.94 | 2 | 64.8 | 15.9 | 2 | 369-381 | K.AFYCCSSARRHER.M | Carbamidomethyl: 4 |

# Detailed Protein Report

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## Protein 1014: absent in melanoma 1 protein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|62988361 | **Score:** | 15.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 188.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 0.5 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MEKRSSGRRS GRRRGSQKST DSPGADAELP ESAARDDAVF DDEVAPNAAS DNASAEKKVK SPRAALDGGV ASAASPESKP
        90        100        110        120        130        140        150        160
SPGTKGQLRG ESDRSKQPPP ASSPTKRKGR SRALEAVPAP PASGPRAPAK ESPPKRVPDP SPVTKGTAAE SGEEAARAIP
       170        180        190        200        210        220        230        240
RELPVKSSSL LPEIKPEHKR GPLPNHFNGR AEGGRSRELG RAAGAPGASD ADGLKPRNHF GVGRSTVTTK VTLPAKPKHV
       250        260        270        280        290        300        310        320
ELNLKTPKNL DSLGNEHNPF SQPVHKGNTA TKISLFENKR TNSSPRHTDI RGQRNTPASS KTFVGRAKLN LAKKAKEMEQ
       330        340        350        360        370        380        390        400
PEKKVMPNSP QNGVLVKETA IETKVTVSEE EILPATRGMN GDSSENQALG PQPNQDDKAD VQTDAGCLSE PVASALIPVK
       410        420        430        440        450        460        470        480
DHKLLEKEDS EAADSKSLVL ENVTDTAQDI PTTVDTKDLP PTAMPKPQHT FSDSQSPAES SPGPSLSLSA PAPGDVPKDT
       490        500        510        520        530        540        550        560
CVQSPISSFP CTDLKVSENH KGCVLPVSRQ NNEKMPLLEL GGETTPPLST ERSPEAVGSE CPSRVLVQVR SFVLPVESTQ
       570        580        590        600        610        620        630        640
DVSSQVIPES SEVREVQLPT CHSNEPEVVS VASCAPPQEE VLGNEHSHCT AELAAKSGPQ VIPPASEKTL PIQAQSQGSR
       650        660        670        680        690        700        710        720
TPLMAESSPT NSPSSGNHLA TPQRPDQTVT NGQDSPASLL NISAGSDDSV FDSSSDMEKF TEIIKQMDSA VCMPMKRKKA
       730        740        750        760        770        780        790        800
RMPNSPAPHF AMPPIHEDHL EKVFDPKVFT FGLGKKKESQ PEMSPALHLM QNLDTKSKLR PKRASAEQSV LFKSLHTNTN
       810        820        830        840        850        860        870        880
GNSEPLVMPE INDKENRDVT NGGIKRSRLE KSALFSSLLS SLPQDKIFSP SVTSVNTMTT AFSTSQNGSL SQSSVSQPTT
       890        900        910        920        930        940        950        960
EGAPPCGLNK EQSNLLPDNS LKVFNFNSSS TSHSSLKSPS HMEKYPQKEK TKEDLDSRSN LHLPETKFSE LSKLKNDDME
       970        980        990       1000       1010       1020       1030       1040
KANHIESVIK SNLPNCANSD TDFMGLFKSS RYDPSISFSG MSLSDTMTLR GSVQNKLNPR PGKVVIYSEP DVSEKCIEVF
      1050       1060       1070       1080       1090       1100       1110       1120
SDIQDCSSWS LSPVILIKVV RGCWILYEQP NFEGHSIPLE EGELELSGLW GIEDILERHE EAESDKPVVI GSIRHVVQDY
      1130       1140       1150       1160       1170       1180       1190       1200
RVSHIDLFTE PEGLGILSSY FDDTEEMQGF GVMQKTCSMK VHWGTWLIYE EPGFQGVPFI LEPGEYPDLS FWDTEAAYIG
      1210       1220       1230       1240       1250       1260       1270       1280
SMRPLKMGGR KVEFPTDPKV VVYEKPFFEG KCVELETGMC SFVMEGGETE EATGDDHLPF TSVGSMKVLR GIWVAYEKPG
      1290       1300       1310       1320       1330       1340       1350       1360
FTGHQYLLEE GEYRDWKAWG GYNGELQSLR PILGDFSNAH MIMYSEKNFG SKGSSIDVLG IVANLKETGY GVKTQSINVL
      1370       1380       1390       1400       1410       1420       1430       1440
SGVWVAYENP DFTGEQYILD KGFYTSFEDW GGKNCKISSV QPICLDSFTG PRRRNQIHLF SEPQFQGHSQ SFEETTSQID
      1450       1460       1470       1480       1490       1500       1510       1520
DSFSTKSCRV SGGSWVVYDG ENFTGNQYVL EEGHYPCLSA MGCPPGATFK SLRFIDVEFS EPTIILFERE DFKGKKIELN
      1530       1540       1550       1560       1570       1580       1590       1600
AETVNLRSLG FNTQIRSVQV IGGIWVTYEY GSYRGRQFLL SPAEVPNWYE FSGCRQIGSL RPFVQKRIYF RLRNKATGLF
      1610       1620       1630       1640       1650       1660       1670       1680
MSTNGNLEDL KLLRIQVMED VGADDQIWIY QEGCIKCRIA EDCCLTIVGS LVTSGSKLGL ALDQNADSQF WSLKSDGRIY
      1690       1700       1710       1720       1730
SKLKPNLVLD IKGGTQYDQN HIILNTVSKE KFTQVWEAMV LYT
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 284 | 2 | 939.2416 | -290.57 | 1 | 33.2 | 15.9 | 0 | 137-145 | R.VPDPSPVTK.G | |

# Detailed Protein Report

## Protein 1015: uncharacterized protein KIAA0355 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|46276868 | **Score:** | 15.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 115.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530417641 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: uncharacterized protein KIAA0355 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MYCCSAQDSK | MDYKRRFLLG | GSKQKVQQHQ | QYPMPELGRA | LSAPLASTAT | TAPLGSLTAA | GSCHHAMPHT | TPIADIQQGI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SKYLDALNVF | CRASTFLTDL | FSTVFRNSHY | SKAATQLKDV | QEHVMEAASR | LTSAIKPEIA | KMLMELSAGA | ANFTDQKEFS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LQDIEVLGRC | FLTVVQVHFQ | FLTHALQKVQ | PVAHSCFAEV | IVPEKKNSGS | GGGLSGMGHT | PEVEEAVRSW | RGAAEATSRL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RERGCDGCLA | GIEVQQLFCS | QSAAIPEHQL | KELNIKIDSA | LQAYKIALES | LGHCEYAMKA | GFHLNPKAIE | ASLQGCCSEA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EAQQTGRRQT | PPQPMQCELP | TVPVQIGSHF | LKGVSFNESA | ADNLKLKTHT | MLQLMKEAGC | YNGITSRDDF | PVTEVLNQVC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PSTWRGACKT | AVQLLFGQAG | LVVVDTAQIE | NKEAYAPQIS | LEGSRIVVQV | PSTWCLKEDP | ATMSLLQRSL | DPEKTLGLVD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VLYTAVLDLN | RWRAGREQAL | PCIQIQLQRE | ICDFGNQADL | PSGNGNKSSG | GLQKTFSKLT | SRFTKKASCT | SSSSSTNYSI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QNTPSKNIFI | AGCSEEKAKM | PGNIDTRLQS | ILNIGNFPRT | TDPSQSAQNS | SNTVANGFLM | ERRENFLHGD | DGKDEKGMNL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PTDQEMQEVI | DFLSGFNMGQ | SHQGSPLVTR | HNSAATAMVT | EQKAGAMQPQ | QPSLPVPPPP | RAPQAGAHTP | LTPQPGLAPQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QQSPKQQQPQ | VQYYQHLLQP | IGPQQPPPQP | RAPGKWVHGS | SQQPAQAVGA | GLSPLGQWPG | ISDLSSDLYS | LGLVSSYMDN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VMSEVLGQKP | QGPRNNTWPN | RDQSDGVFGM | LGEILPFDPA | VGSDPEFARY | VAGVSQAMQQ | KRQAQHGRRP | GNPRGNWPPM |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DDAHRTWPFP | EFFTEGDGLH | GGWSGAQGDS | ASSSDETSSA | NGDSLFSMFS | GPDLVAAVKQ | RRKHSSGEQD | TSTLPSPPLL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TTVEDVNQDN | KTKTWPPKAP | WQHPSPLPST | LPSPSAPLYA | VTSPGSQWND | TMQMLQSPVW | AATNDCSAAA | FSYVQTPPQP |
| 1050 | 1060 | 1070 | 1080 | | | | |
| PPPPAHKAAP | KGFKAFPGKG | ERRPAYLPQY | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1382 | 1 | 873.4411 | 120.85 | 2 | 45.6 | 15.8 | 1 | 1-14 | -.MYCCSAQDSKMDYK.R | Carbamidomethyl: 3;<br>Oxidation: 11 |

# Detailed Protein Report

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## Protein 1016: isoleucine--tRNA ligase, cytoplasmic [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|94721239 | **Score:** | 15.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 144.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
|  |  | **Sequence Coverage [%]:** | 1.3 |
|  |  | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|94721241 | refseq_huma (refseq_human_20140103.fasta) | isoleucine--tRNA ligase, cytoplasmic [Homo sapiens] |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLQQVPENIN | FPAEEEKILE | FWTEFNCFQE | CLKQSKHKPK | FTFYDGPPFA | TGLPHYGHIL | AGTIKDIVTR | YAHQSGFHVD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RRFGWDCHGL | PVEYEIDKTL | GIRGPEDVAK | MGITEYNNQC | RAIVMRYSAE | WKSTVSRLGR | WIDFDNDYKT | LYPQFMESVW |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WVFKQLYDKG | LVYRGVKVMP | FSTACNTPLS | NFESHQNYKD | VQDPSVFVTF | PLEEDETVSL | VAWTTTPWTL | PSNLAVCVNP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EMQYVKIKDV | ARGRLLILME | ARLSALYKLE | SDYEILERFP | GAYLKGKKYR | PLFDYFLKCK | ENGAFTVLVD | NYVKEEEGTG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VVHQAPYFGA | EDYRVCMDFN | IIRKDSLPVC | PVDASGCFTT | EVTDFAGQYV | KDADKSIIRT | LKEQGRLLVA | TTFTHSYPFC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| WRSDTPLIYK | AVPSWFVRVE | NMVDQLLRNN | DLCYWVPELV | REKRFGNWLK | DARDWTISRN | RYWGTPIPLW | VSDDFEEVVC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IGSVAELEEL | SGAKISDLHR | ESVDHLTIPS | RCGKGSLHRI | SEVFDCWFES | GSMPYAQVHY | PFENKREFED | AFPADFIAEG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IDQTRGWFYT | LLVLATALFG | QPPFKNVIVN | GLVLASDGQK | MSKRKKNYPD | PVSIIQKYGA | DALRLYLINS | PVVRAENLRF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KEEGVRDVLK | DVLLPWYNAY | RFLIQNVLRL | QKEEEIEFLY | NENTVRESPN | ITDRWILSFM | QSLIGFFETE | MAAYRLYTVV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PRLVKFVDIL | TNWYVRMNRR | RLKGENGMED | CVMALETLFS | VLLSLCRLMA | PYTPFLTELM | YQNLKVLIDP | VSVQDKDTLS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IHYLMLPRVR | EELIDKKTES | AVSQMQSVIE | LGRVIRDRKT | IPIKYPLKEI | VVIHQDPEAL | KDIKSLEKYI | IEELNVRKVT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LSTDKNKYGI | RLRAEPDHMV | LGKRLKGAFK | AVMTSIKQLS | SEELEQFQKT | GTIVVEGHEL | HDEDIRLMYT | FDQATGGTAQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FEAHSDAQAL | VLLDVTPDQS | MVDEGMAREV | INRIQKLRKK | CNLVPTDEIT | VYYKAKSEGT | YLNSVIESHT | EFIFTTIKAP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LKPYPVSPSD | KVLIQEKTQL | KGSELEITLT | RGSSLPGPAC | AYVNLNICAN | GSEQGGVLLL | ENPKGDNRLD | LLKLKSVVTS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| IFGVKNTELA | VFHDETEIQN | QTDLLSLSGK | TLCVTAGSAP | SLINSSSTLL | CQYINLQLLN | AKPQECLMGT | VGTLLLENPL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 |  |
| GQNGLTHQGL | LYEAAKVFGL | RSRKLKLFLN | ETQTQEITED | IPVKTLNMKT | VYVSVLPTTA | DF |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1672 | 1 | 942.9746 | 4.27 | 2 | 51.2 | 15.8 | 0 | 2-17 | M.LQQVPENINFPAEEEK.I |  |

# Detailed Protein Report

**Protein 1017:** **PREDICTED: disintegrin and metalloproteinase domain-containing protein 10 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530405298 | **Score:** | 15.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 80.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MVLLRVLILL LSWAAGMGGQ YGNPLNKYIR HYEGLSYNVD SLHQKHQRAK RAVSHEDQFL RLDFHAHGRH FNLRMKRDTS
        90        100        110        120        130        140        150        160
LFSDEFKVET SNKVLDYDTS HIYTGHIYGE EGSFSHGSVI DGRFEGFIQT RGGTFYVEPA ERYIKDRTLP FHSVIYHEDD
       170        180        190        200        210        220        230        240
INYPHKYGPQ GGCADHSVFE RMRKYQMTGV EEVTQIPQEE HAANGPELLR KKRTTSAEKN TCQLYIQTDH LFFKYYGTRE
       250        260        270        280        290        300        310        320
AVIAQINTTA DEKDPTNPFR FPNIGVEKFL ELNSEQNHDD YCLAYVFTDR DFDDGVLGLA WVGAPSGSSG GICEKSKLYS
       330        340        350        360        370        380        390        400
DGKKKSLNTG IITVQNYGSH VPPKVSHITF AHEVGHNFGS PHDSGTECTP GESKNLGQKE NGNYIMYARA TSGDKLNNNK
       410        420        430        440        450        460        470        480
FSLCSIRNIS QVLEKKRNNC FVESGQPICG NGMVEQGEEC DCGYSDQCKD ECCFDANQPE GRKCKLKPGK QCSPSQGPCC
       490        500        510        520        530        540        550        560
TAQCAFKSKS EKCRDDSDCA REGICNGFTA LCPASDPKPN FTDCNRHTQV CINGQCAGSI CEKYGLEECT CASSDGKDDK
       570        580        590        600        610        620        630        640
ELCHVCCMKK MDPSTCASTG SVQWSRHFSG RTITLQPGSP CNDFRGYCDV FMRCRLVDAD GPLARLKKAI FSPELYENIA
       650        660        670        680        690        700        710        720
EWIVAHWWAV LLMGIALIML MAGFIKICSV HTPSSNPKLP PPKPLPGTLK RRRPPQPIQQ PQRQRPRESY QMGHMRR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1896 | 1 | 1056.6778 | -73.07 | 3 | 52.0 | 15.8 | 2 | 544-569 | K.YGLEECTCASSDGKDDKELCHVCCMK.K | Carbamidomethyl: 6, 8, 20, 23, 24; Oxidation: 25 |

# Detailed Protein Report

## Protein 1018: IGF-like family receptor 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|13375913 | **Score:** | 15.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 37.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.9 |
| | | **Sequence Coverage [%]:** | 5.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGPGRCLLTA | LLLLALAPPP | EASQYCGRLE | YWNPDNKCCS | SCLQRFGPPP | CPDYEFRENC | GLNDHGDFVT | PPFRKCSSGQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CNPDGAELCS | PCGGGAVTPT | PAAGGGRTPW | RCRERPVPAK | GHCPLTPGNP | GAPSSQERSS | PASSIAWRTP | EPVPQQAWPN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FLPLVVLVLL | LTLAVIAILL | FILLWHLCWP | KEKADPYPYP | GLVCGVPNTH | TPSSSHLSSP | GALETGDTWK | EASLLPLLSR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ELSSLASQPL | SRLLDELEVL | EELIVLLDPE | PGPGGGMAHG | TTRHLAARYG | LPAAWSTFAY | SLRPSRSPLR | ALIEMVVARE |
| 330 | 340 | 350 | 360 | | | | |
| PSASLGQLGT | HLAQLGRADA | LRVLSKLGSS | GVCWA | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1323 | 1 | 918.0778 | 93.29 | 2 | 46.7 | 15.8 | 0 | 320-337 | R.EPSASLGQLGTHLAQLGR.A | |

# Detailed Protein Report

## Protein 1019: PREDICTED: transcription factor HES-4 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530360364 | **Score:** | 15.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 19.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.9 |
| | | **Sequence Coverage [%]:** | 7.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAADTPGKPS | ASPMAGAPAS | ASRTPDKPRS | AAEHRKSSRH | SKLEKADILE | MTVRHLRSLR | RVQVTAALSA | DPAVLGKYRA |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| GFHECLAEVN | RFLAGCEGVP | ADVRSRLLGH | LAACLRQLGP | SRRPASLSPA | APAEAPAPEV | YAGRPLLPSL | GGPFPLLAPP |
| **170** | **180** | **190** | | | | | |
| LLPGLTRALP | AAPRAGPQGP | GGPWRPWLR | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2181 | 1 | 885.4041 | -88.63 | 2 | 57.7 | 15.7 | 2 | 40-54 | R.HSKLEKADILEMTVR.H | |

# Detailed Protein Report

**Protein 1020:** **PREDICTED: translation initiation factor eIF-2B subunit delta isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578803252 | **Score:** | 15.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.27 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.88 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MKAELPPGPG AVGREMTKEE KLQLRKEKKQ QKKKRKEEKG AEPETGSAVS AAQCQGPTRE LPESGIQLGT PREKVPAGRS
        90        100        110        120        130        140        150        160
KAELRAERRA KQEAERALKQ ARKGEQGGPP PKASPSTAGE TPSGVKRLPE YPQVDDLLLR RLVKKPERQQ VPTRKDYGSK
       170        180        190        200        210        220        230        240
VSLFSHLPQY SRQNSLTQFM SIPSSVIHPA MVRLGLQYSQ GLVSGSNARC IALLRALQQV IQDYTTPPNE ELSRDLVNKL
       250        260        270        280        290        300        310        320
KPYMSFLTQC RPLSASMHNA IKFLNKEITS VGSSKREEEA KSELRAAIDR YVQEKIVLAA QAISRFAYQK ISNGDVILVY
       330        340        350        360        370        380        390        400
GCSSLVSRIL QEAWTEGRRF RVVVVDSRPW LEGRHTLRSL VHAGVPASYL LIPAASYVLP EVSKVLLGAH ALLANGSVMS
       410        420        430        440        450        460        470        480
RVGTAQLALV ARAHNVPVLV CCETYKFCER VQTDAFVSNE LDDPDDLQCK RGEHVALANW QNHASLRLLN LVYDVTPPEL
       490        500        510
VDLVITELGM IPCSSVPVVL RVKSSDQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2075 | 1 | 698.3348 | -56.57 | 2 | 56.3 | 15.7 | 1 | 1-14 | -.MKAELPPGPGAVGR.E | Oxidation: 1 | WUP:QUP 0.88<br>QU:MU 2.27 |

# Detailed Protein Report

## Protein 1021: PREDICTED: pre-B-cell leukemia transcription factor 3 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578817531 | **Score:** | 15.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MDDQSRMLQT LAGVNLAGHS VQGGMALPPP PHGHEGADGD GRKQDIGDIL HQIMTITDQS LDEAQAKKHA LNCHRMKPAL
        90        100        110        120        130        140        150        160
FSVLCEIKEK TGLSIRGAQE EDPPDPQLMR LDNMLLAEGV SGPEKGGGSA AAAAAAAASG GSSDNSIEHS DYRAKLTQIR
       170        180        190        200        210        220        230        240
QIYHTELEKY EQACNEFTTH VMNLLREQSR TRPISPKEIE RMVGIIHRKF SSIQMQLKQS TCEAVMILRS RFLDARRKRR
       250        260        270        280        290        300        310        320
NFSKQATEIL NEYFYSHLSN PYPSEEAKEE LAKKCSITVS QVSNWFGNKR IRYKKNIGKF QEEANLYAAK TAVTAAHAVA
       330        340        350        360
AAVQNNQTNS PTTPNSGGYP PSCYQSDGRL Q
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1938 | 1 | 618.9208 | -90.90 | 3 | 52.6 | 15.7 | 1 | 274-289 | K.KCSITVSQVSNWFGNK.R | Carbamidomethyl: 2 |

# Detailed Protein Report

## Protein 1022: putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 [Homo sapiens]

**Accession:** gi|68509926
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 15.7
**MW [kDa]:** 90.9
**pI:** 7.4
**Sequence Coverage [%]:** 1.4
**No. of unique Peptides:** 1

## Quantitation

***QU:MU*** **Median:** 0.41 **CV:** 0.00 % **No. of Peptides:** 1
***WUP:QUP*** **Median:** 8.56 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSKRHRLDLG | EDYPSGKKRA | GTDGKDRDRD | RDREDRSKDR | DRERDRGDRE | REREKEKEKE | LRASTNAMLI | SAGLPPLKAS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HSAHSTHSAH | STHSTHSAHS | THAGHAGHTS | LPQCINPFTN | LPHTPRYYDI | LKKRLQLPVW | EYKDRFTDIL | VRHQSFVLVG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ETGSGKTTQI | PQWCVEYMRS | LPGPKRGVAC | TQPRRVAAMS | VAQRVADEMD | VMLGQEVGYS | IRFEDCSSAK | TILKYMTDGM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LLREAMNDPL | LERYGVIILD | EAHERTLATD | ILMGVLKEVV | RQRSDLKVIV | MSATLDAGKF | QIYFDNCPLL | TIPGRTHPVE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IFYTPEPERD | YLEAAIRTVI | QIHMCEEEEG | DLLLFLTGQE | EIDEACKRIK | REVDDLGPEV | GDIKIIPLYS | TLPPQQQQRI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FEPPPPKKQN | GAIGRKVVVS | TNIAETSLTI | DGVVFVIDPG | FAKQKVYNPR | IRVESLLVTA | ISKASAQQRA | GRAGRTRPGK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CFRLYTEKAY | KTEMQDNTYP | EILRSNLGSV | VLQLKKLGID | DLVHFDFMDP | PAPETLMRAL | ELLNYLAALN | DDGDLTELGS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MMAEFPLDPQ | LAKMVIASCD | YNCSNEVLSI | TAMLSVPQCF | VRPTEAKKAA | DEAKMRFAHI | DGDHLTLLNV | YHAFKQNHES |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VQWCYDNFIN | YRSLMSADNV | RQQLSRIMDR | FNLPRRSTDF | TSRDYYINIR | KALVTGYFMQ | VAHLERTGHY | LTVKDNQVVQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LHPSTVLDHK | PEWVLYNEFV | LTTKNYIRTC | TDIKPEWLVK | IAPQYYDMSN | FPQCEAKRQL | DRIIAKLQSK | EYSQY |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 226 | 1 | 739.8495 | -36.72 | 2 | 32.8 | 15.7 | 2 | 481-491 | K.CFRLYTEKAYK.T | Carbamidomethyl: 1 | WUP:QUP 8.56<br>QU:MU 0.41 |

# Detailed Protein Report

## Protein 1023: wee1-like protein kinase 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|157738687 | **Score:** | 15.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 62.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.84 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDDKDIDKEL | RQKLNFSYCE | ETEIEGQKKV | EESREASSQT | PEKGEVQDSE | AKGTPPWTPL | SNVHELDTSS | EKDKESPDQI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LRTPVSHPLK | CPETPAQPDS | RSKLLPSDSP | STPKTMLSRL | VISPTGKLPS | RGPKHLKLTP | APLKDEMTSL | ALVNINPFTP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ESYKKLFLQS | GGKRKIRGDL | EEAGPEEGKG | GLPAKRCVLR | ETNMASRYEK | EFLEVEKIGV | GEFGTVYKCI | KRLDGCVYAI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KRSMKTFTEL | SNENSALHEV | YAHAVLGHHP | HVVRYYSSWA | EDDHMIIQNE | YCNGGSLQAA | ISENTKSGNH | FEEPKLKDIL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LQISLGLNYI | HNSSMVHLDI | KPSNIFICHK | MQSESSGVIE | EVENEADWFL | SANVMYKIGD | LGHATSINKP | KVEEGDSRFL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ANEILQEDYR | HLPKADIFAL | GLTIAVAAGA | ESLPTNGAAW | HHIRKGNFPD | VPQELSESFS | SLLKNMIQPD | AEQRPSAAAL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ARNTVLRPSL | GKTEELQQQL | NLEKFKTATL | ERELREAQQA | QSPQGYTHHG | DTGVSGTHTG | SRSTKRLVGG | KSARSSSFTS |
| 570 | | | | | | | |
| GEREPLH | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1865 | 1 | 785.9040 | -18.42 | 2 | 51.7 | 15.7 | 1 | 218-231 | K.IGVGEFGTVYKCIK.R | Carbamidomethyl: 12 | WUP:QUP 0.84 |

# Detailed Protein Report

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## Protein 1024: PREDICTED: telomeric repeat-binding factor 2 isoform X4 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|530424267 | **Score:** | 15.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 50.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
|  |  | **Sequence Coverage [%]:** | 2.8 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAGAGTAGP | ASGPGVVRDP | AASQPRKRPG | REGGEGARRS | DTMAGGGGSS | DGSGRAAGRR | ASRSSGRARR | GRHEPGLGGP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AERGAGEARL | EEAVNRWVLK | FYFHEALRAF | RGSRYGDFRQ | IRDIMQALLV | RPLGKEHTVS | RLLRVMQCLS | RIEEGENLDC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SFDMEAELTP | LESAINVLEM | IKTEFTLTEA | VVESSRKLVK | EAMAKKALKS | ESAASSTGKE | DKQPAPGPVE | KPPREPARQL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RNPPTTIGMM | TLKAAFKTLS | GAQDSEAAFA | KLDQKDLVLP | TQALPASPAL | KNKRPRKDEN | ESSAPADGEG | GSELQPKNKR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MTISRLVLEE | DSQSTEPSAG | LNSSQEAASA | PPSKPTVLNQ | PLPGEKNPKV | PKGKWNSSNG | VEEKETWVEE | DELFQVQAAP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 |  |
| DEDSTTNITK | KQKWTVEESE | WVKAGVQKYG | EGNWAAISKN | YPFVNRTAVM | IKDRWRTMKR | LGMN |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 455 | 1 | 666.9184 | 114.60 | 2 | 35.3 | 15.7 | 1 | 71-83 | R.GRHEPGLGGPAER.G |  |

# Detailed Protein Report

## Protein 1025: visinin-like protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21361559 | **Score:** | 15.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 22.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| | | **Sequence Coverage [%]:** | 7.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.76 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.52 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MGKQNSKLAP EVMEDLVKST EFNEHELKQW YKGFLKDCPS GRLNLEEFQQ LYVKFFPYGD ASKFAQHAFR TFDKNGDGTI
        90        100        110        120        130        140        150        160
DFREFICALS ITSRGSFEQK LNWAFNMYDL DGDGKITRVE MLEIIEAIYK MVGTVIMMKM NEDGLTPEQR VDKIFSKMDK
       170        180        190        200
NKDDQITLDE FKEAAKSDPS IVLLLQCDIQ K
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1378 | 4 | 816.3763 | -14.76 | 2 | 46.8 | 15.7 | 1 | 140-153 | K.MNEDGLTPEQRVDK.I | | QU:MU 0.76<br>WUP:QUP 1.52 |

# Detailed Protein Report

## Protein 1026: PREDICTED: coiled-coil domain-containing protein 158 isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578809093 | **Score:** | 15.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 122.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MESKAWESNN | EDLLSSSGVT | SNGGSSSSFF | VSSIRGTIIE | NTSSAGTLTQ | VPFFPKYEVE | LDSPRKIIPS | PGKEHFERVL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EEYSHQVKDL | QRRLNESNEL | HEKQKFYLRQ | SVIDLQTKLQ | EMQMERDAMA | DIRRRESQSQ | EDLRNQLQNT | VHELEAAKCL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KEDMLKDSNT | QIEQLRKMML | SHEGVLQEIR | SILVDFEEAS | GKKICEHDSM | STLHFRSLGS | AISKILRELD | TEISYLKGRI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FPVEDQLEAL | KSESQNKIEL | LLQQHQDRIE | QLISEHEVEI | TGLTEKASSA | RSQANSIQSQ | MEIIQEQARN | QNSMYMRQLS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DLESTVSQLR | SELREAKRMY | EDKTEELEKQ | LVLANSELTE | ARTERDQFSQ | ESGNLDDQLQ | KLLADLHKRE | KELSLEKEQN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KRLWDRDTGN | SITIDHLRRE | LDNRNMEVQR | LEALLKALKS | ECQGQMERQM | AAIQGKNESL | EKVSSLTAQL | ESTKEMLRKV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VEELTAKKMT | LESSERTISD | LTTSLQEKER | AIEATNAEIT | KLRSRVDLKL | QELQHLKNEG | DHLRNVQTEC | EALKLQMTEK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DKVIEILRQQ | IENMTQLVGQ | HGRTAGAMQV | EKAQLEKEIN | DRRMELKELK | ILKDKKDAKI | RELEARVSDL | ELEKVKLVNA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GSERLRAVKD | IKQERDQLLN | EVKTSRSELN | NLSAMKVAMG | MQKQITAKRG | QIDALQSKIQ | FLEEAMTNAN | KEKHFLKEEK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SKLSQELSTV | ATEKNKMAGE | LEVLRSQERR | LKEKVTNMEV | ALDKASLQFA | ECQDIIQRQE | QESVRLKLQH | TLDIKELQGP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GYTSNSSLKP | RLLQPASVTR | SHSNVPSSQS | TASFLSHHST | KANTLKEDPT | RDLKQLLQEL | RSVINEEPAV | SLSKTEEDGR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TSLGALYVAV | EDRVRDCITE | SSLRSDMCHR | SNNSLRDSTE | GSKSSETLSR | EPVTLHAGDR | EDPSGCFTFT | SAASPSVKNS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ASRSFNSSPK | KSPVHSLLTS | SVEGSIGSTS | QYRSAKPIHS | SDSVKVSANR | NNRKNMQEAS | EQTRKLANSG | RRFTAEEPSN |
| 1050 | 1060 | 1070 | 1080 | | | | |
| VFNDQKSRKE | DTESKRPGKN | VTKMTRCLPI | LYRGMRPN | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1840 | 1 | 781.3073 | -162.78 | 2 | 53.4 | 15.7 | 2 | 475-487 | K.EMLRKVVEELTAK.K | Oxidation: 2 |

# Detailed Protein Report

## Protein 1027: PREDICTED: spidroin-1-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530356740 | **Score:** | 15.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.6 |
| | | **Sequence Coverage [%]:** | 11.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLRPRARADC | GVRGRGALGG | VPGRAASRGA | GSRGGRGPGE | GGVPGGRGGA | WGALSGGRVS | RGEGLRLLGA | TGGGCGAWGR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PGLPAAAPKG | LSGGSGGRGS | SQGLSYGRTR | GEAAKSRRAW | TGPRADRTVL | GELRGAAGDR | GVRLPRGDAQ | RPGQNLDGAE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SPARAPAAST | WEDTQGPGAR | SGRRAASAVS | TDGQKPQRVP | SCSRRGSITI | GPGLPGGASE | GSMLRQELGT | AGDEMRLFGQ |
| 250 | 260 | 270 | 280 | | | | |
| GVCFRAMRQP | GSWATGGRPG | VRALQPVPAP | AFHGRRVLP | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1604 | 2 | 978.1044 | -91.99 | 3 | 48.4 | 15.7 | 2 | 59-89 | R.VSRGEGLRLLGATGGGCGAWGRPGLPAAAPK.G | |

# Detailed Protein Report

## Protein 1028: guanine nucleotide-binding protein subunit alpha-15 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|156104883 | **Score:** | 15.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 43.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 4.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MARSLTWRCC | PWCLTEDEKA | AARVDQEINR | ILLEQKKQDR | GELKLLLLGP | GESGKSTFIK | QMRIIHGAGY | SEEERKGFRP |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| LVYQNIFVSM | RAMIEAMERL | QIPFSRPESK | HHASLVMSQD | PYKVTTFEKR | YAAAMQWLWR | DAGIRAYYER | RREFHLLDSA |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| VYYLSHLERI | TEEGYVPTAQ | DVLRSRMPTT | GINEYCFSVQ | KTNLRIVDVG | GQKSERKKWI | HCFENVIALI | YLASLSEYDQ |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| CLEENNQENR | MKESLALFGT | ILELPWFKST | SVILFLNKTD | ILEEKIPTSH | LATYFPSFQG | PKQDAEAAKR | FILDMYTRMY |
| **330** | **340** | **350** | **360** | **370** | **380** | | |
| TGCVDGPEGS | KKGARSRRLF | SHYTCATDTQ | NIRKVFKDVR | DSVLARYLDE | INLL | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1346 | 1 | 955.6732 | 140.57 | 2 | 46.4 | 15.7 | 2 | 38-55 | K.QDRGELKLLLLGPGESGK.S | |

# Detailed Protein Report

## Protein 1029: mas-related G-protein coupled receptor member X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|125660451 | **Score:** | 15.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 36.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 8.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDPTISTLDT | ELTPINGTEE | TLCYKQTLSL | TVLTCIVSLV | GLTGNAVVLW | LLGCRMRRNA | FSIYILNLAA | ADFLFLSGRL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IYSLLSFISI | PHTISKILYP | VMMFSYFAGL | SFLSAVSTER | CLSVLWPIWY | RCHRPTHLSA | VVCVLLWALS | LLRSILEWML |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CGFLFSGADS | AWCQTSDFIT | VAWLIFLCVV | LCGSSLVLLI | RILCGSRKIP | LTRLYVTILL | TVLVFLLCGL | PFGIQFFLFL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| WIHVDREVLF | CHVHLVSIFL | SALNSSANPI | IYFFVGSFRQ | RQNRQNLKLV | LQRALQDASE | VDEGGGQLPE | EILELSGSRL |
| 330 | | | | | | | |
| EQ | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2182 | 1 | 900.3512 | -96.83 | 3 | 57.2 | 15.7 | 0 | 294-319 | R.ALQDASEVDEGGGQLPEEILELSGSR.L | |

# Detailed Protein Report

## Protein 1030: PREDICTED: cadherin-11 isoform X6 [Homo sapiens]

**Accession:** gi|530423519
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 15.6
**MW [kDa]:** 62.7
**pI:** 5.0
**Sequence Coverage [%]:** 3.2
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKENYCLQAA | LVCLGMLCHS | HAFAPERRGH | LRPSFHGHHE | KGKEGQVLQR | SKRGWVWNQF | FVIEEYTGPD | PVLVGRLHSD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IDSGDGNIKY | ILSGEGAGTI | FVIDDKSGNI | HATKTLDREE | RAQYTLMAQA | VDRDTNRPLE | PPSEFIVKVQ | DINDNPPEFL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HETYHANVPE | RSNVGTSVIQ | VTASDADDPT | YGNSAKLVYS | ILEGQPYFSV | EAQTGIIRTA | LPNMDREAKE | EYHVVIQAKD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MGGHMGGLSG | TTKVTITLTD | VNDNPPKFPQ | SVYQMSVSEA | AVPGEEVGRV | KAKDPDIGEN | GLVTYNIVDG | DGMESFEITT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DYETQEGVIK | LKKPVDFETK | RAYSLKVEAA | NVHIDPKFIS | NGPFKDTVTV | KISVEDADEP | PMFLAPSYIH | EVQENAAAGT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VVGRVHAKDP | DAANSPIRYS | IDRHTDLDRF | FTINPEDGFI | KTTKPLDREE | TAWLNITVFA | AEIHNRHQEA | KVPVAIRVLD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VNDNAPKFAA | PYEGFICESD | QTKPLSNQPI | VTISADDKDD | TANGPRFIFS | LPPEIIHNPN | FTVRDNRDAV | EPHGHNHIIM |
| 570 | | | | | | | |
| VLKEF | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2302 | 1 | 701.2728 | -116.45 | 3 | 58.7 | 15.6 | 1 | 548-565 | R.DAVEPHGHNHIIMVLKEF.- | Oxidation: 13 |

# Detailed Protein Report

## Protein 1031: PREDICTED: mono [ADP-ribose] polymerase PARP16 isoform X3 [Homo sapiens]

**Accession:** gi|530406133
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 15.6
**MW [kDa]:** 28.5
**pI:** 10.2
**Sequence Coverage [%]:** 6.7
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQPSGWAAAR | EAAGRDMLAA | DLRCSLFASA | LQSYKRDSVL | RPFPASYARG | DCKDFEALLA | DASKLPNLKE | LLQSSGDNHK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RAWDLVSWIL | SSKVLTIHSA | GKAETSLFGE | GTYLTSDLSL | ALIYSPHGHG | WQHSLLGPIL | SCVAVCEVID | HPDVKCQTKK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KDSKEIDRRR | ARIKHSEGGD | IPPKYFVVTN | NQLLRVKYLL | VYSQKPPKSR | ASSQLSWFSS | HWFTVMISLY | LLLLLIVSVI |
| 250 | 260 | | | | | | |
| NSSAFQHFWN | RAKR | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2526 | 1 | 941.5692 | 108.04 | 2 | 62.2 | 15.6 | 1 | 37-53 | R.DSVLRPFPASYARGDCK.D | |

# Detailed Protein Report

## Protein 1032: inactive heparanase-2 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|261878505 | **Score:** | 15.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 53.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.6 |
| | | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MRVLCAFPEA | MPSSNSRPPA | CLAPGALYLA | LLLHLSLSSQ | AGDRRPLPVD | RAAGLKEKTL | ILLDVSTKNP | VRTVNENFLS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LQLDPSIIHD | GWLDFLSSKR | LVTLARGLSP | AFLRFGGKRT | DFLQFQNLRN | PAKSRGGPGP | DYYLKNYEDE | PNNYRTMHGR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AVNGSQLGKD | YIQLKSLLQP | IRIYSRASLY | GPNIGRPRKN | VIALLDGFMK | VAGSTVDAVT | WQHCYIDGRV | VKVMDFLKTR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LLDTLSDQIR | KIQKVVNTYT | PGKKIWLEGV | VTTSAGGTNN | LSDSYAAGFL | WLNTLGMLAN | QGIDVVIRHS | FFDHGYNHLV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DQNFNPLPDY | WLSLLYKRLI | GPKVLAVHVA | GLQRKPRPGR | VIRDKLRIYA | HCTNHHNHNY | VRGSITLFII | NLHRSRKKIK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LAGTLRDKLV | HQYLLQPYGQ | EGLKSKSVQL | NGQPLVMVDD | GTLPELKPRP | LRAGRTLVIP | PVTMGFYVVK | NVNALACRYR |
| 490 | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2517 | 1 | 913.4734 | -73.94 | 2 | 62.1 | 15.6 | 2 | 57-72 | K.EKTLILLDVSTKNPVR.T | |

# Detailed Protein Report

## Protein 1033: PREDICTED: NAD-dependent protein deacetylase sirtuin-7 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578832025 | **Score:** | 15.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 35.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.8 |
| | | **Sequence Coverage [%]:** | 6.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSSNREKLA | FKAALRFFLL | KKRNDQNLPK | AASIPDYRGP | NGVWTLLQKG | RSVSAADLSE | AEPTLTHMSI | TRLHEQKLVQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HVVSQNCDGL | HLRSGLPRTA | ISELHGNMYI | EVCTSCVPNR | EYVRVFDVTE | RTALHRHQTG | RTCHKCGTQL | RDTIVHFGER |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GTLGQPLNWE | AATEAASRAD | TILCLGSSLK | VLKKYPRLWC | MTKPPSRRPK | LYIVNLQWTP | KDDWAALKLH | GKCDDVMRLL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MAELGLEIPA | YSRWQDPIFS | LATPLRAGEE | GSHSRKSLCR | SREEAPPGDR | GAPLSSAPIL | GGWFGRGCTK | RTKRKKVT |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 192 | 1 | 1043.5843 | 25.50 | 2 | 32.4 | 15.6 | 1 | 31-49 | K.AASIPDYRGPNGVWTLLQK.G | |

# Detailed Protein Report

## Protein 1034: PREDICTED: LOW QUALITY PROTEIN: ubiquitin-conjugating enzyme E2 variant 1-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578818188 | **Score:** | 15.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 15.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578844793 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: LOW QUALITY PROTEIN: ubiquitin-conjugating enzyme E2 variant 1-like [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLGENQNPLN | VSLPFYIRNL | GLWTLLWAQT | TYENRTHSLK | IECRPKTPKN | TXLCKIVTKI | NTNGVDSSNV | VVDPKAILVL |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | |
| AKGQNSHSII | VVLQELWHLV | MSKADIKLPQ | PPEGQCCSNS | SKRKTTGPSF | LPFDLTGLHF | PQ | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1326 | 1 | 946.6005 | 108.67 | 2 | 46.7 | 15.6 | 2 | 0-0 | .IECRPKTPKNTFLCK. | Carbamidomethyl: 3, 14 |

# Detailed Protein Report

## Protein 1035: PREDICTED: coiled-coil domain-containing protein 92-like [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|578830217 | **Score:** | 15.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 47.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.9 |
|  |  | **Sequence Coverage [%]:** | 2.5 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVSTCSQRSP | QAKGPPLAEI | KGLFGWLDAV | AHARGAQAWV | AMDTVSLEHQ | IQSVQRHISF | LKKEQMALLR | DLHLEILRLQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KRCSELTHDL | EMREAQSHQQ | EAASRELESK | CRALESQLEA | RAAANAELRR | EVAQREALVS | ALRCSLRTEE | RRFLEELRRR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SHRATVLGTE | LQKHTEAAAY | LSCQLHAARQ | RLQAPRPGPG | ATAEPRPRRR | ALRARRPPAA | HEAAAKGPGR | DWAAWDRGAG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ALDDADPMPD | PALFLYARRP | LRPSARSPRQ | PPPQEPPDRA | GPQPAPSQPS | APGDPEQVPG | RRAAAPPPGS | GARRPRLPPN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PRTASLLYFP | TFPKLRALSS | RESSSAGPSG | GTFSTERTRR | PDPGLVPPAC | ETGGAGATPF | PGKADNPWWG | GEGWARLRKG |
| 410 | 420 | 430 | 440 |  |  |  |  |
| TQSGIGAPGP | LAPHPPPPPP | PRRRPSRQAF | FLPRRGPG |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 454 | 1 | 646.8079 | -121.57 | 2 | 35.7 | 15.6 | 1 | 259-269 | R.RPLRPSARSPR.Q |  |

# Detailed Protein Report

**Protein 1036:** **PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1 isoform X5 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578813467 | **Score:** | 15.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 33.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 5.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEKTLETVPL | ERKKREKEQF | RKLFIGGLSF | ETTEESLRNY | YEQWGKLTDC | VVMRDPASKR | SRGFGFVTFS | SMAEVDAAMA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ARPHSIDGRV | VEPKRAVARE | ESGKPGAHVT | VKKLFVGGIK | EDTEEHHLRD | YFEEYGKIDT | IEIITDRQSG | KKRGFGFVTF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DDHDPVDKIV | LQKYHTINGH | NAEVRKALSR | QEMQEVQSSR | SGRGGNFGFG | DSRGGGGNFG | PGPGSNFRGG | SDGYGSGRGF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GDGYNGYGGG | PGGNYGSGNY | NDFGNYNQQP | SNYGPMKSGN | FGGSRNMGGP | YGGGNYGPGG | SGGSGGYGGR | SRY |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1128 | 1 | 983.3895 | -134.59 | 2 | 44.2 | 15.5 | 2 | 174-190 | K.YHTINGHNAEVRKALSR.Q | |

# Detailed Protein Report

## Protein 1037: ER lumen protein retaining receptor 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5803048 | **Score:** | 15.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 5.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 2.16 **CV:** 0.00 % **No. of Peptides:** 1

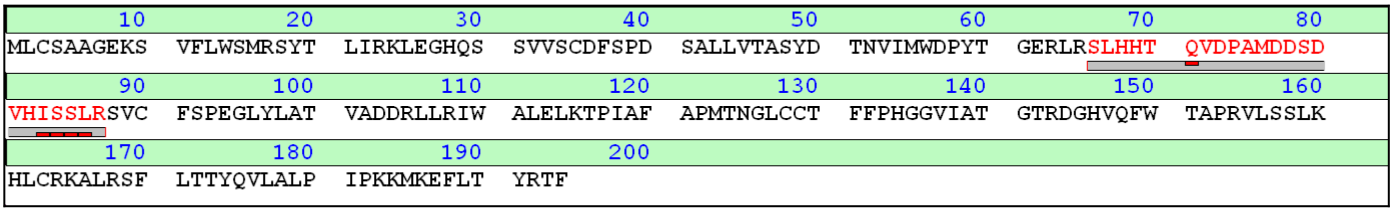
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MNLFRFLGDL | SHLLAIILLL | LKIWKSRSCA | GISGKSQVLF | AVVFTARYLD | LFTNYISLYN | TCMKVVYIAC | SFTTVWLIYS |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| KFKATYDGNH | DTFRVEFLVV | PTAILAFLVN | HDFTPLEILW | TFSIYLESVA | ILPQLFMVSK | TGEAETITSH | YLFALGVYRT |
| **170** | **180** | **190** | **200** | **210** | **220** | | |
| LYLFNWIWRY | HFEGFFDLIA | IVAGLVQTVL | YCDFFYLYIT | KVLKGKKLSL | PA | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 453 | 1 | 669.3289 | -79.98 | 2 | 35.6 | 15.5 | 0 | 36-47 | K.SQVLFAVVFTAR.Y | | WUP:QUP 2.16 |

# Detailed Protein Report

## Protein 1038: WD repeat and SOCS box-containing protein 2 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|514052675 | **Score:** | 15.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 11.3 |
| | | **No. of unique Peptides:** | 1 |



```
        10         20         30         40         50         60         70         80
MLCSAAGEKS VFLWSMRSYT LIRKLEGHQS SVVSCDFSPD SALLVTASYD TNVIMWDPYT GERLRSLHHT QVDPAMDDSD
        90        100        110        120        130        140        150        160
VHISSLRSVC FSPEGLYLAT VADDRLLRIW ALELKTPIAF APMTNGLCCT FFPHGGVIAT GTRDGHVQFW TAPRVLSSLK
       170        180        190        200
HLCRKALRSF LTTYQVLALP IPKKMKEFLT YRTF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 642 | 1 | 820.7414 | 21.33 | 3 | 37.6 | 15.5 | 0 | 66-87 | R.SLHHTQVDPAMDDSDVHISSLR.S | |

# Detailed Protein Report

## Protein 1039: protein SOGA2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|163644316 | **Score:** | 15.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 177.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEEMRDSYLE | EDVYQLQELR | RELDRANKNC | RILQYRLRKA | EQKSLKVAET | GQVDGELIRS | LEQDLKVAKD | VSVRLHHELK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TVEEKRAKAE | DENETLRQQM | IEVEISKQAL | QNELERLKES | SLKRRSTREM | YKEKKTFNQD | DSADLRCQLQ | FAKEEAFLMR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KKMAKLGREK | DELEQELQKY | KSLYGDVDSP | LPTGEAGGPP | STREAELKLR | LKLVEEEANI | LGRKIVELEV | ENRGLKAEME |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DMRGQQEREG | PGRDHAPSIP | TSPFGDSLES | STELRRHLQF | VEEEAELLRR | SISEIEDHNR | QLTHELSKFK | FEPPREPGWL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GEGASPGAGG | GAPLQEELKS | ARLQISELSG | KVLKLQHENH | ALLSNIQRCD | LAAHLGLRAP | SPRDSDAESD | AGKKESDGEE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SRLPQPKREG | PVGGESDSEE | MFEKTSGFGS | GKPSEASEPC | PTELLKARED | SEYLVTLKHE | AQRLERTVER | LITDTDSFLH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DAGLRGGAPL | PGPGLQGEEE | QGEGDQQEPQ | LLGTINAKMK | AFKKELQAFL | EQVNRIGDGL | SPLPHLTESS | SFLSTVTSVS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RDSPIGNLGK | ELGPDLQSRL | KEQLEWQLGP | ARGDERESLR | LRAARELHRR | ADGDTGSHGL | GGQTCFSLEL | RGPPVLPEQS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VSIEELQGQL | VQAARLHQEE | TETFTNKIHK | MEEEHLYALR | WKELEMHSLA | LQNTLHERTW | SDEKNLMQQE | LRSLKQNIFL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| FYVKLRWLLK | HWRQGKQMEE | EGEEFTEGEH | PETLSRLGEL | GVQGGHQADG | PDHDSDRGCG | FPVGEHSPHS | RVQIGDHSLR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LQTADRGQPH | KQVVENQQLF | SAFKALLEDF | RAELREDERA | RLRLQQQYAS | DKAAWDVEWA | VLKCRLEQLE | EKTENKLGEL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GSSAESKGAL | KKEREVHQKL | LADSHSLVMD | LRWQIHHSEK | NWNREKVELL | DRLDRDRQEW | ERQKKEFLWR | IEQLQKENSP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RRGGSFLCDQ | KDGNVRPFPH | QGSLRMPRPV | AMWPCADADS | IPFEDRPLSK | LKESDRCSAS | ENLYLDALSL | DDEPEEPPAH |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RPEREFRNRL | PEEEENHKGN | LQRAVSVSSM | SEFQRLMDIS | PFLPEKGLPS | TSSKEDVTPP | LSPDDLKYIE | EFNKSWDYTP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| NRGHNGGGPD | LWADRTEVGR | AGHEDSTEPF | PDSSWYLTTS | VTMTTDTMTS | PEHCQKQPLR | SHVLTEQSGL | RVLHSPPAVR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| RVDSITAAGG | EGPFPTSRAR | GSPGDTKGGP | PEPMLSRWPC | TSPRHSRDYV | EGARRPLDSP | LCTSLGFASP | LHSLEMSKNL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SDDMKEVAFS | VRNAICSGPG | ELQVKDMACQ | TNGSRTMGTQ | TVQTISVGLQ | TEALRGSGVT | SSPHKCLTPK | AGGGATPVSS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PSRSLRSRQV | APAIEKVQAK | FERTCCSPKY | GSPKLQRKPL | PKADQPNNRT | SPGMAQKGYS | ESAWARSTTT | RESPVHTTIN |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DGLSSLFNII | DHSPVVQDPF | QKGLRAGSRS | RSAEPRPELG | PGQETGTNSR | GRSPSPIGVG | SEMCREEGGE | GTPVKQDLSA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | |
| PPGYTLTENV | ARILNKKLLE | HALKEERRQA | AHGPPGLHSD | SHSLGDTAEP | GPMENQTVLL | TAPWGL | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1525 | 1 | 1022.9446 | -77.80 | 2 | 49.3 | 15.5 | 2 | 447-463 | K.AREDSEYLVTLKHEAQR.L | |

BRUKER

# Detailed Protein Report

## Protein 1040: PREDICTED: WD repeat-containing protein 19 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578808579 | **Score:** | 15.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 144.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKRIFSLLEK | TWLGAPIQFA | WQKTSGNYLA | VTGADYIVKI | FDRHGQKRSE | INLPGNCVAM | DWDKDGDVLA | VIAEKSSCIY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LWDANTNKTS | QLDNGMRDQM | SFLLWSKVGS | FLAVGTVKGN | LLIYNHQTSR | KIPVLGKHTK | RITCGCWNAE | NLLALGGEDK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MITVSNQEGD | TIRQTQVRSE | PSNMQFFLMK | MDDRTSAAES | MISVVLGKKT | LFFLNLNEPD | NPADLEFQQD | FGNIVCYNWY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GDGRIMIGFS | CGHFVVISTH | TGELGQEIFQ | ARNHKDNLTS | IAVSQTLNKV | ATCGDNCIKI | QDLVDLKDMY | VILNLDEENK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GLGTLSWTDD | GQLLALSTQR | GSLHVFLTKL | PILGDACSTR | IAYLTSLLEV | TVANPVEGEL | PITVSVDVEP | NFVAVGLYHL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AVGMNNRAWF | YVLGENAVKK | LKDMEYLGTV | ASICLHSDYA | AALFEGKVQL | HLIESEILDA | QEERETRLFP | AVDDKCRILC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HALTSDFLIY | GTDTGVVQYF | YIEDWQFVND | YRHPVSVKKI | FPDPNGTRLV | FIDEKSDGFV | YCPVNDATYE | IPDFSPTIKG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VLWENWPMDK | GVFIAYDDDK | VYTYVFHKDT | IQGAKVILAG | STKVPFAHKP | LLLYNGELTC | QTQSGKVNNI | YLSTHGFLSN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LKDTGPDELR | PMLAQNLMLK | RFSDAWEMCR | ILNDEAAWNE | LARACLHHME | VEFAIRVYRR | IGNVGIVMSL | EQIKGIEDYN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LLAGHLAMFT | NDYNLAQDLY | LASSCPIAAL | EMRRDLQHWD | SALQLAKHLA | PDQIPFISKE | YAIQLEFAGD | YVNALAHYEK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GITGDNKEHD | EACLAGVAQM | SIRMGDIRRG | VNQALKHPSR | VLKRDCGAIL | ENMKQFSEAA | QLYEKGLYYD | KAASVYIRSK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| NWAKVGDLLP | HVSSPKIHLQ | YAKAKEADGR | YKEAVVAYEN | AKQWQSVIRI | YLDHLNNPEK | AVNIVRETQS | LDGAKMVARF |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FLQLGDYGSA | IQFLVMSKCN | NEAFTLAQQH | NKMEIYADII | GSEDTTNEDY | QSIALYFEGE | KRYLQAGKFF | LLCGQYSRAL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KHFLKCPSSE | DNVAIEMAIE | TVGQAKDELL | TNQLIDHLLG | ENDGMPKDAK | YLFRLYMALK | QYREAAQTAI | IIAREEQSAG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| NYRNAHDVLF | SMYAELKSQK | IKIPSEMATN | LMILHSYILV | KIHVKNGDHM | KGARMLIRVA | NNISKFPSHI | VPILTSTVIE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| CHRAGLKNSA | FSFAAMLMRP | EYRSKIDAKY | KKKIEGMVRE | RQRENTKLTT | PVAQEERRPQ | DLPMLSAVEC | AMNSSSQRWP |
| 1290 | | | | | | | |
| M | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 690 | 2 | 733.4795 | 128.10 | 3 | 38.6 | 15.5 | 1 | 643-661 | K.DTGPDELRPMLAQNLMLKR.F | |

# Detailed Protein Report

## Protein 1041: phosphatidylinositol 3-kinase regulatory subunit gamma [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|166795245 | **Score:** | 15.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|166795247 | refseq_human(refseq_human_20140103.fasta) | phosphatidylinositol 3-kinase regulatory subunit gamma [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MYNTVWSMDR | DDADWREVMM | PYSTELIFYI | EMDPPALPPK | PPKPMTSAVP | NGMKDSSVSL | QDAEWYWGDI | SREEVNDKLR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DMPDGTFLVR | DASTKMQGDY | TLTLRKGGNN | KLIKIYHRDG | KYGFSDPLTF | NSVVELINHY | HHESLAQYNP | KLDVKLMYPV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SRYQQDQLVK | EDNIDAVGKK | LQEYHSQYQE | KSKEYDRLYE | EYTRTSQEIQ | MKRTAIEAFN | ETIKIFEEQC | HTQEQHSKEY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IERFRREGNE | KEIERIMMNY | DKLKSRLGEI | HDSKMRLEQD | LKNQALDNRE | IDKKMNSIKP | DLIQLRKIRD | QHLVWLNHKG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VRQKRLNVWL | GIKNEDADEN | YFINEEDENL | PHYDEKTWFV | EDINRVQAED | LLYGKPDGAF | LIRESSKKGC | YACSVVADGE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | |
| VKHCVIYSTA | RGYGFAEPYN | LYSSLKELVL | HYQQTSLVQH | NDSLNVRLAY | PVHAQMPSLC | R | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2317 | 1 | 1002.9127 | -128.18 | 2 | 58.8 | 15.4 | 0 | 366-383 | R.VQAEDLLYGKPDGAFLIR.E | |

# Detailed Protein Report

## Protein 1042: histone deacetylase 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|13128860 | **Score:** | 15.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 55.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.38 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAQTQGTRRK | VCYYYDGDVG | NYYYGQGHPM | KPHRIRMTHN | LLLNYGLYRK | MEIYRPHKAN | AEEMTKYHSD | DYIKFLRSIR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PDNMSEYSKQ | MQRFNVGEDC | PVFDGLFEFC | QLSTGGSVAS | AVKLNKQQTD | IAVNWAGGLH | HAKKSEASGF | CYVNDIVLAI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LELLKYHQRV | LYIDIDIHHG | DGVEEAFYTT | DRVMTVSFHK | YGEYFPGTGD | LRDIGAGKGK | YYAVNYPLRD | GIDDESYEAI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FKPVMSKVME | MFQPSAVVLQ | CGSDSLSGDR | LGCFNLTIKG | HAKCVEFVKS | FNLPMLMLGG | GGYTIRNVAR | CWTYETAVAL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DTEIPNELPY | NDYFEYFGPD | FKLHISPSNM | TNQNTNEYLE | KIKQRLFENL | RMLPHAPGVQ | MQAIPEDAIP | EESGDEDEDD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PDKRISICSS | DKRIACEEEF | SDSEEEGEGG | RKNSSNFKKA | KRVKTEDEKE | KDPEEKKEVT | EEEKTKEEKP | EAKGVKEEVK |
| 490 | | | | | | | |
| LA | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 184 | 1 | 530.6117 | 41.73 | 3 | 31.2 | 15.4 | 2 | 452-464 | K.DPEEKKEVTEEEK.T | | WUP:QUP 0.38 |

# Detailed Protein Report

## Protein 1043: WD repeat-containing protein 74 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|221219004 | **Score:** | 15.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 42.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530396902 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: WD repeat-containing protein 74 isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAAAAARWNH | VWVGTETGIL | KGVNLQRKQA | ANFTAGGQPR | REEAVSALCW | GTGGETQMLV | GCADRTVKHF | STEDGIFQGQ |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| RHCPGGEGMF | RGLAQADGTL | ITCVDSGILR | VWHDKDKDTS | SDPLLELRVG | PGVCRMRQDP | AHPHVVATGG | KENALKIWDL |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| QGSEEPVFRA | KNVRNDWLDL | RVPIWDQDIQ | FLPGSQKLVT | CTGYHQVRVY | DPASPQRRPV | LETTYGEYPL | TAMTLTPGGN |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| SVIVGNTHGQ | LAEIDLRQGR | LLGCLKGLAG | SVRGLQCHPS | KPLLASCGLD | RVLRIHRIQN | PRGLEHKVYL | KSQLNCLLLS |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | |
| GRDNWEDEPQ | EPQEPNKVPL | EDTETDELWA | SLEAAAKRKL | SGLEQPQGAL | QTRRRKKKRP | GSTSP | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1187 | 1 | 918.4360 | 17.92 | 3 | 43.1 | 15.4 | 1 | 41-65 | R.REEAVSALCWGTGGETQMLVGCADR.T | Carbamidomethyl: 9, 22 |

# Detailed Protein Report

## Protein 1044: PREDICTED: Golgin subfamily A member 8A isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578826741 | **Score:** | 15.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 67.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| | | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAEETGQSKL | AAAKKKFKEY | WQRNRPGVPA | AAKRNTKANG | SSPETAASGG | CHSSEASSSA | SSSLHARQSP | CQEQAAVLNS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RSIKISRLND | TIKSLKQQKK | QVEHQLEEEK | KANNEKQKAE | RELEGQIQRL | NTEKKKLNTD | LYHMKHSLRY | FEEESKDLAG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RLQRSSQRIG | ELEWSLCAVA | ATQKKKPDGF | SSRSKALLKR | QLEQSIREQI | LLKGHVTQLK | ESLKEVQLER | DQYAEQIKGE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RAQWQQRMRK | MSQEVCTLKE | EKKHDTHRVE | ELERSLSRLK | NQMAEPLPPD | APAVSSEVEL | QDLRKELERV | AGELQAQVEN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NQCISLLNRG | QKERLREQEE | RLQEQQERLR | EREKRLQQLA | EPQSDLEELH | ENKSALQLEQ | QVKELQEKLG | QVMETLTSAE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KEPEAAVPAS | GTGGESSGLM | DLLEEKADLR | EHVEKLELGF | IQYRRERCHQ | KVHRLLTEPG | DSAKDASPGG | GHHQAGPGQG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GEEGEAAGAA | GDGVAACGSY | SEGHGKFLAA | ARNPAAEPSP | GAPAPQELGA | ADKHGDLCEA | SLTNSVEPAQ | GEAREGSSQD |
| 570 | 580 | 590 | 600 | 610 | | | |
| NPTAQPVVQL | LGEMQDHQEH | PGLGSNCCVP | CFCWAWLPRR | RR | | | |

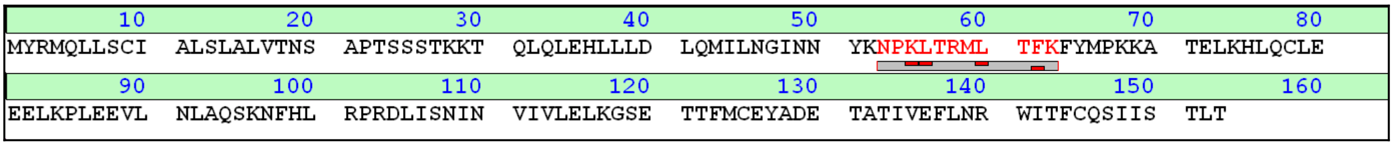
| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 865 | 1 | 647.7984 | -105.89 | 2 | 40.3 | 15.4 | 1 | 436-445 | K.LELGFIQYRR.E | |

# Detailed Protein Report

## Protein 1045: interleukin-2 precursor [Homo sapiens]

**Accession:** gi|28178861
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 15.4
**MW [kDa]:** 17.6
**pI:** 9.0
**Sequence Coverage [%]:** 7.2
**No. of unique Peptides:** 1



```
        10         20         30         40         50         60         70         80
MYRMQLLSCI ALSLALVTNS APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE
        90        100        110        120        130        140        150        160
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2286 | 1 | 682.7901 | -145.71 | 2 | 58.5 | 15.4 | 2 | 53-63 | K.NPKLTRMLTFK.F | Oxidation: 7 |

## Protein 1046: PREDICTED: phosphorylase b kinase regulatory subunit alpha, liver isoform isoform X6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578837920 | **Score:** | 15.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 118.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWERGDKTNQ | GIPELNASSV | GMAKAALEAI | DELDLFGAHG | GRKSVIHVLP | DEVEHCQSIL | FSMLPRASTS | KEIDAGLLSI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ISFPAFAVED | VNLVNVTKNE | IISKLQGRYG | CCRFLRDGYK | TPREDPNRLH | YDPAELKLFE | NIECEWPVFW | TYFIIDGVFS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GDAVQVQEYR | EALEGILIRG | KNGIRLVPEL | YAVPPNKVDE | EYKNPHTVDR | VPMGKVPHLW | GQSLYILSSL | LAEGFLAAGE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IDPLNRRFST | SVKPDVVVQV | TVLAENNHIK | DLLRKHGVNV | QSIADIHPIQ | VQPGRILSHI | YAKLGRNKNM | NLSGRPYRHI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GVLGTSKLYV | IRNQIFTFTP | QFTDQHHFYL | ALDNEMIVEM | LRIELAYLCT | CWRMTGRPTL | TFPISRTMLT | NDGSDIHSAV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LSTIRKLEDG | YFGGARVKLG | NLSEFLTTSF | YTYLTFLDPD | CDEKLFDNAS | EGTFSPDSDS | DLVGYLEDTC | NQESQDELDH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YINHLLQSTS | LRSYLPPLCK | NTEDRHVFSA | IHSTRDILSV | MAKAKGLEVP | FVPMTLPTKV | LSAHRKSLNL | VDSPQPLLEK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VPESDFQWPR | DDHGDVDCEK | LVEQLKDCSN | LQDQADILYI | LYVIKGPSWD | TNLSGQHGVT | VQNLLGELYG | KAGLNQEWGL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IRYISGLLRK | KVEVLAEACT | DLLSHQKQLT | VGLPPEPREK | IISAPLPPEE | LTKLIYEASG | QDISIAVLTQ | EIVVYLAMYV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RAQPSLFVEM | LRLRIGLIIQ | VMATELARSL | NCSGEEASES | LMNLSPFDMK | NLLHHILSGK | EFGVERSVRP | IHSSTSSPTI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SIHEVGHTGV | TKTERSGINR | LRSEMKQMTR | RFSADEQFFS | VGQAASSSAH | SSKSAVTVPR | DYCRSSTPSS | PTGTSSSDSG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GHHIGWGERQ | GQWLRRRRLD | GAINRVPVGF | YQRVWKILQK | CHGLSIDGYV | LPSSTTREMT | PHEIKFAVHV | ESVLNRVPQP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| EYRQLLVEAI | MVLTLLSDTE | MTSIGGIIHV | DQIVQMASQL | FLQDQVSIGA | MDTLEKDQAT | GICHFFYDSA | PSGAYGTMTY |
| 1050 | 1060 | 1070 | | | | | |
| LTRAVASYLQ | ELLPNSGCQM | Q | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1271 | 1 | 927.4170 | -45.41 | 2 | 46.0 | 15.4 | 2 | 99-113 | K.NEIISKLQGRYGCCR.F | Carbamidomethyl: 13, 14 |

# Detailed Protein Report

## Protein 1047: zinc finger protein 667 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|268607677 | **Score:** | 15.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 70.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.9 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPSARGKSKS | KAPITFGDLA | IYFSQEEWEW | LSPIQKDLYE | DVMLENYRNL | VSLGLSFRRP | NVITLLEKGK | APWMVEPVRR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RRAPDSGSKC | ETKKLPPNQC | NKSGQSICQK | LVSAQQKAPT | RKSGCNKNSV | LVKPKKGHSG | KKPLKCNDCG | KTFSRSFSLK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LHQNIHTGEK | PFECSNCRKA | FRQISSILLH | QRIHSGKKSH | ECNKCGESFN | QRTTLILHMR | IHDGKEILDC | GKALSQCQSF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NIHQKIHVVG | NVCQCRKCGK | AFNQMSSLLL | HKKIHNGKKT | HKYNKCGRGF | KKKSVFVVHK | RIHAGEKIPE | NAKALSQSLQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QRSHHLENPF | KCRKCGKLFN | RISPLMLHQR | IHTSEKPYKC | DKCDKFFRRL | STLILHLRIH | NGEKLYRCNK | CEKVCNRHSS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LIQHQKVHTK | KKKLFECKEC | GKMFSGTANL | KIHQNIHSEE | KPFKCNKCSK | VFGRQSFLIE | HQRIHTGEKP | YQCEECGKAF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SHRISLTRHK | RIHTEDRPYE | CDQCGKAFSQ | SAHLAQHERI | HTGEKPYTCK | TCGKAFSQRT | SLILHERSHT | GEKPYECNEC |
| 570 | 580 | 590 | 600 | 610 | 620 | | |
| GKAFSSGSDL | IRHQRSHSSE | KPYECSKCGK | AYSRSSSLIR | HQNTHSEEKA | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 58 | 2 | 779.3515 | -98.67 | 2 | 30.4 | 15.4 | 1 | 535-547 | K.AFSQRTSLILHER.S | |

# Detailed Protein Report

## Protein 1048: zinc finger C2HC domain-containing protein 1C isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|109452611 | **Score:** | 15.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 51.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530404614 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger C2HC domain-containing protein 1C isoform X1 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MAGLQRLASH LPVGVMLPHN TTEAPGPHSA KQDSYEQGDS SQQSLKGHLR NNFQKQLLSN KELILDKVYT HPKWNTQTKA
        90        100        110        120        130        140        150        160
RSYSYPHCTG ISQQDPESDS QGQGNGLFYS SGPQSWYPKA NNQDFIPFTK KRVGVDRAFP LKPMVHRKSC STGEAGTDGD
       170        180        190        200        210        220        230        240
HNVYPRPPEP REFSSRNFGV RNQGNFSVVG TVLAATQAEK AVANFDRTEW VQIRRLEAAG ESLEEEIRRK QILLRGKLKK
       250        260        270        280        290        300        310        320
TEEELRRIQT QKEQAKENEN GELQKIILPR SRVKGNKSNT MYKPIFSPEF EFEEEFSRDR REDETWGRSQ QNSGPFQFSD
       330        340        350        360        370        380        390        400
YRIQRLKRER LVASNNKIRD PVSEPSVEKF SPPSETPVGA LQGSARNSSL SMAPDSSGSS GSIEEPQLGE CSHCGRKFLS
       410        420        430        440        450        460
FRLERHSNIC SRMRGSKRKV FDSSRARAKG TELEQYLNWK GPASAKAEPP QKSNWR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2078 | 1 | 862.3310 | -134.98 | 2 | 55.9 | 15.3 | 2 | 441-456 | K.GPASAKAEPPQKSNWR.- | |

# Detailed Protein Report

## Protein 1049: zinc finger protein 559 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|320202974 | **Score:** | 15.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.4 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MLENYKNLVA VDWESHINTK WSAPQQNFLQ GKTSSVVEME RNHFGEELFD FNQCEKALSE HSCLKTHRRT YFRKKTCECN
        90        100        110        120        130        140        150        160
QCEKAFRKPS IFTLHKKTDI GEELPNCNQC ETAFSQHLHL VCKKTSQNLH LVCKKTHTQE KPYKCSDCEK GLPSSSHLRE
       170        180        190        200        210        220        230        240
CVRIYGGERP YTHKEYVETF SHSTALFVHM QTQDGEKFYE CKACGKPFTE SSYLTQHLRT HSRVLPIEHK KFGKAFAFSP
       250        260        270        280        290        300        310        320
DLAKHIRLRT RGKHYVCNEC GKEFTCFSKL NIHIRVHTGE KPYECNKCGK AFTDSSGLIK HRRTHTGEKP YECKECGKAF
       330        340        350        360        370        380        390        400
ANSSHLTVHM RTHTGEKPYQ CKECGKAFIN SSSFKSHMQT HPGVKPYDCQ QCGKAFIRSS FLIRHLRSHS AERPFECEEC
       410        420        430        440        450        460        470        480
GKAFRYSSHL SQHKRIHTGE RPYKCQKCGQ AFSISSGLTV HMRTHTGERP FECQECGKAF TRSTYLIRHL RSHSVEKPYK
       490        500
ECGQTFSNSS CLTECV
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2542 | 1 | 973.0571 | 97.74 | 2 | 62.4 | 15.3 | 1 | 315-331 | K.ECGKAFANSSHLTVHMR.T | Carbamidomethyl: 2 |

# Detailed Protein Report

## Protein 1050: PREDICTED: RING finger protein 207 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578799105 | **Score:** | 15.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.2 |
| | | **Sequence Coverage [%]:** | 4.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPEEASPAGH | PEDTRRGIPR | VGVRRGRRGH | GRGRPRAEWE | PSPGAGLNFQ | GRLLLGRATA | RCLRARPGAA | LRALDGGREA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RRTGSSQQSG | PADVGSYLRA | PGGPELPGCP | EHPPAGVPAV | PRAVRAPVSS | GLFPRLLCRL | PAWPRDRRPP | HLPAVPDVET |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TYFCNTCGQP | LCARCRDETH | RARMFARHDI | VALGQRSRDV | PQKCTLHAEP | YLLFSTDKKL | LLCIRCFRDM | QKESRAHCVD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LESAYVQGCE | RLEQAVLAVK | ALQTATREAI | ALLQAMVEEV | RHSAAEEEDA | IHALFGSMQA | GREESAAAAG | CAEPIRREGQ |
| 330 | 340 | 350 | 360 | | | | |
| GLQGAALSLG | HLAAHPAGPP | GHLLLLPQLG | QQG | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2534 | 1 | 921.5697 | 42.92 | 2 | 62.3 | 15.3 | 2 | 123-139 | R.AVRAPVSSGLFPRLLCR.L | |

BRUKER

# Detailed Protein Report

## Protein 1051: PREDICTED: kazrin isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530360946 | **Score:** | 15.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 51.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTNTKDPKRA | MESTLATSNS | ATGPVTFSHV | FGQQCQLMQA | AVQSLHTLND | QISHFIVTKS | KALEEDKDPF | LPTEKETLKS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SMILMRHLLM | DAQAKILSMM | EDNKQLALRI | DGAVQSASQE | VTNLRAELTA | TNRRLAELSG | GGGPGPGPGA | AASASAAGDS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AATNMENPQL | GAQVLLREEV | SRLQEEVHLL | RQMKEMLAKD | LEESQGGKSS | EVLSATELRV | QLAQKEQELA | RAKEALQAMK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ADRKRLKGEK | TDLVSQMQQL | YATLESREEQ | LRDFIRNYEQ | HRKESEDAVK | ALAKEKDLLE | REKWELRRQA | KEATDHATAL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RSQLDLKDNR | MKELEAELAM | AKQSLATLTK | DVPKRHSLAM | PGETVLNGNQ | EWVVQADLPL | TAAIRQSQQT | LYHSHPPHPA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | |
| DRQAVRVSPC | HSRQPSVISD | ASAAEGDRSS | TPSDINSPRH | RTHSLWRQSR | PSSEEPAQPY | CTVTRGS | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 989 | 1 | 540.6455 | -205.92 | 2 | 40.7 | 15.3 | 0 | 96-104 | K.ILSMMEDNK.Q | |

# Detailed Protein Report

## Protein 1052: protein KIAA1045 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|149944593 | **Score:** | 15.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 4.8 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530389814 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein KIAA1045 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGVLMSKRQT | VEQVQKVSLA | VSAFKDGLRD | RPSIRRTGEL | PGSRRGTVEG | SVQEVQEEKE | AEAGTSVVQE | ESSAGRAAWE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RLRDGRGVEP | EEFDRTSRFT | PPAFIRPTRK | LDDDKPPEIC | LEPREPVVND | EMCDVCEVWT | AESLFPCRVC | TRVFHDGCLR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RMGYIQGDSA | AEVTEMAHTE | TGWSCHYCDN | INLLLTEEEM | YSLTETFQRC | KVIPDCSLTL | EDFLRYRHQA | AKRGDRDRAL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SEEQEEQAAR | QFAALDPEHR | GHIEWPDFLS | HESLLLLQQL | RPQNSLLRLL | TVKERERARA | AFLARGSGST | VSEAECRRAQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HSWFCKRFPE | APSCSVSISH | VGPIADSSPA | SSSSKSQDKT | LLPTEQESRF | VDWPTFLQEN | VLYILAARPN | SAAIHLKPPG |
| 410 | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2572 | 1 | 1044.0320 | -55.24 | 2 | 62.1 | 15.3 | 2 | 17-35 | K.VSLAVSAFKDGLRDRPSIR.R | |

# Detailed Protein Report

## Protein 1053: metastasis-associated protein MTA1 isoform MTA1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|115527080 | **Score:** | 15.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 80.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAANMYRVGD | YVYFENSSSN | PYLIRRIEEL | NKTANGNVEA | KVVCFYRRRD | ISSTLIALAD | KHATLSVCYK | AGPGADNGEE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GEIEEEMENP | EMVDLPEKLK | HQLRHRELFL | SRQLESLPAT | HIRGKCSVTL | LNETESLKSY | LEREDFFFYS | LVYDPQQKTL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LADKGEIRVG | NRYQADITDL | LKEGEEDGRD | QSRLETQVWE | AHNPLTDKQI | DQFLVVARSV | GTFARALDCS | SSVRQPSLHM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SAAAASRDIT | LFHAMDTLHK | NIYDISKAIS | ALVPQGGPVL | CRDEMEEWSA | SEANLFEEAL | EKYGKDFTDI | QQDFLPWKSL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TSIIEYYYMW | KTTDRYVQQK | RLKAAEAESK | LKQVYIPNYN | KPNPNQISVN | NVKAGVVNGT | GAPGQSPGAG | RACESCYTTQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SYQWYSWGPP | NMQCRLCASC | WTYWKKYGGL | KMPTRLDGER | PGPNRSNMSP | HGLPARSSGS | PKFAMKTRQA | FYLHTTKLTR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IARRLCREIL | RPWHAARHPY | LPINSAAIKA | ECTARLPEAS | QSPLVLKQAV | RKPLEAVLRY | LETHPRPPKP | DPVKSVSSVL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SSLTPAKVAP | VINNGSPTIL | GKRSYEQHNG | VDGNMKKRLL | MPSRGLANHG | QARHMGPSRN | LLLNGKSYPT | KVRLIRGGSL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PPVKRRRMNW | IDAPDDVFYM | ATEETRKIRK | LLSSSETKRA | ARRPYKPIAL | RQSQALPPRP | PPPAPVNDEP | IVIED |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 301 | 1 | 638.3361 | -39.53 | 2 | 33.8 | 15.3 | 0 | 555-567 | K.SVSSVLSSLTPAK.V | |

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# Detailed Protein Report

## Protein 1054: tumor necrosis factor alpha-induced protein 8-like protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|269846912 | **Score:** | 15.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 20.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| | | **Sequence Coverage [%]:** | 5.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530425099 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: tumor necrosis factor alpha-induced protein 8-like protein 1 isoform X1 [Homo sapiens] |
| gi\|269846918 | refseq_human (refseq_human_20140103.fasta) | tumor necrosis factor alpha-induced protein 8-like protein 1 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MDTFSTKSLA LQAQKKLLSK MASKAVVAVL VDDTSSEVLD ELYRATREFT RSRKEAQKML KNLVKVALKL GLLLRGDQLG
        90        100        110        120        130        140        150        160
GEELALLRRF RHRARCLAMT AVSFHQVDFT FDRRVLAAGL LECRDLLHQA VGPHLTAKSH GRINHVFGHL ADCDFLAALY
       170        180        190
GPAEPYRSHL RRICEGLGRM LDEGSL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1438 | 1 | 1095.6551 | -96.87 | 1 | 46.4 | 15.3 | 1 | 66-75 | K.VALKLGLLLR.G | |

# Detailed Protein Report

## Protein 1055: patatin-like phospholipase domain-containing protein 5 isoform 1 [Homo sapiens]

**Accession:** gi|20304127
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 15.3
**MW [kDa]:** 47.9
**pI:** 6.3
**Sequence Coverage [%]:** 4.2
**No. of unique Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGFLEEEGRW | NLSFSGAGYL | GAHHVGATEC | LRQRAPRLLQ | GARRIYGSSS | GALNAVSIVC | GKSVDFCCSH | LLGMVGQLER |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LSLSILHPAY | APIEHVKQQL | QDALPPDAHV | LASQRLGISL | TRWPDGRNFL | VTDFATCDEL | IQALVCTLYF | PFYCGLIPPE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FRGERYIDGA | LSNNLPFADC | PSTITVSPFH | GTVDICPQST | SPNLHELNVF | NFSFQISTEN | FFLGLICLIP | PSLEVVADNC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RQGYLDALRF | LERRGLTKEP | VLWTLVSKEP | PAPADGNWDA | GCDQRWKGGL | SLNWKVPHVQ | VKDVPNFEQL | SPELEAALKK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ACTRDPSRWA | RFWHSGPGQV | LTYLLLPCTL | PFEYIYFRSR | RLVVWLPDVP | ADLWWMQGLL | RNMALEVFSR | TKAQLLGPIS |
| 410 | 420 | 430 | | | | | |
| PPATRVLETS | PLQPQIAPHR | EELGPTHQA | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 958 | 1 | 684.2638 | -84.66 | 3 | 40.3 | 15.3 | 0 | 63-80 | K.SVDFCCSHLLGMVGQLER.L | Carbamidomethyl: 5 |

# Detailed Protein Report

## Protein 1056: charged multivesicular body protein 1b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|31542306 | **Score:** | 15.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 22.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 7.0 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSNMEKHLFN | LKFAAKELSR | SAKKCDKEEK | AEKAKIKKAI | QKGNMEVARI | HAENAIRQKN | QAVNFLRMSA | RVDAVAARVQ |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| TAVTMGKVTK | SMAGVVKSMD | ATLKTMNLEK | ISALMDKFEH | QFETLDVQTQ | QMEDTMSSTT | TLTTPQNQVD | MLLQEMADEA |
| **170** | **180** | **190** | **200** | | | | |
| GLDLNMELPQ | GQTGSVGTSV | ASAEQDELSQ | RLARLRDQV | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 99 | 1 | 837.3495 | -153.38 | 2 | 31.2 | 15.3 | 2 | 7-20 | K.HLFNLKFAAKELSR.S | |

# Detailed Protein Report

## Protein 1057: 40S ribosomal protein S16 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4506691 | **Score:** | 15.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 16.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.8 |
| | | **Sequence Coverage [%]:** | 11.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MPSKGPLQSV QVFGRKKTAT AVAHCKRGNG LIKVNGRPLE MIEPRTLQYK LLEPVLLLGK ERFAGVDIRV RVKGGGHVAQ
        90        100        110        120        130        140        150
IYAIRQSISK ALVAYYQKYV DEASKKEIKD ILIQYDRTLL VADPRRCESK KFGGPGARAR YQKSYR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2194 | 1 | 682.1269 | 129.64 | 3 | 57.8 | 15.2 | 1 | 34-50 | K.VNGRPLEMIEPRTLQYK.L | |

# Detailed Protein Report

## Protein 1058: protein DJ-1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|31543380 | **Score:** | 15.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 19.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| | | **Sequence Coverage [%]:** | 13.8 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530360487 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein DJ-1 isoform X1 [Homo sapiens] |
| gi\|183227678 | refseq_human (refseq_human_20140103.fasta) | protein DJ-1 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MASKRALVIL AKGAEEMETV IPVDVMRRAG IKVTVAGLAG KDPVQCSRDV VICPDASLED AKKEGPYDVV VLPGGNLGAQ
        90        100        110        120        130        140        150        160
NLSESAAVKE ILKEQENRKG LIAAICAGPT ALLAHEIGFG SKVTTHPLAK DKMMNGGHYT YSENRVEKDG LILTSRGPGT
       170        180        190
SFEFALAIVE ALNGKEVAAQ VKAPLVLKD
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1638 | 1 | 882.8299 | 23.17 | 3 | 50.7 | 15.2 | 1 | 157-182 | R.GPGTSFEFALAIVEALNGKEVAAQVK.A | |

# Detailed Protein Report

## Protein 1059: small G protein signaling modulator 2 isoform 1 [Homo sapiens]

**Accession:** gi|148612795
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 15.2
**MW [kDa]:** 118.2
**pI:** 6.1
**Sequence Coverage [%]:** 0.9
**No. of unique Peptides:** 1

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.15 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.35 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGSAEDAVKE | KLLWNVKKEV | KQIMEEAVTR | KFVHEDSSHI | IALCGAVEAC | LLHQLRRRAA | GFLRSDKMAA | LFTKVGKTCP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VAGEICHKVQ | ELQQQAEGRK | PSGVSQEALR | RQGSASGKAP | ALSPQALKHV | WVRTALIEKV | LDKVVQYLAE | NCSKYYEKEA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLADPVFGPI | LASLLVGPCA | LEYTKLKTAD | HYWTDPSADE | LVQRHRIRGP | PTRQDSPAKR | PALGIRKRHS | SGSASEDRLA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ACARECVESL | HQNSRTRLLY | GKNHVLVQPK | EDMEAVPGYL | SLHQSAESLT | LKWTPNQLMN | GTLGDSELEK | SVYWDYALVV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PFSQVVCIHC | HQQKSGGTLV | LVSQDGIQRP | PLHFPQGGHL | LSFLSCLENG | LLPRGQLEPP | LWTQQGKGKV | FPKLRKRSSI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RSVDMEEMGT | GRATDYVFRI | IYPGHRHEHI | TINYHHLAAS | RAASVDDDEE | EEDKLHAMLS | MICSRNLTAP | NPMKDAGDMI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EMQGFGPSLP | AWHLEPLCSQ | GSSCLSCSSS | SSPHATPSHC | SCIPDRLPLR | LLCESMKRQI | VSRAFYGWLA | HCRHLSTVRT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HLSALVHHSV | IPPDRPPGAS | AGLTKDVWSK | YQKDKKNYKE | LELLRQVYYG | GIEHEIRKDV | WPFLLGHYKF | GMSKKEMEQV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DAVVAARYQQ | VLAEWKACEV | VVRQREREAH | PATRTKFSSG | SSIDSHVQRL | IHRDSTISND | VFISVDDLEP | PEPQDPEDSR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PKPEQEAGPG | TPGTAVVEQQ | HSVEFDSPDS | GLPSSRNYSV | ASGIQSSLDE | GQSVGFEEED | GGGEEGSSGP | GPAAHTLREP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QDPSQEKPQA | GELEAGEELA | AVCAAAYTIE | LLDTVALNLH | RIDKDVQRCD | RNYWYFTPPN | LERLRDVMCS | YVWEHLDVGY |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VQGMCDLLAP | LLVTLDNDQL | AYSCFSHLMK | RMSQNFPNGG | AMDTHFANMR | SLIQILDSEL | FELMHQNGDY | THFYFCYRWF |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LLDFKRELLY | EDVFAVWEVI | WAARHISSEH | FVLFIALALV | EAYREIIRDN | NMDFTDIIKF | FNERAEHHDA | QEILRIARDL |
| 1050 | 1060 | | | | | | |
| VHKVQMLIEN | K | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 527 | 1 | 501.2730 | 30.20 | 2 | 36.6 | 15.2 | 0 | 466-474 | R.NLTAPNPMK.D | Oxidation: 8 | WUP:QUP 0.35<br>QU:MU 1.15 |

# Detailed Protein Report

## Protein 1060: PREDICTED: dapper homolog 3 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530415784 | **Score:** | 15.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MRSPRPCGRP | PTDSPDAGGA | GRPLDGYISA | LLRRRRRRGA | GQPRTSPGGA | DGGPRRQNSV | RQRPPDASPS | PGSARPAREP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SLERVGGHPT | SPAALSRAWA | SSWESEAAPE | PAAPPAAPSP | PDSPAEGRLV | KAQYIPGAQA | ATRGLPGRAA | RRKPPPLTRG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RSVEQSPPRE | RPRAAGRRGR | MAEASGRRGS | PRARKASRSQ | SETSLLGRAS | AVPSGPPKYP | TAEREEPRPP | RPRRGPAPTL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AAQAAGSCRR | WRSTAEIDAA | DGRRVRPRAP | AARVPGPGPS | PSAPQRRLLY | GCAGSDSECS | AGRLGPLGRR | GPAGGVGGGY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GESESSASEG | ESPAFSSASS | DSDGSGGLVW | PQQLVAATAA | SGGGAGAGAP | AGPAKVFVKI | KASHALKKKI | LRFRSGSLKV |
| 410 | | | | | | | |
| MTTV | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1795 | 1 | 823.3199 | -37.56 | 2 | 52.8 | 15.2 | 0 | 288-303 | R.LLYGCAGSDSECSAGR.L | Carbamidomethyl: 5 |

# Detailed Protein Report

## Protein 1061: PREDICTED: glucose-6-phosphate 1-dehydrogenase isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530422749 | **Score:** | 15.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAEQVALSRT | QVCGILREEL | FQGDAFHQSD | THIFIIMGAS | GDLAKKKIYP | TIWWLFRDGL | LPENTFIVGY | ARSRLTVADI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RKQSEPFFKA | TPEEKLKLED | FFARNSYVAG | QYDDAASYQR | LNSHMNALHL | GSQANRLFYL | ALPPTVYEAV | TKNIHESCMS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QIRGWNRIIV | EKPFGRDLQS | SDRLSNHISS | LFREDQIYRI | DHYLGKEMVQ | NLMVLRFANR | IFGPIWNRDN | IACVILTFKE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PFGTEGRGGY | FDEFGIIRDV | MQNHLLQMLC | LVAMEKPAST | NSDDVRDEKV | KVLKCISEVQ | ANNVVLGQYV | GNPDGEGEAT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KGYLDDPTVP | RGSTTATFAA | VVLYVENERW | DGVPFILRCG | KALNERKAEV | RLQFHDVAGD | IFHQQCKRNE | LVIRVQPNEA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VYTKMMTKKP | GMFFNPEESE | LDLTYGNRYK | NVKLPDAYER | LILDVFCGSQ | MHFVRSDELR | EAWRIFTPLL | HQIELEKPKP |
| 490 | 500 | 510 | 520 | | | | |
| IPYIYGSRGP | TEADELMKRV | GFQYEGTYKW | VNPHKL | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2614 | 1 | 659.1695 | -206.35 | 2 | 61.0 | 15.2 | 0 | 153-163 | K.NIHESCMSQIR.G | |

# Detailed Protein Report

## Protein 1062: PREDICTED: DNA mismatch repair protein Msh2 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530367623 | **Score:** | 15.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 103.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 4.45 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.60 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAVQPKETLQ | LESAAEVGFV | RFFQGMPEKP | TTTVRLFDRG | DFYTAHGEDA | LLAAREVFKT | QGVIKYMGPA | GAKNLQSVVL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SKMNFESFVK | DLLLVRQYRV | EVYKNRAGNK | ASKENDWYLA | YKASPGNLSQ | FEDILFGNND | MSASIGVVGV | KMSAVDGQRQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VGVGYVDSIQ | RKLGLCEFPD | NDQFSNLEAL | LIQIGPKECV | LPGGETAGDM | GKLRQIIQRG | GILITERKKA | DFSTKDIYQD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LNRLLKGKKG | EQMNSAVLPE | MENQVAVSSL | SAVIKFLELL | SDDSNFGQFE | LTTFDFSQYM | KLDIAAVRAL | NLFQGSVEDT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TGSQSLAALL | NKCKTPQGQR | LVNQWIKQPL | MDKNRIEERL | NLVEAFVEDA | ELRQTLQEDL | LRRFPDLNRL | AKKFQRQAAN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LQDCYRLYQG | INQLPNVIQA | LEKHEGKHQK | LLLAVFVTPL | TDLRSDFSKF | QEMIETTLDM | DQVENHEFLV | KPSFDPNLSE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LREIMNDLEK | KMQSTLISAA | RDLGLDPGKQ | IKLDSSAQFG | YYFRVTCKEE | KVLRNNKNFS | TVDIQKNGVK | FTNSKLTSLN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EEYTKNKTEY | EEAQDAIVKE | IVNISSGYVE | PMQTLNDVLA | QLDAVVSFAH | VSNGAPVPYV | RPAILEKGQG | RIILKASRHA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CVEVQDEIAF | IPNDVYFEKD | KQMFHIITGP | NMGGKSTYIR | QTGVIVLMAQ | IGCFVPCESA | EVSIVDCILA | RVGAGDSQLK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GVSTFMAEML | ETASILRSAT | KDSLIIIDEL | GRGTSTYDGF | GLAWAISEYI | ATKIGAFCMF | ATHFHELTAL | ANQIPTVNNL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| HVTALTTEET | LTMLYQVKKG | VCDQSFGIHV | AELANFPKHV | IECAKQKALE | LEEFQYIGES | QGYDIMEPAA | KKCYLERENL |
| 890 | 900 | 910 | 920 | 930 | | | |
| RVTEPKDQCL | ILLTWKRKLR | GGKRSACSRP | ERQNQGSGEL | S | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 151 | 1 | 981.4369 | -27.53 | 2 | 31.6 | 15.2 | 2 | 904-921 | K.RSACSRPERQNQGSGELS.- | | QU:MU 4.45<br>WUP:QUP 0.60 |

# Detailed Protein Report

## Protein 1063: PREDICTED: stAR-related lipid transfer protein 5 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578827450 | **Score:** | 15.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 16.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.7 |
| | | **Sequence Coverage [%]:** | 8.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 1.30 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MDPALAAQMS EAVAEKMLQY RRDTAGWKIC REGVSEELGG KGSRRRLRGA RVPRSPQAPP LPVVFCSPIP WTRLRGIPMG
         90        100        110        120        130        140        150
IVFFFKKKIG PVMLTMTSGE WSFSFLEAIC GVSREPVPRR RHCIWDTRGG VGLCEASCWR PTSEVG
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 189 | 1 | 652.8289 | 4.93 | 2 | 32.3 | 15.1 | 1 | 32-44 | R.EGVSEELGGKGSR.R | | QU:MU 1.30 |

# Detailed Protein Report

## Protein 1064: PREDICTED: FH1/FH2 domain-containing protein 3 isoform X6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530413959 | **Score:** | 15.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 170.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MATLACRVQF | LDDTDPFNST | NFPEPSRPPL | FTFREDLALG | TQLAGVHRLL | QAPHKLDDCT | LQLSHNGAYL | DLEATLAEQR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DELEGFQDDA | GRGKKHSIIL | RTQLSVRVHA | CIEKLYNSSG | RDLRRALFSL | KQIFQDDKDL | VHEFVVAEGL | TCLIKVGAEA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DQNYQNYILR | ALGQIMLYVD | GMNGVINRNE | TIQWLYTLIG | SKFRLVVKTA | LKLLLVFVEY | SESNAPLLIQ | AVTAVDTKRG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VKPWSNIMEI | LEEKDGVDTE | LLVYAMTLVN | KTLSGLPDQD | TFYDVVDCLE | ELGIAAVSQR | HLNKKGTDLD | LVEQLNIYEV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ALRHEDGDET | TEPPPSGCRD | RRRASVCSSG | GGEHRGLDRR | RSRRHSVQSI | KSTLSAPTSP | CSQSAPSFKP | NQVRDLREKE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EEEEEEQPIT | EPSSEEERED | DASCQGKDSK | VGAASGQSPT | GRDAAPKSSA | LPAVSNASSQ | GKPLLVGTAG | GTTWHSGSSG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SEATPSALLS | PPASAARPSS | ATPGSLKVSP | TIDKLPYVPH | SPFHLFSYDF | EDSSLSTKEK | EAESQKENSS | SDSFSLSTYS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ASEPYHFRSF | SSNRYSNFGN | NSYHSSRPSS | GSSVPTTPTS | SVSPPQEARL | ERSSPSGLLT | SSFRQHQESL | AAERERRRQE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| REERLQRIER | EERNKFSRDY | LDKREEQRQA | REERYKYLEQ | LAAEEHEKEL | RSRSVSRGRA | DLSLDLTSPA | APACLAPLSH |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SPSSSDSQEA | LTVSASSPGT | PHHPQASAGD | PEPESEAEPE | AEAGAGQVAD | EAGQDIASAH | EGAETEVEQA | LEQEPEERAS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LSEKERQNEG | VNERDNCSAS | SVSSSSSTLE | REEKEDKLSR | DRTTGLWPAG | VQDAGVNGQC | GDILTNKRFM | LDMLYAHNRK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SPDDEEKGDG | EAGRTQQEAE | AVASLATRIS | TLQANSQTQD | ESVRRVDVGC | LDNRGSVKAF | AEKFNSGDLG | RGSISPDAEP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NDKVPETAPV | QPKTESDYIW | DQLMANPREL | RIQDMDFTDL | GEEDDIDVLD | VDLGHREAPG | PPPPPPPTFL | GLPPPPPPPL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LDSIPPPPVP | GNLLVPPPPV | FNAPQGLGWS | QVPRGQPTFT | KKKKTIRLFW | NEVRPFDWPC | KNNRRCREFL | WSKLEPIKVD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TSRLEHLFES | KSKELSVSKK | TAADGKRQEI | IVLDSKRSNA | INIGLTVLPP | PRTIKIAILN | FDEYALNKEG | IEKILTMIPT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| DEEKQKIQEA | QLANPEIPLG | SAEQFLLTLS | SISELSARLH | LWAFKMDYET | TEKEVAEPLL | DLKEGIDQLE | NNKTLGFILS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TLLAIGNFLN | GTNAKAFELS | YLEKVPEVKD | TVHKQSLLHH | VCTMVVENFP | DSSDLYSEIG | AITRSAKVDF | DQLQDNLCQM |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ERRCKASWDH | LKAIAKHEMK | PVLKQRMSEF | LKDCAERIII | LKIVHRRIIN | RFHSFLLFMG | HPPYAIREVN | INKFCRIISE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| FALEYRTTRE | RVLQQKQKRA | NHRERNKTRG | KMITDDPLVP | GLWELMTRPM | SQMMQLMRSW | TASSSQPPKC | PVSEWCRGRG |
| 1530 | 1540 | | | | | | |
| NDPGPTGNLC | EEP | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 876 | 1 | 835.2166 | -178.08 | 2 | 40.5 | 15.1 | 1 | 1518-1533 | R.GRGNDPGPTGNLCEEP.- | Carbamidomethyl: 13 |

# Detailed Protein Report

## Protein 1065: solute carrier family 13 member 3 isoform e [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|301069353 | **Score:** | 15.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| | | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASAIEEWNL | HRRIALKILM | LVGVQPARLI | LGMMVTTSFL | SMWLSNTAST | AMMLPIANAI | LKSLFGQKEV | RKDPSQESEE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NTAAVRRNGL | HTVPTEMQFL | ASTEAKDHPG | ETEVPLDLPA | DSRKEDEYRR | NIWKGFLISI | PYSASIGGTA | TLTGTAPNLI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLGQLKSFFP | QCDVVNFGSW | FIFAFPLMLL | FLLAGWLWIS | FLYGGLSFRG | WRKNKSEIRT | NAEDRARAVI | REEYQNLGPI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KFAEQAVFIL | FCMFAILLFT | RDPKFIPGWA | SLFNPGFLSD | AVTGVAIVTI | LFFFPSQRPS | LKWWFDFKAP | NTETEPLLTW |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KKAQETVPWN | IILLLGGGFA | MAKGCEESGL | SVWIGGQLHP | LENVPPALAV | LLITVVIAFF | TEFASNTATI | IIFLPVLAEL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AIRLRVHPLY | LMIPGTVGCS | FAFMLPVSTP | PNSIAFASGH | LLVKDMVRTG | LLMNLMGVLL | LSLAMNTWAQ | TIFQLGTFPD |
| 490 | 500 | 510 | | | | | |
| WADMYSVNVT | ALPPTLANDT | FRTL | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2339 | 1 | 682.2881 | -68.27 | 3 | 59.7 | 15.1 | 2 | 69-86 | K.EVRKDPSQESEENTAAVR.R | |

# Detailed Protein Report

## Protein 1066: PREDICTED: tetratricopeptide repeat protein 25 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578831507 | **Score:** | 15.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 58.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKHLLHPTKG | EPKWKASLKS | EKTVRQLLGE | LYVDKEYLEK | LLLDEDLIKG | TMKGGLTVED | LIMTGINYLD | THSNFWRQQK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PIYARERDRK | LMQEKWLRDH | KRRPSQTAHY | ILKSLEDIDM | LLTSGSAEGS | LQKAEKVLKK | VLEWNKEEVP | NKDELVGNLY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SCIGNAQIEL | GQMEAALQSH | RKDLEIAKEY | DLPDAKSRAL | DNIGRVFARV | GKFQQAIDTW | EEKIPLAKTT | LEKTWLFHEI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GRCYLELDQA | WQAQNYGEKS | QQCAEEEGDI | EWQLNASVLV | AQAQVKLRDF | ESAVNNFEKA | LERAKLVHNN | EAQQAIISAL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DDANKGIIRE | LRKTNYVENL | KEKSEGEASL | YEDRIITREK | DMRRVRDEPE | KVVKQWDHSE | DEKETDEDDE | AFGEALQSPA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SGKQSVEAGK | ARSDLGAVAK | GLSGELGTRS | GETGRKLLEA | GRRESREIYR | RPSGELEQRL | SGEFSRQEPE | ELKKLSEVGR |
| 490 | 500 | 510 | | | | | |
| REPEELGKTQ | FGEIGETKKT | GNEMEKEYE | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1482 | 1 | 619.9673 | -68.13 | 3 | 46.9 | 15.1 | 2 | 411-429 | K.ARSDLGAVAKGLSGELGTR.S | |

# Detailed Protein Report

## Protein 1067: mdm2-binding protein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21630257 | **Score:** | 15.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 102.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.8 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDRYLLLVIW | GEGKFPSAAS | REAEHGPEVS | SGEGTENQPD | FTAANVYHLL | KRSISASINP | EDSTFPACSV | GGIPGSKKWF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FAVQAIYGFY | QFCSSDWQEI | HFDTEKDKIE | DVLQTNIEEC | LGAVECFEEE | DSNSRESLSL | ADLYEEAAEN | LHQLSDKLPA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PGRAMVDIIL | LLSDKDPPKL | KDYLPTVGAL | KHLREWYSAK | ITIAGNHCEI | NCQKIAEYLS | ANVVSLEDLR | NVIDSKELWR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GKIQIWERKF | GFEISFPEFC | LKGVTLKNFS | TSNLNTDFLA | KKIIPSKDKN | ILPKVFHYYG | PALEFVQMIK | LSDLPSCYMS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DIEFELGLTN | STKQNSVLLL | EQISSLCSKV | GALFVLPCTI | SNILIPPPNQ | LSSRKWKEYI | AKKPKTISVP | DVEVKGECSS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YYLLLQGNGN | RRCKATLIHS | ANQINGSFAL | NLIHGKMKTK | TEEAKLSFPF | DLLSLPHFSG | EQIVQREKQL | ANVQVLALEE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CLKRRKLAKQ | PETVSVAELK | SLLVLTRKHF | LDYFDAVIPK | MILRKMDKIK | TFNILNDFSP | VEPNSSSLME | TNPLEWPERH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VLQNLETFEK | TKQKMRTGSL | PHSSEQLLGH | KEGPRDSITL | LDAKELLKYF | TSDGLPIGDL | QPLPIQKGEK | TFVLTPELSP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GKLQVLPFEK | ASVCHYHGIE | YCLDDRKALE | RDGGFSELQS | RLIRYETQTT | CTRESFPVPT | VLSPLPSPVV | SSDPGSVPDG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EVLQNELRTE | VSRLKRRSKD | LNCLYPRKRL | VKSESSESLL | SQTTGNSNHY | HHHVTSRKPQ | TERSLPVTCP | LVPIPSCETP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KLATKTSSGQ | KSMHESKTSR | QIKESRSQKH | TRILKEVVTE | TLKKHSITET | HECFTACSQR | LFEISKFYLK | DLKTSRGLFE |
| 890 | 900 | 910 | | | | | |
| EMKKTANNNA | VQVIDWVLEK | TSKK | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1646 | 1 | 1011.4579 | -81.06 | 3 | 50.8 | 15.0 | 2 | 215-240 | K.IAEYLSANVVSLEDLRNVIDSKELWR.G | |

# Detailed Protein Report

## Protein 1068: PREDICTED: serine protease 44 [Homo sapiens]

**Accession:** gi|530357996
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 15.0
**MW [kDa]:** 14.4
**pI:** 12.2
**Sequence Coverage [%]:** 9.2
**No. of unique Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530434688 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: serine protease 44 [Homo sapiens] |
| gi\|530373565 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: serine protease 44 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MASQSGSSLG | LLAWFLLLQP | WLEEARAGRV | GAQGGVALLF | PSALPSGPGG | QDPGASGWEP | PPVGAPGSPA | APQSRGNAVR |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | |
| PASVLLPSAC | GQRTSRITGG | LPAPDRKWPW | QVSLQTSNRH | ICGGSLIARH | WVLTAAHCIS | G | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1082 | 1 | 670.8357 | -47.72 | 2 | 43.6 | 15.0 | 1 | 94-106 | R.TSRITGGLPAPDR.K | |

# Detailed Protein Report

## Protein 1069: PREDICTED: ruvB-like 2 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530415520 | **Score:** | 15.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVGQLAARRA | AGVVLEMIRE | GKIAGRAVLI | AGQPGTGKTA | IAMGMAQALG | PDTPFTAIAG | SEIFSLEMSK | TEALTQAFRR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SIGVRIKEET | EIIEGEVVEI | QIDRPATGTG | SKVGKLTLKT | TEMETIYDLG | TKMIESLTKD | KVQAGDVITI | DKATGKISKL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GRSFTRARDY | DAMGSQTKFV | QCPDGELQKR | KEVVHTVSLH | EIDVINSRTQ | GFLALFSGDT | GEIKSEVREQ | INAKVAEWRE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EGKAEIIPGV | LFIDEVHMLD | IESFSFLNRA | LESDMAPVLI | MATNRGITRI | RGTSYQSPHG | IPIDLLDRLL | IVSTTPYSEK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DTKQILRIRC | EEEDVEMSED | AYTVLTRIGL | ETSLRYAIQL | ITAASLVCRK | RKGTEVQVDD | IKRVYSLFLD | ESRSTQYMKE |
| 410 | 420 | | | | | | |
| YQDAFLFNEL | KGETMDTS | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1247 | 1 | 419.0865 | -325.47 | 2 | 43.9 | 15.0 | 0 | 133-139 | K.MIESLTK.D | Oxidation: 1 |

# Detailed Protein Report

## Protein 1070: uncharacterized protein KIAA1751 [Homo sapiens]

**Accession:** gi|122937416
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 15.0
**MW [kDa]:** 86.9
**pI:** 5.3
**Sequence Coverage [%]:** 1.4
**No. of unique Peptides:** 1

## Quantitation

***WUP:QUP*** **Median:** 3.80 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEDDGSLLPE | DELLADALLL | EDERDELEDP | EFDIKCLLQE | AEDDVDPGHS | SSVKELDTDA | DKLKKKTAED | RTQAFHLRQN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LSALDKMHEE | QELFTEKMRG | ELRACRQRRD | LIDKQQEAVA | AEIATEEEAG | NMAAVGRLQA | VSRRLFAELE | NERDLQSRTE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AVLKESENTM | WHIEIQEGRL | EAFRTADREE | VEATGRRLQV | RAAEQLCREQ | EALGKVERNR | LLRIRKSLNT | QKELGLRHQK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LLEDARKNHK | VAVRFLKASL | GRIREQEKKE | EMECHEYMRR | RMDAVVALKG | SISANRDTLR | KFQAWDRAKA | ELAEQRVQAE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KKAILAQGRD | AFRHLVHQRR | RQELEAQKRA | FEEEQKLRKQ | EIISRILKEE | AEEEKRKKQH | PPTSARHRLT | LRDKTWNYIS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DFCKKTTVPT | NTYTLDYEAA | AGPGPSRLLE | VVSSELIQGD | PGASSEEETL | AEPEISGLWN | EDYKPYQVPK | EDVDRKPVGG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TKMDKDILER | TVERLRSRVV | HKQVVWGREF | QGRPFNSKPE | LLHFQDFDIG | KVYKKKITLV | NTTYTINYCK | LVGVEEHLRD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FIHVDFDPPG | PLSAGMSCEV | LVTFKPMINK | DLEGNISFLA | QTGEFSVPLK | CSTKKCSLSL | DKELIDFGSY | VVGETTSRTI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TLTNVGGLGT | TFKFLPASEP | CEMDDSQSAL | KLSSLLTYED | KSLYDKAATS | FSEQQLEGTE | SSQADMQSRK | ELEKLDKEQE |
| 730 | 740 | 750 | 760 | 770 | | | |
| EEQPAGEPGC | QAKPGWAGGE | GLRAAFQGAE | GPRGGLESRE | FS | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2144 | 1 | 687.4001 | 47.83 | 2 | 55.2 | 15.0 | 2 | 366-376 | R.ILKEEAEEEKR.K | | WUP:QUP 3.80 |

# Detailed Protein Report

## Protein 1071: cyclin-dependent kinase 5 activator 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4502737 | **Score:** | 15.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 5.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGTVLSLSPS | YRKATLFEDG | AATVGHYTAV | QNSKNAKDKN | LKRHSIISVL | PWKRIVAVSA | KKKNSKKVQP | NSSYQNNITH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LNNENLKKSL | SCANLSTFAQ | PPPAQPPAPP | ASQLSGSQTG | GSSSVKKAPH | PAVTSAGTPK | RVIVQASTSE | LLRCLGEFLC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RRCYRLKHLS | PTDPVLWLRS | VDRSLLLQGW | QDQGFITPAN | VVFLYMLCRD | VISSEVGSDH | ELQAVLLTCL | YLSYSYMGNE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | |
| ISYPLKPFLV | ESCKEAFWDR | CLSVINLMSS | KMLQINADPH | YFTQVFSDLK | NESGQEDKKR | LLLGLDR | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2666 | 1 | 945.9810 | -33.71 | 2 | 61.6 | 15.0 | 1 | 168-183 | K.HLSPTDPVLWLRSVDR.S | |

# Detailed Protein Report

## Protein 1072: GEM-interacting protein isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|573014822 | **Score:** | 15.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 103.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| | | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDAAEPGLPP | GPEGRKRYSD | IFRSLDNLEI | SLGNVTLEML | AGDPLLSEDP | EPDKTPTATV | TNEASCWSGP | SPEGPVPLTG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EELDLRLIRT | KGGVDAALEY | AKTWSRYAKE | LLAWTEKRAS | YELEFAKSTM | KIAEAGKVSI | QQQSHMPLQY | IYTLFLEHDL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SLGTLAMETV | AQQKRDYYQP | LAAKRTEIEK | WRKEFKEQWM | KEQKRMNEAV | QALRRAQLQY | VQRSEDLRAR | SQGSPEDSAP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QASPGPSKQQ | ERRRRSREEA | QAKAQEAEAL | YQACVREANA | RQQDLEIAKQ | RIVSHVRKLV | FQGDEVLRRV | TLSLFGLRGA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QAERGPRAFA | ALAECCAPFE | PGQRYQEFVR | ALRPEAPPPP | PPAFSFQEFL | PSLNSSPLDI | RKKLSGPLPP | RLDENSAEPG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PWEDPGTGWR | WQGPTPGSDV | DSVGGGSESR | SLDSPTSSPD | LGDGLENGLG | SPFGKWTLSS | AAQTHQLRRL | RGPAKCRECE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AFMVSGTECE | ECFLTCHKRC | LETLLILCGH | RRLPARTPLF | GVDFLQLPRD | FPEEVPFVVT | KCTAEIEHRA | LDVQGIYRVS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GSRVRVERLC | QAFENGRALV | ELSGNSPHDV | SSVLKRFLQE | LTEPVIPFHL | YDAFISLAKT | LHADPGDDPG | TPSPSPEVIR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SLKTLLVQLP | DSNYNTLRHL | VAHLFRVAAR | FMENKMSANN | LGIVFGPTLL | RPPDGPRAAS | AIPVTCLLDS | GHQAQLVEFL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| IVHYEQIFGM | DELPQATEPP | PQDSSPAPGP | LTTSSQPPPP | HLDPDSQPPV | LASDPGPDPQ | HHSTLEQHPT | ATPTEIPTPQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SDQREDVAED | TKDGGGEVSS | QGPEDSLLGT | QSRGHFSRQP | VKYPRGGVRP | VTHQLSSLAL | VASKLCEETP | ITSVPRGSLR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | |
| GRGPSPAAAS | PEGSPLRRTP | LPKHFEITQE | TARLLSKLDS | EAVPRATCCP | DVQPEEAEDH | L | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1688 | 1 | 745.8381 | -60.85 | 2 | 50.9 | 15.0 | 1 | 2-16 | M.DAAEPGLPPGPEGRK.R | |

# Detailed Protein Report

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## Protein 1073: toll-like receptor 9 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|8394456 | **Score:** | 14.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 115.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.45 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.23 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGFCRSALHP | LSLLVQAIML | AMTLALGTLP | AFLPCELQPH | GLVNCNWLFL | KSVPHFSMAA | PRGNVTSLSL | SSNRIHHLHD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SDFAHLPSLR | HLNLKWNCPP | VGLSPMHFPC | HMTIEPSTFL | AVPTLEELNL | SYNNIMTVPA | LPKSLISLSL | SHTNILMLDS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ASLAGLHALR | FLFMDGNCYY | KNPCRQALEV | APGALLGLGN | LTHLSLKYNN | LTVVPRNLPS | SLEYLLLSYN | RIVKLAPEDL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ANLTALRVLD | VGGNCRRCDH | APNPCMECPR | HFPQLHPDTF | SHLSRLEGLV | LKDSSLSWLN | ASWFRGLGNL | RVLDLSENFL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YKCITKTKAF | QGLTQLRKLN | LSFNYQKRVS | FAHLSLAPSF | GSLVALKELD | MHGIFFRSLD | ETTLRPLARL | PMLQTLRLQM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NFINQAQLGI | FRAFPGLRYV | DLSDNRISGA | SELTATMGEA | DGGEKVWLQP | GDLAPAPVDT | PSSEDFRPNC | STLNFTLDLS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RNNLVTVQPE | MFAQLSHLQC | LRLSHNCISQ | AVNGSQFLPL | TGLQVLDLSH | NKLDLYHEHS | FTELPRLEAL | DLSYNSQPFG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MQGVGHNFSF | VAHLRTLRHL | SLAHNNIHSQ | VSQQLCSTSL | RALDFSGNAL | GHMWAEGDLY | LHFFQGLSGL | IWLDLSQNRL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HTLLPQTLRN | LPKSLQVLRL | RDNYLAFFKW | WSLHFLPKLE | VLDLAGNQLK | ALTNGSLPAG | TRLRRLDVSC | NSISFVAPGF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| FSKAKELREL | NLSANALKTV | DHSWFGPLAS | ALQILDVSAN | PLHCACGAAF | MDFLLEVQAA | VPGLPSRVKC | GSPGQLQGLS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IFAQDLRLCL | DEALSWDCFA | LSLLAVALGL | GVPMLHHLCG | WDLWYCFHLC | LAWLPWRGRQ | SGRDEDALPY | DAFVVFDKTQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SAVADWVYNE | LRGQLEECRG | RWALRLCLEE | RDWLPGKTLF | ENLWASVYGS | RKTLFVLAHT | DRVSGLLRAS | FLLAQQRLLE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DRKDVVVLVI | LSPDGRRSRY | VRLRQRLCRQ | SVLLWPHQPS | GQRSFWAQLG | MALTRDNHHF | YNRNFCQGPT | AE |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1392 | 3 | 698.8594 | -48.59 | 2 | 45.8 | 14.9 | 0 | 235-247 | K.LAPEDLANLTALR.V | | WUP:QUP 1.23<br>QU:MU 1.45 |

# Detailed Protein Report

## Protein 1074: PREDICTED: androglobin isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578812976 | **Score:** | 14.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 189.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| | | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.47 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.80 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASKQTKKKE | VHRINSAHGS | DKSKDFYPFG | SNVQSGSTEQ | KKGKFPLWPE | WSEADINSEK | WDAGKGAKEK | DKTGKSPVFH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FFEDPEGKIE | LPPSLKIYSW | KRPQDILFSQ | TPVVVKNEIT | FDLFSANEHL | LCSELMRWII | SEIYAVWKIF | NGGILSNYFK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GTSGEPPLLP | WKPWEHIYSL | CKAVKGHMPL | FNSYGKYVVK | LYWMGCWRKI | TIDDFLPFDE | DNNLLLPATT | YEFELWPMLL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SKAIIKLANI | DIHVADRREL | GEFTVIHALT | GWLPEVISLH | PGYMDKVWEL | LKEILPEFKL | SDEASSESKI | AVLDSKLKEP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GKEGKEGKEI | KDGKEVKDVK | EFKPESSLTT | LKAPEKSDKV | PKEKADARDI | GKKRSKDGEK | EKFKFSLHGS | RPSSEVQYSV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QSLSDCSSAI | QTSHMVVYAT | FTPLYLFENK | IFSLEKMADS | AEKLREYGLS | HICSHPVLVT | RSRSCPLVAP | PKPPPLPPWK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LIRQKKETVI | TDEAQELIVK | KPERFLEISS | PFLNYRMTPF | TIPTEMHFVR | SLIKKGIPPG | SDLPSVSETD | ETATHSQTDL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SQITKATSQG | NTASQVILGK | GTDEQTDFGL | GDAHQSDGLN | LEREIVSQTT | ATQEKSQEEL | PTTNNSVSKE | IWLDFEDFCV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CFQNIYIFHK | PSSYCLNFQK | SEFKFSEERV | SYYLFVDSLK | PIELLVCFSA | LVRWGEYGAL | TKDSPPIEPG | LLTAETFSWK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SLKPGSLVLK | IHTYATKATV | VRLPVGRHML | LFNAYSPVGH | SIHICSMVSF | VIGDEHVVLP | NFEPESCRFT | EQSLLIMKAI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GNVIANFKDK | GKLSAALKDL | QTAHYPVPFH | DKELTAQHFR | VFHLSLWRLM | KKVQITKPPP | NFKFAFRAMV | LDLELLNSSL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EEVSLVEWLD | VKYCMPTSDK | EYSAEEVAAA | IKIQAMWRGT | YVRLLMKARI | PDTKENISVA | DTLQKVWAVL | EMNLEQYAVS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LLRLMFKSKC | KSLESYPCYQ | DEETKIAFAD | YTVTYQEQPP | NSWFIVFRET | FLVHQDMILV | PKVYTTLPIC | ILHIVNNDTM |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EQVPKVFQKV | VPYLYTKNKK | GYTFVAEAFT | GDTYVAASRW | KLRLIGSSAP | LPCLSRDSPC | NSFAIKEIRD | YYIPNDKKIL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| FRYSVKVLTP | QPATIQVRTS | KPDAFIKLQV | LENEETMVSS | TGKGQAIIPA | FHFLKSEKGL | SSQSSKHILS | FHSASKKEQE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VYVKKKAAQG | IQKSPKGRAV | SAIQDIGLPL | VEEETTSTPT | REDSSSTPLQ | NYKYIIQCSV | LYNSWPLTES | QLTFVQALKD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LKKSNTKAYG | ERHEELINLG | SPDSHTISEG | QKSSVTSKTT | RKGKEKSSEK | EKTAKEKQAP | RFEPQISTVH | PQQEDPNKPY |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| WILRLVTEHN | ESELFEVKKD | TERADEIRAM | KQAWETTEPG | RAIKASQARL | HYLSGFIKKT | SDAESPPISE | SQTKPKEEVE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| TAARGVKEPN | SKNSAGSESK | EMTQTGSGSA | VWKKWQLTKG | LRDVAKSTSS | ESGGVSSPGK | EEREQSTRKE | NIQTGPRTRS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PTILETSPRL | IRKALEFMDL | SQYVRKTDTD | PLLQTDELNQ | QQAMQKAEEI | HQFRQHRTRV | LSIRNIDQEE | RLKLKDEVLD |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | |
| MYKEMQDSLD | EARQKIFDIR | EEYRNKLLEA | EHLKLEALSA | QEAAMKLETE | KMTPAPDTQK | KKKGKKK | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2431 | 1 | 590.4218 | 113.13 | 3 | 60.3 | 14.9 | 2 | 849-863 | R.LMKKVQITKPPPNFK.F |  | WUP:QUP 1.80<br>QU:MU 0.47 |

# Detailed Protein Report

## Protein 1075: PREDICTED: zinc finger protein 608 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530380059 | **Score:** | 14.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 133.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.48 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.29 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQLEGKGQLD | PIQTVDPLFT | VPAPPPPISS | SLTPQILPSY | FSPSSSNIAA | PVEQLLVRTR | SVGVNTCEVG | VVTEPECLGP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CEPGTSVNLE | GIVWHETEEG | VLVVNVTWRN | KTYVGTLLDC | TKHDWAPPRF | CESPTSDLEM | RGGRGRGKRA | RSAAAAPGSE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ASFTESRGLQ | NKNRGGANGK | GRRGSLNASG | RRTPPNCAAE | DIKASPSSTN | KRKNKPPMEL | DLNSSSEDNK | PGKRVRTNSR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| STPTTPQGKP | ETTFLDQGCS | SPVLIDCPHP | NCNKKYKHIN | GLRYHQAHAH | LDPENKLEFE | PDSEDKISDC | EEGLSNVALE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CSEPSTSVSA | YDQLKAPASP | GAGNPPGTPK | GKRELMSNGP | GSIIGAKAGK | NSGKKKGLNN | ELNNLPVISN | MTAALDSCSA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ADGSLAAEMP | KLEAEGLIDK | KNLGDKEKGK | KATNCKTDKN | LSKLKSARPI | APAPAPTPPQ | LIAIPTATFT | TTTTGTIPGL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PSLTTTVVQA | TPKSPPLKPI | QPKPTIMGEP | ITVNPALVSL | KDKKKKEKRK | LKDKEGKETG | SPKMDAKLGK | LEDSKGASKD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LPGHFLKDHL | NKNEGLANGL | SESQESRMAS | IKAEADKVYT | FTDNAPSPSI | GSASRLECST | LVNGQAPMAP | LHVLTQNGAE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SSAAKTSSPA | YSDISDAADD | GGSDSRSEGM | RSKASSPSDI | ISSKDSVVKG | HSSTTAQSSQ | LKESHSPYYH | SYDPYYSPSY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| MHPGQVGAPA | AGNSGSTQGM | KIKKESEEDA | EKKDKAEQLD | SKKVDHNSAS | LQPQHQSVIT | QRHPALAQSL | YYGQYAYGLY |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| MDQKSLMATS | PAYRQQYEKY | YEDQRLAEQK | MAQTGRGDCE | RKSELPLKEL | GKEETKQKNM | PSATISKAPS | TPEPNKNHSK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LGPSVPNKTE | ETGKSQLLSN | HQQQLQADSF | KAKQMENHQL | IKEAVEMKSV | MDSMKQTGVD | PTSRFKQDPD | SRTWHHYVYQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PKYLDQQKSE | ELDREKKLKE | DSPRKTPNKE | SGVPSLPVSL | TSIKEEPKEA | KHPDSQSMEE | SKLKNDDRKT | PVNWKDSRGT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RVAVSSPMSQ | HQSYIQYLHA | YPYPQMYDPS | HPAYRAVSPV | LMHSYPGAYL | SPGFHYPVYG | KMSGREETEK | VNTSPSVNTK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TTTESKALDL | LQQHANQYRS | KSPAPVEKAT | AEREREAERE | RDRHSPFGQR | HLHTHHHTHV | GMGYPLIPGQ | YDPFQGLTSA |
| 1210 | 1220 | 1230 | | | | | |
| ALVASQQVAA | QASASGMFPG | QRRE | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 131 | 2 | 635.8171 | -6.20 | 2 | 30.6 | 14.9 | 0 | 112-122 | K.TYVGTLLDCTK.H | Carbamidomethyl: 9 | WUP:QUP 0.29<br>QU:MU 2.48 |

# Detailed Protein Report

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## Protein 1076: nuclear body protein SP140 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|52487277 | **Score:** | 14.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 20.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| | | **Sequence Coverage [%]:** | 7.6 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

***WUP:QUP*** **Median:** 4.90 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MAQQGQQGQM ASGDSNLNFR MVAEIQNVEG QNLQEQVCPE PIFRFFRENK VEIASAITRP FPFLMGLRDR SFISEQMYEH
         90        100        110        120        130        140        150        160
FQEAFRNLVP VTRVMYCVLS ELEKTFGWSH LEALFSRINL MAYPDLNEIY RSFQNENLSS SAVLCQLVSP NKDWRSHEES
        170        180
LAHTGTLRRS CM
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1971 | 2 | 719.2914 | -92.19 | 2 | 54.5 | 14.9 | 0 | 156-168 | R.SHEESLAHTGTLR.R | | WUP:QUP 4.90 |

# Detailed Protein Report

## Protein 1077: prolyl 3-hydroxylase 3 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|28466983 | **Score:** | 14.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 81.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MLRLLRPLLL LLLLPPPGSP EPPGLTQLSP GAPPQAPDLL YADGLRAYAA GAWAPAVALL REALRSQAAL GRVRLDCGAS
        90        100        110        120        130        140        150        160
CAADPGAALP AVLLGAPEPD SGPGPTQGSW ERQLLRAALR RADCLTQCAA RRLGPGGAAR LRVGSALRDA FRRREPYNYL
       170        180        190        200        210        220        230        240
QRAYYQLKKL DLAAAAAHTF FVANPMHLQM REDMAKYRRM SGVRPQSFRD LETPPHWAAY DTGLELLGRQ EAGLALPRLE
       250        260        270        280        290        300        310        320
EALQGSLAQM ESCRADCEGP EEQQGAEEEE DGAASQGGLY EAIAGHWIQV LQCRQRCVGE TATRPGRSFP VPDFLPNQLR
       330        340        350        360        370        380        390        400
RLHEAHAQVG NLSQAIENVL SVLLFYPEDE AAKRALNQYQ AQLGEPRPGL GPREDIQRFI LRSLGEKRQL YYAMEHLGTS
       410        420        430        440        450        460        470        480
FKDPDPWTPA ALIPEALREK LREDQEKRPW DHEPVKPKPL TYWKDVLLLE GVTLTQDSRQ LNGSERAVLD GLLTPAECGV
       490        500        510        520        530        540        550        560
LLQLAKDAAG AGARSGYRGR RSPHTPHERF EGLTVLKAAQ LARAGTVGSQ GAKLLLEVSE RVRTLTQAYF SPERPLHLSF
       570        580        590        600        610        620        630        640
THLVCRSAIE GEQEQRMDLS HPVHADNCVL DPDTGECWRE PPAYTYRDYS GLLYLNDDFQ GGDLFFTEPN ALTVTARVRP
       650        660        670        680        690        700        710        720
RCGRLVAFSS GVENPHGVWA VTRGRRCALA LWHTWAPEHR EQEWIEAKEL LQESQEEEEE EEEEMPSKDP SPEPPSRRHQ
       730        740
RVQDKTGRAP RVREEL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1015 | 1 | 967.4606 | -122.98 | 1 | 42.3 | 14.9 | 1 | 133-142 | R.LGPGGAARLR.V | |

# Detailed Protein Report

## Protein 1078: granulysin isoform 519 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|157502222 | **Score:** | 14.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 14.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 14.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MEGLVFSRLS PEYYDLARAH LRDEEKSCPC LAQEGPQGDL LTKTQELGRD YRTCLTIVQK LKKMVDKPTQ RSVSNAATRV
        90        100        110        120        130        140
CRTGRSRWRD VCRNFMRRYQ SRVTQGLVAG ETAQQICEDL RLCIPSTGPL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1089 | 1 | 712.4579 | 130.18 | 3 | 43.7 | 14.8 | 2 | 64-82 | K.MVDKPTQRSVSNAATRVCR.T | Oxidation: 1 |

BRUKER

# Detailed Protein Report

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## Protein 1079: olfactory receptor 56A1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|284172508 | **Score:** | 14.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 35.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 9.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MIQPMASPSN | SSTVPVSEFL | LICFPNFQSW | QHWLSLPLSL | LFLLAMGANT | TLLITIQLEA | SLHQPLYYLL | SLLSLLDIVL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CLTVIPKVLA | IFWYDLRSIS | FPACFLQMFI | MNSFLPMESC | TFMVMAYDRY | VAICHPLRYP | SIITNQFVAK | ASVFIVVRNA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLTAPIPILT | SLLHYCGENV | IENCICANLS | VSRLSCDNFT | LNRIYQFVAG | WTLLGSDLFL | IFLSYTFILR | AVLRFKAEGA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AVKALSTCGS | HFILILFFST | ILLVVVLTNV | ARKKVPMDIL | ILLNVLHHLI | PPALNPIVYG | VRTKEIKQGI | QKLLQRGR |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2787 | 1 | 1086.6653 | 15.08 | 3 | 65.2 | 14.8 | 1 | 274-302 | K.KVPMDILILLNVLHHLIPPALNPIVYGVR.T | |

# Detailed Protein Report

## Protein 1080: PREDICTED: choline transporter-like protein 3 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530361747 | **Score:** | 14.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 64.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MHCLGAEYLV | SAEGAPRQRE | WRPQIYRKCT | DTAWLFLFFL | FWTGLVFIMG | YSVVAGAAGR | LLFGYDSFGN | MCGKKNSPVE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GAPLSGQDMT | LKKHVFFMNS | CNLEVKGTQL | NRMALCVSNC | PEEQLDSLEE | VQFFANTSGS | FLCVYSLNSF | NYTHSPKADS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LCPRLPVPPS | KSFPLFNRCV | PQTPECYSLF | ASVLINDVDT | LHRILSGIMS | GRDTILGLCI | LALALSLAMM | FTFRFITTLL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VHIFISLVIL | GLLFVCGVLW | WLYYDYTNDL | SIELDTEREN | MKCVLGFAIV | STGITAVLLV | LIFVLRKRIK | LTVELFQITN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KAISSAPFLL | FQPLWTFAIL | IFFWVLWVAV | LLSLGTAGAA | QVMEGGQVEY | KPLSGIRYMW | SYHLIGLIWT | SEFILACQQM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TIAGAVVTCY | FNRSKNDPPD | HPILSSLSIL | FFYHQGTVVK | GSFLISVVRI | PRIIVMYMQN | ALKEQQHGAL | SRYLFRCCYC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CFWCLDKYLL | HLNQNAYTTT | AINGTDFCTS | AKDAFKILSK | NSSHFTSINC | FGDFIIFLGK | SFVKRSNKLN | NARAQQDKHS |
| 570 | 580 | | | | | | |
| LRNEEGTELQ | AIVR | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2747 | 1 | 1044.5342 | 23.81 | 2 | 64.7 | 14.8 | 1 | 1-19 | -.MHCLGAEYLVSAEGAPRQR.E | |

# Detailed Protein Report

**Protein 1081:** **ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|7242140 | **Score:** | 14.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPSCGACTCG | AAAVRLITSS | LASAQRGISG | GRIHMSVLGR | LGTFETQILQ | RAPLRSFTET | PAYFASKDGI | SKDGSGDGNK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KSASEGSSKK | SGSGNSGKGG | NQLRCPKCGD | LCTHVETFVS | STRFVKCEKC | HHFFVVLSEA | DSKKSIIKEP | ESAAEAVKLA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FQQKPPPPPK | KIYNYLDKYV | VGQSFAKKVL | SVAVYNHYKR | IYNNIPANLR | QQAEVEKQTS | LTPRELEIRR | REDEYRFTKL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LQIAGISPHG | NALGASMQQQ | VNQQIPQEKR | GGEVLDSSHD | DIKLEKSNIL | LLGPTGSGKT | LLAQTLAKCL | DVPFAICDCT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TLTQAGYVGE | DIESVIAKLL | QDANYNVEKA | QQGIVFLDEV | DKIGSVPGIH | QLRDVGGEGV | QQGLLKLLEG | TIVNVPEKNS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RKLRGETVQV | DTTNILFVAS | GAFNGLDRII | SRRKNEKYLG | FGTPSNLGKG | RRAAAAADLA | NRSGESNTHQ | DIEEKDRLLR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HVEARDLIEF | GMIPEFVGRL | PVVVPLHSLD | EKTLVQILTE | PRNAVIPQYQ | ALFSMDKCEL | NVTEDALKAI | ARLALERKTG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ARGLRSIMEK | LLLEPMFEVP | NSDIVCVEVD | KEVVEGKKEP | GYIRAPTKES | SEEEYDSGVE | EEGWPRQADA | ANS |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 524 | 1 | 817.7754 | 49.53 | 3 | 35.0 | 14.8 | 1 | 2-26 | M.PSCGACTCGAAAVRLITSSLASAQR.G | Carbamidomethyl: 3 |

# Detailed Protein Report

## Protein 1082: PREDICTED: serine/threonine-protein phosphatase with EF-hands 2 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578809184 | **Score:** | 14.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGSGTSTQHH | FAFQNAERAF | KAAALIQRWY | RRYVARLEMR | RRCTWSIFQS | IEYAGQQDQV | KLHDFFSYLM | DHFIPSSHND |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RDFLTRIFTE | DRFAQDSEMK | KCSDYESIEV | PDSYTGPRLS | FPLLPDHATA | LVEAFRLKQQ | LHARYVLNLL | YETKKHLVQL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PNINRVSTCY | SEEITVCGDL | HGQLDDLIFI | FYKNGLPSPE | RSYVFNGDFV | DRGKDSVEIL | MILFAFMLVY | PKEFHLNRGN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HEDHMVNLRY | GFTKEVMNKY | KVHGKEILRT | LQDVFCWLPL | ATLIDEKVLI | LHGGVSDITD | LELLDKIERS | KIVSTMRCKT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RQKSEKQMEE | KRRANQKSSA | QGPIPWFLPE | SRSLPSSPLR | LGSYKAQKTS | RSSSIPCSGS | LDGRELSRQV | RSSVELELER |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CRQQAGLLVT | GEKEEPSRSA | SEADSEAGEL | RKPTQEEWRQ | VVDILWSDPM | AQEGCKANTI | RGGGCYFGPD | VTQQLLQKYN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| MQFLIRSHEC | KPEGYEFCHN | RKVLTIFSAS | NYYEVGSNRG | AYVKLGPALT | PHIVQYQANK | VTHTLTMRQR | ISRVEESALR |
| 570 | 580 | 590 | 600 | | | | |
| ALREKLFAHS | SDLLSEFKKH | DADKVGLASS | QLCYYQQK | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2068 | 1 | 946.8198 | -78.17 | 2 | 55.7 | 14.8 | 0 | 487-501 | R.SHECKPEGYEFCHNR.K | Carbamidomethyl: 4 |

# Detailed Protein Report

## Protein 1083: glycolipid transfer protein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|7705987 | **Score:** | 14.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 23.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.7 |
| | | **Sequence Coverage [%]:** | 7.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MALLAEHLLK | PLPADKQIET | GPFLEAVSHL | PPFFDCLGSP | VFTPIKADIS | GNITKIKAVY | DTNPAKFRTL | QNILEVEKEM |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| YGAEWPKVGA | TLALMWLKRG | LRFIQVFLQS | ICDGERDENH | PNLIRVNATK | AYEMALKKYH | GWIVQKIFQA | ALYAAPYKSD |
| **170** | **180** | **190** | **200** | **210** | | | |
| FLKALSKGQN | VTEEECLEKI | RLFLVNYTAT | IDVIYEMYTQ | MNAELNYKV | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1016 | 1 | 983.1678 | 145.88 | 2 | 42.3 | 14.8 | 2 | 131-146 | K.AYEMALKKYHGWIVQK.I | |

# Detailed Protein Report

## Protein 1084: uncharacterized protein C11orf94 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|148229481 | **Score:** | 14.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 10.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 15.3 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MVLAMLGALH PRAGLSLFLH LILAVALLRS QPLRSQRSVP EAFSAPLELS QPLSGLVDDY GILPKHPRPR GPRPLLSRAQ
        90        100
QRKRDGPDLA EYYYDAHL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2213 | 1 | 899.3247 | -92.16 | 2 | 57.5 | 14.8 | 1 | 84-98 | K.RDGPDLAEYYYDAHL.- | |

# Detailed Protein Report

## Protein 1085: long-chain-fatty-acid--CoA ligase 5 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|42794758 | **Score:** | 14.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 75.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|42794760 | refseq_human (refseq_human_20140103.fasta) | long-chain-fatty-acid--CoA ligase 5 isoform b [Homo sapiens] |

```
         10         20         30         40         50         60         70         80
MLFIFNFLFS PLPTPALICI LTFGAAIFLW LITRPQPVLP LLDLNNQSVG IEGGARKGVS QKNNDLTSCC FSDAKTMYEV
         90        100        110        120        130        140        150        160
FQRGLAVSDN GPCLGYRKPN QPYRWLSYKQ VSDRAEYLGS CLLHKGYKSS PDQFVGIFAQ NRPEWIISEL ACYTYSMVAV
        170        180        190        200        210        220        230        240
PLYDTLGPEA IVHIVNKADI AMVICDTPQK ALVLIGNVEK GFTPSLKVII LMDPFDDDLK QRGEKSGIEI LSLYDAENLG
        250        260        270        280        290        300        310        320
KEHFRKPVPP SPEDLSVICF TSGTTGDPKG AMITHQNIVS NAAAFLKCVE HAYEPTPDDV AISYLPLAHM FERIVQAVVY
        330        340        350        360        370        380        390        400
SCGARVGFFQ GDIRLLADDM KTLKPTLFPA VPRLLNRIYD KVQNEAKTPL KKFLLKLAVS SKFKELQKGI IRHDSFWDKL
        410        420        430        440        450        460        470        480
IFAKIQDSLG GRVRVIVTGA APMSTSVMTF FRAAMGCQVY EAYGQTECTG GCTFTLPGDW TSGHVGVPLA CNYVKLEDVA
        490        500        510        520        530        540        550        560
DMNYFTVNNE GEVCIKGTNV FKGYLKDPEK TQEALDSDGW LHTGDIGRWL PNGTLKIIDR KKNIFKLAQG EYIAPEKIEN
        570        580        590        600        610        620        630        640
IYNRSQPVLQ IFVHGESLRS SLVGVVVPDT DVLPSFAAKL GVKGSFEELC QNQVVREAIL EDLQKIGKES GLKTFEQVKA
        650        660        670        680        690
IFLHPEPFSI ENGLLTPTLK AKRGELSKYF RTQIDSLYEH IQD
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1866 | 1 | 938.3231 | -159.47 | 2 | 53.7 | 14.8 | 1 | 110-125 | K.QVSDRAEYLGSCLLHK.G | Carbamidomethyl: 12 |

# Detailed Protein Report

**Protein 1086:** **PREDICTED: phosphorylase b kinase gamma catalytic chain, liver/testis isoform isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530408225 | **Score:** | 14.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.83 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.53 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578828573 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: phosphorylase b kinase gamma catalytic chain, liver/testis isoform isoform X4 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MRKGELFDYL | TEKVALSEKE | TRSIMRSLLE | AVSFLHANNI | VHRDLKPENI | LLDDNMQIRL | SDFGFSCHLE | PGEKLRELCG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TPGYLAPEIL | KCSMDETHPG | YGKEVDLLFP | SWACGVILFT | LLAGSPPFWH | RRQILMLRMI | MEGQYQFSSP | EWDDRSSTVK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DLISRLLQVD | PEARLTAEQA | LQHPFFERCE | GSQPWNLTPR | QRFRVAVWTV | LAAGRVALST | HRVRPLTKNA | LLRDPYALRS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | |
| VRHLIDNCAF | RLYGHWVKKG | EQQNRAALFQ | HRPPGPFPIM | GPEEEGDSAA | ITEDEAVLVL | G | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 258 | 1 | 512.5885 | -45.54 | 3 | 33.2 | 14.8 | 2 | 14-26 | K.VALSEKETRSIMR.S | Oxidation: 12 | QU:MU 0.83<br>WUP:QUP 1.53 |

# Detailed Protein Report

**Protein 1087:** **mediator of RNA polymerase II transcription subunit 6 isoform 2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|42544155 | **Score:** | 14.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 28.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| | | **Sequence Coverage [%]:** | 6.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAAVDIRDNL | LGISWVDSSW | IPILNSGSVL | DYFSERSNPF | YDRTCNNEVV | KMQRLTLEHL | NQMVGIEYIL | LHAQEPILFI |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| IRKQQRQSPA | QVIPLADYYI | IAGVIYQAPD | LGSVINSRVL | TAVHGIQSAF | DEAMSYCRYH | PSKGYWWHFK | DHEEQDKVRP |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| KAKRKEEPSS | IFQRQRVDAL | LLDLRQKFPP | KFVQLKPGEK | PVPVDQTKKE | AEPIPETVKP | EEKETTKNVQ | QTVSAKGPPE |
| **250** | | | | | | | |
| KRMRLQ | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1210 | 1 | 955.6887 | 154.62 | 2 | 44.7 | 14.8 | 0 | 192-208 | K.FVQLKPGEKPVPVDQTK.K | |

# Detailed Protein Report

## Protein 1088: PREDICTED: WD repeat-containing protein 88 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578833944 | **Score:** | 14.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 0.61 | **CV:** 0.00 % | **No. of Peptides:** 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASPPRCSPT | AHDRECKLPP | PSAPASEYCP | GKLSWGTMAR | ALGRFKLSIP | HTHLLATLDP | LALDREPPPH | LLPEKHQVPE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KLIWGDQDPL | SKIPFKILSG | HEHAVSTCHF | CVDDTKLLSG | SYDCTVKLWD | PVDGSVVRDF | EHRPKAPVVE | CSITGDSSRV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IAASYDKTVR | AWDLETGKLL | WKVRYDTFIV | SCKFSPDGKY | VVSGFDVDHG | ICIMDAENIT | TVSVIKDHHT | RSITSCCFDP |
| 250 | 260 | 270 | 280 | | | | |
| DSQRVASVSL | DRCIKIWDVT | SQATLLTITK | LFSHFWRV | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1628 | 1 | 882.4156 | -3.95 | 2 | 48.7 | 14.8 | 1 | 185-199 | R.YDTFIVSCKFSPDGK.Y | Carbamidomethyl: 8 | QU:MU 0.61 |

# Detailed Protein Report

## Protein 1089: PREDICTED: coiled-coil domain-containing protein 114 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530417580 | **Score:** | 14.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 52.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGLLRERAEK | EEAQSEMEAQ | VLQRQILHLE | QLHHFLKLKN | NDRQPDPDVL | EKREKQAGEV | AEGVWKTSQE | RLVLCYEDAL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NKLSQLMGES | DPDLLVQKYL | EIEERNFAEF | NFINEQNLEL | EHVQEEIKEM | QEALVSARAS | KDDQHLLQEQ | QQKVLQQRMD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KVHSEAERLE | ARFQDVRGQL | EKLKADIQLL | FTKAHCDSSM | IDDLLGVKTS | MGDRDMGLFL | SLIEKRLVEL | LTVQAFLHAQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SFTSLADAAL | LVLGQSLEDL | PKKMAPLQPP | DTLEDPPGFE | ASDDYPMSRE | ELLSQVEKLV | ELQEQAEAQR | QKDLAAAAAK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LDGTLSVDLA | STQRAGSSTV | LVPTRHPHAI | PGSILSHKTS | RDRGSLGHVT | FGGLSSSTGH | LPSHITHGDP | NTGHVTFGST |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SASSGGHVTF | RPVSASSYLG | STGYVGSSRG | GENTEGGVES | GGTASDSSGG | LGSSRDHVSS | TGPASSTGPG | SSTSKDSRG |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 188 | 1 | 793.9104 | -9.49 | 2 | 32.3 | 14.8 | 2 | 53-66 | K.REKQAGEVAEGVWK.T | |

# Detailed Protein Report

## Protein 1090: PREDICTED: keratin, type I cuticular Ha1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530412192 | **Score:** | 14.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 42.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.68 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530431086 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: keratin, type I cuticular Ha1 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPYNFCLPSL | SCRTSCSSRP | CVPPSCHSCT | LPGACNIPAN | VSNCNWFCEG | SFNGSEKETM | QFLNDRLASY | LEKVRQLERD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NAELENLIRE | RSQQQEPLLC | PSYQSYFKTI | EELQQKILCT | KSENARLVVQ | IDNAKLAADD | FRTKYQTELS | LRQLVESDIN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GLRRILDELT | LCKSDLEAQV | ESLKEELLCL | KSNHEQEVNT | LRCQLGDRLN | VEVDAAPTVD | LNRVLNETRS | QYEALVETNR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| REVEQWFTTQ | TEELNKQVVS | SSEQLQSYQA | EIIELRRTVN | ALEIELQAQH | NLRDSLENTL | TESEARYSSQ | LSQVQSLITN |
| 330 | 340 | 350 | 360 | 370 | | | |
| VESQLAEIRS | DLERQNQEYQ | VLLDVRARLE | CEINTYRSLL | ESEDCK | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 881 | 1 | 512.1602 | -149.56 | 2 | 39.4 | 14.7 | 0 | 358-366 | R.SLLESEDCK.- | | QU:MU 1.68 |

# Detailed Protein Report

## Protein 1091: guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|20357529 | **Score:** | 14.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 37.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 5.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSELEQLRQE | AEQLRNQIRD | ARKACGDSTL | TQITAGLDPV | GRIQMRTRRT | LRGHLAKIYA | MHWGTDSRLL | VSASQDGKLI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IWDSYTTNKV | HAIPLRSSWV | MTCAYAPSGN | FVACGGLDNI | CSIYSLKTRE | GNVRVSRELP | GHTGYLSCCR | FLDDNQIITS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SGDTTCALWD | IETGQQTVGF | AGHSGDVMSL | SLAPDGRTFV | SGACDASIKL | WDVRDSMCRQ | TFIGHESDIN | AVAFFPNGYA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FTTGSDDATC | RLFDLRADQE | LLMYSHDNII | CGITSVAFSR | SGRLLLAGYD | DFNCNIWDAM | KGDRAGVLAG | HDNRVSCLGV |
| 330 | 340 | 350 | | | | | |
| TDDGMAVATG | SWDSFLKIWN | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2534 | 1 | 1051.5171 | 26.06 | 2 | 60.0 | 14.7 | 0 | 284-301 | R.LLLAGYDDFNCNIWDAMK.G | |

# Detailed Protein Report

## Protein 1092: melanoma-associated antigen C3 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|20162568 | **Score:** | 14.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 71.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLLPCHWVLD | ATFSDGSLGQ | WVKNTCATYA | LSPVVLPPQP | QPRKKATDKD | YSAFHLGHLR | EVRLFLRGGT | SDQRMDSLVL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CPTYFKLWRT | LSGSPGLQLS | DLHFGSQPEG | KFSLRRAVSV | KQREEPQDWP | LNEKRTLWKD | SDLPTWRRGT | GYTLSLPAVS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PGKRLWGEKA | GSLPESEPLF | TYTLDEKVDK | LVQFLLLKYQ | AKEPLTRAEM | QMNVINTYTG | YFPMIFRKAR | EFIEILFGIS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LTEVDPDHFY | VFVNTLDLTC | EGSLSDEQGM | PQNRLLILIL | SVIFIKGNCA | SEEVIWEVLN | AIGPWSALAG | FADVLSRLAL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WESEGPEAFC | EESGLRSAEG | SVLDLANPQG | LAGHRQEDGR | RGLTEASPQQ | KKGGEDEDMP | AAGMPPLPQS | PPEIPPQGPP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KISPQGPPQS | PPQSPLDSCS | SPLLWTRLDE | ESSSEEEDTA | TWHALPESES | LPRYALDEKV | AELVQFLLLK | YQTKEPVTKA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EMLTTVIKKY | KDYFPMIFGK | AHEFIELIFG | IALTDMDPDN | HSYFFEDTLD | LTYEGSLIDD | QGMPKNCLLI | LILSMIFIKG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SCVPEEVIWE | VLSAIGPIQR | PAREVLEFLS | KLSSIIPSAF | PSWYMDALKD | MEDRAQAIID | TTDDATAMAS | ASPSVMSTNF |
| 650 | | | | | | | |
| CPE | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2527 | 1 | 913.0731 | 131.56 | 2 | 62.2 | 14.7 | 2 | 122-135 | K.QREEPQDWPLNEKR.T | |

# Detailed Protein Report

## **Protein 1093:** PREDICTED: uncharacterized protein CXorf65 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530421697 | **Score:** | 14.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 18.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.1 |
| | | **Sequence Coverage [%]:** | 8.8 |
| | | **No. of unique Peptides:** | 1 |

```
         10         20         30         40         50         60         70         80
MFIFIKHGDN QQFLVNTNCA VVVLLYYIRS KVKLPKTNTI DLCEQTGKMK MLFLMKPNHA EYASKYLTAR STYYVCKVER
         90        100        110        120        130        140        150        160
GPPVALRIQC DALERRRIQM LKMKEAKKVV IIEPPASVPS KQSGRSDKKK STRKSPTFRN RPDFRKNKGR QLNKTTKQKK
        170
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2029 | 1 | 732.3134 | -180.02 | 2 | 53.8 | 14.7 | 1 | 108-121 | K.KVVIIEPPASVPSK.Q | |

# Detailed Protein Report

## Protein 1094: sodium/potassium-transporting ATPase subunit alpha-2 proprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4502271 | **Score:** | 14.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 112.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 2.96 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGRGAGREYS | PAATTAENGG | GKKKQKEKEL | DELKKEVAMD | DHKLSLDELG | RKYQVDLSKG | LTNQRAQDVL | ARDGPNALTP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PPTTPEWVKF | CRQLFGGFSI | LLWIGAILCF | LAYGIQAAME | DEPSNDNLYL | GVVLAAVVIV | TGCFSYYQEA | KSSKIMDSFK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NMVPQQALVI | REGEKMQINA | EEVVVGDLVE | VKGGDRVPAD | LRIISSHGCK | VDNSSLTGES | EPQTRSPEFT | HENPLETRNI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CFFSTNCVEG | TARGIVIATG | DRTVMGRIAT | LASGLEVGRT | PIAMEIEHFI | QLITGVAVFL | GVSFFVLSLI | LGYSWLEAVI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FLIGIIVANV | PEGLLATVTV | CLTLTAKRMA | RKNCLVKNLE | AVETLGSTST | ICSDKTGTLT | QNRMTVAHMW | FDNQIHEADT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TEDQSGATFD | KRSPTWTALS | RIAGLCNRAV | FKAGQENISV | SKRDTAGDAS | ESALLKCIEL | SCGSVRKMRD | RNPKVAEIPF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NSTNKYQLSI | HEREDSPQSH | VLVMKGAPER | ILDRCSTILV | QGKEIPLDKE | MQDAFQNAYM | ELGGLGERVL | GFCQLNLPSG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KFPRGFKFDT | DELNFPTEKL | CFVGLMSMID | PPRAAVPDAV | GKCRSAGIKV | IMVTGDHPIT | AKAIAKGVGI | ISEGNETVED |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IAARLNIPMS | QVNPREAKAC | VVHGSDLKDM | TSEQLDEILK | NHTEIVFART | SPQQKLIIVE | GCQRQGAIVA | VTGDGVNDSP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ALKKADIGIA | MGISGSDVSK | QAADMILLDD | NFASIVTGVE | EGRLIFDNLK | KSIAYTLTSN | IPEITPFLLF | IIANIPLPLG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TVTILCIDLG | TDMVPAISLA | YEAAESDIMK | RQPRNSQTDK | LVNERLISMA | YGQIGMIQAL | GGFFTYFVIL | AENGFLPSRL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LGIRLDWDDR | TMNDLEDSYG | QEWTYEQRKV | VEFTCHTAFF | ASIVVVQWAD | LIICKTRRNS | VFQQGMKNKI | LIFGLLEETA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | |
| LAAFLSYCPG | MGVALRMYPL | KVTWWFCAFP | YSLLIFIYDE | VRKLILRRYP | GGWVEKETYY | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2397 | 1 | 805.8341 | -70.08 | 2 | 60.4 | 14.7 | 0 | 580-593 | K.LCFVGLMSMIDPPR.A | Oxidation: 7, 9 | WUP:QUP 2.96 |

**BRUKER**

# Detailed Protein Report

## Protein 1095: BTB/POZ domain-containing protein 9 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|151108435 | **Score:** | 14.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 61.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| | | **Sequence Coverage [%]:** | 4.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRESQPEAEI | PLQDTTAEAF | TMLLKYIYTG | RATLTDEKEE | VLLDFLSLAH | KYGFPELEDS | TSEYLCTILN | IQNVCMTFDV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ASLYSLPKLT | CMCCMFMDRN | AQEVLSSEGF | LSLSKTALLN | IVLRDSFAAP | EKDIFLALLN | WCKHNSKENH | AEIMQAVRLP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LMSLTELLNV | VRPSGLLSPD | AILDAIKVRS | ESRDMDLNYR | GMLIPEENIA | TMKYGAQVVK | GELKSALLDG | DTQNYDLDHG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FSRHPIDDDC | RSGIEIKLGQ | PSIINHIRIL | LWDRDSRSYS | YFIEVSMDEL | DWVRVIDHSQ | YLCRSWQKLY | FPARVCRYIR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IVGTHNTVNK | IFHIVAFECM | FTNKTFTLEK | GLIVPMENVA | TIADCASVIE | GVSRSRNALL | NGDTKNYDWD | SGYTCHQLGS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GAIVVQLAQP | YMIGSIRLLL | WDCDDRSYSY | YVEVSTNQQQ | WTMVADRTKV | SCKSWQSVTF | ERQPASFIRI | VGTHNTANEV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | |
| FHCVHFECPE | QQSSQKEENS | EESGTGDTSL | AGQQLDSHAL | RAPSGSSLPS | SPGSNSRSPN | RQHQ | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2400 | 1 | 938.4644 | 18.43 | 3 | 59.9 | 14.7 | 2 | 190-213 | R.SESRDMDLNYRGMLIPEENIATMK.Y | |

# Detailed Protein Report

## Protein 1096: PREDICTED: patatin-like phospholipase domain-containing protein 7 isoform X7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530426740 | **Score:** | 14.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 81.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEEEKDDSPQ | ADFCLGTALH | SWGLWFTEEG | SPSTMLTGIA | VGALLALALV | GVLILFMFRR | LRQFRQAQPT | PQYRFRKRDK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VMFYGRKIMR | KVTTLPNTLV | ENTALPRQRA | RKRTKVLSLA | KRILRFKKEY | PALQPKEPPP | SLLEADLTEF | DVKNSHLPSE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VLYMLKNVRV | LGHFEKPLFL | ELCKHIVFVQ | LQEGEHVFQP | REPDPSICVV | QDGRLEVCIQ | DTDGTEVVVK | EVLAGDSVHS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LLSILDIITG | HAAPYKTVSV | RAAIPSTILR | LPAAAFHGVF | EKYPETLVRV | VQIIMVRLQR | VTFLALHNYL | GLTTELFNAE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SQAIPLVSVA | SVAAGKAKKQ | VFYGEEERLK | KPPRLQESCD | SADHGGGRPA | AAGPLLKRSH | SVPAPSIRKQ | ILEELEKPGA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GDPDPSAPQG | GPGSATSDLG | MACDRARVFL | HSDEHPGSSV | ASKSRKSVMV | AEIPSTVSQH | SESHTDETLA | SRKSDAIFRA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AKKDLLTLMK | LEDSSLLDGR | VALLHVPAGT | VVSRQGDQDA | SILFVVSGLL | HVYQRKIGSQ | EDTCLFLTRP | GEMVGQLAVL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TGEPLIFTVK | ANRDCSFLSI | SKAHFYEIMR | KQPTVVLGVA | HTVVKRMSSF | VRQIDFALDW | VEVEAGRAIY | RQGDKSDCTY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IMLSGRLRSV | IRKDDGKKRL | AGEYGRGDLV | GVVETLTHQA | RATTVHAVRD | SELAKLPAGA | LTSIKRRYPQ | VVTRLIHLLG |
| 730 | 740 | 750 | | | | | |
| EKILGSLQQG | PVTADWKKET | G | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2108 | 1 | 1052.4312 | -68.35 | 2 | 56.7 | 14.6 | 1 | 574-590 | R.DCSFLSISKAHFYEIMR.K | Carbamidomethyl: 2 |

# Detailed Protein Report

## Protein 1097: ATP-binding cassette sub-family A member 5 [Homo sapiens]

**Accession:** gi|27262624
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 14.6
**MW [kDa]:** 186.4
**pI:** 6.5
**Sequence Coverage [%]:** 0.9
**No. of unique Peptides:** 1

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.54 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.27 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|27262626 | refseq_human (refseq_human_20140103.fasta) | ATP-binding cassette sub-family A member 5 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSTAIREVGV | WRQTRTLLLK | NYLIKCRTKK | SSVQEILFPL | FFLFWLILIS | MMHPNKKYEE | VPNIELNPMD | KFTLSNLILG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YTPVTNITSS | IMQKVSTDHL | PDVIITEEYT | NEKEMLTSSL | SKPSNFVGVV | FKDSMSYELR | FFPDMIPVSS | IYMDSRAGCS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KSCEAAQYWS | SGFTVLQASI | DAAIIQLKTN | VSLWKELEST | KAVIMGETAV | VEIDTFPRGV | ILIYLVIAFS | PFGYFLAIHI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VAEKEKKIKE | FLKIMGLHDT | AFWLSWVLLY | TSLIFLMSLL | MAVIATASLL | FPQSSSIVIF | LLFFLYGLSS | VFFALMLTPL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FKKSKHVGIV | EFFVTVAFGF | IGLMIILIES | FPKSLVWLFS | PFCHCTFVIG | IAQVMHLEDF | NEGASFSNLT | AGPYPLIITI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IMLTLNSIFY | VLLAVYLDQV | IPGEFGLRRS | SLYFLKPSYW | SKSKRNYEEL | SEGNVNGNIS | FSEIIEPVSS | EFVGKEAIRI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SGIQKTYRKK | GENVEALRNL | SFDIYEGQIT | ALLGHSGTGK | STLMNILCGL | CPPSDGFASI | YGHRVSEIDE | MFEARKMIGI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| CPQLDIHFDV | LTVEENLSIL | ASIKGIPANN | IIQEVQKVLL | DLDMQTIKDN | QAKKLSGGQK | RKLSLGIAVL | GNPKILLLDE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PTAGMDPCSR | HIVWNLLKYR | KANRVTVFST | HFMDEADILA | DRKAVISQGM | LKCVGSSMFL | KSKWGIGYRL | SMYIDKYCAT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ESLSSLVKQH | IPGATLLQQN | DQQLVYSLPF | KDMDKFSGLF | SALDSHSNLG | VISYGVSMTT | LEDVFLKLEV | EAEIDQADYS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VFTQQPLEEE | MDSKSFDEME | QSLLILSETK | AALVSTMSLW | KQQMYTIAKF | HFFTLKRESK | SVRSVLLLLL | IFFTVQIFMF |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LVHHSFKNAV | VPIKLVPDLY | FLKPGDKPHK | YKTSLLLQNS | ADSDISDLIS | FFTSQNIMVT | MINDSDYVSV | APHSAALNVM |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| HSEKDYVFAA | VFNSTMVYSL | PILVNIISNY | YLYHLNVTET | IQIWSTPFFQ | EITDIVFKIE | LYFQAALLGI | IVTAMPPYFA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| MENAENHKIK | AYTQLKLSGL | LPSAYWIGQA | VVDIPLFFII | LILMLGSLLA | FHYGLYFYTV | KFLAVVFCLI | GYVPSVILFT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| YIASFTFKKI | LNTKEFWSFI | YSVAALACIA | ITEITFFMGY | TIATILHYAF | CIIIPIYPLL | GCLISFIKIS | WKNVRKNVDT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| YNPWDRLSVA | VISPYLQCVL | WIFLLQYYEK | KYGGRSIRKD | PFFRNLSTKS | KNRKLPEPPD | NEDEDEDVKA | ERLKVKELMG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| CQCCEEKPSI | MVSNLHKEYD | DKKDFLLSRK | VKKVATKYIS | FCVKKGEILG | LLGPNGAGKS | TIINILVGDI | EPTSGQVFLG |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| DYSSETSEDD | DSLKCMGYCP | QINPLWPDTT | LQEHFEIYGA | VKGMSASDMK | EVISRITHAL | DLKEHLQKTV | KKLPAGIKRK |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LCFALSMLGN | PQITLLDEPS | TGMDPKAKQH | MWRAIRTAFK | NRKRAAILTT | HYMEEAEAVC | DRVAIMVSGQ | LRCIGTVQHL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| KSKFGKGYFL | EIKLKDWIEN | LEVDRLQREI | QYIFPNASRQ | ESFSSILAYK | IPKEDVQSLS | QSFFKLEEAK | HAFAIEEYSF |
| 1610 | 1620 | 1630 | 1640 | 1650 | | | |
| SQATLEQVFV | ELTKEQEEED | NSCGTLNSTL | WWERTQEDRV | VF | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2136 | 1 | 805.8396 | -128.42 | 2 | 55.1 | 14.6 | 1 | 1560-1573 | R.QESFSSILAYKIPK.E |  | WUP:QUP 1.27<br>QU:MU 2.54 |

# Detailed Protein Report

## Protein 1098: PREDICTED: general transcription factor 3C polypeptide 1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578828542 | **Score:** | 14.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 231.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDALESLLDE | VALEGLDGLC | LPALWSRLET | RVPPFPLPLE | PCTQEFLWRA | LATHPGISFY | EEPRERPDLQ | LQDRYEEIDL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ETGILESRRD | PVALEDVYPI | HMILENKDGI | QGSCRYFKER | KNITNDIRTK | SLQPRCTMVE | AFDRWGKKLI | IVASQAMRYR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ALIGQEGDPD | LKLPDFSYCI | LERLGRSRWQ | GELQRDLHTT | AFKVDAGKLH | YHRKILNKNG | LITMQSHVIR | LPTGAQQHSI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LLLLNRFHVD | RRSKYDILME | KLSVMLSTRT | NHIETLGKLR | EELGLCERTF | KRLYQYMLNA | GLAKVVSLRL | QEIHPECGPC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KTKKGTDVMV | RCLKLLKEFK | RNDHDDDEDE | EVISKTVPPV | DIVFERDMLT | QTYDLIERRG | TKGISQAEIR | VAMNVGKLEA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RMLCRLLQRF | KVVKGFMEDE | GRQRTTKYIS | CVFAEESDLS | RQYQREKARS | ELLTTVSLAS | MQEESLLPEG | EDTFLSESDS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EEERSSSKRR | GRGSQKDTRA | SANLRPKTQP | HHSTPTKGGW | KVVNLHPLKK | QPPSFPGAAE | ERACQSLASR | DSLLDTSSVS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EPNVSFVSHC | ADSNSGDIAV | IEEVRMENPK | ESSSSLKTGR | HSSGQDKPHE | TYRLLKRRNL | IIEAVTNLRL | IESLFTIQKM |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IMDQEKQEGV | STKCCKKSIV | RLVRNLSEEG | LLRLYRTTVI | QDGIKKKVDL | VVHPSMDQND | PLVRSAIEQV | RFRISNSSTA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NRVKTSQPPV | PQGEAEEDSQ | GKEGPSGSGD | SQLSASSRSE | SGRMKKSDNK | MGITPLRNYH | PIVVPGLGRS | LGFLPKMPRL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RVVHMFLWYL | IYGHPASNTV | EKPSFISERR | TIKQESGRAG | VRPSSSGSAW | EACSEAPSKG | SQDGVTWEAE | VELATETVYV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DDASWMRYIP | PIPVHRDFGF | GWALVSDILL | CLPLSIFIQI | VQVSYKVDNL | EEFLNDPLKK | HTLIRFLPRP | IRQQLLYKRR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| YIFSVVENLQ | RLCYMGLLQF | GPTEKFQDKD | QVFIFLKKNA | VIVDTTICDP | HYNLARSSRP | FERRLYVLNS | MQDVENYWFD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LQCVCLNTPL | GVVRCPRVRK | NSSTDQGSDE | EGSLQKEQES | AMDKHNLERK | CAMLEYTTGS | REVVDEGLIP | GDGLGAAGLD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SSFYGHLKRN | WIWTSYIINQ | AKKENTAAEN | GLTVRLQTFL | SKRPMPLSAR | GEFPGEKSKR | LRYHDEADQS | ALQRMTRLRV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TWSMQEDGLL | VLCRIASNVL | NTKVKGPFVT | WQVVRDILHA | TFEESLDKTS | HSVGRRARYI | VKNPQAYLNY | KVCLAEVYQD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KALVGDFMNR | RGDYDDPKVC | ANEFKEFVEK | LKEKFSSALR | NSNLEIPDTL | QELFARYRVL | AIGDEKDQTR | KEDELNSVDD |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| IHFLVLQNLI | QSTLALSDSQ | MKSYQSFQTF | RLYREYKDHV | LVKAFMECQK | RSLVNRRRVN | HTLGPKKNRA | LPFVPMSYQL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SQTYYRIFTW | RFPSTICTES | FQFLDRMRAA | GKLDQPDRFS | FKDQDNNEPT | NDMVAFSLDG | PGGNCVAVLT | LFSLGLISVD |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| VRIPEQIIVV | DSSMVENEVI | KSLGKDGSLE | DDEDEEDDLD | EGVGGKRRSM | EVKPAQASHT | NYLLMRGYYS | PGIVSTRNLN |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| PNDSIVVNSC | QMKFQLRCTP | VPARLRPAAA | PLEELTMGTS | CLPDTFTKLI | NPQENTCSLE | EFVLQLELSG | YSPEDLTAAL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| EILEAIIATG | CFGIDKEELR | RRFSALEKAG | GGRTRTFADC | IQALLEQHQV | LEVGGNTARL | VAMGSAWPWL | LHSVRLKDRE |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| DADIQREDPQ | ARPLEGSSSE | DSPPEGQAPP | SHSPRGTKRR | ASWASENGET | DAEGTQMTPA | KRPALQDSNL | APSLGPGAED |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| GAEAQAPSPP | PALEDTAAAG | AAQEDQEGVG | EFSSPGQEQL | SGQAQPPEGS | EDPRGFTESF | GAANISQAAR | ERDCESVCFI |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| GRPWRVVDGH | LNLPVCKGMM | EAMLYHIMTR | PGIPESSLLR | HYQGVLQPVA | VLELLQGLES | LGCIRKRWLR | KPRPVSLFST |
| 2010 | 2020 | 2030 | 2040 | 2050 | | | |
| PVVEEVEVPS | SLDESPMAFY | EPTLDCTLRL | GRVFPHEVNW | NKWIHL | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2710 | 1 | 941.5667 | 103.70 | 2 | 62.3 | 14.6 | 2 | 129-144 | R.TKSLQPRCTMVEAFDR.W | |

# Detailed Protein Report

## Protein 1099: ankyrin repeat and BTB/POZ domain-containing protein 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|300796386 | **Score:** | 14.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 113.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| | | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAGTYSSTLK | TLEDLTLDSG | YGAGDSCRSL | SLSSSKSNSQ | ALNSSAQQHR | GAAWWCYSGS | MNSRHNSWDT | VNTVLPEDPE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VADLFSRCPR | LPELEEFPWT | EGDVARVLRK | GAGGRRLPQF | SAEAVRRLAG | LLRRALIRVA | REAQRLSVLH | AKCTRFEVQS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AVRLVHSWAL | AESCALAAVK | ALSLYSMSAG | DGLRRGKSAR | CGLTFSVGRF | FRWMVDTRIS | VRIHEYAAIS | LTACMENLVE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EIRARVMASH | SPDGGGAGGG | EVSAEALEMV | INNDAELWGV | LQPYEHLICG | KNANGVLSLP | AYFSPYNGGS | LGHDERADAY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AQLELRTLEQ | SLLATCVGSI | SELSDLVSRA | MHHMQGRHPL | CPGASPARQA | RQPPQPITWS | PDALHTLYYF | LRCPQMESME |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NPNLDPPRMT | LNNERPFMLL | PPLMEWMRVA | ITYAEHRRSL | TVDSGDIRQA | ARLLLPGLDC | EPRQLKPEHC | FSSFRRLDAR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AATEKFNQDL | GFRMLNCGRT | DLINQAIEAL | GPDGVNTMDD | QGMTPLMYAC | AAGDEAMVQM | LIDAGANLDI | QVPSNSPRHP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SIHPDSRHWT | SLTFAVLHGH | ISVVQLLLDA | GAHVEGSAVN | GGEDSYAETP | LQLASAAGNY | ELVSLLLSRG | ADPLLSMLEA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HGMGSSLHED | MNCFSHSAAH | GHRNVLRKLL | TQPQQAKADV | LSLEEILAEG | VEESDASSQG | SGSEGPVRLS | RTRTKALQEA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| MYYSAEHGYV | DITMELRALG | VPWKLHIWIE | SLRTSFSQSR | YSVVQSLLRD | FSSIREEEYN | EELVTEGLQL | MFDILKTSKN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DSVIQQLATI | FTHCYGSSPI | PSIPEIRKTL | PARLDPHFLN | NKEMSDVTFL | VEGKLFYAHK | VLLVTASNRF | KTLMTNKSEQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DGDSSKTIEI | SDMKYHIFQM | MMQYLYYGGT | ESMEIPTTDI | LELLSAASLF | QLDALQRHCE | ILCSQTLSME | SAVNTYKYAK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | |
| IHNAPELALF | CEGFFLKHMK | ALLEQDAFRQ | LIYGRSSKVQ | GLDPLQDLQN | TLAERVHSVY | ITSRV | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1098 | 1 | 955.4548 | -49.92 | 2 | 43.8 | 14.6 | 0 | 999-1015 | K.VQGLDPLQDLQNTLAER.V | |

BRUKER

# Detailed Protein Report

## Protein 1100: zinc finger protein 775 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|116256460 | **Score:** | 14.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MESGLAGNGT | GAGLVMKVKQ | EKPERLLQTL | APQAMLVEKD | KENIFQQHRG | LPPRQTMGRP | RALGGQEESG | SPRWAPPTEQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DAGLAGRAPG | SASGPLSPSL | SSGEGHFVCL | DCGKRFSWWS | SLKIHQRTHT | GEKPYLCGKC | GKSFSQKPNL | ARHQRHHTGE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RPFCCPECAR | RFSQKQHLLK | HQKTHSRPAT | HSCPECERCF | RHQVGLRIHQ | RAHARDRQGS | RAGLHELIQD | AAARRACRLQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PGPPRGRPEW | AWLGLCQGWW | GQPGARAAVS | GPEGPGEPRQ | FICNECGKSF | TWWSSLNIHQ | RIHTGERPYA | CPECGRRFSQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KPNLTRHLRN | HTGERPHPCP | HCGRGFRQKQ | HLLKHLRTHL | PGAQAAPCPS | CGKSCRSRAA | LRAHQRAHAV | AEPAVPAGEP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GDQPQAEAIP | GLAARPRSSQ | RSPGARDTLW | GRGQAGLAGP | GEPRQFICNE | CGKSFSWWSA | LTIHQRIHTG | ERPYPCPECG |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| RRFSQKPNLT | RHRRNHTGER | PYLCPACGRG | FSQKQHLLKH | QRVHRAAPAC | SPKEEAR | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 122 | 1 | 1029.4533 | -54.70 | 2 | 31.5 | 14.6 | 1 | 355-373 | K.HLRTHLPGAQAAPCPSCGK.S | Carbamidomethyl: 14, 17 |

## Protein 1101: arylsulfatase F precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|31742482 | **Score:** | 14.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 65.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|319996606 | refseq_human (refseq_human_20140103.fasta) | arylsulfatase F precursor [Homo sapiens] |
| gi\|319996604 | refseq_human (refseq_human_20140103.fasta) | arylsulfatase F precursor [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRPRRPLVFM | SLVCALLNTC | QAHRVHDDKP | NIVLIMVDDL | GIGDLGCYGN | DTMRTPHIDR | LAREGVRLTQ | HISAASLCSP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SRSAFLTGRY | PIRSGMVSSG | NRRVIQNLAV | PAGLPLNETT | LAALLKKQGY | STGLIGKWHQ | GLNCDSRSDQ | CHHPYNYGFD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YYYGMPFTLV | DSCWPDPSRN | TELAFESQLW | LCVQLVAIAI | LTLTFGKLSG | WVSVPWLLIF | SMILFIFLLG | YAWFSSHTSP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LYWDCLLMRG | HEITEQPMKA | ERAGSIMVKE | AISFLERHSK | ETFLLFFSFL | HVHTPLPTTD | DFTGTSKHGL | YGDNVEEMDS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MVGKILDAID | DFGLRNNTLV | YFTSDHGGHL | EARRGHAQLG | GWNGIYKGGK | GMGGWEGGIR | VPGIVRWPGK | VPAGRLIKEP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TSLMDILPTV | ASVSGGSLPQ | DRVIDGRDLM | PLLQGNVRHS | EHEFLFHYCG | SYLHAVRWIP | KDDSGSVWKA | HYVTPVFQPP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ASGGCYVTSL | CRCFGEQVTY | HNPPLLFDLS | RDPSESTPLT | PATEPLHDFV | IKKVANALKE | HQETIVPVTY | QLSELNQGRT |
| 570 | 580 | 590 | 600 | | | | |
| WLKPCCGVFP | FCLCDKEEEV | SQPRGPNEKR | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1746 | 1 | 672.9041 | -110.19 | 3 | 52.1 | 14.5 | 0 | 560-576 | R.TWLKPCCGVFPFCLCDK.E | Carbamidomethyl: 13 |

# Detailed Protein Report

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## Protein 1102: glutamate--cysteine ligase catalytic subunit isoform a [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|4557625 | **Score:** | 14.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 72.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
|  |  | **Sequence Coverage [%]:** | 1.4 |
|  |  | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 1.60 **CV:** 0.00 % **No. of Peptides:** 1

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGLLSQGSPL | SWEETKRHAD | HVRRHGILQF | LHIYHAVKDR | HKDVLKWGDE | VEYMLVSFDH | ENKKVRLVLS | GEKVLETLQE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KGERTNPNHP | TLWRPEYGSY | MIEGTPGQPY | GGTMSEFNTV | EANMRKRRKE | ATSILEENQA | LCTITSFPRL | GCPGFTLPEV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KPNPVEGGAS | KSLFFPDEAI | NKHPRFSTLT | RNIRHRRGEK | VVINVPIFKD | KNTPSPFIET | FTEDDEASRA | SKPDHIYMDA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MGFGMGNCCL | QVTFQACSIS | EARYLYDQLA | TICPIVMALS | AASPFYRGYV | SDIDCRWGVI | SASVDDRTRE | ERGLEPLKNN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NYRISKSRYD | SIDSYLSKCG | EKYNDIDLTI | DKEIYEQLLQ | EGIDHLLAQH | VAHLFIRDPL | TLFEEKIHLD | DANESDHFEN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IQSTNWQTMR | FKPPPPNSDI | GWRVEFRPME | VQLTDFENSA | YVVFVVLLTR | VILSYKLDFL | IPLSKVDENM | KVAQKRDAVL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QGMFYFRKDI | CKGGNAVVDG | CGKAQNSTEL | AAEEYTLMSI | DTIINGKEGV | FPGLIPILNS | YLENMEVDVD | TRCSILNYLK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LIKKRASGEL | MTVARWMREF | IANHPDYKQD | SVITDEMNYS | LILKCNQIAN | ELCECPELLG | SAFRKVKYSG | SKTDSSN |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2754 | 1 | 557.9575 | 265.47 | 2 | 65.6 | 14.5 | 1 | 183-191 | K.HPRFSTLTR.N |  | WUP:QUP 1.60 |

# Detailed Protein Report

## Protein 1103: protein EURL homolog isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|154426270 | **Score:** | 14.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 25.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 10.0 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MNEEEQFVNI DLNDDNICSV CKLGTDKETL SFCHICFELN IEGVPKSDLL HTKSLRGHKD CFEKYHLIAN QGCPRSKLSK
        90        100        110        120        130        140        150        160
STYEEVKTIL SKKINWIVQY AQNKDLDSDS ECSKNPQHHL FNFRHKPEEK LLPQFDSQVP KYSAKWIDGS AGGISNCTQR
       170        180        190        200        210        220        230
ILEQRENTDF GLSMLQDSGA TLCRNSVLWP HSHNQAQKKE ETISSPEANV QTQHPHYSRE E
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 175 | 1 | 877.0244 | -23.87 | 3 | 31.9 | 14.5 | 0 | 1-22 | -.MNEEEQFVNIDLNDDNICSVCK.L | Carbamidomethyl: 18 |

# Detailed Protein Report

## Protein 1104: PREDICTED: cGMP-inhibited 3',5'-cyclic phosphodiesterase A isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578822894 | **Score:** | 14.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 118.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.51 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAVPGDAARV | RDKPVHSGVS | QAPTAGRDCH | HRADPASPRD | SGCRGCWGDL | VLQPLRSSRK | LSSALCAGSL | SFLLALLVRL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VRGEVGCDLE | QCKEAAAAEE | EEAAPGAEGG | VFPGPRGGAP | GGGARLSPWL | QPSALLFSLL | CAFFWMGLYL | LRAGVRLPLA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VALLAACCGG | EALVQIGLGV | GEDHLLSLPA | AGVVLSCLAA | ATWLVLRLRL | GVLMIALTSA | VRTVSLISLE | RFKVAWRPYL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AYLAGVLGIL | LARYVEQILP | QSAEAAPREH | LGSQLIAGTK | EDIPVFKRRR | RSSSVVSAEM | SGCSSKSHRR | TSLPCIPREQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LMGHSEWDHK | RGPRGSQSSG | TSITVDIAVM | GEAHGLITDL | LADPSLPPNV | CTSLRAVSNL | LSTQLTFQAI | HKPRVNPVTS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LSENYTCSDS | EESSEKDKLA | IPKRLRRSLP | PGLLRRVSST | WTTTTSATGL | PTLEPAPVRR | DRSTSIKLQE | APSSSPDSWN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NPVMMTLTKS | RSFTSSYAIS | AANHVKAKKQ | SRPGALAKIS | PLSSPCSSPL | QGTPASSLVS | KISAVQFPES | ADTTAKQSLG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SHRALTYTQS | APDLSPQILT | PPVICSSCGR | PYSQGNPADE | PLERSGVATR | TPSRTDDTAQ | VTSDYETNNN | SDSSDIVQNE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DETECLREPL | RKASACSTYA | PETMMFLDKP | ILAPEPLVMD | NLDSIMEQLN | TWNFPIFDLV | ENIGRKCGRI | LSQVSYRLFE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DMGLFEAFKI | PIREFMNYFH | ALEIGYRDIP | YHNRIHATDV | LHAVWYLTTQ | PIPGLSTVIN | DHGSTSDSDS | DSGFTHGHMG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| YVFSKTYNVT | DDKYGCLSGN | IPALELMALY | VAAAMHDYDH | PGRTNAFLVA | TSAPQAVLYN | DRSVLENHHA | AAAWNLFMSR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PEYNFLINLD | HVEFKHFRFL | VIEAILATDL | KKHFDFVAKF | NGKVNDDVGI | DWTNENDRLL | VCQMCIKLAD | INGPAKCKEL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| HLQWTDGIVN | EFYEQGDEEA | SLGLPISPFM | DRSAPQLANL | QESFISHIVG | PLCNSYDSAG | LMPGKWVEDS | DESGDTDDPE |
| 1050 | 1060 | 1070 | 1080 | 1090 | | | |
| EEEEEAPAPN | EEETCENNES | PSKYQMPLAY | RLEDTLQDKF | LKGGMLR | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 645 | 1 | 647.6267 | -227.08 | 2 | 36.5 | 14.5 | 0 | 83-93 | R.GEVGCDLEQCK.E | Carbamidomethyl: 5, 10 | WUP:QUP 0.51 |

# Detailed Protein Report

## Protein 1105: T-cell activation inhibitor, mitochondrial isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|544710724 | **Score:** | 14.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 5.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578806007 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: T-cell activation inhibitor, mitochondrial isoform X1 [Homo sapiens] |
| gi\|544710792 | refseq_human (refseq_human_20140103.fasta) | T-cell activation inhibitor, mitochondrial isoform 3 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MHTQPLKEAK | RMPDRPIKWD | KSYYSFTGFK | DPDEDLEQVS | RVETTLTSWL | DNNGKSAVKK | LKNSLPLRKE | LDRLKDELSH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QLQLSDIRWQ | RSWGIAHRCS | QLHSLSRLAQ | QNLETLKKAK | GCTIIFTDRS | GMSAVGHVML | GTMDVHHHWT | KLFERLPSYF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DLQRRLMILE | DQISYLLGGI | QVVYIEELQP | VLTLEEYYSL | LDVFYNRLLK | SRILFHPRSL | RGLQMILNSD | RYAPSLHELG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HFNIPTLCDP | ANLQWFILTK | AQQARENMKR | KEELKVIENE | LIQASTKKFS | LEKLYKEPSI | SSIQMVDCCK | RLLEQSLPYL |
| 330 | 340 | 350 | 360 | | | | |
| HGMHLCISHF | YSVMQDGDLC | IPWNWKNGEA | IK | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1560 | 1 | 724.9960 | -32.87 | 3 | 49.7 | 14.5 | 2 | 294-311 | K.LYKEPSISSIQMVDCCKR.L | Carbamidomethyl: 15;<br>Oxidation: 12 |

# Detailed Protein Report

## Protein 1106: NHL repeat-containing protein 2 [Homo sapiens]

**Accession:** gi|42476013
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 14.5
**MW [kDa]:** 79.4
**pI:** 5.2
**Sequence Coverage [%]:** 2.1
**No. of unique Peptides:** 1

## Quantitation

***QU:MU*** **Median:** 0.70 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MAAPGGRGRS LSGLLPAQTS LEYALLDAVT QQEKDSLVYQ YLQKVDGWEQ DLSVPEFPEG LEWLNTEEPI SVYKDLCGKI

        90        100        110        120        130        140        150        160
VVLDFFTYCC INCIHLLPDL HALEHTYSDK DGLLIIGVHS AKFPNEKVLD NIKSAVLRYN ITHPMVNDAD ASLWQELEVS

       170        180        190        200        210        220        230        240
CWPTLVILGP RGNMLFSLIG EGHKDKLFLY TSIALKYYKD RGQIRDNKIG IKLYKDSLPP SPLLFPGKVT VDQVTDRLVI

       250        260        270        280        290        300        310        320
ADTGHHRILV VWKNGQIQYS IGGPNPGRKD GIFSESTFNS PQGVAIMNNI IYVADTENHL IRKIDLEAEK VSTVAGIGIQ

       330        340        350        360        370        380        390        400
GTDKEGGAKG EQQPISSPWD VVFGTSGSEV QRGDILWIAM AGTHQIWALL LDSGKLPKKN ELTKGTCLRF AGSGNEENRN

       410        420        430        440        450        460        470        480
NAYPHKAGFA QPSGLSLASE DPWSCLFVAD SESSTVRTVS LKDGAVKHLV GGERDPMNLF AFGDVDGVGI NAKLQHPLGV

       490        500        510        520        530        540        550        560
TWDKKRNLLY VADSYNHKIK VVDPKTKNCT TLAGTGDTNN VTSSSFTEST FNEPGGLCIG ENGELLYVAD TNNHQIKVMD

       570        580        590        600        610        620        630        640
LETKMVSVLP IFRSENAVVD GPFLVEKQKT LPKLPKSAPS IRLSPVTACA GQTLQFKLRL DLPSGSKLTE GVSSCWFLTA

       650        660        670        680        690        700        710        720
EGNEWLLQGQ IAAGDIENIS SQPTISLQIP DDCLSLEAIV SVSVFLYYCS ADSSACMMKA ILFSQPLQIT DTQQGCIAPV

       730
ELRYVF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 330 | 1 | 782.3795 | -43.66 | 2 | 34.1 | 14.5 | 0 | 603-617 | R.LSPVTACAGQTLQFK.L | | QU:MU 0.70 |

# Detailed Protein Report

## Protein 1107: PREDICTED: target of Nesh-SH3 isoform X33 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530374326 | **Score:** | 14.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 148.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| | | **Sequence Coverage [%]:** | 0.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRGGKCNMLS | SLGCLLLCGS | ITLALGNAQK | LPKGKRPNLK | VHINTTSDSI | LLKFLRPSPN | VKLEGLLLGY | GSNVSPNQYF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PLPAEGKFTE | AIVDAEPKYL | IVVRPAPPPS | QKKSCSGKTR | SRKPLQLVVG | TLTPSSVFLS | WGFLINPHHD | WTLPSHCPND |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RFYTIRYREK | DKEKKWIFQI | CPATETIVEN | LKPNTVYEFG | VKDNVEGGIW | SKIFNHKTVV | GSKKVNGKIQ | STYDQDHTVP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AYVPRKLIPI | TIIKQVIQNV | THKDSAKSPE | KAPLGGVILV | HLIIPGLNET | TVKLPASLMF | EISDALKTQL | AKNETLALPA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ESKTPEVEKI | SARPTTVTPE | TVPRSTKPTT | SSALDVSETT | LVLSKRTPET | LQTILIPQFE | LPLSTLAPKS | LPEFPEAKTP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FPFEKPRGTL | ASSEKPWIVP | TAKISEDSKV | LQPQTATYDV | FSSPTTSDEP | EISDSYTATS | DRILDSIPPK | TSRTLEQPRA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TLAPSETPFV | PQKLEIFTSP | EMQPTTPAPQ | QTTSIPSTPK | RRPRPKPPRT | KPERTTSAGT | ITPKISKSPE | PTWTTPAPGK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TQFISLKPKI | PLSPEVTHTK | PAPEPQTLLP | SQSTIGPETP | GTKPSTTLAP | RKTKRPGRRP | RPRPRPKTTP | SPEVPKSKPA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LEPATIQPEP | LVPTTASKPS | ERPKTTHRPD | APQIQPGSKP | PKQLLPKPQT | TAEPDMPPTK | SVSEPVPFET | EAPSMTIVPT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TDIEPVTVRT | EATVTTLAPK | TSQRTRTRRP | RPKHKTTPRP | ETLQTKLDFG | PITPGTSSAP | TTTTKRTRRP | HPKPKTTPHP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EVPQTKLAPK | QTPRAPPKPK | TSPRPRIPQT | QPVPKVPQRV | TAKPKTSPSP | EVSYTTPAPK | DVLLPHKPYP | EVSQSEPAPL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ETRGIPFIPM | ISPSPSQEEL | QTTLEETDQS | TQEPFTTKIP | RTTELAKTTQ | APHRFYTTVR | PRTSDKPHIR | PGVKQAPRPS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GADRNVSVDS | THPTKKPGTR | RPPLPPRPTH | PRRKPLPPNN | VTGKPGSAGI | ISSGPITTPP | LRSTPRPTGT | PLERIETDIK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QPTVPASGEE | LENITDFSSS | PTRETDPLGK | PRFKGPHVRY | IQKPDNSPCS | ITDSVKRFPK | EEATEGNATS | PPQNPPTNLT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| VVTVEGCPSF | VILDWEKPLN | DTVTEYEVIS | RENGSFSGKN | KSIQMTNQTF | STVENLKPNT | SYEFQVKPKN | PLGEGPVSNT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VAFSTESADP | RVSEPVSAGR | DAIWTERPFN | SDSYSECKGK | QYVKRTWYKK | FVGVQLCNSL | RYKIYLSDSL | TGKFYNIGDQ |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| RGHGEDHCQF | VDSFLDGRTG | QQLTSDQLPI | KEGYFRAVRQ | EPVQFGEIGG | HTQINYVQWY | ECGTTIPGKW | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 986 | 1 | 955.6747 | 172.89 | 1 | 41.9 | 14.5 | 0 | 628-636 | K.TTPSPEVPK.S | |

# Detailed Protein Report

## Protein 1108: PREDICTED: transcription factor COE4 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578835491 | **Score:** | 14.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 61.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQGAGILDAS | TAAQSGVGLA | RAHFEKQPPS | NLRKSNFFHF | VLAMYDRQGQ | PVEVERTAFI | DFVEKDREPG | AEKTNNGIHY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RLRLVYNNGL | RTEQDLYVRL | IDSMSKQAII | YEGQDKNPEM | CRVLLTHEIM | CSRCCDRKSC | GNRNETPSDP | VIIDRFFLKF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FLKCNQNCLK | NAGNPRDMRR | FQVVVSTTVS | VDGHVLAVSD | NMFVHNNSKH | GRRARRLDPS | EAATPCIKAI | SPGEGWTTGG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ATVIVIGDNF | FDGLQVVFGN | VLVWSELITP | HAIRVQTPPR | HIPGVVEVTL | SYKSKQFCKG | CPGRFVYTAL | NEPTIDYGFQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RLQKVIPRHP | GDPERLPKEV | LLKRAADLAE | ALYGVPGSNQ | ELLLKRAADV | AEALYSTPRA | PGPLAPLAPS | HPHPAVVGIN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AFSSPLAIAV | GDATPGPEPG | YARSCSSASP | RGFAPSPGSQ | QSGYGGGLGA | GLGGYGAPGV | AGLGVPGSPS | FLNGSTATSP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FAIMPSSPPL | AAASSMSLPA | AAPTTSVFSF | SPVNMISAVK | QRSAFAPVLR | PPSSPPQACP | RAHGEGLPDQ | SFEDSDKFHS |
| 570 | 580 | | | | | | |
| PARGLQGLAY | S | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2275 | 1 | 899.3236 | -147.38 | 2 | 56.8 | 14.4 | 1 | 92-106 | R.TEQDLYVRLIDSMSK.Q | |

# Detailed Protein Report

## Protein 1109: PREDICTED: small nuclear protein PRAC2-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578795609 | **Score:** | 14.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 12.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.6 |
| | | **Sequence Coverage [%]:** | 13.6 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578844002 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: small nuclear protein PRAC2-like [Homo sapiens] |
| gi\|578813255 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: small nuclear protein PRAC2-like [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MDRRWMALRP GSRRRTAFFF HSRSLVPNLL AFFLGLSGAG PIHLPMPWPN GRRRRVLDPH TQLSTHEAPG CWKPVALPGM
        90        100        110        120
KACPQFLLEW SASAGRGRPC LFNGPSTLVE
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2421 | 1 | 818.3153 | -104.73 | 2 | 60.7 | 14.4 | 0 | 82-96 | K.ACPQFLLEWSASAGR.G | |

# Detailed Protein Report

## Protein 1110: serpin H1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|32454741 | **Score:** | 14.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| | | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578821832 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: serpin H1 isoform X3 [Homo sapiens] |
| gi\|578821830 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: serpin H1 isoform X2 [Homo sapiens] |
| gi\|578821828 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: serpin H1 isoform X1 [Homo sapiens] |
| gi\|333360851 | refseq_human (refseq_human_20140103.fasta) | serpin H1 precursor [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MRSLLLLSAF CLLEAALAAE VKKPAAAAAP GTAEKLSPKA ATLAERSAGL AFSLYQAMAK DQAVENILVS PVVVASSLGL
        90        100        110        120        130        140        150        160
VSLGGKATTA SQAKAVLSAE QLRDEEVHAG LGELLRSLSN STARNVTWKL GSRLYGPSSV SFADDFVRSS KQHYNCEHSK
       170        180        190        200        210        220        230        240
INFRDKRSAL QSINEWAAQT TDGKLPEVTK DVERTDGALL VNAMFFKPHW DEKFHHKMVD NRGFMVTRSY TVGVMMMHRT
       250        260        270        280        290        300        310        320
GLYNYYDDEK EKLQIVEMPL AHKLSSLIIL MPHHVEPLER LEKLLTKEQL KIWMGKMQKK AVAISLPKGV VEVTHDLQKH
       330        340        350        360        370        380        390        400
LAGLGLTEAI DKNKADLSRM SGKKDLYLAS VFHATAFELD TDGNPFDQDI YGREELRSPK LFYADHPFIF LVRDTQSGSL
       410        420
LFIGRLVRPK GDKMRDEL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1592 | 1 | 910.3836 | -67.04 | 2 | 49.6 | 14.4 | 0 | 168-184 | R.SALQSINEWAAQTTDGK.L | |

# Detailed Protein Report

## Protein 1111: UPF0609 protein C4orf27 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|157388914 | **Score:** | 14.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVGGGGKRRP | GGEGPQCEKT | TDVKKSKFCE | ADVSSDLRKE | VENHYKLSLP | EDFYHFWKFC | EELDPEKPSD | SLSASLGLQL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VGPYDILAGK | HKTKKKSTGL | NFNLHWRFYY | DPPEFQTIII | GDNKTQYHMG | YFRDSPDEFP | VYVGINEAKK | NCIIVPNGDN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VFAAVKLFLT | KKLREITDKK | KINLLKNIDE | KLTEAARELG | YSLEQRTVKM | KQRDKKVVTK | TFHGAGLVVP | VDKNDVGYRE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LPETDADLKR | ICKTIVEAAS | DEERLKAFAP | IQEMMTFVQF | ANDECDYGMG | LELGMDLFCY | GSHYFHKVAG | QLLPLAYNLL |
| 330 | 340 | 350 | | | | | |
| KRNLFAEIIE | EHLANRSQEN | IDQLAA | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1471 | 1 | 620.4233 | 145.55 | 3 | 48.1 | 14.4 | 1 | 150-166 | K.KNCIIVPNGDNVFAAVK.L | Carbamidomethyl: 3 |

# Detailed Protein Report

## Protein 1112: beta-1-syntrophin [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|11321640 | **Score:** | 14.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 58.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAVAAAAAAA | GPAGAGGGRA | QRSGLLEVLV | RDRWHKVLVN | LSEDALVLSS | EEGAAAYNGI | GTATNGSFCR | GAGAGHPGAG |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| GAQPPDSPAG | VRTAFTDLPE | QVPESISNQK | RGVKVLKQEL | GGLGISIKGG | KENKMPILIS | KIFKGLAADQ | TQALYVGDAI |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| LSVNGADLRD | ATHDEAVQAL | KRAGKEVLLE | VKYMREATPY | VKKGSPVSEI | GWETPPPESP | RLGGSTSDPP | SSQSFSFHRD |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| RKSIPLKMCY | VTRSMALADP | ENRQLEIHSP | DAKHTVILRS | KDSATAQAWF | SAIHSNVNDL | LTRVIAEVRE | QLGKTGIAGS |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| REIRHLGWLA | EKVPGESKKQ | WKPALVVLTE | KDLLIYDSMP | RRKEAWFSPV | HTYPLLATRL | VHSGPGKGSP | QAGVDLSFAT |
| **410** | **420** | **430** | **440** | **450** | **460** | **470** | **480** |
| RTGTRQGIET | HLFRAETSRD | LSHWTRSIVQ | GCHNSAELIA | EISTACTYKN | QECRLTIHYE | NGFSITTEPQ | EGAFPKTIIQ |
| **490** | **500** | **510** | **520** | **530** | **540** | | |
| SPYEKLKMSS | DDGIRMLYLD | FGGKDGEIQL | DLHSCPKPIV | FIIHSFLSAK | ITRLGLVA | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2302 | 1 | 703.3364 | -29.47 | 2 | 57.1 | 14.4 | 0 | 388-401 | K.GSPQAGVDLSFATR.T | |

# Detailed Protein Report

## Protein 1113: granzyme A precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5453676 | **Score:** | 14.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 28.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.65 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.71 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MRNSYRFLAS SLSVVVSLLL IPEDVCEKII GGNEVTPHSR PYMVLLSLDR KTICAGALIA KDWVLTAAHC NLNKRSQVIL
        90        100        110        120        130        140        150        160
GAHSITREEP TKQIMLVKKE FPYPCYDPAT REGDLKLLQL TEKAKINKYV TILHLPKKGD DVKPGTMCQV AGWGRTHNSA
       170        180        190        200        210        220        230        240
SWSDTLREVN ITIIDRKVCN DRNHYNFNPV IGMNMVCAGS LRGGRDSCNG DSGSPLLCEG VFRGVTSFGL ENKCGDPRGP
       250        260        270
GVYILLSKKH LNWIIMTIKG AV
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 92 | 1 | 566.5853 | -66.20 | 3 | 30.1 | 14.4 | 1 | 62-75 | K.DWVLTAAHCNLNKR.S | Carbamidomethyl: 9 | WUP:QUP 0.71<br>QU:MU 1.65 |

# Detailed Protein Report

## Protein 1114: E3 ubiquitin-protein ligase DTX3L [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|19923717 | **Score:** | 14.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 83.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| | | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASHLRPPSP | LLVRVYKSGP | RVRRKLESYF | QSSKSSGGGE | CTVSTQEHEA | PGTFRVEFSE | RAAKERVLKK | GEHQILVDEK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PVPIFLVPTE | NSIKKNTRPQ | ISSLTQSQAE | TPSGDMHQHE | GHIPNAVDSC | LQKIFLTVTA | DLNCNLFSKE | QRAYITTLCP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SIRKMEGHDG | IEKVCGDFQD | IERIHQFLSE | QFLESEQKQQ | FSPSMTERKP | LSQQERDSCI | SPSEPETKAE | QKSNYFEVPL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PYFEYFKYIC | PDKINSIEKR | FGVNIEIQES | SPNMVCLDFT | SSRSGDLEAA | RESFASEFQK | NTEPLKQECV | SLADSKQANK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FKQELNHQFT | KLLIKEKGGE | LTLLGTQDDI | SAAKQKISEA | FVKIPVKLFA | ANYMMNVIEV | DSAHYKLLET | ELLQEISEIE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KRYDICSKVS | EKGQKTCILF | ESKDRQVDLS | VHAYASFIDA | FQHASCQLMR | EVLLLKSLGK | ERKHLHQTKF | ADDFRKRHPN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VHFVLNQESM | TLTGLPNHLA | KAKQYVLKGG | GMSSLAGKKL | KEGHETPMDI | DSDDSKAASP | PLKGSVSSEA | SELDKKEKGI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| CVICMDTISN | KKVLPKCKHE | FCAPCINKAM | SYKPICPTCQ | TSYGIQKGNQ | PEGSMVFTVS | RDSLPGYESF | GTIVITYSMK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AGIQTEEHPN | PGKRYPGIQR | TAYLPDNKEG | RKVLKLLYRA | FDQKLIFTVG | YSRVLGVSDV | ITWNDIHHKT | SRFGGPEMYG |
| 730 | 740 | 750 | | | | | |
| YPDPSYLKRV | KEELKAKGIE | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1498 | 1 | 982.5825 | 15.99 | 2 | 48.4 | 14.4 | 1 | 1-17 | -.MASHLRPPSPLLVRVYK.S | |

# Detailed Protein Report

## Protein 1115: PREDICTED: dipeptidyl peptidase 9 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530425489 | **Score:** | 14.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 91.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRKVKKLRLD | KENTGSWRSF | SLNSEGAERM | ATTGTPTADR | GDAAATDDPA | ARFQVQKHSW | DGLRSIIHGS | RKYSGLIVNK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| APHDFQFVQK | TDESGPHSHR | LYYLGMPYGS | RENSLLYSEI | PKKVRKEALL | LLSWKQMLDH | FQATPHHGVY | SREEELLRER |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KRLGVFGITS | YDFHSESGLF | LFQASNSLFH | CRDGGKNGFM | VSPMKPLEIK | TQCSGPRMDP | KICPADPAFF | SFINNSDLWV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ANIETGEERR | LTFCHQGLSN | VLDDPKSAGV | ATFVIQEEFD | RFTGYWWCPT | ASWEGSEGLK | TLRILYEEVD | ESEVEVIHVP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SPALEERKTD | SYRYPRTGSK | NPKIALKLAE | FQTDSQGKIV | STQEKELVQP | FSSLFPKVEY | IARAGWTRDG | KYAWAMFLDR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PQQWLQLVLL | PPALFIPSTE | NEEQRLASAR | AVPRNVQPYV | VYEEVTNVWI | NVHDIFYPFP | QSEGEDELCF | LRANECKTGF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CHLYKVTAVL | KSQGYDWSEP | FSPGEDEFKC | PIKEEIALTS | GEWEVLARHG | SKIWVNEETK | LVYFQGTKDT | PLEHHLYVVS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YEAAGEIVRL | TTPGFSHSCS | MSQNFDMFVS | HYSSVSTPPC | VHVYKLSGPD | DDPLHKQPRF | WASMMEAASC | PPDYVPPEIF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HFHTRSDVRL | YGMIYKPHAL | QPGKKHPTVL | FVYGGPQVQL | VNNSFKGIKY | LRLNTLASLG | YAVVVIDGRG | SCQRGLRFEG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ALKNQMGQVE | IEDQVEGLQF | VAEKYGFIDL | SRVAIHGWSY | GGFLSLMGLI | HKPQVFKQPH | GAEPPSSLPA | TADRRMASGC |
| 810 | 820 | | | | | | |
| TKPRQQLSVG | G | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2196 | 1 | 994.6661 | 122.52 | 2 | 57.8 | 14.4 | 2 | 341-358 | K.NPKIALKLAEFQTDSQGK.I | |

# Detailed Protein Report

## Protein 1116: 1,4-alpha-glucan-branching enzyme [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|189458812 | **Score:** | 14.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 80.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAPMTPAAR | PEDYEAALNA | ALADVPELAR | LLEIDPYLKP | YAVDFQRRYK | QFSQILKNIG | ENEGGIDKFS | RGYESFGVHR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CADGGLYCKE | WAPGAEGVFL | TGDFNGWNPF | SYPYKKLDYG | KWELYIPPKQ | NKSVLVPHGS | KLKVVITSKS | GEILYRISPW |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AKYVVREGDN | VNYDWIHWDP | EHSYEFKHSR | PKKPRSLRIY | ESHVGISSHE | GKVASYKHFT | CNVLPRIKGL | GYNCIQLMAI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MEHAYYASFG | YQITSFFAAS | SRYGTPEELQ | ELVDTAHSMG | IIVLLDVVHS | HASKNSADGL | NMFDGTDSCY | FHSGPRGTHD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LWDSRLFAYS | SWEVLRFLLS | NIRWWLEEYR | FDGFRFDGVT | SMLYHHHGVG | QGFSGDYSEY | FGLQVDEDAL | TYLMLANHLV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HTLCPDSITI | AEDVSGMPAL | CSPISQGGGG | FDYRLAMAIP | DKWIQLLKEF | KDEDWNMGDI | VYTLTNRRYL | EKCIAYAESH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DQALVGDKSL | AFWLMDAEMY | TNMSVLTPFT | PVIDRGIQLH | KMIRLITHGL | GGEGYLNFMG | NEFGHPEWLD | FPRKGNNESY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HYARRQFHLT | DDDLLRYKFL | NNFDRDMNRL | EERYGWLAAP | QAYVSEKHEG | NKIIAFERAG | LLFIFNFHPS | KSYTDYRVGT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | |
| ALPGKFKIVL | DSDAAEYGGH | QRLDHSTDFF | SEAFEHNGRP | YSLLVYIPSR | VALILQNVDL | PN | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2742 | 1 | 729.3802 | 64.57 | 2 | 65.4 | 14.4 | 1 | 579-589 | K.FLNNFDRDMNR.L | Oxidation: 9 |

# Detailed Protein Report

## Protein 1117: serine palmitoyltransferase 1 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|30474871 | **Score:** | 14.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 16.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 7.7 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MATATEQWVL VEMVQALYEA PAYHLILEGI LILWIIRLLF SKTYKLQERS DLTVKEKEEL IEEWQPEPLV PPVPKDHPAL
        90        100        110        120        130        140        150
NYNIVSGPPS HKTVVNGKEC INFASFNFLG LLDNPRVKAA ALASLKKYGV GTCGPRGFYG TFE
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2660 | 1 | 550.5095 | 265.16 | 2 | 64.3 | 14.3 | 2 | 117-127 | R.VKAAALASLKK.Y | |

# Detailed Protein Report

## Protein 1118: proprotein convertase subtilisin/kexin type 9 preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|31317307 | **Score:** | 14.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 74.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGTVSSRRSW | WPLPLLLLLL | LLLGPAGARA | QEDEDGDYEE | LVLALRSEED | GLAEAPEHGT | TATFHRCAKD | PWRLPGTYVV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VLKEETHLSQ | SERTARRLQA | QAARRGYLTK | ILHVFHGLLP | GFLVKMSGDL | LELALKLPHV | DYIEEDSSVF | AQSIPWNLER |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ITPPRYRADE | YQPPDGGSLV | EVYLLDTSIQ | SDHREIEGRV | MVTDFENVPE | EDGTRFHRQA | SKCDSHGTHL | AGVVSGRDAG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VAKGASMRSL | RVLNCQGKGT | VSGTLIGLEF | IRKSQLVQPV | GPLVVLLPLA | GGYSRVLNAA | CQRLARAGVV | LVTAAGNFRD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DACLYSPASA | PEVITVGATN | AQDQPVTLGT | LGTNFGRCVD | LFAPGEDIIG | ASSDCSTCFV | SQSGTSQAAA | HVAGIAAMML |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SAEPELTLAE | LRQRLIHFSA | KDVINEAWFP | EDQRVLTPNL | VAALPPSTHG | AGWQLFCRTV | WSAHSGPTRM | ATAVARCAPD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EELLSCSSFS | RSGKRRGERM | EAQGGKLVCR | AHNAFGGEGV | YAIARCCLLP | QANCSVHTAP | PAEASMGTRV | HCHQQGHVLT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GCSSHWEVED | LGTHKPPVLR | PRGQPNQCVG | HREASIHASC | CHAPGLECKV | KEHGIPAPQE | QVTVACEEGW | TLTGCSALPG |
| 650 | 660 | 670 | 680 | 690 | 700 | | |
| TSHVLGAYAV | DNTCVVRSRD | VSTTGSTSEG | AVTAVAICCR | SRHLAQASQE | LQ | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2788 | 1 | 714.6895 | 34.37 | 3 | 66.0 | 14.3 | 0 | 660-680 | R.DVSTTGSTSEGAVTAVAICCR.S | Carbamidomethyl: 19, 20 |

# Detailed Protein Report

## Protein 1119: G protein-activated inward rectifier potassium channel 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|25121970 | **Score:** | 14.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 44.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.3 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578800900 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: G protein-activated inward rectifier potassium channel 3 isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAQENAAFSP | GQEEPPRRRG | RQRYVEKDGR | CNVQQGNVRE | TYRYLTDLFT | TLVDLQWRLS | LLFFVLAYAL | TWLFFGAIWW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LIAYGRGDLE | HLEDTAWTPC | VNNLNGFVAA | FLFSIETETT | IGYGHRVITD | QCPEGIVLLL | LQAILGSMVN | AFMVGCMFVK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ISQPNKRAAT | LVFSSHAVVS | LRDGRLCLMF | RVGDLRSSHI | VEASIRAKLI | RSRQTLEGEF | IPLHQTDLSV | GFDTGDDRLF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LVSPLVISHE | IDAASPFWEA | SRRALERDDF | EIVVILEGMV | EATGMTCQAR | SSYLVDEVLW | GHRFTSVLTL | EDGFYEVDYA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SFHETFEVPT | PSCSARELAE | AAARLDAHLY | WSIPSRLDEK | VEEEGAGEGA | GGEAGADKEQ | NGCLPPPESE | SKV |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1255 | 1 | 937.9577 | 39.66 | 2 | 45.3 | 14.3 | 0 | 1-17 | -.MAQENAAFSPGQEEPPR.R | Oxidation: 1 |

# Detailed Protein Report

## Protein 1120: anaphase-promoting complex subunit 11 isoform 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|574956971 | **Score:** | 14.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 14.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 21.3 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MKVKIKCWNG VATWLWVAND ENCGICRMAF NGCCPDCPLH GESISRCLGW CPQPVPVLGG RAHPQARCPA TTARWCGASA
        90        100        110        120        130        140        150
PTASTCIASS SGCTHSRCSS TAPCAARNGS SRSEARPGSR WRGILRLLPH AGADGCWGQR P
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1140 | 1 | 1019.2076 | 93.06 | 3 | 43.8 | 14.3 | 1 | 68-97 | R.CPATTARWCGASAPTASTCIASSSGCTHSR.C | Carbamidomethyl: 9, 19 |

# Detailed Protein Report

**Protein 1121:** **PREDICTED: zinc finger CCCH domain-containing protein 6 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578804313 | **Score:** | 14.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 101.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTQEFINQHT | VEHKGKQICK | YFLEGRCIKG | DQCKFDHDAE | LEKRKEICKF | YLQGYCTKGE | NCIYMHNEFP | CKFYHSGAKC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YQGDNCKFSH | DDLTKETKKL | LDKVLNTDEE | LINEDERELE | ELRKRGITPL | PKPPPGVGLL | PTPPEHFPFS | DPEDDFQTDF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SDDFRKIPSL | FEIVVKPTVD | LAHKIGRKPP | AFYTSASPPG | PQFQGSSPHP | QHIYSSGSSP | GPGPNMSQGH | SSPVMHPGSP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GHHPCAGPPG | LPVPQSPPLP | PGPPEIVGPQ | NQAGVLVQPD | TSLTPPSMGG | AYHSPGFPGH | VMKVPRENHC | SPGSSYQQSP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GEMQLNTNYE | SLQNPAEFYD | NYYAQHSIHN | FQPPNNSGDG | MWHGEFAQQQ | PPVVQDSPNH | GSGSDGSSTR | TGHGPLPVPG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LLPAVQRALF | VRLTQRYQED | EEQTSTQPHR | APSKEEDDTV | NWYSSSEEEE | GSSVKSILKT | LQKQTETLRN | QQQPSTELST |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PTDPRLAKEK | SKGNQVVDPR | LRTIPRQDIR | KPSESAPLDL | RLAWDPRKLR | GNGSGHIGSS | VGGAKFDLHH | ANAGTNVKHK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RGDDDDEDTE | RELREKAFLI | PLDASPGIML | QDPRSQLRQF | SHIKMDITLT | KPNFAKHIVW | APEDLLPVPL | PKPDPVSSIN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LPLPPLIADQ | RLNRLWNTKS | DLHQNTVSID | PKLAAKAKIN | TTNREGYLEQ | FGDSHGSGAK | LGDPRLQKNF | DPRLHRLPNT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ESHQVVMKDS | HASKGAPHLP | RSNPGSSQPS | GAGTSNSGSG | ALPPYAPKLS | SSAGLPLGTS | TSVLSGISLY | DPRDHGSSST |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SELATASSGE | NSKNQKKSGG | LKSSDKTEPS | PGEAILPQKP | SPNVGVTLEG | PADPQADVPR | SSGKVQVPAV | HSLPVQALTG |
| 890 | 900 | 910 | 920 | 930 | 940 | | |
| LIRPQYSDPR | QARQPGQGSP | TPDNDPGRET | DDKSLKEVFK | TFDPTASPFC | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1396 | 7 | 830.0815 | 105.87 | 2 | 47.6 | 14.3 | 2 | 456-469 | K.SILKTLQKQTETLR.N | |

# Detailed Protein Report

## Protein 1122: probable ATP-dependent RNA helicase DHX58 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|149408122 | **Score:** | 14.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 76.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.1 |
| | | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MELRSYQWEV | IMPALEGKNI | IIWLPTGAGK | TRAAAYVAKR | HLETVDGAKV | VVLVNRVHLV | TQHGEEFRRM | LDGRWTVTTL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SGDMGPRAGF | GHLARCHDLL | ICTAELLQMA | LTSPEEEEHV | ELTVFSLIVV | DECHHTHKDT | VYNVIMSQYL | ELKLQRAQPL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PQVLGLTASP | GTGGASKLDG | AINHVLQLCA | NLDTWCIMSP | QNCCPQLQEH | SQQPCKQYNL | CHRRSQDPFG | DLLKKLMDQI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HDHLEMPELS | RKFGTQMYEQ | QVVKLSEAAA | LAGLQEQRVY | ALHLRRYNDA | LLIHDTVRAV | DALAALQDFY | HREHVTKTQI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LCAERRLLAL | FDDRKNELAH | LATHGPENPK | LEMLEKILQR | QFSSSNSPRG | IIFTRTRQSA | HSLLLWLQQQ | QGLQTVDIRA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QLLIGAGNSS | QSTHMTQRDQ | QEVIQKFQDG | TLNLLVATSV | AEEGLDIPHC | NVVVRYGLLT | NEISMVQARG | RARADQSVYA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FVATEGSREL | KRELINEALE | TLMEQAVAAV | QKMDQAEYQA | KIRDLQQAAL | TKRAAQAAQR | ENQRQQFPVE | HVQLLCINCM |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VAVGHGSDLR | KVEGTHHVNV | NPNFSNYYNV | SRDPVVINKV | FKDWKPGGVI | SCRNCGEVWG | LQMIYKSVKL | PVLKVRSMLL |
| 650 | 660 | 670 | 680 | | | | |
| ETPQGRIQAK | KWSRVPFSVP | DFDFLQHCAE | NLSDLSLD | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1926 | 1 | 618.9091 | -113.75 | 3 | 52.4 | 14.3 | 1 | 614-629 | R.NCGEVWGLQMIYKSVK.L | |

# Detailed Protein Report

## Protein 1123: upstream stimulatory factor 2 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|46877105 | **Score:** | 14.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 30.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDMLDPGLDP | AASATAAAAA | SHDKGPEAEE | GVELQEGGDG | PGAEEQTAVA | ITSVQQAAFG | DHNIQYQFRT | ETNGGQAVIQ |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| NPFSNGGSPA | AEAVSGEARF | AYFPASSVGD | TTAVSVQTTD | QSLQAGGQFY | VMMTPQDVLQ | TGTQRTIAPR | THPYSPKIDG |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| TRTPRDERRR | AQHNEVERRR | RDKINNWIVQ | LSKIIPDCNA | DNSKTGASKG | GILSKACDYI | RELRQTNQRM | QETFKEAERL |
| **250** | **260** | **270** | **280** | | | | |
| QMDNELLRQQ | IEELKNENAL | LRAQLQQHNL | EMVGEGTRQ | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1816 | 2 | 898.8604 | -121.72 | 2 | 52.5 | 14.3 | 2 | 205-221 | K.TGASKGGILSKACDYIR.E | Carbamidomethyl: 13 |

# Detailed Protein Report

## Protein 1124: PREDICTED: polyamine-modulated factor 1-binding protein 1 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578829261 | **Score:** | 14.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 118.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.7 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578829263 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: polyamine-modulated factor 1-binding protein 1 isoform X4 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKDEAGERDR | EVSSLNSKLL | SLQLDIKNLH | DVCKRQRKTL | QDNQLCMEEA | MNSSHDKKQA | QALAFEESEV | EFGSSKQCHL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RQLQQLKKKL | LVLQQELEFH | TEELQTSYYS | LRQYQSILEK | QTSDLVLLHH | HCKLKEDEVI | LYEEEMGNHN | ENTGEKLHLA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QEQLALAGDK | IASLERSLNL | YRDKYQSSLS | NIELLECQVK | MLQGELGGIM | GQEPENKGDH | SKVRIYTSPC | MIQEHQETQK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RLSEVWQKVS | QQDDLIQELR | NKLACSNALV | LEREKALIKL | QADFASCTAT | HRYPPSSSEE | CEDIKKILKH | LQEQKDSQCL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HVEEYQNLVK | DLRVELEAVS | EQKRNIMKDM | MKLELDLHGL | REETSAHIER | KDKDITILQC | RLQELQLEFT | ETQKLTLKKD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KFLQEKDEML | QELEKKLTQV | QNSLLKKEKE | LEKQQCMATE | LEMTVKEAKQ | DKSKEAECKA | LQAEVQKLKN | SLEEAKQQER |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LAAQQAAQCK | EEAALAGCHL | EDTQRKLQKG | LLLDKQKADT | IQELQRELQM | LQKESSMAEK | EQTSNRKRVE | ELSLELSEAL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RKLENSDKEK | RQLQKTVAEQ | DMKMNDMLDR | IKHQHREQGS | IKCKLEEDLQ | EATKLLEDKR | EQLKKSKEHE | KLMEGELEAL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RQEFKKKDKT | LKENSRKLEE | ENENLRAELQ | CCSTQLESSL | NKYNTSQQVI | QDLNKEIALQ | KESLMSLQAQ | LDKALQKEKH |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YLQTTITKEA | YDALSRKSAA | CQDDLTQALE | KLNHVTSETK | SLQQSLTQTQ | EKKAQLEEEI | IAYEERMKKL | NTELRKLRGF |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| HQESELEVHA | FDKKLEEMSC | QVLQWQKQHQ | NDLKMLAAKE | EQLREFQEEM | AALKENLLED | DKEPCCLPQW | SVPKDTCRLY |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RGNDQIMTNL | EQWAKQQKVA | NEKLGNQLRE | QVKYIAKLSG | EKDHLHSVMV | HLQQENKKLK | KEIEEKKMKA | ENTRLCTKAL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | | |
| GPSRTESTQR | EKVCGTLGWK | GLPQDMGQRM | DLTKYIGMPH | CPGTSAICQK | NKCDFFL | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1491 | 1 | 472.2634 | 90.28 | 2 | 48.8 | 14.3 | 1 | 1011-1017 | K.NKCDFFL.- | Carbamidomethyl: 3 |

# Detailed Protein Report

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## Protein 1125: probable ATP-dependent RNA helicase DHX36 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|167830436 | **Score:** | 14.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 113.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.3 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSYDYHQNWG | RDGGPRSSGG | GYGGGPAGGH | GGNRGSGGGG | GGGGGGRGGR | GRHPGHLKGR | EIGMWYAKKQ | GQKNKEAERQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ERAVVHMDER | REEQIVQLLN | SVQAKNDKES | EAQISWFAPE | DHGYGTEVST | KNTPCSENKL | DIQEKKLINQ | EKKMFRIRNR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SYIDRDSEYL | LQENEPDGTL | DQKLLEDLQK | KKNDLRYIEM | QHFREKLPSY | GMQKELVNLI | DNHQVTVISG | ETGCGKTTQV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TQFILDNYIE | RGKGSACRIV | CTQPRRISAI | SVAERVAAER | AESCGSGNST | GYQIRLQSRL | PRKQGSILYC | TTGIILQWLQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SDPYLSSVSH | IVLDEIHERN | LQSDVLMTVV | KDLLNFRSDL | KVILMSATLN | AEKFSEYFGN | CPMIHIPGFT | FPVVEYLLED |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VIEKIRYVPE | QKEHRSQFKR | GFMQGHVNRQ | EKEEKEAIYK | ERWPDYVREL | RRRYSASTVD | VIEMMEDDKV | DLNLIVALIR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YIVLEEEDGA | ILVFLPGWDN | ISTLHDLLMS | QVMFKSVNQT | QVFKRTPPGV | RKIVIATNIA | ETSITIDDVV | YVIDGGKIKE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| THFDTQNNIS | TMSAEWVSKA | NAKQRKGRAG | RVQPGHCYHL | YNGLRASLLD | DYQLPEILRT | PLEELCLQIK | ILRLGGIAYF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LSRLMDPPSN | EAVLLSIRHL | MELNALDKQE | ELTPLGVHLA | RLPVEPHIGK | MILFGALFCC | LDPVLTIAAS | LSFKDPFVIP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LGKEKIADAR | RKELAKDTRS | DHLTVVNAFE | GWEEARRRGF | RYEKDYCWEY | FLSSNTLQML | HNMKGQFAEH | LLGAGFVSSR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NPKDPESNIN | SDNEKIIKAV | ICAGLYPKVA | KIRLNLGKKR | KMVKVYTKTD | GLVAVHPKSV | NVEQTDFHYN | WLIYHLKMRT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SSIYLYDCTE | VSPYCLLFFG | GDISIQKDND | QETIAVDEWI | VFQSPARIAH | LVKELRKELD | ILLQEKIESP | HPVDWNDTKS |
| 970 | 980 | 990 | 1000 | | | | |
| RDCAVLSAII | DLIKTQEKAT | PRNFPPRFQD | GYYS | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 338 | 1 | 686.9336 | 150.15 | 2 | 32.9 | 14.3 | 2 | 35-52 | R.GSGGGGGGGGGGRGGRGR.H | |

# Detailed Protein Report

## Protein 1126: PREDICTED: cyclin-dependent kinase inhibitor 2A isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530389655 | **Score:** | 14.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 11.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 11.4 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MMMGSARVAE LLLLHGAEPN CADPATLTRP VHDAAREGFL DTLVVLHRAG ARLDVRDAWG RLPVDLAEEL GHRDVARYLR
        90        100        110
AAAGGTRGSN HARIDAAEGP SDIPD
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 704 | 1 | 600.1941 | -134.67 | 2 | 38.4 | 14.3 | 0 | 94-105 | R.IDAAEGPSDIPD.- | |

# Detailed Protein Report

## Protein 1127: PREDICTED: integrin alpha-7 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530400184 | **Score:** | 14.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 126.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.72 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAGARSRDPW | GASGICYLFG | SLLVELLFSR | AVAFNLDVMG | ALRKEGEPGS | LFGFSVALHR | QLQPRPQSWL | LVGAPQALAL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PGQQANRTGG | LFACPLSLEE | TDCYRVDIDQ | GADMQKESKE | NQWLGVSVRS | QGPGGKIVTC | AHRYEARQRV | DQILETRDMI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GRCFVLSQDL | AIRDELDGGE | WKFCEGRPQG | HEQFGFCQQG | TAAAFSPDSH | YLLFGAPGTY | NWKGTARVEL | CAQGSADLAH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LDDGPYEAGG | EKEQDPRLIP | VPANSYFGLL | FVTNIDSSDP | DQLVYKTLDP | ADRLPGPAGD | LALNSYLGFS | IDSGKGLVRA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EELSFVAGAP | RANHKGAVVI | LRKDSASRLV | PEVMLSGERL | TSGFGYSLAV | ADLNSDGWPD | LIVGAPYFFE | RQEELGGAVY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VYLNQGGHWA | GISPLRLCGS | PDSMFGISLA | VLGDLNQDGF | PDIAVGAPFD | GDGKVFIYHG | SSLGVVAKPS | QVLEGEAVGI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KSFGYSLSGS | LDMDGNQYPD | LLVGSLADTA | VLFRARPILH | VSHEVSIAPR | SIDLEQPNCA | GGHSVCVDLR | VCFSYIAVPS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SYSPTVALDY | VLDADTDRRL | RGQVPRVTFL | SRNLEEPKHQ | ASGTVWLKHQ | HDRVCGDAMF | QLQENVKDKL | RAIVVTLSYS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LQTPRLRRQA | PGQGLPPVAP | ILNAHQPSTQ | RAEIHFLKQG | CGEDKICQSN | LQLVRARFCT | RVSDTEFQPL | PMDVDGTTAL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| FALSGQPVIG | LELMVTNLPS | DPAQPQADGD | DAHEAQLLVM | LPDSLHYSGV | RALDPAEKPL | CLSNENASHV | ECELGNPMKR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GAQVTFYLIL | STSGISIETT | ELEVELLLAT | ISEQELHPVS | ARARVFIELP | LSIAGMAIPQ | QLFFSGVVRG | ERAMQSERDV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GSKVKYEVTV | SNQGQSLRTL | GSAFLNIMWP | HEIANGKWLL | YPMQVELEGG | QGPGQKGLCS | PRPNILHLDV | DSRDRRRREL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| EPPEQQEPGE | RQEPSMSWWP | VSSAEKKKNI | TLDCARGTAN | CVVFSCPLYS | FDRAAVLHVW | GRLWNSTFLE | EYSAVKSLEV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| IVRANITVKS | SIKNLMLRDA | STVIPVMVYL | DPMAVVAEGV | PWWVILLAVL | AGLLVLALLV | LLLWKCGFFH | RSSQSSSFPT |
| 1130 | 1140 | 1150 | 1160 | 1170 | | | |
| NYHRACLAVQ | PSAMEVGGPG | TVGWDSSNGR | STPRPPCPST | MR | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1967 | 3 | 665.2921 | -47.52 | 2 | 55.0 | 14.3 | 0 | 1151-1162 | R.STPRPPCPSTMR.- | | QU:MU 0.72 |

# Detailed Protein Report

## Protein 1128: noggin precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4885523 | **Score:** | 14.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 25.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 9.9 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MERCPSLGVT LYALVVVLGL RATPAGGQHY LHIRPAPSDN LPLVDLIEHP DPIFDPKEKD LNETLLRSLL GGHYDPGFMA
        90        100        110        120        130        140        150        160
TSPPEDRPGG GGGAAGGAED LAELDQLLRQ RPSGAMPSEI KGLEFSEGLA QGKKQRLSKK LRRKLQMWLW SQTFCPVLYA
       170        180        190        200        210        220        230        240
WNDLGSRFWP RYVKVGSCFS KRSCSVPEGM VCKPSKSVHL TVLRWRCQRR GGQRCGWIPI QYPIISECKC SC
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1566 | 1 | 862.7593 | -26.29 | 3 | 47.9 | 14.3 | 2 | 182-204 | K.RSCSVPEGMVCKPSKSVHLTVLR.W | Carbamidomethyl: 11;<br>Oxidation: 9 |

# Detailed Protein Report

## Protein 1129: selenium-binding protein 1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|385137128 | **Score:** | 14.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MATKCGNCGP | GYSTPLEAMK | GPREEIVYLP | CIYRNTGTEA | PDYLATVDVD | PKSPQYCQVI | EPKDIHAKCE | LAFLHTSHCL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ASGEVMISSL | GDVKGNGKGG | FVLLDGETFE | VKGTWERPGG | AAPLGYDFWY | QPRHNVMIST | EWAAPNVLRD | GFNPADVEAG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LYGSHLYVWD | WQRHEIVQTL | SLKDGLIPLE | IRFLHNPDAA | QGFVGCALSS | TIQRFYKNEG | GTWSVEKVIQ | VPPKKVKGWL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LPEMPGLITD | ILLSLDDRFL | YFSNWLHGDL | RQYDISDPQR | PRLTGQLFLG | GSIVKGGPVQ | VLEDEELKSQ | PEPLVVKGKR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VAGGPQMIQL | SLDGKRLYIT | TSLYSAWDKQ | FYPDLIREGS | VMLQVDVDTV | KGGLKLNPNF | LVDFGKEPLG | PALAHELRYP |
| 410 | 420 | | | | | | |
| GGDCSSDIWI | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1766 | 1 | 1045.8477 | -101.94 | 2 | 50.4 | 14.3 | 1 | 1-20 | -.MATKCGNCGPGYSTPLEAMK.G | Oxidation: 1, 19 |

# Detailed Protein Report

## Protein 1130: LON peptidase N-terminal domain and RING finger protein 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|148528975 | **Score:** | 14.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 83.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSPEPVPPPP | PPQCPGCDRA | EPIAQRLEEG | DEAFRAGDYE | MAAELFRSML | AGLAQPDRGL | CLRLGDALAR | AGRLPEALGA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FRGAARLGAL | RPEELEELAG | GLVRAVGLRD | RPLSAENPGG | EPEAPGEGGP | APEPRAPRDL | LGCPRCRRLL | HKPVTLPCGL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TVCKRCVEPG | PARPQVRRVN | VVLSGLLEKC | FPAECRLRRL | AGQARSLQRQ | QQPEAALLRC | DQALELAPDD | NSLLLLRAEL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YLTMKNYEQA | LQDASAACQN | EPLLIKGHQV | KAQALSGLGR | SKEVLKEFLY | CLALNPECNS | VKKEAQKVMC | EVLFSATANV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HENLTSSIQS | RLKAQGHSHM | NAQALLEEGD | AGSSENSSEK | SDMLGNTNSS | VLYFILGLHF | EEDKKALESI | LPTAPSAGLK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RQFPDDVEDA | PDLNAPGKIP | KKDLSLQRSP | NSETEESQGL | SLDVTDFECA | LCMRLLFEPV | TTPCGHTFCL | KCLERCLDHA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PHCPLCKDKL | SELLASRNFN | ITVLAEELIF | RYLPDELSDR | KRIYDEEMSE | LSNLTRDVPI | FVCAMAFPTV | PCPLHVFEPR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YRLMIRRCME | TGTKRFGMCL | SAEHAGLSEY | GCMLEIKDVR | TFPDGSSVVD | AIGISRFRVL | SHRHRDGYNT | ADIEYLEDEK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VEGPEYEELA | ALHDSVHQQS | VSWFASLQDR | MKEQILSHFG | VMPDREPEPQ | SNPSGPAWSW | WILAVLPLER | KAQLAILGMT |
| 730 | 740 | 750 | 760 | | | | |
| SLKERLLAIR | RILVIITRKM | NSRQELANAR | ERNN | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 899 | 1 | 491.6498 | -154.78 | 2 | 40.8 | 14.2 | 1 | 568-575 | R.CMETGTKR.F | Carbamidomethyl: 1 |

# Detailed Protein Report

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## Protein 1131: chymotrypsinogen B precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|118498341 | **Score:** | 14.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.7 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 10.6 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MASLWLLSCF | SLVGAAFGCG | VPAIHPVLSG | LSRIVNGEDA | VPGSWPWQVS | LQDKTGFHFC | GGSLISEDWV | VTAAHCGVRT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SDVVVAGEFD | QGSDEENIQV | LKIAKVFKNP | KFSILTVNND | ITLLKLATPA | RFSQTVSAVC | LPSADDDFPA | GTLCATTGWG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KTKYNANKTP | DKLQQAALPL | LSNAECKKSW | GRRITDVMIC | AGASGVSSCM | GDSGGPLVCQ | KDGAWTLVGI | VSWGSDTCST |
| 250 | 260 | 270 | | | | | |
| SSPGVYARVT | KLIPWVQKIL | AAN | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 323 | 1 | 939.4727 | 58.29 | 3 | 32.7 | 14.2 | 0 | 194-221 | R.ITDVMICAGASGVSSCMGDSGGPLVCQK.D | Carbamidomethyl: 16, 26;<br>Oxidation: 17 |

# Detailed Protein Report

## Protein 1132: PREDICTED: NADPH oxidase activator 1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578817006 | **Score:** | 14.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 35.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSKWPEGSLN | GLDSALDQVQ | RRGSLPPRQV | PRGEVFRPHR | WHLKHLEPVD | FLGKAKVVAS | AIPDDQGWGV | RPQQPQGPGA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NHDARSLIMD | SPRAGTHQGP | LDAETEVGAD | RCTSTAYQEQ | RPQVEQVGKQ | APLSPGLPAM | GGPGPGPCED | PAGAGGAGAG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GSEPLVTVTV | QCAFTVALRA | RRGADLSSLR | ALLGQALPHQ | AQLGQLSYLA | PGEDGHWVPI | PEEESLQRAW | QDAAACPRGL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QLQCRGAGGR | PVLYQVVAQH | SYSAQGPEDL | GFRQGDTVDV | LCEEPDVPLA | VDQAWLEGHC | DGRIGIFPKC | FVVPAGPRMS |
| 330 | 340 | | | | | | |
| GAPGRLPRSQ | QGDQP | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2321 | 1 | 1002.7244 | 204.94 | 1 | 59.5 | 14.2 | 0 | 310-318 | K.CFVVPAGPR.M | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 1133: PREDICTED: putative uncharacterized protein FLJ46235-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530359082 | **Score:** | 14.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 13.0 |
| | | **Sequence Coverage [%]:** | 6.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530435845 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: putative uncharacterized protein FLJ46235-like [Homo sapiens] |
| gi\|530386771 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: putative uncharacterized protein FLJ46235-like [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPSPSLQTAA | SDSARAQIPA | AFVRPKPPPA | QLSRPTCGLA | VASPGPDLAS | RWPSPAVFLP | ASQRPRQAHR | MPLTGLWRSS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SSLTVASPGP | APARPDGVSR | PRVSQVGPSR | AQLLPPGRWP | VRAQSVLKSA | SPGPAPACRR | PLDLRHGLCL | LTVDPHQAQL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LPQHGRLRPG | SCSACGQPPR | ARLSPLAILS | RPRSVSSQPL | QAQLSLPAAP | AGPAPASQQP | RSAQLLPSSW | QPL |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2544 | 1 | 694.4688 | 179.47 | 2 | 60.1 | 14.2 | 0 | 2-15 | M.PSPSLQTAASDSAR.A | |

# Detailed Protein Report

## Protein 1134: leucine-rich repeat-containing protein 10 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|63003903 | **Score:** | 14.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| | | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGNTIRALVA | FIPADRCQNY | VVRDLREMPL | DKMVDLSGSQ | LRRFPLHVCS | FRELVKLYLS | DNHLNSLPPE | LGQLQNLQIL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ALDFNNFKAL | PQVVCTLKQL | CILYLGNNKL | CDLPSELSLL | QNLRTLWIEA | NCLTQLPDVV | CELSLLKTLH | AGSNALRLLP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GQLRRLQELR | TIWLSGNRLT | DFPTVLLHMP | FLEVIDVDWN | SIRYFPSLAH | LSSLKLVIYD | HNPCRNAPKV | AKGVRRVGRW |
| 250 | 260 | 270 | 280 | | | | |
| AEETPEPDPR | KARRYALVRE | ESQELQAPVP | LLPPTNS | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 611 | 1 | 536.1729 | -265.36 | 2 | 37.2 | 14.2 | 0 | 89-98 | K.ALPQVVCTLK.Q | |

# Detailed Protein Report

## Protein 1135: 60S acidic ribosomal protein P0 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4506667 | **Score:** | 14.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|16933546 | refseq_human (refseq_human_20140103.fasta) | 60S acidic ribosomal protein P0 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPREDRATWK | SNYFLKIIQL | LDDYPKCFIV | GADNVGSKQM | QQIRMSLRGK | AVVLMGKNTM | MRKAIRGHLE | NNPALEKLLP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HIRGNVGFVF | TKEDLTEIRD | MLLANKVPAA | ARAGAIAPCE | VTVPAQNTGL | GPEKTSFFQA | LGITTKISRG | TIEILSDVQL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IKTGDKVGAS | EATLLNMLNI | SPFSFGLVIQ | QVFDNGSIYN | PEVLDITEET | LHSRFLEGVR | NVASVCLQIG | YPTVASVPHS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IINGYKRVLA | LSVETDYTFP | LAEKVKAFLA | DPSAFVAAAP | VAAATTAAPA | AAAAPAKVEA | KEESEESDED | MGFGLFD |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1927 | 1 | 918.3436 | -0.04 | 2 | 54.0 | 14.2 | 0 | 302-317 | K.EESEESDEDMGFGLFD.- | |

# Detailed Protein Report

## Protein 1136: PREDICTED: nuclear receptor subfamily 4 group A member 1 isoform X2 [Homo sapiens]

**Accession:** gi|530400145
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 14.2
**MW [kDa]:** 70.4
**pI:** 8.9
**Sequence Coverage [%]:** 2.8
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTSAQYKIKI | LIEGLHHGQR | PGPAPPRQPG | SFCWALKADG | IMWLAKACWS | IQSEMPCIQA | QYGTPAPSPG | PRDHLASDPL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TPEFIKPTMD | LASPEAAPAA | PTALPSFSTF | MDGYTGEFDT | FLYQLPGTVQ | PCSSASSSAS | STSSSSATSP | ASASFKFEDF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QVYGCYPGPL | SGPVDEALSS | SGSDYYGSPC | SAPSPSTPSF | QPPQLSPWDG | SFGHFSPSQT | YEGLRAWTEQ | LPKASGPPQP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PAFFSFSPPT | GPSPSLAQSP | LKLFPSQATH | QLGEGESYSM | PTAFPGLAPT | SPHLEGSGIL | DTPVTSTKAR | SGAPGGSEGR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CAVCGDNASC | QHYGVRTCEG | CKGFFKRTVQ | KNAKYICLAN | KDCPVDKRRR | NRCQFCRFQK | CLAVGMVKEV | VRTDSLKGRR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GRLPSKPKQP | PDASPANLLT | SLVRAHLDSG | PSTAKLDYSK | FQELVLPHFG | KEDAGDVQQF | YDLLSGSLEV | IRKWAEKIPG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FAELSPADQD | LLLESAFLEL | FILRLAYRSK | PGEGKLIFCS | GLVLHRLQCA | RGFGDWIDSI | LAFSRSLHSL | LVDVPAFACL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SALVLITDRH | GLQEPRRVEE | LQNRIASCLK | EHVAAVAGEP | QPASCLSRLL | GKLPELRTLC | TQGLQRIFYL | KLEDLVPPPP |
| 650 | 660 | | | | | | |
| IIDKIFMDTL | PF | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2308 | 1 | 973.1508 | 106.11 | 2 | 58.7 | 14.2 | 0 | 10-27 | K.ILIEGLHHGQRPGPAPPR.Q | |

# Detailed Protein Report

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## Protein 1137: telomerase-binding protein EST1A isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|378744171 | **Score:** | 14.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| | | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.63 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.19 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530410170 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: telomerase-binding protein EST1A isoform X3 [Homo sapiens] |
| gi\|378744173 | refseq_human (refseq_human_20140103.fasta) | telomerase-binding protein EST1A isoform 3 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| METFPAVAEK | VLKEFQVLLQ | HSPSPIGSTR | MLQLMTINMF | AVHNSQLKDC | FSEECRSVIQ | EQAAALGLAM | FSLLVRRCTC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LLKESAKAQL | SSPEDQDDQD | DIKVSSFVPD | LKELLPSVKV | WSDWMLGYPD | TWNPPPTSLD | LPSHVAVDVW | STLADFCNIL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TAVNQSEVPL | YKDPDDDLTL | LILEEDRLLS | GFVPLLAAPQ | DPCYVEKTSD | KVIAADCKRV | TVLKYFLEAL | CGQEEPLLAF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KGGKYVSVAP | VPDTMGKEMG | SQEGTRLEDE | EEDVVIEDFE | EDSEAEGSGG | EDDIRELRAK | KLALARKIAE | QQRRQEKIQA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VLEDHSQMRQ | MELEIRPLFL | VPDTNGFIDH | LASLARLLES | RKYILVVPLI | VINELDGLAK | GQETDHRAGG | YARVVQEKAR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KSIEFLEQRF | ESRDSCLRAL | TSRGNELESI | AFRSEDITGQ | LGNNDDLILS | CCLHYCKDKA | KDFMPASKEE | PIRLLREVVL |
| 490 | 500 | 510 | 520 | | | | |
| LTDDRNLRVK | ALTRNVPVRD | IPAFLTWAQV | G | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2172 | 1 | 666.3077 | -111.59 | 2 | 57.5 | 14.2 | 1 | 2-13 | M.ETFPAVAEKVLK.E | | WUP:QUP 0.19<br>QU:MU 0.63 |

# Detailed Protein Report

## Protein 1138: PREDICTED: dedicator of cytokinesis protein 6 isoform X5 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|578833406 | **Score:** | 14.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 130.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
|  |  | **Sequence Coverage [%]:** | 1.1 |
|  |  | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.44 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MKASLWAAEL GWAVTGCGLL HEELALQWVV SSSAVREAIL QHAWFFFQLM VKSMALHLLL GQRLDTPRKL RFPGRFLDDI

        90        100        110        120        130        140        150        160
TALVGSVGLE VITRVHKDVE LAEHLNASLA FFLSDLLSLV DRGFVFSLVR AHYKQVATRL QSSPNPAALL TLRMEFTRIL

       170        180        190        200        210        220        230        240
CSHEHYVTLN LPCCPLSPPA SPSPSVSSTT SQSSTFSSQA PDPKVTSMFE LSGPFRQQHF LAGLLLTELA LALEPEAEGA

       250        260        270        280        290        300        310        320
FLLHKKAISA VHSLLCGHDT DPRYAEATVK ARVAELYLPL LSIARDTLPR LHDFAEGPGQ RSRLASMLDS DTEGEGDIAG

       330        340        350        360        370        380        390        400
TINPSVAMAI AGGPLAPGSR ASISQGPPTA SRAGCALSAE SSRTLLACVL WVLKNTEPAL LQRWATDLTL PQLGRLLDLL

       410        420        430        440        450        460        470        480
YLCLAAFEYK GKKAFERINS LTFKKSLDMK ARLEEAILGT IGARQEMVRR SRERSPFGNP ENVRWRKSVT HWKQTSDRVD

       490        500        510        520        530        540        550        560
KTKDEMEHEA LVEGNLATEA SLVVLDTLEI IVQTVMLSEA RESVLGAVLK VVLYSLGSAQ SALFLQHGLA TQRALVSKFP

       570        580        590        600        610        620        630        640
ELLFEEDTEL CADLCLRLLR HCGSRISTIR THASASLYLL MRQNFEIGHN FARVKMQVTM SLSSLVGTTQ NFSEEHLRRS

       650        660        670        680        690        700        710        720
LKTILTYAEE DMGLRDSTFA EQVQDLMFNL HMILTDTVKM KEHQEDPEML IDLMYRIARG YQGSPDLRLT WLQNMAGKHA

       730        740        750        760        770        780        790        800
ELGNHAEAAQ CMVHAAALVA EYLALLEDHR HLPVGCVSFQ NISSNVLEES AISDDILSPD EEGFCSGKHF TELGLVGLLE

       810        820        830        840        850        860        870        880
QAAGYFTMGG LYEAVNEVYK NLIPILEAHR DYKKLAAVHG KLQEAFTKIM HQSSGWERVF GTYFRVGFYG AHFGDLDEQE

       890        900        910        920        930        940        950        960
FVYKEPSITK LAEISHRLEE FYTERFGDDV VEIIKDSNPV DKSKLDSQKA YIQITYVEPY FDTYELKDRV TYFDRNYGLR

       970        980        990       1000       1010       1020       1030       1040
TFLFCTPFTP DGRAHGELPE QHKRKTLLST DHAFPYIKTR IRVCHREETV LTPVEVAIED MQKKTRELAF ATEQDPPDAK

      1050       1060       1070       1080       1090       1100       1110       1120
MLQMVLQGSV GPTVNQGPLE VAQVFLAEIP EDPKLFRHHN KLRLCFKDFC KKCEDALRKN KALIGPDQKE YHRELERNYC

      1130       1140       1150       1160
RLREALQPLL TQRLPQLMAP TPPGLRNSLN RASFRKADL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1355 | 1 | 695.8559 | -59.65 | 2 | 46.5 | 14.1 | 0 | 1134-1146 | R.LPQLMAPTPPGLR.N |  | QU:MU | 0.44 |

BRUKER

# Detailed Protein Report

## Protein 1139: POU domain, class 2, transcription factor 3 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|148664218 | **Score:** | 14.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 47.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.41 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MVNLESMHTD | IKMSGDVADS | TDARSTLSQV | EPGNDRNGLD | FNRQIKTEDL | SDSLQQTLSH | RPCHLSQGPA | MMSGNQMSGL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NASPCQDMAS | LHPLQQLVLV | PGHLQSVSQF | LLSQTQPGQQ | GLQPNLLPFP | QQQSGLLLPQ | TGPGLASQAF | GHPGLPGSSL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EPHLEASQHL | PVPKHLPSSG | GADEPSDLEE | LEKFAKTFKQ | RRIKLGFTQG | DVGLAMGKLY | GNDFSQTTIS | RFEALNLSFK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NMCKLKPLLE | KWLNDAESSP | SDPSVSTPSS | YPSLSEVFGR | KRKKRTSIET | NIRLTLEKRF | QDNPKPSSEE | ISMIAEQLSM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EKEVVRVWFC | NRRQKEKRIN | CPVATPIKPP | VYNSRLVSPS | GSLGPLSVPP | VHSTMPGTVT | SSCSPGNNSR | PSSPGSGLHA |
| 410 | 420 | 430 | 440 | | | | |
| SSPTASQNNS | KAAVNSASSF | NSSGSWYRWN | HSTYLH | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 465 | 1 | 643.8361 | 18.68 | 2 | 35.8 | 14.1 | 0 | 2-12 | M.VNLESMHTDIK.M | | WUP:QUP 0.41 |

# Detailed Protein Report

## Protein 1140: zinc finger imprinted 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|33354273 | **Score:** | 14.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 61.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|226423929 | refseq_human (refseq_human_20140103.fasta) | zinc finger imprinted 2 [Homo sapiens] |
| gi\|226423927 | refseq_human (refseq_human_20140103.fasta) | zinc finger imprinted 2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MYQPEDDNNS | DVTSDDDMTR | NRRESSPPHS | VHSFSGDRDW | DRRGRSRDME | PRDRWSHTRN | PRSRMPPRDL | SLPVVAKTSF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EMDREDDRDS | RAYESRSQDA | ESYQNVVDLA | EDRKPHNTIQ | DNMENYRKLL | SLGFLAQDSV | PAEKRNTEML | DNLPSAGSQF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PDFKHLGTFL | VFEELVTFED | VLVDFSPEEL | SSLSAAQRNL | YREVMLENYR | NLVSLGHQFS | KPDIISRLEE | EESYAMETDS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RHTVICQGES | HDDPLEPHQG | NQEKLLTPIT | MNDPKTLTPE | RSYGSDEFER | SSNLSKQSKD | PLGKDPQEGT | APGICTSPQS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ASQENKHNRC | EFCKRTFSTQ | VALRRHERIH | TGKKPYECKQ | CAEAFYLMPH | LNRHQKTHSG | RKTSGCNEGR | KPSVQCANLC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ERVRIHSQED | YFECFQCGKA | FLQNVHLLQH | LKAHEAARVL | PPGLSHSKTY | LIRYQRKHDY | VGERACQCCD | CGRVFSRNSY |
| 490 | 500 | 510 | 520 | 530 | | | |
| LIQHYRTHTQ | ERPYQCQLCG | KCFGRPSYLT | QHYQLHSQEK | TVECDHC | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2843 | 1 | 616.8649 | -144.67 | 3 | 64.2 | 14.1 | 0 | 487-501 | R.THTQERPYQCQLCGK.C | Carbamidomethyl: 13 |

# Detailed Protein Report

## Protein 1141: homeobox protein Hox-D8 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|315075340 | **Score:** | 14.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 4.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSSYFVNPLY | SKYKAAAAAA | AAAGEAINPT | YYDCHFAPEV | GGRHAAAAAA | LQLYGNSAAG | FPHAPPQAHA | HPHPSPPPSG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TGCGGREGRG | QEYFHPGGGS | PAAAYQAAPP | PPPHPPPPPP | PPPCGGIACH | GEPAKFYGYD | NLQRQPIFTT | QQEAELVQYP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DCKSSSGNIG | EDPDHLNQSS | SPSQMFPWMR | PQAPGRRRGR | QTYSRFQTLE | LEKEFLFNPY | LTRKRRIEVS | HALALTERQV |
| 250 | 260 | 270 | 280 | 290 | | | |
| KIWFQNRRMK | WKKENNKDKF | PVSRQEVKDG | ETKKEAQELE | EDRAEGLTN | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1773 | 1 | 798.3031 | -132.50 | 2 | 52.5 | 14.1 | 1 | 2-14 | M.SSYFVNPLYSKYK.A | |

# Detailed Protein Report

## Protein 1142: heterogeneous nuclear ribonucleoprotein U isoform b [Homo sapiens]

**Accession:** gi|14141161

**Database:** refseq_human(refseq_human_20140103.fasta)

**Database Date:** 2015-11-30

**Score:** 14.1

**MW [kDa]:** 88.9

**pI:** 5.5

**Sequence Coverage [%]:** 1.4

**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSSPVNVKK | LKVSELKEEL | KKRRLSDKGL | KAELMERLQA | ALDDEEAGGR | PAMEPGNGSL | DLGGDSAGRS | GAGLEQEAAA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GGDEEEEEEE | EEEEGISALD | GDQMELGEEN | GAAGAADSGP | MEEEEAASED | ENGDDQGFQE | GEDELGDEEE | GAGDENGHGE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QQPQPPATQQ | QQPQQQRGAA | KEAAGKSSGP | TSLFAVTVAP | PGARQGQQQA | GGDGKTEQKG | GDKKRGVKRP | REDHGRGYFE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YIEENKYSRA | KSPQPPVEEE | DEHFDDTVVC | LDTYNCDLHF | KISRDRLSAS | SLTMESFAFL | WAGGRASYGV | SKGKVCFEMK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VTEKIPVRHL | YTKDIDIHEV | RIGWSLTTSG | MLLGEEEFSY | GYSLKGIKTC | NCETEDYGEK | FDENDVITCF | ANFESDEVEL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SYAKNGQDLG | VAFKISKEVL | AGRPLFPHVL | CHNCAVEFNF | GQKEKPYFPI | PEEYTFIQNV | PLEDRVRGPK | GPEEKKDCEV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VMMIGLPGAG | KTTWVTKHAA | ENPGKYNILG | TNTIMDKMMV | AGFKKQMADT | GKLNTLLQRA | PQCLGKFIEI | AARKKRNFIL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DQTNVSAAAQ | RRKMCLFAGF | QRKAVVVCPK | DEDYKQRTQK | KAEVEGKDLP | EHAVLKMKGN | FTLPEVAECF | DEITYVELQK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EEAQKLLEQY | KEESKKALPP | EKKQNTGSKK | SNKNKSGKNQ | FNRGGGHRGR | GGFNMRGGNF | RGGAPGNRGG | YNRRGNMPQR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GGGGGGSGGI | GYPYPRAPVF | PGRGSYSNRG | NYNRGGMPNR | GNYNQNFRGR | GNNRGYKNQS | QGYNQWQQGQ | FWGQKPWSQH |
| 810 | | | | | | | |
| YHQGYY | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 437 | 2 | 658.3928 | -3.68 | 2 | 35.1 | 14.1 | 2 | 11-21 | K.LKVSELKEELK.K | |

# Detailed Protein Report

## Protein 1143: beta-Ala-His dipeptidase precursor [Homo sapiens]

**Accession:** gi|21071039
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 14.1
**MW [kDa]:** 56.7
**pI:** 5.0
**Sequence Coverage [%]:** 6.7
**No. of unique Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDPKLGRMAA | SLLAVLLLLL | ERGMFSSPSP | PPALLEKVFQ | YIDLHQDEFV | QTLKEWVAIE | SDSVQPVPRF | RQELFRMMAV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AADTLQRLGA | RVASVDMGPQ | QLPDGQSLPI | PPVILAELGS | DPTKGTVCFY | GHLDVQPADR | GDGWLTDPYV | LTEVDGKLYG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RGATDNKGPV | LAWINAVSAF | RALEQDLPVN | IKFIIEGMEE | AGSVALEELV | EKEKDRFFSG | VDYIVISDNL | WISQRKPAIT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YGTRGNSYFM | VEVKCRDQDF | HSGTFGGILH | EPMADLVALL | GSLVDSSGHI | LVPGIYDEVV | PLTEEEINTY | KAIHLDLEEY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RNSSRVEKFL | FDTKEEILMH | LWRYPSLSIH | GIEGAFDEPG | TKTVIPGRVI | GKFSIRLVPH | MNVSAVEKQV | TRHLEDVFSK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RNSSNKMVVS | MTLGLHPWIA | NIDDTQYLAA | KRAIRTVFGT | EPDMIRDGST | IPIAKMFQEI | VHKSVVLIPL | GAVDDGEHSQ |
| 490 | 500 | 510 | | | | | |
| NEKINRWNYI | EGTKLFAAFF | LEMAQLH | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2217 | 1 | 1288.9464 | -38.66 | 3 | 57.6 | 14.1 | 2 | 335-368 | K.EEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGR.V | Oxidation: 5 |

# Detailed Protein Report

## Protein 1144: PREDICTED: urea transporter 1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530413917 | **Score:** | 14.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 43.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.65 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNGRSLIGGA | GDARHGPVWK | DPFGTKAGDA | ARRGIARLSL | ALADGSQEQE | PEEEIAMEDS | PTMVRVDSPT | MVRGENQVSP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CQGRRCFPKA | LGYVTGDMKE | LANQLKDKPV | VLQFIDWILR | GISQVVFVNN | PVSGILILVG | LLVQNPWWAL | TGWLGTVVST |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LMALLLSQDR | SLIASGLYGY | NATLVGVLMA | VFSDKGDYFW | WLLLPVCAMS | MTCPIFSSAL | NSMLSKWDLP | VFTLPFNMAL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SMYLSATGHY | NPFFPAKLVI | PITTAPNISW | SDLSALELLK | SIPVGVGQIY | GCDNPWTGGI | FLGAILLSSP | LMCLHAAIGS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LLGIAAGLSL | SAPFEDIYFG | LWGFNSSLAC | IAMGGMFMAL | TWQTHLLALG | CALFTAYLGV | GMANFMAEGT | CERRIVGKKK |
| 410 | | | | | | | |
| QA | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1091 | 1 | 622.3184 | -16.57 | 2 | 43.8 | 14.1 | 1 | 2-14 | M.NGRSLIGGAGDAR.H | | QU:MU | 0.65 |

# Detailed Protein Report

## Protein 1145: nitric oxide synthase, inducible [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|24041029 | **Score:** | 14.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 131.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 1.2 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MACPWKFLFK | TKFHQYAMNG | EKDINNNVEK | APCATSSPVT | QDDLQYHNLS | KQQNESPQPL | VETGKKSPES | LVKLDATPLS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SPRHVRIKNW | GSGMTFQDTL | HHKAKGILTC | RSKSCLGSIM | TPKSLTRGPR | DKPTPPDELL | PQAIEFVNQY | YGSFKEAKIE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EHLARVEAVT | KEIETTGTYQ | LTGDELIFAT | KQAWRNAPRC | IGRIQWSNLQ | VFDARSCSTA | REMFEHICRH | VRYSTNNGNI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RSAITVFPQR | SDGKHDFRVW | NAQLIRYAGY | QMPDGSIRGD | PANVEFTQLC | IDLGWKPKYG | RFDVVPLVLQ | ANGRDPELFE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IPPDLVLEVA | MEHPKYEWFR | ELELKWYALP | AVANMLLEVG | GLEFPGCPFN | GWYMGTEIGV | RDFCDVQRYN | ILEEVGRRMG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LETHKLASLW | KDQAVVEINI | AVLHSFQKQN | VTIMDHHSAA | ESFMKYMQNE | YRSRGGCPAD | WIWLVPPMSG | SITPVFHQEM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LNYVLSPFYY | YQVEAWKTHV | WQDEKRRPKR | REIPLKVLVK | AVLFACMLMR | KTMASRVRVT | ILFATETGKS | EALAWDLGAL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FSCAFNPKVV | CMDKYRLSCL | EEERLLLVVT | STFGNGDCPG | NGEKLKKSLF | MLKELNNKFR | YAVFGLGSSM | YPRFCAFAHD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IDQKLSHLGA | SQLTPMGEGD | ELSGQEDAFR | SWAVQTFKAA | CETFDVRGKQ | HIQIPKLYTS | NVTWDPHHYR | LVQDSQPLDL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SKALSSMHAK | NVFTMRLKSR | QNLQSPTSSR | ATILVELSCE | DGQGLNYLPG | EHLGVCPGNQ | PALVQGILER | VVDGPTPHQT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VRLEALDESG | SYWVSDKRLP | PCSLSQALTY | FLDITTPPTQ | LLLQKLAQVA | TEEPERQRLE | ALCQPSEYSK | WKFTNSPTFL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EVLEEFPSLR | VSAGFLLSQL | PILKPRFYSI | SSSRDHTPTE | IHLTVAVVTY | HTRDGQGPLH | HGVCSTWLNS | LKPQDPVPCF |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VRNASGFHLP | EDPSHPCILI | GPGTGIAPFR | SFWQQRLHDS | QHKGVRGGRM | TLVFGCRRPD | EDHIYQEEML | EMAQKGVLHA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VHTAYSRLPG | KPKVYVQDIL | RQQLASEVLR | VLHKEPGHLY | VCGDVRMARD | VAHTLKQLVA | AKLKLNEEQV | EDYFFQLKSQ |
| 1130 | 1140 | 1150 | 1160 |  |  |  |  |
| KRYHEDIFGA | VFPYEAKKDR | VAVQPSSLEM | SAL |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2767 | 1 | 841.9071 | -64.44 | 2 | 65.0 | 14.1 | 1 | 517-530 | K.VLVKAVLFACMLMR.K | Carbamidomethyl: 10;<br>Oxidation: 11, 13 |

# Detailed Protein Report

## Protein 1146: abhydrolase domain-containing protein 16A isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|294660765 | **Score:** | 14.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 4.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPPPALFLSS | LYPRLEFQND | FYRSCIRRSS | PQPPPNLAWR | PESLYSGELA | GGGYLSLSKV | VPFSHYAGTL | LLLLAGVACL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RGIGRWTNPQ | YRQFITILEA | THRNQSSENK | RQLANYNFDF | RSWPVDFHWE | EPSSRKESRG | GPSRRGVALL | RPEPLHRGTA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DTLLNRVKKL | PCQITSYLVA | HTLGRRMLYP | GSVYLLQKAL | MPVLLQGQAR | LVEECNGRRA | KLLACDGNEI | DTMFVDRRGT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AEPQGQKLVI | CCEGNAGFYE | VGCVSTPLEA | GYSVLGWNHP | GFAGSTGVPF | PQNEANAMDV | VVQFAIHRLG | FQPQDIIIYA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WSIGGFTATW | AAMSYPDVSA | MILDASFDDL | VPLALKVMPD | SWRGLVTRTV | RQHLNLNNAE | QLCRYQGPVL | LIRRTKDEII |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TTTVPEDIMS | NRGNDLLLKL | LQHRYPRVMA | EEGLRVVRQW | LEASSQLEEA | SIYSRWEVEE | DWCLSVLRSY | QAEHGPDFPW |
| 490 | 500 | 510 | 520 | 530 | | | |
| SVGEDMSADG | RRQLALFLAR | KHLHNFEATH | CTPLPAQNFQ | MPWHL | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1466 | 1 | 846.6175 | -88.48 | 3 | 48.0 | 14.1 | 0 | 469-491 | R.SYQAEHGPDFPWSVGEDMSADGR.R | |

# Detailed Protein Report

## Protein 1147: krev interaction trapped protein 1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|61742817 | **Score:** | 14.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 78.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578814707 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: krev interaction trapped protein 1 isoform X15 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MGNPENIEDA YYVAVIRPKNT ASLNSREYRA KSYEILLHEV PIEGQKKKRK KVLLETKLQG NSEITQGILD YVVETTKPIS
        90        100        110        120        130        140        150        160
PANQGIRGKR VVLMKKFPLD GEKMGREASL FIVPSVVKDN TKYTYTPGCP IFYCLQDIMR VCSESSTHFA TLTARMLIAL
       170        180        190        200        210        220        230        240
DKWLDERHAQ SHFIPALFRP SPLERIKTNV INPAYATESG QTENSLHMGY SALEIKSKML ALEKADTCIY NPLFGSDLQY
       250        260        270        280        290        300        310        320
TNRVDKVVIN PYFGLGAPDY SKIQIPKQEK WQRSMSSVTE DKYGKVEATR ILLEKGKCNP NLLNGQLSSP LHFAAGGGHA
       330        340        350        360        370        380        390        400
EIVQILLNHP ETDRHITDQQ GRSPLNICEE NKQNNWEEAA KLLKEAINKP YEKVRIYRMD GSYRSVELKH GNNTTVQQIM
       410        420        430        440        450        460        470        480
EGMRLSQETQ QYFTIWICSE NLSLQLKPYH KPLQHVRDWP EILAELTNLD PQRETPQLFL RRDVRLPLEV EKQIEDPLAI
       490        500        510        520        530        540        550        560
LILFDEARYN LLKGFYTAPD AKLITLASLL LQIVYGNYES KKHKQGFLNE ENLKSIVPVT KLKSKAPHWT NRILHEYKNL
       570        580        590        600        610        620        630        640
STSEGVSKEM HHLQRMFLQN CWEIPTYGAA FFTGQIFTKA SPSNHKVIPV YVGVNIKGLH LLNMETKALL ISLKYGCFMW
       650        660        670        680        690
QLGDTDTCFQ IHSMENKMSF IVHTKQAGLV VKLLMKLNGQ LMPTERNS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1509 | 1 | 829.3458 | -157.64 | 2 | 49.1 | 14.1 | 1 | 658-672 | K.MSFIVHTKQAGLVVK.L | |

# Detailed Protein Report

## Protein 1148: contactin-2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4827022 | **Score:** | 14.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 113.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.9 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGTATRRKPH | LLLVAAVALV | SSSAWSSALG | SQTTFGPVFE | DQPLSVLFPE | ESTEEQVLLA | CRARASPPAT | YRWKMNGTEM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KLEPGSRHQL | VGGNLVIMNP | TKAQDAGVYQ | CLASNPVGTV | VSREAILRFG | FLQEFSKEER | DPVKAHEGWG | VMLPCNPPAH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YPGLSYRWLL | NEFPNFIPTD | GRHFVSQTTG | NLYIARTNAS | DLGNYSCLAT | SHMDFSTKSV | FSKFAQLNLA | AEDTRLFAPS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IKARFPAETY | ALVGQQVTLE | CFAFGNPVPR | IKWRKVDGSL | SPQWTTAEPT | LQIPSVSFED | EGTYECEAEN | SKGRDTVQGR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IIVQAQPEWL | KVISDTEADI | GSNLRWGCAA | AGKPRPTVRW | LRNGEPLASQ | NRVEVLAGDL | RFSKLSLEDS | GMYQCVAENK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HGTIYASAEL | AVQALAPDFR | LNPVRRLIPA | ARGGEILIPC | QPRAAPKAVV | LWSKGTEILV | NSSRVTVTPD | GTLIIRNISR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SDEGKYTCFA | ENFMGKANST | GILSVRDATK | ITLAPSSADI | NLGDNLTLQC | HASHDPTMDL | TFTWTLDDFP | IDFDKPGGHY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RRTNVKETIG | DLTILNAQLR | HGGKYTCMAQ | TVVDSASKEA | TVLVRGPPGP | PGGVVVRDIG | DTTIQLSWSR | GFDNHSPIAK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| YTLQARTPPA | GKWKQVRTNP | ANIEGNAETA | QVLGLTPWMD | YEFRVIASNI | LGTGEPSGPS | SKIRTREAAP | SVAPSGLSGG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GGAPGELIVN | WTPMSREYQN | GDGFGYLLSF | RRQGSTHWQT | ARVPGADAQY | FVYSNESVRP | YTPFEVKIRS | YNRRGDGPES |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LTALVYSAEE | EPRVAPTKVW | AKGVSSSEMN | VTWEPVQQDM | NGILLGYEIR | YWKAGDKEAA | ADRVRTAGLD | TSARVSGLHP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| NTKYHVTVRA | YNRAGTGPAS | PSANATTMKP | PPRRPPGNIS | WTFSSSSLSI | KWDPVVPFRN | ESAVTGYKML | YQNDLHLTPT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LHLTGKNWIE | IPVPEDIGHA | LVQIRTTGPG | GDGIPAEVHI | VRNGGTSMMV | ENMAVRPAPH | PGTVISHSVA | MLILIGSLEL |
| 1050 | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 159 | 1 | 619.6506 | -71.74 | 3 | 31.7 | 14.0 | 1 | 599-617 | K.EATVLVRGPPGPPGGVVVR.D | |

# Detailed Protein Report

## Protein 1149: cytokine receptor common subunit beta precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4559408 | **Score:** | 14.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 97.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVLAQGLLSM | ALLALCWERS | LAGAEETIPL | QTLRCYNDYT | SHITCRWADT | QDAQRLVNVT | LIRRVNEDLL | EPVSCDLSDD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MPWSACPHPR | CVPRRCVIPC | QSFVVTDVDY | FSFQPDRPLG | TRLTVTLTQH | VQPPEPRDLQ | ISTDQDHFLL | TWSVALGSPQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SHWLSPGDLE | FEVVYKRLQD | SWEDAAILLS | NTSQATLGPE | HLMPSSTYVA | RVRTRLAPGS | RLSGRPSKWS | PEVCWDSQPG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DEAQPQNLEC | FFDGAAVLSC | SWEVRKEVAS | SVSFGLFYKP | SPDAGEEECS | PVLREGLGSL | HTRHHCQIPV | PDPATHGQYI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VSVQPRRAEK | HIKSSVNIQM | APPSLNVTKD | GDSYSLRWET | MKMRYEHIDH | TFEIQYRKDT | ATWKDSKTET | LQNAHSMALP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ALEPSTRYWA | RVRVRTSRTG | YNGIWSEWSE | ARSWDTESVL | PMWVLALIVI | FLTIAVLLAL | RFCGIYGYRL | RRKWEEKIPN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PSKSHLFQNG | SAELWPPGSM | SAFTSGSPPH | QGPWGSRFPE | LEGVFPVGFG | DSEVSPLTIE | DPKHVCDPPS | GPDTTPAASD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LPTEQPPSPQ | PGPPAASHTP | EKQASSFDFN | GPYLGPPHSR | SLPDILGQPE | PPQEGGSQKS | PPPGSLEYLC | LPAGGQVQLV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PLAQAMGPGQ | AVEVERRPSQ | GAAGSPSLES | GGGPAPPALG | PRVGGQDQKD | SPVAIPMSSG | DTEDPGVASG | YVSSADLVFT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PNSGASSVSL | VPSLGLPSDQ | TPSLCPGLAS | GPPGAPGPVK | SGFEGYVELP | PIEGRSPRSP | RNNPVPPEAK | SPVLNPGERP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ADVSPTSPQP | EGLLVLQQVG | DYCFLPGLGP | GPLSLRSKPS | SPGPGPEIKN | LDQAFQVKKP | PGQAVPQVPV | IQLFKALKQQ |
| 890 | 900 | | | | | | |
| DYLSLPPWEV | NKPGEVC | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2606 | 1 | 495.0590 | 111.94 | 4 | 60.9 | 14.0 | 0 | 601-619 | R.SLPDILGQPEPPQEGGSQK.S | |

# Detailed Protein Report

## Protein 1150: PREDICTED: proline-rich protein PRCC isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530365026 | **Score:** | 14.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 48.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSLVAYASSD | ESEPDEAEPE | PEEEEAVAPT | SGPALGGLFA | SLPAPKGPAL | LPPPPQMLAP | AFPPPLLLPP | PTGDPRLQPP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PPLPFGLGGF | PPPPGVSPAE | AAGVGEGLGL | GLPSPRGPGL | NLPPPIGGAG | PPLGLPKPKK | RKEPVKIAAP | ELHKGDSDSE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EDEPTKKKTI | LQGSSEGTGL | SALLPQPKNL | TVKETNRLLL | PHAFSRKPSD | GSPDTKPSRL | ASKTKTSSLA | PVVGTTTTTP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SPSAIKAAAK | SAALQVTKQI | TQEEDDSDEE | VAPENFFSLP | EKAEPPGVEP | YPYPIPTVPE | ELPPGTEPEP | AFQDDAANAP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LEFKMAAGSS | GAPWMPKPGD | DYSYNQFSTY | GDANAAGAYY | QFKRLQGKRN | RGREEINFVE | IKGDDQLSGA | QQWMTKSLTE |
| 410 | 420 | 430 | 440 | 450 | 460 | | |
| EKTMKSFSKK | KGEQPTGQQR | RKHQITYLIH | QAKERELELK | NTWSENKLSR | RQTQAKYGF | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2229 | 1 | 666.3544 | -49.99 | 2 | 56.2 | 14.0 | 1 | 143-154 | K.EPVKIAAPELHK.G | |

# Detailed Protein Report

## Protein 1151: PREDICTED: guanine nucleotide-binding protein G(olf) subunit alpha isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578832131 | **Score:** | 14.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 26.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 8.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGLCYSLRPL | LFGGPGDDPC | AASEPPVEDA | QPAPAPALAP | VRAAARDTAR | TLLPRGGEGS | PACARPKADK | PKEKRQRTEQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LSAEEREAAK | EREAVKEARK | VSRGIDRMLR | DQKRDLQQTH | RLLLLGAGES | GKSTIVKQMR | ILHVNGFNPE | EKKQKILDIR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KNVKDAIVTI | VSAMSTIIPP | VPLANPENQF | RSDYIKSIAP | ITDFEYSQEF | FDHVKKLWDD | EGVKACFERS | NEYQLIDCAQ |
| 250 | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 826 | 1 | 737.3742 | -17.03 | 3 | 40.3 | 14.0 | 2 | 47-67 | R.DTARTLLPRGGEGSPACARPK.A | Carbamidomethyl: 17 |

# Detailed Protein Report

## Protein 1152: F-box only protein 31 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|83035136 | **Score:** | 13.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 60.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAVCARLCGV | GPSRGCRRRQ | QRRGPAETAA | ADSEPDTDPE | EERIEASAGV | GGGLCAGPSP | PPPRCSLLEL | PPELLVEIFA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SLPGTDLPSL | AQVCTKFRRI | LHTDTIWRRR | CREEYGVCEN | LRKLEITGVS | CRDVYAKLLH | RYRHILGLWQ | PDIGPYGGLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NVVVDGLFII | GWMYLPPHDP | HVDDPMRFKP | LFRIHLMERK | AATVECMYGH | KGPHHGHIQI | VKKDEFSTKC | NQTDHHRMSG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GRQEEFRTWL | REEWGRTLED | IFHEHMQELI | LMKFIYTSQY | DNCLTYRRIY | LPPSRPDDLI | KPGLFKGTYG | SHGLEIVMLS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FHGRRARGTK | ITGDPNIPAG | QQTVEIDLRH | RIQLPDLENQ | RNFNELSRIV | LEVRERVRQE | QQEGGHEAGE | GRGRQGPRES |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QPSPAQPRAE | APSKGPDGTP | GEDGGEPGDA | VAAAEQPAQC | GQGQPFVLPV | GVSSRNEDYP | RTCRMCFYGT | GLIAGHGFTS |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| PERTPGVFIL | FDEDRFGFVW | LELKSFSLYS | RVQATFRNAD | APSPQAFDEM | LKNIQSLTS | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2106 | 1 | 925.3145 | -137.61 | 2 | 56.2 | 13.9 | 2 | 1-17 | -.MAVCARLCGVGPSRGCR.R | Carbamidomethyl: 4, 8 |

# Detailed Protein Report

## Protein 1153: PREDICTED: Na(+)/H(+) exchange regulatory cofactor NHE-RF2 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530409419 | **Score:** | 13.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 35.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSPPPSGGPW GLRAGVRGDS SAGGGCVVGA RCLRGLPGFP GSCSSGASTG PSCVLGPGLL PVPSALGPGA GQGLPAASFL
        90        100        110        120        130        140        150        160
PFLGRKPSWV GGARLEPSQG SGLSHHPAPQ SDSAPTSPPI PGEPGPQREV DKWGGSLGRP ESSGHPGRTP ATCCHCAAVM
       170        180        190        200        210        220        230        240
ARSGSATPPA RAPGAPPRSP PQRLVQDVSG PLRELRPRLC HLRKGPQGYG FNLHSDKSRP GQYIRSVDPG SPAARSGLRA
       250        260        270        280        290        300        310        320
QDRLIEVNGQ NVEGLRHAEV VASIKAREDE ARLLVVDPET DEHFKRLRVT PTEEHVEGPL PSPVTNGTSP AQLNGGSACS
       330        340        350
SRSDLPGSDK DTEEGPPSGV WD
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 513 | 1 | 746.2002 | -160.22 | 2 | 36.4 | 13.9 | 0 | 149-162 | R.TPATCCHCAAVMAR.S | Carbamidomethyl: 6 |

# Detailed Protein Report

## Protein 1154: bisphosphoglycerate mutase [Homo sapiens]

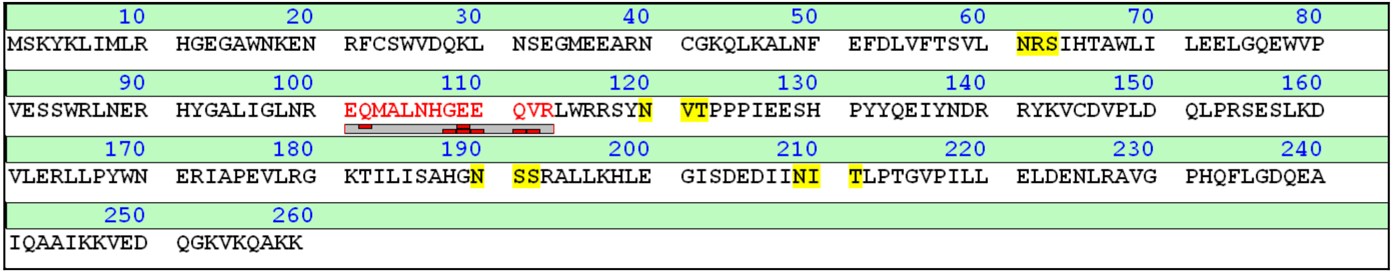
| | | | |
|---|---|---|---|
| **Accession:** | gi\|4502445 | **Score:** | 13.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 30.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.78 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.04 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578814542 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: bisphosphoglycerate mutase isoform X1 [Homo sapiens] |
| gi\|40353764 | refseq_human (refseq_human_20140103.fasta) | bisphosphoglycerate mutase [Homo sapiens] |



```
        10         20         30         40         50         60         70         80
MSKYKLIMLR HGEGAWNKEN RFCSWVDQKL NSEGMEEARN CGKQLKALNF EFDLVFTSVL NRSIHTAWLI LEELGQEWVP
        90        100        110        120        130        140        150        160
VESSWRLNER HYGALIGLNR EQMALNHGEE QVRLWRRSYN VTPPPIEESH PYYQEIYNDR RYKVCDVPLD QLPRSESLKD
       170        180        190        200        210        220        230        240
VLERLLPYWN ERIAPEVLRG KTILISAHGN SSRALLKHLE GISDEDIINI TLPTGVPILL ELDENLRAVG PHQFLGDQEA
       250        260
IQAAIKKVED QGKVKQAKK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 875 | 1 | 770.8392 | -29.89 | 2 | 39.4 | 13.9 | 0 | 101-113 | R.EQMALNHGEEQVR.L | | WUP:QUP 1.04<br>QU:MU 0.78 |

# Detailed Protein Report

## Protein 1155: tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|239788462 | **Score:** | 13.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 72.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAEGTAEAPL | ENGGGGDSGA | GALERGVAPI | KRQYLTTKEQ | FHQFLEAKGQ | EKTCRETEVG | DPAGNELAEP | EAKRIRLEDG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QTADGQTEEA | AEPGEQLQTQ | KRARGQNKGR | PHVKPTNYDK | NRLCPSLIQE | SAAKCFFGDR | CRFLHDVGRY | LETKPADLGP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RCVLFETFGR | CPYGVTCRFA | GAHLRPEGQN | LVQEELAARG | TQPPSIRNGL | DKALQQQLRK | REVRFERAEQ | ALRRFSQGPT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PAAAVPEGTA | AEGAPRQENC | GAQQVPAGPG | TSTPPSSPVR | TCGPLTDEDV | VRLRPCEKKR | LDIRGKLYLA | PLTTCGNLPF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RRICKRFGAD | VTCGEMAVCT | NLLQGQMSEW | ALLKRHQCED | IFGVQLEGAF | PDTMTKCAEL | LSRTVEVDFV | DINVGCPIDL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VYKKGGGCAL | MNRSTKFQQI | VRGMNQVLDV | PLTVKIRTGV | QERVNLAHRL | LPELRDWGVA | LVTLHGRSRE | QRYTKLADWQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YIEECVQAAS | PMPLFGNGDI | LSFEDANRAM | QTGVTGIMIA | RGALLKPWLF | TEIKEQRHWD | ISSSERLDIL | RDFTNYGLEH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| WGSDTQGVEK | TRRFLLEWLS | FLCRYVPVGL | LERLPQRINE | RPPYYLGRDY | LETLMASQKA | ADWIRISEML | LGPVPPSFAF |
| 650 | 660 | | | | | | |
| LPKHKANAYK | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1713 | 1 | 1108.3609 | -134.91 | 2 | 51.7 | 13.9 | 1 | 53-73 | K.TCRETEVGDPAGNELAEPEAK.R | |

# Detailed Protein Report

## Protein 1156: heterogeneous nuclear ribonucleoprotein D-like isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|332801090 | **Score:** | 13.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| | | **Sequence Coverage [%]:** | 5.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEVPPRLSHV | PPPLFPSAPA | TLASRSLSHW | RPRPPRQLAP | LLPSLAPSSA | RQGARRAQRH | VTAQQPSRLA | GGAAIKGGRR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RRPDLFRRHF | KSSSIQRSAA | AAAATRTARQ | HPPADSSVTM | EDMNEYSNIE | EFAEGSKINA | SKNQQDDGKM | FIGGLSWDTS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KKDLTEYLSR | FGEVVDCTIK | TDPVTGRSRG | FGFVLFKDAA | SVDKVLELKE | HKLDGKLIDP | KRAKALKGKE | PPKKVFVGGL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SPDTSEEQIK | EYFGAFGEIE | NIELPMDTKT | NERRGFCFIT | YTDEEPVKKL | LESRYHQIGS | GKCEIKVAQP | KEVYRQQQQQ |
| 330 | 340 | 350 | 360 | 370 | | | |
| QKGGRGAAAG | GRGGTRGRGR | GQQSTYGKAS | RGGGNHQNNY | QPY | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1687 | 1 | 1044.9895 | -108.72 | 2 | 50.9 | 13.9 | 2 | 37-56 | R.QLAPLLPSLAPSSARQGARR.A | |

# Detailed Protein Report

## Protein 1157: copine-2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|30181236 | **Score:** | 13.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 61.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAHIPSGGAP | AAGAAPMGPQ | YCVCKVELSV | SGQNLLDRDV | TSKSDPFCVL | FTENNGRWIE | YDRTETAINN | LNPAFSKKFV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LDYHFEEVQK | LKFALFDQDK | SSMRLDEHDF | LGQFSCSLGT | IVSSKKITRP | LLLLNDKPAG | KGLITIAAQE | LSDNRVITLS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LAGRRLDKKD | LFGKSDPFLE | FYKPGDDGKW | MLVHRTEVIK | YTLDPVWKPF | TVPLVSLCDG | DMEKPIQVMC | YDYDNDGGHD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FIGEFQTSVS | QMCEARDSVP | LEFECINPKK | QRKKKNYKNS | GIIILRSCKI | NRDYSFLDYI | LGGCQLMFTV | GIDFTASNGN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PLDPSSLHYI | NPMGTNEYLS | AIWAVGQIIQ | DYDSDKMFPA | LGFGAQLPPD | WKVSHEFAIN | FNPTNPFCSG | VDGIAQAYSA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CLPHIRFYGP | TNFSPIVNHV | ARFAAQATQQ | RTATQYFILL | IITDGVISDM | EETRHAVVQA | SKLPMSIIIV | GVGNADFAAM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | |
| EFLDGDSRML | RSHTGEEAAR | DIVQFVPFRE | FRNAAKETLA | KAVLAELPQQ | VVQYFKHKNL | PPTNSEPA | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 909 | 1 | 578.3188 | -12.36 | 3 | 41.4 | 13.9 | 0 | 522-536 | K.AVLAELPQQVVQYFK.H | |

# Detailed Protein Report

## Protein 1158: PREDICTED: uncharacterized protein LOC101928589 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530422285 | **Score:** | 13.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 18.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 9.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.11 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.41 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MACIWGIGEH KASELGSPHI CPVPALYCPS FGTGVREKLE LAHPVASGAV FPAPPQGFPV SAKPVPQPGF RVPFASVWEL
        90        100        110        120        130        140        150        160
CACVRVFVEE GSFLSNGLRK GKEYSLQPLG SLGQGCGPRT VCGAGQLVAS TPNSRDPVTP ASGPPCPQYL VLYTKDDLAH
       170        180
LPPRGTTVTC SSVSL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 94 | 1 | 809.4140 | 12.04 | 2 | 31.1 | 13.9 | 0 | 120-135 | R.TVCGAGQLVASTPNSR.D | Carbamidomethyl: 3 | WUP:QUP 0.41<br>QU:MU 2.11 |

# Detailed Protein Report

## Protein 1159: PREDICTED: polycystin-1-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530437735 | **Score:** | 13.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 33.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGWHDAEDAG | APLVYALLLQ | RCRQGHCEEF | CVYKGSLSGY | GAVLPPGFRP | HFEVGLAVVV | QDQLGAAVVA | LNRSLAITLP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EPNGSAMGLT | VWLHGLTASV | LPGLLRQADP | QHVIEYSLAL | VTVLNEYERA | LDVAAEPKHE | RQRRAQIRKN | ITETLVSLRV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HTVDDIQQIA | AALAQCMGPS | RELVCRSCLK | QTLHKLEAMM | RILQAETTAG | TVTPTAIGDS | ILNITGDLIH | LASSDVRAPQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RSELGAESPL | RMVASQAYNL | TSALMRILTR | SRVLNEEPVT | LAGEEIMAQG | KRSDPRSLLC | YGGAPGPGCH | FSIP |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1831 | 1 | 1057.3580 | -212.11 | 1 | 52.7 | 13.9 | 1 | 187-195 | R.SCLKQTLHK.L | |

# Detailed Protein Report

## Protein 1160: PREDICTED: oral-facial-digital syndrome 1 protein isoform X11 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530421293 | **Score:** | 13.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 63.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 2.10 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLNEKVKEMS | DYSLLKEEKL | ELLAQNKLLK | QQLEESRNEN | LRLLNRLAQP | APELAVFQKE | LRKAEKAIVV | EHEEFESCRQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ALHKQLQDEI | EHSAQLKAQI | LGYKASVKSL | TTQVADLKLQ | LKQTQTALEN | EVYCNPKQSV | IDRSVNGLIN | GNVVPCNGEI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SGDFLNNPFK | QENVLARMVA | SRITNYPTAW | VEGSSPDSDL | EFVANTKARV | KELQQEAERL | EKAFRSYHRR | VIKNSAKSPL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AAKSPPSLHL | LEAFKNITSS | SPERHIFGED | RVVSEQPQVG | TLEERNDVVE | ALTGSAASRL | RGGTSSRRLS | STPLPKAKRS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LESEMYLEGL | GRSHIASPSP | CPDRMPLPSP | TESRHSLSIP | PVSSPPEQKV | GLYRRQTELQ | DKSEFSDVDK | LAFKDNEEFE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SSFECVDQKQ | IEEQKEEEKI | REQQVKERRQ | REERRQSNLQ | EVLERERREL | EKLYQERKMI | EESLKIKIKK | ELEMENELEM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SNQEIKDKSA | HSENPLEKYM | KIIQQEQDQE | SADKSSKKMV | QEGSLVDTLQ | SSDKVESLTG | FSHEELDDSW | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 564 | 2 | 599.3063 | -105.08 | 2 | 37.0 | 13.9 | 2 | 308-318 | R.RLSSTPLPKAK.R | | WUP:QUP 2.10 |

# Detailed Protein Report

**Protein 1161:** **PREDICTED: zinc finger protein with KRAB and SCAN domains 4 isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530381975 | **Score:** | 13.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| | | **Sequence Coverage [%]:** | 4.3 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530381977 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein with KRAB and SCAN domains 4 isoform X4 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MAREPRKNAA LDAQSAEDQT GLLTVKVEKE EASALTAEVP VGDQGQELLC CKMALLTQTQ GSQSSQCQPM KALFKHESLG
        90        100        110        120        130        140        150        160
SQPLHDRVLQ VPGLAQGGCC REDAMVASRL TPGSQGLLKM EDVALTLTPG WTQLDSSQVN LYRDEKQENH SSLVSLGGEI
       170        180        190        200        210        220        230        240
QTKSRDLPPV KKLPEKEHGK ICHLREDIAQ IPTHAEAGEQ EGRLQRKQKN AIGSRRHYCH ECGKSFAQSS GLTKHRRIHT
       250        260        270        280        290        300        310        320
GEKPYECEDC GKTFIGSSAL VIHQRVHTGE KPYECEECGK VFSHSSNLIK HQRTHTGEKP YECDDCGKTF SQSCSLLEHH
       330        340        350        360        370        380        390        400
KIHTGEKPYQ CNMCGKAFRR NSHLLRHQRI HGDKNVQNPE HGESWESQGR TESQWENTEA PVSYKCNECE RSFTRNRSLI
       410        420        430        440        450
EHQKIHTGEK PYQCDTCGKG FTRTSYLVQH QRSHVGKKTL SQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2244 | 1 | 972.9601 | -38.26 | 2 | 56.4 | 13.9 | 0 | 8-26 | K.NAALDAQSAEDQTGLLTVK.V | |

# Detailed Protein Report

## Protein 1162: protein FAM222B isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|568786296 | **Score:** | 13.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578831131 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein FAM222B isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRSSFPLASA | KKNLRVGTNL | EQRDSSTHQG | DTTQKMRTAH | YPTPAELDAY | AKKVANNPLT | IKIFPNSVKV | PQRKHVRRTV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NGLDTSAQRY | SPYPTQAATK | AGLLAIVKVP | AKSILKDFDG | TRARLLPEAI | MNPPVAPYAT | VAPSTLAHPQ | AQALARQQAL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QHAQTLAHAP | PQTLQHPQGI | PPPQALSHPQ | SLQQPQGLGH | PQPMAQTQGL | VHPQALAHQG | LQHPHNPLLH | GGRKMPDSDA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PPNVTVSTST | IPLSMAATLQ | HSQPPDLSSI | VHQINQFCQT | RAGISTTSVC | EGQIANPSPI | SRSLLINAST | RVSTHSVPTP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MPSCVVNPME | HTHAATAALP | AAGPVNLPTG | ISRVPTGYPS | DLKPVTWNQH | QLAHLQQMCS | EASGTPAPGL | TGKHAAGREL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AGPGFVGKAP | AYPQELCLAQ | SFHLKPPLEK | PTPSPPVNGM | AAPLAYPNGH | YFQPLWNNIL | PTPNSDSSGS | QDLAMPFHGG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QPTGAPLDCA | AAPGAHYRAG | TGGGPVASQN | SLMQTVDYLS | GDFQQACFRE | QSLAMLSKAH | RAPGNRAPDP | TESRSLHIQH |
| 570 | | | | | | | |
| PGYR | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 7 | 1 | 804.3526 | -6.18 | 2 | 29.0 | 13.9 | 1 | 24-37 | R.DSSTHQGDTTQKMR.T | Oxidation: 13 |

# Detailed Protein Report

**Protein 1163:** **succinate-semialdehyde dehydrogenase, mitochondrial isoform 2 precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4507229 | **Score:** | 13.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MATCIWLRSC | GARRLGSTFP | GCRLRPRAGG | LVPASGPAPG | PAQLRCYAGR | LAGLSAALLR | TDSFVGGRWL | PAAATFPVQD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PASGAALGMV | ADCGVREARA | AVRAAYEAFC | RWREVSAKER | SSLLRKWYNL | MIQNKDDLAR | IITAESGKPL | KEAHGEILYS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AFFLEWFSEE | ARRVYGDIIH | TPAKDRRALV | LKQPIGVAAV | ITPWNFPSAM | ITRKVGAALA | AGCTVVVKPA | EDTPFSALAL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AELASQAGIP | SGVYNVIPCS | RKNAKEVGEA | ICTDPLVSKI | SFTGSTTTGK | ILLHHAANSV | KRVSMELGGL | APFIVFDSAN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VDQAVAGAMA | SKFRNTGQTC | VCSNQFLVQR | GIHDAFVKAF | AEAMKKNLRV | GNGFEEGTTQ | GPLINEKAVE | KVEKQVNDAV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SKGATVVTGG | KRHQLGKNFF | EPTLLCNVTQ | DMLCTHEETF | GPLAPVIKFD | TEEEAIAIAN | AADVGLAGYF | YSQDPAQIWR |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| VAEQLEVGMV | GVNEGLISSV | ECPFGGVKQS | GLGREGSKYG | IDEYLELKYV | CYGGL | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2507 | 1 | 822.4446 | 39.86 | 2 | 61.9 | 13.9 | 1 | 515-528 | R.EGSKYGIDEYLELK.Y | |

# Detailed Protein Report

## Protein 1164: dynein assembly factor 3, axonemal isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|73476319 | **Score:** | 13.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 64.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLPLLDSSKR | AGTLGSGCGV | PRVHSAALSR | EEGASRDIWR | IKVWARVMTT | PAGSGSGFGS | VSWWGLSPAL | DLQAESPPVD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PDSQADTVHS | NPELDVLLLG | SVDGRHLLRT | LSRAKFWPRR | RFNFFVLENN | LEAVARHMLI | FSLALEEPEK | MGLQERSETF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LEVWGNALLR | PPVAAFVRAQ | ADLLAHLVPE | PDRLEEQLPW | LSLRALKFRE | RDALEAVFRF | WAGGEKGPQA | FPMSRLWDSR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LRHYLGSRYD | ARRGVSDWDL | RMKLHDRGAQ | VIHPQEFRRW | RDTGVAFELR | DSSAYHVPNR | TLASGRLLSY | RGERVAARGY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WGDIATGPFV | AFGIEADDES | LLRTSNGQPV | KTAGEITQHN | VTELLRDVAA | WGRARATGGD | LEEQQHAEGS | PEPGTPAAPT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PESFTVHFLP | LNSAQTLHHK | SCYNGRFQLL | YVACGMVHLL | IPELGACVAP | GGNLIVELAR | YLVDVRQEQL | QGFNTRVREL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AQAAGFAPQT | GARPSETFAR | FCKSQESALG | NTVPAVEPGT | PPLDILAQPL | EASNPALEGL | TQPLQGGTPH | CEPCQLPSES |
| 570 | 580 | 590 | | | | | |
| PGSLSEVLAQ | PQGALAPPNC | ESDSKTGV | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 436 | 1 | 738.9740 | -117.81 | 3 | 35.1 | 13.9 | 2 | 1-22 | -.MLPLLDSSKRAGTLGSGCGVPR.V | |

# Detailed Protein Report

## **Protein 1165:** protocadherin beta-1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|14195607 | **Score:** | 13.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 90.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAGTRRKSLQ | NRQVGSLLIF | LCISVGDATT | IRYSVAEEME | SGSFVANVAK | DLGLEVGKLA | ARGARLVSEG | NKMHFRLHRK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TGDLFVKEKL | DRESLCGKAD | PCVLHFEVVL | VEPLQSFRAE | VRVFDINDNA | PVFLNKEPLL | KIPESTPLGS | RFPLQSAQDL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DVGLNGLQNY | TLSANGYFHL | HTRFCSHGPK | YAELVLNKPL | DREEQPEVNL | TITAVDGGSP | PKSGTAHIHV | VVLDVNDHVP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QFSRLVYRAQ | VSENSPNGSL | VATVTAVDLD | EGTNKAITYS | LAQNPEAILK | TFQIDPQNGE | VRLRGPLDFE | AIETYDIDIQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ATDGGGLSAH | SKVLVEVVDV | NDNPPEVMVS | SVSSPLPEDS | PPQTVVALFT | IRDRDIRVGG | KVTCFLREDL | PFVIKPTFGN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SYSLVTDRSL | DREEVSGYNI | TIVAMDTGPP | SLSAETMIEV | LISDVNDNPP | IFREDSYILT | VRENNSPAVF | IGKVHAEDLD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LGENAQITYS | LLPPKNGDLS | VFAYISINSG | NGKLYALRTM | DYEAIQDFQF | VVKATDGGFL | SLSSQVTVRV | VVLDDNDNRP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MILYPLQNGT | LPCNDLVPRS | AEAGYLVTKV | VAVDGDSGQN | SWLSYHLLKA | TDLGLFSVQR | QNGEIHTLRQ | ISERDPMMQK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LIILVQDHGQ | PALSTTVSLN | ILLVDGFSEP | YLQFQDPTKH | SRKVNPSTKY | LVISLVILSF | LFLLSVIVIF | IIHVYQKIKY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| REKFTIQEHF | YDDCNFSNNL | VQGQGNGSLS | RPCPYEMCSA | TGTGNSEFRF | LKRFMPNFPF | PHATGEIKME | AGSSLPPNSD |
| 810 | 820 | | | | | | |
| RNKSQRLEGH | DQVSDDYM | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 283 | 1 | 815.0883 | 28.08 | 3 | 33.2 | 13.8 | 2 | 621-640 | R.QNGEIHTLRQISERDPMMQK.L | Oxidation: 17, 18 |

# Detailed Protein Report

## Protein 1166: PREDICTED: apoptosis-resistant E3 ubiquitin protein ligase 1 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530404992 | **Score:** | 13.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 75.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVVPSKTKIV | CHFSTLVLTC | GQPHTLQIVP | RDEYDNPTNN | SMSLRDEHNY | TLSIHELGPQ | EEESTGVSFE | KSVTSNRQTF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QVFLRLTLHS | RGCFHACISY | QNQPINNGEF | DIIVLSEDEK | NIVERNVSTS | GVSIYFEAYL | YNATNCSSTP | WHLPPMHMTS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SQRRPSTAVD | EEDEDSPSEC | HTPEKVKKPK | KVYCYVSPKQ | FSVKEFYLKI | IPWRLYTFRV | CPGTKFSYLG | PDPVHKLLTL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VVDDGIQPPV | ELSCKERNIL | AATFIRSLHK | NIGGSETFQD | KVNFFQRELR | QVHMKRPHSK | VTLKVSRHAL | LESSLKATRN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FSISDWSKNF | EVVFQDEEAL | DWGGPRREWF | ELICKALFDT | TNQLFTRFSD | NNQALVHPNP | NRPAHLRLKM | YEFAGRLVGK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CLYESSLGGA | YKQLVRARFT | RSFLAQIIGL | RMHYKYFETD | DPEFYKSKVC | FILNNDMSEM | ELVFAEEKYN | KSGQLDKVVE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LMTGGAQTPV | TNANKIFYLN | LLAQYRLASQ | VKEEVEHFLK | GLNELVPENL | LAIFDENELE | LLMCGTGDIS | VSDFKAHAVV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VGGSWHFREK | VMRWFWTVVS | SLTQEELARL | LQFTTGSSQL | PPGGFAALCP | SFQIIAAPTH | STLPTAHTCF | NQLCLPTYDS |
| 650 | 660 | 670 | | | | | |
| YEEVHRMLQL | AISEGCEGFG | ML | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2591 | 1 | 557.8482 | 105.51 | 2 | 60.7 | 13.8 | 1 | 388-396 | R.LKMYEFAGR.L | |

# Detailed Protein Report

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## Protein 1167: iodotyrosine dehalogenase 1 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|257743489 | **Score:** | 13.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 28.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 10.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MYFLTPILVA | ILCILVVWIF | KNADRSMEKK | KGEPRTRAEA | RPWVDEDLKD | SSDLHQAEED | ADEWQESEEN | VEHIPFSHNH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YPEKEMVKRS | QEFYELLNKR | RSVRFISNEQ | VPMEVIDNVI | RTAGTAPSGA | HTEPWTFVVV | KDPDVKHKIR | KIIEEEEEIN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YMKRMGHRWV | TDLKKLRTNW | IKEYLDTAPI | LILIFKQVHG | FAANGKKKVH | YYNEISVSIA | CGILLAALQV | FGKIILKELA |
| 250 | | | | | | | |
| LISFLNL | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1605 | 1 | 1008.8011 | -96.76 | 3 | 50.3 | 13.8 | 1 | 1-25 | -.MYFLTPILVAILCILVVWIFKNADR.S | Carbamidomethyl: 13;<br>Oxidation: 1 |

---

# Detailed Protein Report

## Protein 1168: PREDICTED: monoacylglycerol lipase ABHD12 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530425689 | **Score:** | 13.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 29.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MWYEDALASS HPIILYLHGN AGTRGGDHRV ELYKVLSSLG YHVVTFDYRG WGDSVGTPSE RGMTYDALHV FDWIKARSGD

        90        100        110        120        130        140        150        160
NPVYIWGHSL GTGVATNLVR RLCERETPPD ALILESPFTN IREEAKSHPF SVIYRYFPGF DWFFLDPITS SGIKFANDEN

       170        180        190        200        210        220        230        240
VKHISCPLLI LHAEDDPVVP FQLGRKVGPG LCLWCSWHLA HSASVGGPGW EWAGGKAAPA CCITGCAPAT SGSGGHLILP

       250        260        270
ASPPGCFGRT WEVWCKGWGR GPLMLSPRI
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 413 | 2 | 435.7618 | 34.22 | 2 | 35.1 | 13.8 | 0 | 261-268 | R.GPLMLSPR.I | |

# Detailed Protein Report

## Protein 1169: PREDICTED: immunoglobulin superfamily member 8 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578801731 | **Score:** | 13.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 63.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.55 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.73 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRLKGMGCWA | REVLVPEGPL | YRVAGTAVSI | SCNVTGYEGP | AQQNFEWFLY | RPEAPDTALG | IVSTKDTQFS | YAVFKSRVVA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GEVQVQRLQG | DAVVLKIARL | QAQDAGIYEC | HTPSTDTRYL | GSYSGKVELR | VLPDVLQVSA | APPGPRGRQA | PTSPPRMTVH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EGQELALGCL | ARTSTQKHTH | LAVSFGRSVP | EAPVGRSTLQ | EVVGIRSDLA | VEAGAPYAER | LAAGELRLGK | EGTDRYRMVV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GGAQAGDAGT | YHCTAAEWIQ | DPDGSWAQIA | EKRAVLAHVD | VQTLSSQLAV | TVGPGERRIG | PGEPLELLCN | VSGALPPAGR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HAAYSVGWEM | APAGAPGPGR | LVAQLDTEGV | GSLGPGYEGR | HIAMEKVASR | TYRLRLEAAR | PGDAGTYRCL | AKAYVRGSGT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RLREAASARS | RPLPVHVREE | GVVLEAVAWL | AGGTVYRGET | ASLLCNISVR | GGPPGLRLAA | SWWVERPEDG | ELSSVPAQLV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GGVGQDGVAE | LGVRPGGGPV | SVELVGPRSH | RLRLHSLGPE | DEGVYHCAPS | AWVQHADYSW | YQAGSARSGP | VTVYPYMHAL |
| 570 | 580 | 590 | 600 | | | | |
| DTLFVPLLVG | TGVALVTGAT | VLGTITCCFM | KRLRKR | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1931 | 1 | 719.7780 | -145.57 | 2 | 54.5 | 13.8 | 2 | 389-401 | R.CLAKAYVRGSGTR.L | Carbamidomethyl: 1 | WUP:QUP 0.73<br>QU:MU 1.55 |

# Detailed Protein Report

## **Protein 1170:** PREDICTED: mitogen-activated protein kinase kinase kinase 8 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578818254 | **Score:** | 13.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 44.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 1.69 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MEYMSTGSDN KEEIDLLIKH LNVSDVIDIM ENLYASEEPA VYEPSLMTMC QDSNQNDERS KSLLLSGQEV PWLSSVRYGT
        90        100        110        120        130        140        150        160
VEDLLAFANH ISNTAKHFYG QRPQESGILL NMVITPQNGR YQIDSDVLLI PWKLTYRNIG SDFIPRGAFG KVYLAQDIKT
       170        180        190        200        210        220        230        240
KKRMACKLIP VDQFKPSDVE IQACFRHENI AELYGAVLWG ETVHLFMEAG EGGSVLEKLE SCGPMREFEI IWVTKHVLKG
       250        260        270        280        290        300        310        320
LDFLHSKKVI HHDIKPSNIV FMSTKAVLVD FGLSVQMTED VYFPKDLRGT EIYMSPEVIL CRGHSTKADI YSLGATLIHM
       330        340        350        360        370        380        390        400
QTGTPPWVKR YPRSAYPSYL YIILRAQEAP RNLRCSRGNA LSTSTSALWL ATSILFGDHQ RLNMAEGCHV CSKLRQH
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 949 | 1 | 646.1628 | -186.29 | 2 | 41.4 | 13.8 | 0 | 382-393 | R.LNMAEGCHVCSK.L | | QU:MU 1.69 |

# Detailed Protein Report

---

**Protein 1171:** **rho GTPase-activating protein 12 isoform 5 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|398303814 | **Score:** | 13.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 87.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKMADRSGKI | IPGQVYIEVE | YDYEYEAKDR | KIVIKQGERY | ILVKKTNDDW | WQVKPDENSK | AFYVPAQYVK | EVTRKALMPP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VKQVAGLPNN | STKIMQSLHL | QRSTENVNKL | PELSSFGKPS | SSVQGTGLIR | DANQNFGPSY | NQGQTVNLSL | DLTHNNGKFN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NDSHSPKVSS | QNRTRSFGHF | PGPEFLDVEK | TSFSQEQSCD | SAGEGSERIH | QDSESGDELS | SSSTEQIRAT | TPPNQGRPDS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PVYANLQELK | ISQSALPPLP | GSPAIQINGE | WETHKDSSGR | CYYYNRGTQE | RTWKPPRWTR | DASISKGDFQ | NPGDQEWLKH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VDDQGRQYYY | SADGSRSEWE | LPKYNASSQQ | QREIIKSRSL | DRRLQEPIVL | TKWRHSTIVL | DTNDKDQEKY | GLLNVTKIAE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NGKKVRKNWL | SSWAVLQGSS | LLFTKTQGSS | TSWFGSNQSK | PEFTVDLKGA | TIEMASKDKS | SKKNVFELKT | RQGTELLIQS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DNDTVINDWF | KVLSSTINNQ | AVETDEGIEE | EIPDSPGIEK | HDKEKEQKDP | KKLRSFKVSS | IDSSEQKKTK | KNLKKFLTRR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PTLQAVREKG | YIKDQVFGSN | LANLCQRENG | TVPKFVKLCI | EHVEEHGLDI | DGIYRVSGNL | AVIQKLRFAV | NHDEKLDLND |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SKWEDIHVIT | GALKMFFREL | PEPLFTFNHF | NDFVNAIKQE | PRQRVAAVKD | LIRQLPKPNQ | DTMQILFRHL | RRVIENGEKN |
| 730 | 740 | 750 | 760 | 770 | | | |
| RMTYQSIAIV | FGPTLLKPEK | ETGNIAVHTV | YQNQIVELIL | LELSSIFGR | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1695 | 1 | 865.1582 | 65.82 | 3 | 49.5 | 13.8 | 1 | 470-491 | K.TRQGTELLIQSDNDTVINDWFK.V | |

# Detailed Protein Report

## Protein 1172: PREDICTED: RNA-binding protein 6-like [Homo sapiens]

**Accession:** gi|578840146
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 13.8
**MW [kDa]:** 39.4
**pI:** 9.9
**Sequence Coverage [%]:** 3.4
**No. of unique Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEVGAQRLQV | NGGGDTGIRG | QWRWSHREYR | SMEVEHRDYR | SMEVGHRDYR | SMEVGSQGLQ | VNGGGVTGTK | GQWRWKHRDY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RSMEVGAQGL | QVSGGGSQGL | QVNGGGAQRL | QVNGGGGTGT | AGQWRWSTGT | TGQWRWSTGT | TGQWRWVTET | TGQWRWSTET |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TGQWRWSHRD | YRSMEVGHRD | YSSMEVEHRD | YRSMEVGHRD | YWSMEVEHRD | YRSMEVGHRD | YWSMEVEHRD | YRSMEVGHRD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YRSMEVEHRD | YRSMEVGSQR | LQVNGGGAQR | LQVNGGGAQR | LQVNGRGVQG | LQVNGGGVTG | TTGQWRWGHR | DYRSMEVGSQ |
| 330 | 340 | 350 | | | | | |
| RLQVNGGGAQ | GLQVNGGGAQ | GLQVNGRGV | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1137 | 1 | 593.6896 | -206.81 | 2 | 44.3 | 13.8 | 0 | 8-19 | R.LQVNGGGDTGIR.G | |

# Detailed Protein Report

## Protein 1173: PREDICTED: ankyrin repeat and sterile alpha motif domain-containing protein 1B isoform X17 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578824012 | **Score:** | 13.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 117.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.12 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.25 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MGKDQELLEA ARTGNVALVE KLLSGRKGGI LGGGSGPLPL SNLLSIWRGP NVNCTDSSGY TALHHAALNG HKDIVLKLLQ
        90        100        110        120        130        140        150        160
YEASTNVADN KGYFPIHLAA WKGDVEIVKI LIHHGPSHSR VNEQNNENET ALHCAAQYGH SEVVAVLLEE LTDPTIRNSK
       170        180        190        200        210        220        230        240
LETPLDLAAL YGRLRVVKMI ISAHPNLMSC NTRKHTPLHL AARNGHKAVV QVLLEAGMDV SCQTEKGSAL HEAALFGKVD
       250        260        270        280        290        300        310        320
VVRVLLETGI DANIKDSLGR TVLDILKEHP SQKSLQIATL LQEYLEGVGR STVLEEPVQE DATQETHISS PVESPSQKTK
       330        340        350        360        370        380        390        400
SETVTGELSK LLDEIKLCQE KDYSFEDLCH TISDHYLDNL SKISEEELGK NGSQSVRTSS TINLSPGEVE EEDDDENTCG
       410        420        430        440        450        460        470        480
PSGLWEALTP CNGCRNLGFP MLAQESYPKK RNYTMEIVPS ASLDTFPSEN ENFLCDLMDT AVTKKPCSLE IARAPSPRTD
       490        500        510        520        530        540        550        560
NASEVAVTTP GTSNHRNSST GPTPDCSPPS PDTALKNIVK VIRPQPKQRT SIVSSLDFHR MNHNQEYFEI NTSTGCTSFT
       570        580        590        600        610        620        630        640
ASPPASPPTS SVGTTEVKNE GTNHTDDLSR QDDNDPPKEY DPGQFAGLLH GSSPACESPE NPFHLYGKRE QCEKGQDEVS
       650        660        670        680        690        700        710        720
LANSPLPFKQ SPIENNSEPL VKKIKPKVVS RTIFHKKSNQ LENHTIVGTR STRSGSRNGD QWVMNAGGFV ERACTLGRIR
       730        740        750        760        770        780        790        800
SLPKALIDMH LSKSVSKSDS DLIAYPSNEK TSRVNWSESS TAEHSSKGNS ERTPSFTSEW EEIDKIMSSI DVGINNELKE
       810        820        830        840        850        860        870        880
MNGETTRPRC PVQTVGQWLE SIGLPQYENH LMANGFDNVQ FMGSNVMEDQ DLLEIGILNS GHRQRILQAI QLLPKMRPIG
       890        900        910        920        930        940        950        960
HDGYHPTSVA EWLDSIELGD YTKAFLINGY TSMDLLKKIW EVELINVLKI NLIGHRKRIL ASLGDRLHDD PPQKPPRSIT
       970        980        990       1000       1010       1020       1030       1040
LREPSGNHTP PQLSPSLSQS TYTTGGSLDV PHIIMQGDAR RRRNENYFDD IPRSKLERQM AQVQTDVQES SLCLPHLRWE
      1050       1060       1070
SRGENLTVIA LPWLLNIFLN CLVRFYF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1762 | 1 | 916.3154 | -149.52 | 2 | 52.4 | 13.7 | 1 | 179-194 | K.MIISAHPNLMSCNTRK.H | Oxidation: 10 | WUP:QUP 1.25<br>QU:MU 0.12 |

# Detailed Protein Report

## Protein 1174: PREDICTED: PITH domain-containing protein 1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530361255 | **Score:** | 13.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| | | **Sequence Coverage [%]:** | 9.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.54 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.79 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSHGHSHGGG GCRCAAEREE PPEQRGLAYG LYLRIDLERL QCLNESREGS GRGVFKPWEE RTDRSKFVES DADEELLFNI
        90        100        110        120        130        140        150        160
PFTGNVKLKG IIIMGEDDDS HPSEMRLYKN IPQMSFDDTE REPDQTFSLN RDLTGELEYA TKISRFSNVY HLSIHISKNF
       170        180        190
GADTTKVFYI GLRGEWTEPQ FSCSFADTR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2184 | 1 | 951.3370 | -89.38 | 2 | 57.7 | 13.7 | 0 | 90-106 | K.GIIIMGEDDDSHPSEMR.L | | WUP:QUP 0.79<br>QU:MU 1.54 |

# Detailed Protein Report

## Protein 1175: E3 ubiquitin-protein ligase RAD18 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|256818821 | **Score:** | 13.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.6 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDSLAESRWP | PGLAVMKTID | DLLRCGICFE | YFNIAMIIPQ | CSHNYCSLCI | RKFLSYKTQC | PTCCVTVTEP | DLKNNRILDE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LVKSLNFARN | HLLQFALESP | AKSPASSSSK | NLAVKVYTPV | ASRQSLKQGS | RLMDNFLIRE | MSGSTSELLI | KENKSKFSPQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KEASPAAKTK | ETRSVEEIAP | DPSEAKRPEP | PSTSTLKQVT | KVDCPVCGVN | IPESHINKHL | DSCLSREEKK | ESLRSSVHKR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KPLPKTVYNL | LSDRDLKKKL | KEHGLSIQGN | KQQLIKRHQE | FVHMYNAQCD | ALHPKSAAEI | VREIENIEKT | RMRLEASKLN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ESVMVFTKDQ | TEKEIDEIHS | KYRKKHKSEF | QLLVDQARKG | YKKIAGMSQK | TVTITKEDES | TEKLSSVCMG | QEDNMTSVTN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HFSQSKLDSP | EELEPDREED | SSSCIDIQEV | LSSSESDSCN | SSSSDIIRDL | LEEEEAWEAS | HKNDLQDTEI | SPRQNRRTRA |
| 490 | 500 | | | | | | |
| AESAEIEPRN | KRNRN | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 703 | 1 | 847.0893 | 137.09 | 2 | 38.8 | 13.7 | 1 | 262-276 | K.EHGLSIQGNKQQLIK.R | |

# Detailed Protein Report

## Protein 1176: glucose-dependent insulinotropic receptor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|30425400 | **Score:** | 13.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 36.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MESSFSFGVI | LAVLASLIIA | TNTLVAVAVL | LLIHKNDGVS | LCFTLNLAVA | DTLIGVAISG | LLTDQLSSPS | RPTQKTLCSL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RMAFVTSSAA | ASVLTVMLIT | FDRYLAIKQP | FRYLKIMSGF | VAGACIAGLW | LVSYLIGFLP | LGIPMFQQTA | YKGQCSFFAV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FHPHFVLTLS | CVGFFPAMLL | FVFFYCDMLK | IASMHSQQIR | KMEHAGAMAG | GYRSPRTPSD | FKALRTVSVL | IGSFALSWTP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FLITGIVQVA | CQECHLYLVL | ERYLWLLGVG | NSLLNPLIYA | YWQKEVRLQL | YHMALGVKKV | LTSFLLFLSA | RNCGPERPRE |
| 330 | 340 | | | | | | |
| SSCHIVTISS | SEFDG | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1747 | 1 | 1273.4623 | -117.75 | 2 | 51.6 | 13.7 | 2 | 191-213 | K.IASMHSQQIRKMEHAGAMAGGYR.S | Oxidation: 12 |

# Detailed Protein Report

## Protein 1177: metallothionein-2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5174764 | **Score:** | 13.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 6.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 36.1 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70
MDPNCSCAAG DSCTCAGSCK CKECKCTSCK KSCCSCCPVG CAKCAQGCIC KGASDKCSCC A
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1689 | 1 | 1134.8861 | -12.81 | 2 | 51.4 | 13.7 | 1 | 1-22 | -.MDPNCSCAAGDSCTCAGSCKCK.E | Carbamidomethyl: 19, 21 |

# Detailed Protein Report

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## Protein 1178: PREDICTED: STE20-related kinase adapter protein alpha isoform X6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530413123 | **Score:** | 13.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 33.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| | | **Sequence Coverage [%]:** | 5.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSFLVSKPER | IRRWVSEKFI | VEGLRDLELF | GEQPPGDTRR | KTNDASSESI | ASFSKQEVMS | SFLPEGGCYE | LLTVIGKGFE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DLMTVNLARY | KPTGEYVTVR | RINLEACSNE | MVTFLQGELH | VSKLFNHPNI | VPYRATFIAD | NELWVVTSFM | AYGSAKDLIC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| THFMDGMNEL | AIAYILQGVL | KALDYIHHMG | YVHRSVKASH | ILISVDGKVY | LSGLRSNLSM | ISHGQRQRVV | HDFPKYSVKV |
| 250 | 260 | 270 | 280 | 290 | 300 | | |
| LPWLSPEVLQ | QNLQGYDAKS | DIYSVGITAC | ELANGHVPFK | DMPATQGEDS | TVKGI | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 58 | 1 | 516.8847 | -52.61 | 3 | 29.7 | 13.7 | 1 | 281-295 | K.DMPATQGEDSTVKGI.- | |

# Detailed Protein Report

## Protein 1179: activator of basal transcription 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|7019319 | **Score:** | 13.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEAEESEKAA | TEQEPLEGTE | QTLDAEEEQE | ESEEAACGSK | KRVVPGIVYL | GHIPPRFRPL | HVRNLLSAYG | EVGRVFFQAE |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| DRFVRRKKKA | AAAAGGKKRS | YTKDYTEGWV | EFRDKRIAKR | VAASLHNTPM | GARRRSPFRY | DLWNLKYLHR | FTWSHLSEHL |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| AFERQVRRQR | LRAEVAQAKR | ETDFYLQSVE | RGQRFLAADG | DPARPDGSWT | FAQRPTEQEL | RARKAARPGG | RERARLATAQ |
| **250** | **260** | **270** | **280** | | | | |
| DKARSNKGLL | ARIFGAPPPS | ESMEGPSLVR | DS | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2718 | 1 | 905.0001 | 0.91 | 2 | 65.1 | 13.7 | 2 | 117-133 | R.IAKRVAASLHNTPMGAR.R | Oxidation: 14 |

# Detailed Protein Report

## Protein 1180: ret finger protein-like 3 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5730013 | **Score:** | 13.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 32.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAALFQEASS | CPVCSDYLEK | PMSLECGCTV | CLKCINSLQK | EPHGEDLLCC | CCSMVSQRNK | IRPNRQLERL | VSHIKELEPK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LKKILQMNPR | MRKFQVDMTL | DADTANNFLL | ISDDLRSVRS | GLITQNRQDL | AERFDVSVCI | LGSPRFTCGR | HYWEVDVGTS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TEWDLGVCRE | SVHCKGKIQL | TTELGFWTVS | LRDGSRLSAS | TVPLTFLLVD | RKLQRVGIFL | DMGMQNVSFF | DAESGSHVYT |
| 250 | 260 | 270 | 280 | 290 | | | |
| FRSVSAEEPL | RPFLAPSIPP | NGDQGVLSIC | PLMNSGTTDA | PVRPGEAK | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2145 | 2 | 1013.3708 | -30.21 | 2 | 56.7 | 13.7 | 0 | 41-58 | K.EPHGEDLLCCCCSMVSQR.N | Oxidation: 14 |

# Detailed Protein Report

## Protein 1181: PREDICTED: transmembrane protein 74B isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530425788 | **Score:** | 13.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 25.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| | | **Sequence Coverage [%]:** | 5.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578835461 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: transmembrane protein 74B isoform X4 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MASPPGLELK TLSNGPQAPR RSAPLGPVAP TREGVENACF SSEEHETHFQ NPGNTRLGSS PSPPGGVSSL PRSQRDDLSL
        90        100        110        120        130        140        150        160
HSEEGPALEP VSRPVDYGFV SALVFLVSGI LLVVTAYAIP REARVNPDTV TAREMERLEM YYARLGSHLD RCIIAGLGLL
       170        180        190        200        210        220        230        240
TVGGMLLSVL LMVSLCKGEL YRRRTFVPGK GSRKTYGSIN LRMRQLNGDG GQALVENEVV QVSETSHTLQ RS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1546 | 1 | 676.3228 | -78.11 | 2 | 49.5 | 13.6 | 2 | 191-202 | K.GSRKTYGSINLR.M | |

# Detailed Protein Report

## Protein 1182: retinal-specific ATP-binding cassette transporter [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|105990541 | **Score:** | 13.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 255.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 0.5 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGFVRQIQLL | LWKNWTLRKR | QKIRFVVELV | WPLSLFLVLI | WLRNANPLYS | HHECHFPNKA | MPSAGMLPWL | QGIFCNVNNP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CFQSPTPGES | PGIVSNYNNS | ILARVYRDFQ | ELLMNAPESQ | HLGRIWTELH | ILSQFMDTLR | THPERIAGRG | IRIRDILKDE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ETLTLFLIKN | IGLSDSVVYL | LINSQVRPEQ | FAHGVPDLAL | KDIACSEALL | ERFIIFSQRR | GAKTVRYALC | SLSQGTLQWI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EDTLYANVDF | FKLFRVLPTL | LDSRSQGINL | RSWGGILSDM | SPRIQEFIHR | PSMQDLLWVT | RPLMQNGGPE | TFTKLMGILS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DLLCGYPEGG | GSRVLSFNWY | EDNNYKAFLG | IDSTRKDPIY | SYDRRTTSFC | NALIQSLESN | PLTKIAWRAA | KPLLMGKILY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TPDSPAARRI | LKNANSTFEE | LEHVRKLVKA | WEEVGPQIWY | FFDNSTQMNM | IRDTLGNPTV | KDFLNRQLGE | EGITAEAILN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FLYKGPRESQ | ADDMANFDWR | DIFNITDRTL | RLVNQYLECL | VLDKFESYND | ETQLTQRALS | LLEENMFWAG | VVFPDMYPWT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SSLPPHVKYK | IRMDIDVVEK | TNKIKDRYWD | SGPRADPVED | FRYIWGGFAY | LQDMVEQGIT | RSQVQAEAPV | GIYLQQMPYP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CFVDDSFMII | LNRCFPIFMV | LAWIYSVSMT | VKSIVLEKEL | RLKETLKNQG | VSNAVIWCTW | FLDSFSIMSM | SIFLLTIFIM |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HGRILHYSDP | FILFLFLLAF | STATIMLCFL | LSTFFSKASL | AAACSGVIYF | TLYLPHILCF | AWQDRMTAEL | KKAVSLLSPV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AFGFGTEYLV | RFEEQGLGLQ | WSNIGNSPTE | GDEFSFLLSM | QMMLLDAAVY | GLLAWYLDQV | FPGDYGTPLP | WYFLLQESYW |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LGGEGCSTRE | ERALEKTEPL | TEETEDPEHP | EGIHDSFFER | EHPGWVPGVC | VKNLVKIFEP | CGRPAVDRLN | ITFYENQITA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FLGHNGAGKT | TTLSILTGLL | PPTSGTVLVG | GRDIETSLDA | VRQSLGMCPQ | HNILFHHLTV | AEHMLFYAQL | KGKSQEEAQL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EMEAMLEDTG | LHHKRNEEAQ | DLSGGMQRKL | SVAIAFVGDA | KVVILDEPTS | GVDPYSRRSI | WDLLLKYRSG | RTIIMSTHHM |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DEADLLGDRI | AIIAQGRLYC | SGTPLFLKNC | FGTGLYLTLV | RKMKNIQSQR | KGSEGTCSCS | SKGFSTTCPA | HVDDLTPEQV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LDGDVNELMD | VVLHHVPEAK | LVECIGQELI | FLLPNKNFKH | RAYASLFREL | EETLADLGLS | SFGISDTPLE | EIFLKVTEDS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DSGPLFAGGA | QQKRENVNPR | HPCLGPREKA | GQTPQDSNVC | SPGAPAAHPE | GQPPPEPECP | GPQLNTGTQL | VLQHVQALLV |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KRFQHTIRSH | KDFLAQIVLP | ATFVFLALML | SIVIPPFGEY | PALTLHPWIY | GQQYTFFSMD | EPGSEQFTVL | ADVLLNKPGF |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GNRCLKEGWL | PEYPCGNSTP | WKTPSVSPNI | TQLFQKQKWT | QVNPSPSCRC | STREKLTMLP | ECPEGAGGLP | PPQRTQRSTE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ILQDLTDRNI | SDFLVKTYPA | LIRSSLKSKF | WVNEQRYGGI | SIGGKLPVVP | ITGEALVGFL | SDLGRIMNVS | GGPITREASK |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| EIPDFLKHLE | TEDNIKVWFN | NKGWHALVSF | LNVAHNAILR | ASLPKDRSPE | EYGITVISQP | LNLTKEQLSE | ITVLTTSVDA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| VVAICVIFSM | SFVPASFVLY | LIQERVNKSK | HLQFISGVSP | TTYWVTNFLW | DIMNYSVSAG | LVVGIFIGFQ | KKAYTSPENL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| PALVALLLLY | GWAVIPMMYP | ASFLFDVPST | AYVALSCANL | FIGINSSAIT | FILELFENNR | TLLRFNAVLR | KLLIVFPHFC |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| LGRGLIDLAL | SQAVTDVYAR | FGEEHSANPF | HWDLIGKNLF | AMVVEGVVYF | LLTLLVQRHF | FLSQWIAEPT | KEPIVDEDDD |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| VAEERQRIIT | GGNKTDILRL | HELTKIYPGT | SSPAVDRLCV | GVRPGECFGL | LGVNGAGKTT | TFKMLTGDTT | VTSGDATVAG |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| KSILTNISEV | HQNMGYCPQF | DAIDELLTGR | EHLYLYARLR | GVPAEEIEKV | ANWSIKSLGL | TVYADCLAGT | YSGGNKRKLS |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| TAIALIGCPP | LVLLDEPTTG | MDPQARRMLW | NVIVSIIREG | RAVVLTSHSM | EECEALCTRL | AIMVKGAFRC | MGTIQHLKSK |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2411 | 1 | 1045.2315 | -153.98 | 1 | 60.6 | 13.6 | 0 | 1172-1182 | K.GSEGTCSCSSK.G | |

# Detailed Protein Report

## Protein 1183: transmembrane protein 133 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|14042933 | **Score:** | 13.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 14.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 15.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTSHHCVGPG | NHISWSGHEK | EHRLDYCPEV | TFPLTKGFPL | GYTLLFNFAS | YPFLLPSKIK | TLLRNKDSFL | NILCPACLLL |
| **90** | **100** | **110** | **120** | **130** | | | |
| IRRCNIEYSS | TGLNFLNTFT | VSLIVTVIPL | LQNVPVPLGN | NVGKMQVYE | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 101 | 1 | 753.3098 | -36.66 | 3 | 31.2 | 13.6 | 0 | 1-20 | -.MTSHHCVGPGNHISWSGHEK.E | Carbamidomethyl: 6 |

# Detailed Protein Report

## Protein 1184: PREDICTED: urea transporter 1 isoform X6 [Homo sapiens]

**Accession:** gi|578832648

**Database:** refseq_human(refseq_human_20140103.fasta)

**Database Date:** 2015-11-30

**Modification(s):** Oxidation

**Score:** 13.6

**MW [kDa]:** 46.4

**pI:** 5.2

**Sequence Coverage [%]:** 5.7

**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MFVGPDTAPY EIKDQNILMV ALQTLMAKEP EEEIAMEDSP TMVRVDSPTM VRGENQVSPC QGRRCFPKAL GYVTGDMKEL
        90        100        110        120        130        140        150        160
ANQLKDKPVV LQFIDWILRG ISQVVFVNNP VSGILILVGL LVQNPWWALT GWLGTVVSTL MALLLSQDRS LIASGLYGYN
       170        180        190        200        210        220        230        240
ATLVGVLMAV FSDKGDYFWW LLLPVCAMSM TCPIFSSALN SMLSKWDLPV FTLPFNMALS MYLSATGHYN PFFPAKLVIP
       250        260        270        280        290        300        310        320
ITTAPNISWS DLSALELLKS IPVGVGQIYG CDNPWTGGIF LGAILLSSPL MCLHAAIGSL LGIAAGLSLS APFEDIYFGL
       330        340        350        360        370        380        390        400
WGFNSSLACI AMGGMFMALT WQTHLLALGC ALFTAYLGVG MANFMAEVGL PACTWPFCLA TLLFLIMTTK NSNIYKMPLS
       410        420        430
KVTYPEENRI FYLQAKKRMV ESPL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1598 | 1 | 927.4639 | 48.47 | 3 | 49.7 | 13.6 | 1 | 29-52 | K.EPEEEIAMEDSPTMVRVDSPTMVR.G | Oxidation: 14, 22 |

# Detailed Protein Report

## Protein 1185: PREDICTED: EF-hand domain-containing protein D2 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530361370 | **Score:** | 13.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| | | **Sequence Coverage [%]:** | 4.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MATDELATKL SRRLQMEGEG GGETPEQPGL NGAAAAAAGA PDEAAEALGS ADCELSAKLL RRADLNQGIG EPQSPSRRVF
        90        100        110        120        130        140        150        160
NPYTEFKEFS RKQIKDMEKM FKQYDAGRDG FIDLMELKLM MEKLGAPQTH LGLKNMIKEV DEDFDSKLSF REVQAINVSS
       170        180        190        200
RFEEEIKAEQ EERKKQAEEM KQRKAAFKEL QSTFK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 453 | 1 | 572.6547 | -231.51 | 2 | 34.2 | 13.6 | 0 | 79-87 | R.VFNPYTEFK.E | |

# Detailed Protein Report

## Protein 1186: PREDICTED: helicase POLQ-like isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578808747 | **Score:** | 13.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 82.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLQELLCCRK | DVLMILPYVA | IVQEKISGLS | SFGIELGFFV | EEYAGSKGRF | PPTKRREKKS | LYIATIEKGH | SLVNSLIETG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RIDSLGLVVV | DELHMIGEGS | RGATLEMTLA | KILYTSKTTQ | IIGMSATLNN | VEDLQKFLQA | EYYTSQFRPV | ELKEYLKIND |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TIYEVDSKAE | NGMTFSRLLN | YKYSDTLKKM | DPDHLVALVT | EVIPNYSCLV | FCPSKKNCEN | VAEMICKFLS | KEYLKHKEKE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KCEVIKNLKN | IGNGNLCPVL | KRTIPFGVAY | HHSGLTSDER | KLLEEAYSTG | VLCLFTCTST | LAAGVNLPAR | RVILRAPYVA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KEFLKRNQYK | QMIGRAGRAG | IDTIGESILI | LQEKDKQQVL | ELITKPLENC | YSHLVQEFTK | GIQTLFLSLI | GLKIATNLDD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IYHFMNGTFF | GVQQKVLLKE | KSLWEITVES | LRYLTEKGLL | QKDTIYKSEE | EVQYNFHITK | LGRASFKGTI | DLAYCDILYR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DLKKGLEGLV | LESLLHLIYL | TTPYDLVSQC | NPDWMIYFRQ | FSQLSPAEQN | VAAILGVSES | FIGKKASGQA | IGKKVDKNVV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NRLYLSFVLY | TLLKETNIWT | VSEKFNMPRG | YIQNLLTGTA | SFSSCVLHFC | EELEEFWVYR | ALLVELTKKL | TYCVKAELIP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LMEVTGVLEG | RAKQLYSAGY | KSLMHLANAN | PEVLVRTIDH | LSRRQAKQIV | SSAKMLLHEK | AEALQEEVEE | LLRLPSDFPG |
| 730 | | | | | | | |
| AVASSTDKA | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1448 | 1 | 626.6972 | -186.66 | 2 | 46.5 | 13.6 | 1 | 1-10 | -.MLQELLCCRK.D | Oxidation: 1 |

# Detailed Protein Report

## Protein 1187: PREDICTED: programmed cell death protein 4 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530393428 | **Score:** | 13.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 4.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***WUP:QUP*** | **Median:** | 8.46 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578819263 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: programmed cell death protein 4 isoform X2 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLRDLNLGEM | KSGVPVLAVS | LALEGKASHR | EMTSKLLSDL | CGTVMSTTDV | EKSFDKLLKD | LPELALDTPR | APQLVGQFIA |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| RAVGDGILCN | TYIDSYKGTV | DCVQARAALD | KATVLLSMSK | GGKRKDSVWG | SGGGQQSVNH | LVKEIDMLLK | EYLLSGDISE |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| AEHCLKELEV | PHFHHELVYE | AIIMVLESTG | ESTFKMILDL | LKSLWKSSTI | TVDQMKRGYE | RIYNEIPDIN | LDVPHSYSVL |
| **250** | **260** | **270** | **280** | **290** | | | |
| ERFVEECFQA | GIISKQLRDL | CPSRGRKRFV | SEGDGGRLKP | ESY | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2121 | 1 | 797.4163 | -60.05 | 2 | 56.9 | 13.6 | 1 | 57-70 | K.LLKDLPELALDTPR.A | | WUP:QUP 8.46 |

# Detailed Protein Report

## Protein 1188: structural maintenance of chromosomes protein 1B [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|71565160 | **Score:** | 13.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 143.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.99 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAHLELLLVE | NFKSWRGRQV | IGPFRRFTCI | IGPNGSGKSN | VMDALSFVMG | EKIANLRVKN | IQELIHGAHI | GKPISSSASV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KIIYVEESGE | EKTFARIIRG | GCSEFRFNDN | LVSRSVYIAE | LEKIGIIVKA | QNCLVFQGTV | ESISVKKPKE | RTQFFEEIST |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SGELIGEYEE | KKRKLQKAEE | DAQFNFNKKK | NIAAERRQAK | LEKEEAERYQ | SLLEELKMNK | IQLQLFQLYH | NEKKIHLLNT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KLEHVNRDLS | VKRESLSHHE | NIVKARKKEH | GMLTRQLQQT | EKELKSVETL | LNQKRPQYIK | AKENTSHHLK | KLDVAKKSIK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DSEKQCSKQE | DDIKALETEL | ADLDAAWRSF | EKQIEEEILH | KKRDIELEAS | QLDRYKELKE | QVRKKVATMT | QQLEKLQWEQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KTDEERLAFE | KRRHGEVQGN | LKQIKEQIED | HKKRIEKLEE | YTKTCMDCLK | EKKQQEETLV | DEIEKTKSRM | SEFNEELNLI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RSELQNAGID | THEGKRQQKR | AEVLEHLKRL | YPDSVFGRLF | DLCHPIHKKY | QLAVTKVFGR | FITAIVVASE | KVAKDCIRFL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KEERAEPETF | LALDYLDIKP | INERLRELKG | CKMVIDVIKT | QFPQLKKVIQ | FVCGNGLVCE | TMEEARHIAL | SGPERQKTVA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LDGTLFLKSG | VISGGSSDLK | YKARCWDEKE | LKNLRDRRSQ | KIQELKGLMK | TLRKETDLKQ | IQTLIQGTQT | RLKYSQNELE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| MIKKKHLVAF | YQEQSQLQSE | LLNIESQCIM | LSEGIKERQR | RIKEFQEKID | KVEDDIFQHF | CEEIGVENIR | EFENKHVKRQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QEIDQKRLEF | EKQKTRLNVQ | LEYSRSHLKK | KLNKINTLKE | TIQKGSEDID | HLKKAEENCL | QTVNELMAKQ | QQLKDIRVTQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| NSSAEKVQTQ | IEEERKKFLA | VDREVGKLQK | EVVSIQTSLE | QKRLEKHNLL | LDCKVQDIEI | ILLSGSLDDI | IEVEMGTEAE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| STQATIDIYE | KEEAFEIDYS | SLKEDLKALQ | SDQEIEAHLR | LLLQQVASQE | DILLKTAAPN | LRALENLKTV | RDKFQESTDA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| FEASRKEARL | CRQEFEQVKK | RRYDLFTQCF | EHVSISIDQI | YKKLCRNNSA | QAFLSPENPE | EPYLEGISYN | CVAPGKRFMP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| MDNLSGGEKC | VAALALLFAV | HSFRPAPFFV | LDEVDAALDN | TNIGKVSSYI | KEQTQDQFQM | IVISLKEEFY | SRADALIGIY |
| 1210 | 1220 | 1230 | 1240 | | | | |
| PEYDDCMFSR | VLTLDLSQYP | DTEGQESSKR | HGESR | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2132 | 1 | 757.3003 | -55.47 | 2 | 55.0 | 13.6 | 1 | 1117-1129 | K.RFMPMDNLSGGEK.C | Oxidation: 3, 5 | WUP:QUP 0.99 |

# Detailed Protein Report

## Protein 1189: PREDICTED: PR domain zinc finger protein 1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530383954 | **Score:** | 13.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 73.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRYVNPAHSP | REQNLAACQN | GMNIYFYTIK | PIPANQELLV | WYCRDFAERL | HYPYPGELTM | MNLTQTQSSL | KQPSTEKNEL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CPKNVPKREY | SVKEILKLDS | NPSKGKDLYR | SNISPLTSEK | DLDDFRRRGS | PEMPFYPRVV | YPIRAPLPED | FLKASLAYGI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ERPTYITRSP | IPSSTTPSPS | ARSSPDQSLK | SSSPHSSPGN | TVSPVGPGSQ | EHRDSYAYLN | ASYGTEGLGS | YPGYAPLPHL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PPAFIPSYNA | HYPKFLLPPY | GMNCNGLSAV | SSMNGINNFG | LFPRLCPVYS | NLLGGGSLPH | PMLNPTSLPS | SLPSDGARRL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LQPEHPREVL | VPAPHSAFSF | TGAAASMKDK | ACSPTSGSPT | AGTAATAEHV | VQPKATSAAM | AAPSSDEAMN | LIKNKRNMTG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YKTLPYPLKK | QNGKIKYECN | VCAKTFGQLS | NLKVHLRVHS | GERPFKCQTC | NKGFTQLAHL | QKHYLVHTGE | KPHECQVCHK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RFSSTSNLKT | HLRLHSGEKP | YQCKVCPAKF | TQFVHLKLHK | RLHTRERPHK | CSQCHKNYIH | LCSLKVHLKG | NCAAAPAPGL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PLEDLTRINE | EIEKFDISDN | ADRLEDVEDD | ISVISVVEKE | ILAVVRKEKE | ETGLKVSLQR | NMGNGLLSSG | CSLYESSDLP |
| 650 | 660 | 670 | | | | | |
| LMKLPPSNPL | PLVPVKVKQE | TVEPMDP | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1285 | 4 | 598.7793 | 9.10 | 2 | 46.2 | 13.6 | 0 | 129-138 | R.GSPEMPFYPR.V | Oxidation: 5 |

# Detailed Protein Report

## Protein 1190: gelsolin isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|38044288 | **Score:** | 13.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 80.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530391028 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: gelsolin isoform X6 [Homo sapiens] |
| gi\|189083778 | refseq_human(refseq_human_20140103.fasta) | gelsolin isoform b [Homo sapiens] |
| gi\|189083776 | refseq_human(refseq_human_20140103.fasta) | gelsolin isoform b [Homo sapiens] |
| gi\|189083772 | refseq_human(refseq_human_20140103.fasta) | gelsolin isoform b [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MVVEHPEFLK | AGKEPGLQIW | RVEKFDLVPV | PTNLYGDFFT | GDAYVILKTV | QLRNGNLQYD | LHYWLGNECS | QDESGAAAIF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TVQLDDYLNG | RAVQHREVQG | FESATFLGYF | KSGLKYKKGG | VASGFKHVVP | NEVVVQRLFQ | VKGRRVVRAT | EVPVSWESFN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NGDCFILDLG | NNIHQWCGSN | SNRYERLKAT | QVSKGIRDNE | RSGRARVHVS | EEGTEPEAML | QVLGPKPALP | AGTEDTAKED |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AANRKLAKLY | KVSNGAGTMS | VSLVADENPF | AQGALKSEDC | FILDHGKDGK | IFVWKGKQAN | TEERKAALKT | ASDFITKMDY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PKQTQVSVLP | EGGETPLFKQ | FFKNWRDPDQ | TDGLGLSYLS | SHIANVERVP | FDAATLHTST | AMAAQHGMDD | DGTGQKQIWR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IEGSNKVPVD | PATYGQFYGG | DSYIILYNYR | HGGRQGQIIY | NWQGAQSTQD | EVAASAILTA | QLDEELGGTP | VQSRVVQGKE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PAHLMSLFGG | KPMIIYKGGT | SREGGQTAPA | STRLFQVRAN | SAGATRAVEV | LPKAGALNSN | DAFVLKTPSA | AYLWVGTGAS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EAEKTGAQEL | LRVLRAQPVQ | VAEGSEPDGF | WEALGGKAAY | RTSPRLKDKK | MDAHPPRLFA | CSNKIGRFVI | EEVPGELMQE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DLATDDVMLL | DTWDQVFVWV | GKDSQEEEKT | EALTSAKRYI | ETDPANRDRR | TPITVVKQGF | EPPSFVGWFL | GWDDDYWSVD |
| 730 | 740 | | | | | | |
| PLDRAMAELA | A | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 943 | 1 | 660.3451 | -9.44 | 2 | 41.8 | 13.5 | 0 | 534-546 | K.AGALNSNDAFVLK.T | |

# Detailed Protein Report

## Protein 1191: PREDICTED: cyclin-L2 isoform X7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578799847 | **Score:** | 13.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 33.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.5 |
| | | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.16 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNDSLRTDVF | VRFQPESIAC | ACIYLAARTL | EIPLPNRPHW | FLLFGATEEE | IQEICLKILQ | LYARKKVDLT | HLEGEVEKRK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HAIEEAKAQA | RGLLPGGTQV | LDGTSGFSPA | PKLVESPKEG | KGSKPSPLSV | KNTKRRLEGA | KKAKADSPVN | GLPKGRESRS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RSRSREQSYS | RSPSRSASPK | RRKSDSGSTS | GGSKSQSRSR | SRSDSPPRQA | PRSAPYKGSE | IRGSRKSKDC | KYPQKPHKSR |
| 250 | 260 | 270 | 280 | 290 | 300 | | |
| SRSSSRSRSR | SRERADNPGK | YKKKSHYYRD | QRRERSRSYE | RTGRRYERDH | PGHSRHRR | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 510 | 1 | 469.1462 | -224.93 | 2 | 34.8 | 13.5 | 2 | 282-288 | R.TGRRYER.D | | WUP:QUP 0.16 |

# Detailed Protein Report

## Protein 1192: PREDICTED: receptor-type tyrosine-protein phosphatase zeta isoform X2 [Homo sapiens]

**Accession:** gi|578814473
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 13.5
**MW [kDa]:** 207.2
**pI:** 4.7
**Sequence Coverage [%]:** 1.8
**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK QSPINIDEDL TQVNVNLKKL
        90        100        110        120        130        140        150        160
KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV FKASKITFHW GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA
       170        180        190        200        210        220        230        240
DRFSSFEEAV KGKGKLRALS ILFEVGTEEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC
       250        260        270        280        290        300        310        320
TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY TGKEEIHEAV CSSEPENVQA
       330        340        350        360        370        380        390        400
DPENYTSLLV TWERPRVVYD TMIEKFAVLY QQLDGEDQTK HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY
       410        420        430        440        450        460        470        480
SDQLIVDMPT DNPELDLFPE LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN
       490        500        510        520        530        540        550        560
RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPHT VEGTSASLND GSKTVLRSPH MNLSGTAESL
       570        580        590        600        610        620        630        640
NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE
       650        660        670        680        690        700        710        720
ESLKDPSMEG NVWFPSSTDI TAQPDVGSGR ESFLQTNYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP
       730        740        750        760        770        780        790        800
TEVTPHAFTP SSRQQDLVST VNVVYSQTTQ PVYNAVPSDP ILVETPKVDK ISSTMLHLIV SNSASSENML HSTSVPVFDV
       810        820        830        840        850        860        870        880
SPTSHMHSAS LQGLTISYAS EKYEPVLLKS ESSHQVVPSL YSNDELFQTA NLEINQAHPP KGRHVFATPV LSIDEPLNTL
       890        900        910        920        930        940        950        960
INKLIHSDEI LTSTKSSVTG KVFAGIPTVA SDTFVSTDHS VPIGNGHVAI TAVSPHRDGS VTSTKLLFPS KATSELSHSA
       970        980        990       1000       1010       1020       1030       1040
KSDAGLVGGG EDGDTDDDGD DDDDDRGSDG LSIHKCMSCS SYRESQEKVM NDSDTHENSL MDQNNPISYS LSENSEEDNR
      1050       1060       1070       1080       1090       1100       1110       1120
VTSVSSDSQT GMDRSPGKSP SANGLSQKHN DGKEENDIQT GSALLPLSPE SKAWAVLTSD EESGSGQGTS DSLNENETST
      1130       1140       1150       1160       1170       1180       1190       1200
DFSFADTNEK DADGILAAGD SEITPGFPQS PTSSVTSENS EVFHVSEAEA SNSSHESRIG LAEGLESEKK AVIPLVIVSA
      1210       1220       1230       1240       1250       1260       1270       1280
LTFICLVVLV GILIYWRKCF QTAHFYLEDS TSPRVISTPP TPIFPISDDV GAIPIKHFPK HVADLHASSG FTEEFETLKE
      1290       1300       1310       1320       1330       1340       1350       1360
FYQEVQSCTV DLGITADSSN HPDNKHKNRY INIVAYDHSR VKLAQLAEKD GKLTDYINAN YVDGYNRPKA YIAAQGPLKS
      1370       1380       1390       1400       1410       1420       1430       1440
TAEDFWRMIW EHNVEVIVMI TNLVEKGRRK CDQYWPADGS EEYGNFLVTQ KSVQVLAYYT VRNFTLRNTK IKKGSQKGRP
      1450       1460       1470       1480       1490       1500       1510       1520
SGRVVTQYHY TQWPDMGVPE YSLPVLTFVR KAAYAKRHAV GPVVVHCSAG VGRTGTYIVL DSMLQQIQHE GTVNIFGFLK
      1530       1540       1550       1560       1570       1580       1590       1600
HIRSQRNYLV QTEEQYVFIH DTLVEAILSK ETEVLDSHIH AYVNALLIPG PAGKTKLEKQ FQLLSQSNIQ QSDYSAALKQ
      1610       1620       1630       1640       1650       1660       1670       1680
CNREKNRTSS IIPVERSRVG ISSLSGEGTD YINASYIMGY YQSNEFIITQ HPLLHTIKDF WRMIWDHNAQ LVVMIPDGQN
      1690       1700       1710       1720       1730       1740       1750       1760
MAEDEFVYWP NKDEPINCES FKVTLMAEEH KCLSNEEKLI IQDFILEATQ DDYVLEVRHF QCPKWPNPDS PISKTFELIS
      1770       1780       1790       1800       1810       1820       1830       1840
VIKEEAANRD GPMIVHDEHG GVTAGTFCAL TTLMHQLEKE NSVDVYQVAK MINLMRPGVF ADIEQYQFLY KVILSLVSTR
      1850       1860       1870
QEENPSTSLD SNGAALPDGN IAESLESLV
```

| Cmpd. | No. of | m/z meas. |  | z | Rt | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

| | Cmpds. | | Δ m/z [ppm] | | [min] | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 2103 | 1 | 1131.3567 | -83.48 | 3 | 56.2 | 13.5 | 1 | 962-995 | K.SDAGLVGGGEDGDTDDDGDDDDDDRGSDGLSIHK.C | |

# Detailed Protein Report

## Protein 1193: RAS guanyl-releasing protein 4 isoform f [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|226246584 | **Score:** | 13.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 53.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNRKDSKRKS | HQECTGKIGG | RGRPRQVRRH | KTCPSPREIS | KVMASMNLGL | LSEGGCSEDE | LLEKCIQSFD | SAGSLCHEDH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MLNMVLAMHS | WVLPSADLAA | RLLTSYQKAT | GDTQELRRLQ | ICHLVRYWLM | RHPEVMHQDP | QLEEVIGRFW | ATVAREGNSA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QRRLGDSSDL | LSPGGPGPPL | PMSSPGLGKK | RKVSLLFDHL | ETGELAQHLT | YLEFRSFQAI | TLSLDLFYTE | DEIYELSYAR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EPRCPKSLPP | SPFNAPLVVE | WAPGVTPKPD | RVTLGRHVEQ | LVESVFKNYD | PEGRGTISQE | DFERLSGNFP | FACHGLHPPP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RQGRGSFSRE | ELTGYLLRAS | AICSKLGLAF | LHTFHEVTFR | KPTFCDSCSG | FLWGVTKQGY | RCRECGLCCH | KHCRDQVKVE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CKKRPGAKGD | AGPPGAPVPS | TPAPHASCGS | EENHSYTLSL | EPETGCQLRH | AWTQTESPHP | SWETDTVPCP | VMDPPSTASS |
| 490 | | | | | | | |
| KLDS | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1426 | 1 | 817.1045 | 28.93 | 3 | 47.5 | 13.5 | 0 | 164-189 | R.LGDSSDLLSPGGPGPPLPMSSPGLGK.K | Oxidation: 19 |

# Detailed Protein Report

## Protein 1194: PREDICTED: cytochrome P450 2U1 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530377130 | **Score:** | 13.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 37.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| | | **Sequence Coverage [%]:** | 6.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSPGPSQPP | AEDPPWPARL | LRAPLGLLRL | DPSGGALLLC | GLVALLGWSW | LRRRRARGIP | PGPTPWPLVG | NFGHVLLPPF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LRRRSWLSSR | TRAAGIDPSV | IGPQVLLAHL | ARVYGSIFSF | FIGHYLVVVL | SDFHSVREAL | VQQAEVFSDR | PRVPLISIVT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KEKEKVHEEI | ERVIGANRAP | SLTDKAQMPY | TEATIMEVQR | LTVVVPLAIP | HMTSENTVLQ | GYTIPKGTLI | LPNLWSVHRD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PAIWEKPEDF | YPNRFLDDQG | QLIKKETFIP | FGIGKRVCMG | EQLAKMELFL | MFVSLMQSFA | FALPEDSKKP | LLTGRFGLTL |
| 330 | 340 | | | | | | |
| APHPFNITIS | RR | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 332 | 1 | 752.4965 | 78.30 | 3 | 32.8 | 13.5 | 1 | 91-112 | R.TRAAGIDPSVIGPQVLLAHLAR.V | |

# Detailed Protein Report

## Protein 1195: cyclic AMP-responsive element-binding protein 3-like protein 4 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|364023829 | **Score:** | 13.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.7 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578800562 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: cyclic AMP-responsive element-binding protein 3-like protein 4 isoform X1 [Homo sapiens] |
| gi\|364023831 | refseq_human (refseq_human_20140103.fasta) | cyclic AMP-responsive element-binding protein 3-like protein 4 isoform 2 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDLGIPDLLD | AWLEPPEDIF | STGSVLELGL | HCPPPEVPGL | QESEPEDFLK | LFIDPNEVYC | SEASPGSDSG | ISEDPCHPDS |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| PPAPRATSSP | MLYEVVYEAG | ALERMQGETG | PNVGLISIQL | DQWSPAFMVP | DSCMVSELPF | DAHAHILPRA | GTVAPVPCTT |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| LLPCQTLFLT | DEEKRLLGQE | GVSLPSHLPL | TKAEERVLKK | VRRKIRNKQS | AQDSRRRKKE | YIDGLESRVA | ACSAQNQELQ |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| KKVQELERHN | ISLVAQLRQL | QTLIAQTSNK | AAQTSTCVLI | LLFSLALIIL | PSFSPFQSRP | EAGSEDYQPH | GVTSRNILTH |
| **330** | **340** | **350** | **360** | **370** | **380** | | |
| KDVTENLETQ | VVESRLREPP | GAKDANGSTR | TLLEKMGGKP | RPSGRIRSVL | HADEM | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 634 | 1 | 676.8750 | 44.62 | 4 | 37.5 | 13.5 | 0 | 150-174 | R.AGTVAPVPCTTLLPCQTLFLTDEEK.R | Carbamidomethyl: 9 |

# Detailed Protein Report

## Protein 1196: caspase recruitment domain-containing protein 16 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|16751833 | **Score:** | 13.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 10.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 19.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10          20          30          40          50          60          70          80
MADKVLKEKR  KLFIHSMGEG  TINGLLDELL  QTRVLNQEEM  EKVKRENATV  MDKTRALIDS  VIPKGAQACQ  ICITYICEED
        90         100
SYLAETLGLS  AGPIPGN
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1484 | 1 | 1059.1226 | 52.34 | 2 | 48.2 | 13.5 | 2 | 46-64 | R.ENATVMDKTRALIDSVIPK.G | Oxidation: 6 |

# Detailed Protein Report

## Protein 1197: PREDICTED: leucine-rich repeat-containing protein 28 isoform X6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578826607 | **Score:** | 13.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 6.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MCLSLQYLTV | DRNRLWYVPR | HLCQLPSLNE | LSMAGNRLAF | LPLDLGRSRE | LQYVYVDNNI | HLKGLPSYLY | NKVIGCSGCG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| APIQVSEVKL | LSFSSGQRTV | FLPAEVKAIG | TEHDHVLPLQ | ELAMRGLYHT | YHSLLKDLNF | LSPISLPRSL | LELLHCPLGH |
| 170 | 180 | 190 | 200 | 210 | 220 | | |
| CHRCSEPMFT | IVYPKLFPLR | ETPMAGLHQW | KTTVSFVAYC | CSTQCLQTFD | LLS | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2523 | 1 | 856.5611 | 147.82 | 2 | 62.1 | 13.5 | 1 | 1-14 | -.MCLSLQYLTVDRNR.L | |

# Detailed Protein Report

## Protein 1198: PREDICTED: tubby protein homolog isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578820749 | **Score:** | 13.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 48.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVQSSARASA | GPAACEPAPS | PAPPPPAEPR | AEPEAAMEGV | SSHRTLSYSR | WSYDSVLDDE | GRNLRQQKLD | RQRALLEQKQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KKKRQEPLMV | QANADGRPRS | RRARQSEEQA | PLVESYLSSS | GSTSYQVQEA | DSLASVQLGA | TRPTAPASAK | RTKAAATAGG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QGGAARKEKK | GKHKGTSGPA | ALAEDKSEAQ | GPVQILTVGQ | SDHAQDAGET | AAGGGERPSG | QDLRATMQRK | GISSSMSFDE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DEEDEEENSS | SSSQLNSNTR | PSSATSRKSV | REAASAPSPT | APEQPVDVEV | QDLEEFALRP | APQGITIKCR | ITRDKKGMDR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GMYPTYFLHL | DREDGKKVFL | LAGRKRKKSK | TSNYLISVDP | TDLSRGGDSY | IGKLRSNLMG | TKFTVYDNGV | NPQKASSSTL |
| 410 | 420 | 430 | 440 | 450 | 460 | | |
| ESGTLRQELA | AVCYETNVLG | FKGPRKMSVI | VPGMNMVHER | VSIRPRNRTT | S | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1339 | 1 | 661.4013 | 77.79 | 3 | 46.9 | 13.5 | 2 | 83-99 | K.KRQEPLMVQANADGRPR.S | Oxidation: 7 |

# Detailed Protein Report

## Protein 1199: PREDICTED: gastrin/cholecystokinin type B receptor isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530395959 | **Score:** | 13.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 55.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MELLKLNRSV | QGTGPGPGAS | LCRPGAPLLN | SSSVGNLSCE | PPRIRGAGTR | ELELAIRITL | YAVIFLMSVG | GNMLIIVVLG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LSRRLRTVTN | AFLLSLAVSD | LLLAVACMPF | TLLPNLMGTF | IFGTVICKAV | SYLMGVSVSV | STLSLVAIAL | ERYSAICRPL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QARVWQTRSH | AARVIVATWL | LSGLLMVPYP | VYTVVQPVGP | RVLQCVHRWP | SARVRQTWSV | LLLLLLFFIP | GVVMAVAYGL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ISRELYLGLR | FDGDSDSDSQ | SRVRNQGGLP | GGAGPREQNL | GEAELWRATG | PAGVGGTEMK | VRVRRKLEME | LSWERRSGGD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WAGDWGDSPF | SLTAHPLCSG | AVHQNGRCRP | ETGAVGEDSD | GCYVQLPRSR | PALELTALTA | PGPGSGSRPT | QAKLLAKKRV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VRMLLVIVVL | FFLCWLPVYS | ANTWRAFDGP | GAHRALSGAP | ISFIHLLSYA | SACVNPLVYC | FMHRRFRQAC | LETCARCCPR |
| 490 | 500 | 510 | 520 | | | | |
| PPRARPRALP | DEDPPTPSIA | SLSRLSYTTI | STLGPG | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1548 | 1 | 851.5588 | 119.65 | 2 | 47.7 | 13.5 | 2 | 288-304 | R.ATGPAGVGGTEMKVRVR.R | Oxidation: 12 |

# Detailed Protein Report

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## Protein 1200: PREDICTED: PHD finger protein 14 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530385115 | **Score:** | 13.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 76.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MIVQMTVILK | LEMPQDSLIL | EKSQNWSSQK | MDHILICCVC | LGDNSEDADE | IIQCDNCGIT | VHEGCYGVDG | ESDSIMSSAS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ENSTEPWFCD | ACKCGVSPSC | ELCPNQDGIF | KETDAGRWVH | IVCALYVPGV | AFGDIDKLRP | VTLTEMNYSK | YGAKECSFCE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DPRFARTGVC | ISCDAGMCRA | YFHVTCAQKE | GLLSEAAAEE | DIADPFFAYC | KQHADRLDRK | WKRKNYLALQ | SYCKMSLQER |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EKQLSPEAQA | RINARLQQYR | AKAELARSTR | PQAWVPREKL | PRPLTSSASA | IRKLMRKAEL | MGISTDIFPV | DNSDTSSSVD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GRRKHKQPAL | TADFVNYYFE | RNMRMIQIQE | NMAEQKNIKD | KLENEQEKLH | VEYNKLCESL | EELQNLNGKL | RSEGQGIWAL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LGRITGQKLN | IPAILRAPKE | RKPSKKEGGT | QKTSTLPAVL | YSCGICKKNH | DQHLLLLCDT | CKLHYHLGCL | DPPLTRMPRK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TKNSYWQCSE | CDQAGSSDME | ADMAMETLPD | GTKRSRRQIK | EPVKFVPQDV | PPEPKKIPIR | NTRTRGRKRS | FVPEEEKHEE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RVPRERRQRQ | SVLQKKPKAE | DLRTECATCK | GTGDNENLVS | RMRLSETKNR | CDECRLCYHF | GCLDPPLKKS | PKQTGYGWIC |
| 650 | 660 | 670 | 680 | | | | |
| QECDSSSSKE | DENEAERKNI | SQELNMEQKN | PKK | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1204 | 1 | 749.0883 | 185.96 | 2 | 45.2 | 13.5 | 1 | 280-293 | K.LPRPLTSSASAIRK.L | |

# Detailed Protein Report

## Protein 1201: PREDICTED: WD repeat-containing protein 87 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578834971 | **Score:** | 13.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 316.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.9 |
| | | **Sequence Coverage [%]:** | 0.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.98 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.03 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MSSPRLIPLW KDLKLLLNDT INKSKQPSED PKNCLIVLSD RSQVLFKESR YPQNMPCVCY YFSDAHFFAS LSWVTSNTKE
        90        100        110        120        130        140        150        160
IQAVAWMKSK TEDMVEKRTF SMTERLPPIQ SMVHAGSFHI LVVYCGDLIL RLFGDHFRAF KPLGKVPCRF NISCLCYDPE
       170        180        190        200        210        220        230        240
MKMLLSGILG AVVTWVIELG GTGLQIAHMV SMPGDELVQD IVLNGPSGSL LALCETVVRV LMHQGKGQLG EVKRFTSTSS
       250        260        270        280        290        300        310        320
GSSITCCFTC FDQGFLYAGN QAGEIQVWSL QQGHPLHSFQ AHQSGVICIR SRPEAHTLLT AGSDSLIKEW NLTSGSLLRR
       330        340        350        360        370        380        390        400
LELGEELYRL QFIDSITFFC QTAHSFSLHR LPCFYSLFNV CGSAPQQLRR VCCGNNWFRI LCTTEDGLLR FVSPVTGDLL
       410        420        430        440        450        460        470        480
VITWPFSILD QAVDWAYDPG KEELFVATGS SEVLVFDTTR CPCPAKYLLG TSPNSQDFVQ CLAYGHFNLG RGLEGLIFSG
       490        500        510        520        530        540        550        560
HQSGVIRVLS QHSCARLEKF MHFGAVLALS TLSGGIFGGQ GNSLLCSYGM DDYVHLSEAV LDGVKVQLRP LASILSSCHL
       570        580        590        600        610        620        630        640
THLILLPKSV GAITETNCLR LWKFHDFLSS GSQNGLKFIE TLPLHLCAIT SFDVCLSLSL FVTGSADGSV RIWDFHGRLI
       650        660        670        680        690        700        710        720
GILDSSLHFG PVCFANDRGD LLVTFNQSLY LVSCLKLLPP ALLTRLSFMS ISDEVLEVPK PFIPSFFFSF ETMFVPKYIY
       730        740        750        760        770        780        790        800
PGQAQQKLVG LEKLVNNRAI AFDHSVPHVI EEDEEGSPVL LRSSMHYSLQ DMEDWMQVSP ALRSETARRL LNDTTNSNPL
       810        820        830        840        850        860        870        880
IRELAWEGLK RLGMITHLFA MPLAQGLMDK DERVRIKTLS LMAEIGIHSR TSLLQLTQKQ ETFREMQQQM IGEEPLDHLL
       890        900        910        920        930        940        950        960
GMRATDLQIL STQVEQRLNE NLTLSHRDEK PAFSLDVSMP SELKSSLKPP TVSEESEVAI KPSKGQRRGQ AGVKKHSQKW
       970        980        990       1000       1010       1020       1030       1040
LRGLKKTKER DSKQMSTEPG LLEDESGTEA APIEMEEASV YSQWSSSTSV IKLSKDVDSQ EKDISKDHIA LTLKRLQKIR
      1050       1060       1070       1080       1090       1100       1110       1120
DKRDKKATAQ KLKKKHKKKG KEAKVINEET TPPVMEQPVT KKVKIQGRGA SGISGRRSTA GDGSSWRDDL CRLMALRISG
      1130       1140       1150       1160       1170       1180       1190       1200
SQTKMSENLN AELVTFAQEM LVDRHPSWEL FQEICPLLKK ESKVLLEDLD WDVVPPEKKP IFIQEGAIRE DMIQGVTQEV
      1210       1220       1230       1240       1250       1260       1270       1280
IRHKEVMPRE EEQAQKKARD MLGLEETQVI LKKGKKVIFL EPGNVTMGKE ISKKEEKKTF QKSPKQGRKA VQKERKVGKI
      1290       1300       1310       1320       1330       1340       1350       1360
KREMTKEERD MSEEVEEMAT LEEKVVKQEG KLVMIERTPS WQDWKKAWDE WKQVHGETRK SWKAWKEEWE KRLLQEEEKL
      1370       1380       1390       1400       1410       1420       1430       1440
HQAGEKLSPE EEMLQEDKKL KWEEWKQVWE NMLSSKSKEQ QYKDEEEVTL EEEVSREGEE KEQQVTEEQR HIQEEHKWAR
      1450       1460       1470       1480       1490       1500       1510       1520
IHRKRARAEK KRAQEERKLA QEEEKLAQEE RQLAQEERKL AQAYVKITQD DREMAQAEGK FAQKEETLAQ RGEKLSQEAE
      1530       1540       1550       1560       1570       1580       1590       1600
KLAQKRKKLA KKWEKVAREE EKLAKKGGKL AEVKNILAQK VEELPQREQN LDWQEKELAQ ELEELEWDME ELSWKEEELN
      1610       1620       1630       1640       1650       1660       1670       1680
QEEGKLVEEK KKLAEEEEAL AWQREKLSEE ETKLAQEEEL LIQEKEKLAQ HKEKMPEEEE RLGRKREQLI EKKMKLAQKR
      1690       1700       1710       1720       1730       1740       1750       1760
ERWINSMEEL TKNKMILYQK KNLAQEKKNL AQEKEKLAQR KENLLYNKER LTHSKKQLVQ VKNKLGMFNK ILAQVEEKLT
      1770       1780       1790       1800       1810       1820       1830       1840
QEKETVIKKK EKLAETEKKL VQVEDSLAKK QEKLAQEKMK LALEKAMVQG KKRLRGELDI AKEEKALNLE MKRLAEEKMR
      1850       1860       1870       1880       1890       1900       1910       1920
LVEGKETLSK GETPETSRQR KMTQVEQELF ERKLSLEEKI LLHEDRILAM EESEIAKGKL EFTRGQRIFV QGQRKLAKAS
      1930       1940       1950       1960       1970       1980       1990       2000
RKLIKKRESL SKEPAKLNKI LKALQKLTRD ERKLTQEEIK MTKMKRALFV KERRLSIEQS KLDIKEWDFS EKRSELTKDE
      2010       2020       2030       2040       2050       2060       2070       2080
KKLARKQRKL ANKMRRMINK EEKMTEEESK LARKHSEVIL DDEEEGGIEE EEVIPFLKRR WRKRKEAKRG DKPKEKFSSQ
      2090       2100       2110       2120       2130       2140       2150       2160
VDEVESEEHF SEEMESLLDE LEKQESLSSE EEEEREEEEE REEEEEREEE EERKEEEEGE EKQVEKEEEE KKKKKKEKKK
      2170       2180       2190       2200       2210       2220       2230       2240
EEVQEKEEVF EEKEEIMSEE ETESLSDEEE EEESCSLEEE VDREKEILKK EKQFKLQEQR RKSLRGRERV LSILRGVPHG
      2250       2260       2270       2280       2290       2300       2310       2320
KGRAIRLGVL KSPLKKLMST ALEMKEKTPV PVPEKQISWE DKKATVVEIP RKFLGTMDKE REVMGKYEPI PPHVLGTVLE
      2330       2340       2350       2360       2370       2380       2390       2400
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 698 | 1 | 512.1244 | -202.48 | 2 | 38.3 | 13.5 | 0 | 1098-1107 | R.STAGDGSSWR.D |  | WUP:QUP 1.03<br>QU:MU 0.98 |

# Detailed Protein Report

## Protein 1202: integral membrane protein GPR180 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|30725877 | **Score:** | 13.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.2 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGGLRLLAVA | LTCCWWPQGS | QGKTLRGSFS | STAAQDAQGQ | RIGHFEFHGD | HALLCVRINN | IAVAVGKEAK | LYLFQAQEWL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KLQQSSHGYS | CSEKLSKAQL | TMTMNQTEHN | LTVSQIPSPQ | TWHVFYADKY | TCQDDKENSQ | VEDIPFEMVL | LNPDAEGNPF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DHFSAGESGL | HEFFFLLVLV | YFVIACIYAQ | SLWQAIKKGG | PMHMILKVLT | TALLLQAGSA | LANYIHFSSY | SKDGIGVPFM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GSLAEFFDIA | SQIQMLYLLL | SLCMGWTIVR | MKKSQSRPLQ | WDSTPASTGI | AVFIVMTQSV | LLLWEQFEDI | SHHSYHSHHN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LAGILLIVLR | ICLALSLGCG | LYQIITVERS | TLKREFYITF | AKGCILWFLC | HPVLACISVI | FSDYQRDKVI | TIGVILCQSV |
| 410 | 420 | 430 | 440 | 450 | | | |
| SMVILYRLFL | SHSLYWEVSS | LSSVTLPLTI | SSGHKSRPHF | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1390 | 1 | 727.2022 | -165.33 | 2 | 45.7 | 13.5 | 0 | 82-94 | K.LQQSSHGYSCSEK.L | |

# Detailed Protein Report

## Protein 1203: PREDICTED: protein DBF4 homolog B isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578831448 | **Score:** | 13.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.52 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.31 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMMHVQQLSL | ASLCVKKQQP | KKPEGTCPAA | ESRTRKVARL | KAPFLKIEDE | SRKFRPFHHQ | FKSFPEISFL | GPKDASPFEA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PTTLGSMHHT | RESKDGEPSP | RSAAHTMPRR | KKGYCECCQE | AFEELHVHLQ | SAQHRSFALE | AHLYAEVDRI | IAQLSHSFAD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IPFQAGLPRW | SGSPASDCDP | LCPETLHPHQ | PSHPRAASPR | IRKEDSCQAS | GIPEQDGTVD | STQAPAERAG | TGEVPGPIAS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CQDLGVSVDV | FVDPPGIPVS | RSPACQCLLP | SSGFMELSSG | PDLALFGHKR | KVQFPSGSAK | KRVGASWPQA | SFFVPIAPNP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CGTRTTSGKR | LPSLPLTGHE | SRLLASLQPL | CHSQTCLSLP | DPFPWQPTDR | PAEFWATQPS | WLGKGWPPGP | EDSECTATGP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VSQEAGQLLS | CPTAPGWPSA | PLYSATSVQP | SGAPVESRST | SLLQPLPASA | GASCSRCLWA | PQPLQVPCLP | VSQPWSQPQP |
| 490 | 500 | 510 | | | | | |
| QPQPHAGREL | LLRVPKVLGS | SQGQAAPD | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 331 | 1 | 938.4730 | 4.05 | 2 | 34.1 | 13.5 | 0 | 1-16 | -.MMMHVQQLSLASLCVK.K | Carbamidomethyl: 14 | WUP:QUP 1.31<br>QU:MU 0.52 |

# Detailed Protein Report

## Protein 1204: PREDICTED: tubulointerstitial nephritis antigen isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578811605 | **Score:** | 13.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 33.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 5.1 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MTLEDGFKFR LGTLPPSPML LSMNEMTASL PATTDLPEFF VASYKWPGWT HGPLDQKNCA ASWAFSTASV AADRIAIQSK
        90        100        110        120        130        140        150        160
GRYTANLSPQ NLISCCAKNR HGCNSGSIDR AWWYLRKRGL VSHACYPLFK DQNATNNGCA MASRSDGRGK RHATKPCPNN
       170        180        190        200        210        220        230        240
VEKSNRIYQC SPPYRVSSNE TEIMKEIMQN GPVQAIMQVR EDFFHYKTGI YRHVTSTNKE SEKYRKLQTH AVKLTGWGTL
       250        260        270        280        290        300
RGAQGQKEKF WIAANSWGKS WGENGYFRIL RGVNESDIEK LIIAAWGQLT SSDEP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2439 | 1 | 857.4153 | -31.52 | 2 | 61.0 | 13.5 | 0 | 186-200 | K.EIMQNGPVQAIMQVR.E | |

# Detailed Protein Report

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## Protein 1205: alpha-protein kinase 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|115511036 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 201.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.8 |
| | | **Sequence Coverage [%]:** | 0.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.25 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.36 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEVAWLVYVL | GQQPLARQGE | GQSRLVPGRG | LVLWLPGLPR | SSPSWPAVDL | APLAPARPRG | PLICHTGHEQ | AGREPGPGSS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TKGPVLHDQD | TRCAFLPRPP | GPLQTRRYCR | HQGRQGSGLG | AGPGAGTWAP | APPGVSKPRC | PGRARPGEGQ | QQVTTARPPA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| INRGARQPRA | GAAAAGRGPG | AGAWRTGEAA | ASAGPAVGEG | GAMGSRRAPS | RGWGAGGRSG | AGGDGEDDGP | VWIPSPASRS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YLLSVRPETS | LSSNRLSHPS | SGRSTFCSII | AQLTEETQPL | FETTLKSRSV | SEDSDVRFTC | IVTGYPEPEV | TWYKDDTELD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RYCGLPKYEI | THQGNRHTLQ | LYRCREEDAA | IYQASAQNSK | GIVSCSGVLE | VGTMTEYKIH | QRWFAKLKRK | AAAKLREIEQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SWKHEKAVPG | EVDTLRKLSP | DRFQRKRRLS | GAQAPGPSVP | TREPEGGTLA | AWQEGETETA | QHSGLGLINS | FASGEVTTNG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EAAPENGEDG | EHGLLTYICD | AMELGPQRAL | KEESGAKKKK | KDEESKQGLR | KPELEKAAQS | RRSSENCIPS | SDEPDSCGTQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GPVGVEQVQT | QPRGRAARGP | GSSGTDSTRK | PASAVGTPDK | AQKAPGPGPG | QEVYFSLKDM | YLENTQAVRP | LGEEGPQTLS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VRAPGESPKG | KAPLRARSEG | VPGAPGQPTH | SLTPQPTRPF | NRKRFAPPKP | KGEATTDSKP | ISSLSQAPEC | GAQSLGKAPP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QASVQVPTPP | ARRRHGTRDS | TLQGQAGHRT | PGEVLECQTT | TAPTMSASSS | SDVASIGVST | SGSQGIIEPM | DMETQEDGRT |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SANQRTGSKK | NVQADGKIQV | DGRTRGDGTQ | TAQRTRADRK | TQVDAGTQES | KRPQSDRSAQ | KGMMTQGRAE | TQLETTQAGE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KIQEDRKAQA | DKGTQEDRRM | QGEKGMQGEK | GTQSEGSAPT | AMEGQSEQEV | ATSLGPPSRT | PKLPPTAGPR | APLNIECFVQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TPEGSCFPKK | PGCLPRSEEA | VVTASRNHEQ | TVLGPLSGNL | MLPAQPPHEG | SVEQVGGERC | RGPQSSGPVE | AKQEDSPFQC |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PKEERPGGVP | CMDQGGCPLA | GLSQEVPTMP | SLPGTGLTAS | PKAGPCSTPT | SQHGSTATFL | PSEDQVLMSS | APTLHLGLGT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PTQSHPPETM | ATSSEGACAQ | VPDVEGRTPG | PRSCDPGLID | SLKNYLLLLL | KLSSTETSGA | GGESQVGAAT | GGLVPSATLT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PTVEVAGLSP | RTSRRILERV | ENNHLVQSAQ | TLLLSPCTSR | RLTGLLDREV | QAGRQALAAA | RGSWGPGPSS | LTVPAIVVDE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| EDPGLASEGA | SEGEGEVSPE | GPGLLGASQE | SSMAGRLGEA | GGQAAPGQGP | SAESIAQEPS | QEEKFPGEAL | TGLPAATPEE |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LALGARRKRF | LPKVRAAGDG | EATTPEERES | PTVSPRGPRK | SLVPGSPGTP | GRERRSPTQG | RKASMLEVPR | AEEELAAGDL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GPSPKAGGLD | TEVALDEGKQ | ETLAKPRKAK | DLLKAPQVIR | KIRVEQFPDA | SGSLKLWCQF | FNILSDSVLT | WAKDQRPVGE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| VGRSAGDEGP | AALAIVQASP | VDCGVYRCTI | HNEHGSASTD | FCLSPEVLSG | FISREEGEVG | EEIEMTPMVF | AKGLADSGCW |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| GDKLFGRLVS | EELRGGGYGC | GLRKASQAKV | IYGLEPIFES | GRTCIIKVSS | LLVFGPSSET | SLVGRNYDVT | IQGCKIQNMS |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| REYCKIFAAE | ARAAPGFGEV | PEIIPLYLIY | RPANNIPYAT | LEEDLGKPLE | SYCSREWGCA | EAPTASGSSE | AMQKCQTFQH |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| WLYQWTNGSF | LVTDLAGVDW | KMTDVQIATK | LRGYQGLKES | CFPALLDRFA | SSHQCNAYCE | LLGLTPLKGP | EAAHPQAKAK |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | |
| GSKSPSAGRK | GSQLSPQPQK | KGLPSPQGTR | KSAPSSKATP | QASEPVTTQL | LGQPPTQEEG | SKAQGMR | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1359 | 1 | 669.3184 | -65.41 | 2 | 45.3 | 13.4 | 0 | 429-442 | R.LSGAQAPGPSVPTR.E | | WUP:QUP 0.36<br>QU:MU 2.25 |

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# Detailed Protein Report

## Protein 1206: photoreceptor-specific nuclear receptor isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|7706515 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.0 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 6.3 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
METRPTALMS STVAAAAPAA GAASRKESPG RWGLGEDPTG VSPSLQCRVC GDSSSGKHYG IYACNGCSGF FKRSVRRRLI
        90        100        110        120        130        140        150        160
YRCQVGAGMC PVDKAHRNQC QACRLKKCLQ AGMNQDAVQN ERQPRSTAQV HLDSMESNTE SRPESLVAPP APAGRSPRGP
       170        180        190        200        210        220        230        240
TPMSAARALG HHFMASLITA ETCAKLEPED ADENIDVTSN DPEFPSSPYS SSSPCGLDSI HETSARLLFM AVKWAKNLPV
       250        260        270        280        290        300        310        320
FSSLPFRDQV ILLEEAWSEL FLLGAIQWSL PLDSCPLLAP PEASAAGGAQ GRLTLASMET RVLQETISRF RALAVDPTEF
       330        340        350        360        370
ACMKALVLFK PETRGLKDPE HVEALQDQSQ VMLSQHSKAH HPSQPVR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2476 | 1 | 900.2164 | 98.29 | 3 | 59.2 | 13.4 | 2 | 302-324 | R.VLQETISRFRALAVDPTEFACMK.A | Carbamidomethyl: 21;<br>Oxidation: 22 |

# Detailed Protein Report

## Protein 1207: gastric inhibitory polypeptide receptor precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4503999 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 53.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTTSPILQLL | LRLSLCGLLL | QRAETGSKGQ | TAGELYQRWE | RYRRECQETL | AAAEPPSGLA | CNGSFDMYVC | WDYAAPNATA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RASCPWYLPW | HHHVAAGFVL | RQCGSDGQWG | LWRDHTQCEN | PEKNEAFLDQ | RLILERLQVM | YTVGYSLSLA | TLLLALLILS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LFRRLHCTRN | YIHINLFTSF | MLRAAAILSR | DRLLPRPGPY | LGDQALALWN | QALAACRTAQ | IVTQYCVGAN | YTWLLVEGVY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LHSLLVLVGG | SEEGHFRYYL | LLGWGAPALF | VIPWVIVRYL | YENTQCWERN | EVKAIWWIIR | TPILMTILIN | FLIFIRILGI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LLSKLRTRQM | RCRDYRLRLA | RSTLTLVPLL | GVHEVVFAPV | TEEQARGALR | FAKLGFEIFL | SSFQGFLVSV | LYCFINKEVQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | |
| SEIRRGWHHC | RLRRSLGEEQ | RQLPERAFRA | LPSGSGPGEV | PTSRGLSSGT | LPGPGNEASR | ELESYC | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1597 | 4 | 1023.5001 | 6.47 | 1 | 50.2 | 13.4 | 2 | 327-333 | R.TRQMRCR.D | Carbamidomethyl: 6;<br>Oxidation: 4 |

# Detailed Protein Report

## Protein 1208: hematopoietic lineage cell-specific protein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|167234422 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| | | **Sequence Coverage [%]:** | 6.4 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MWKSVVGHDV | SVSVETQGDD | WDTDPDFVND | ISEKEQRWGA | KTIEGSGRTE | HINIHQLRNK | VSEEHDVLRK | KEMESGPKAS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HGYGGRFGVE | RDRMDKSAVG | HEYVAEVEKH | SSQTDAAKGF | GGKYGVERDR | ADKSAVGFDY | KGEVEKHTSQ | KDYSRGFGGR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YGVEKDKWDK | AALGYDYKGE | TEKHESQRDY | AKGFGGQYGI | QKDRVDKSAV | GFNEMEAPTT | AYKKTTPIEA | ASSGTRGLKA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KFESMAEEKR | KREEEEKAQQ | VARRQQERKA | VTKRSPEAPQ | PVIAMEEPAV | PAPLPKKISS | EAWPPVGTPP | SSESEPVRTS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| REHPVPLLPI | RQTLPEDNEE | PPALPPRTLE | GLQVEEEPVY | EAEPEPEPEP | EPEPENDYED | VEEMDRHEQE | DEPEGDYEEV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LEPEDSSFSS | ALAGSSGCPA | GAGAGAVALG | ISAVALYDYQ | GEGSDELSFD | PDDVITDIEM | VDEGWWRGRC | HGHFGLFPAN |
| 490 | | | | | | | |
| YVKLLE | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2470 | 1 | 1131.1745 | 0.11 | 3 | 59.2 | 13.4 | 0 | 4-34 | K.SVVGHDVSVSVETQGDDWDTDPDFVNDISEK.E | |

# Detailed Protein Report

## Protein 1209: complement component C9 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4502511 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 63.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSACRSFAVA | ICILEISILT | AQYTTSYDPE | LTESSGSASH | IDCRMSPWSE | WSQCDPCLRQ | MFRSRSIEVF | GQFNGKRCTD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AVGDRRQCVP | TEPCEDAEDD | CGNDFQCSTG | RCIKMRLRCN | GDNDCGDFSD | EDDCESEPRP | PCRDRVVEES | ELARTAGYGI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NILGMDPLST | PFDNEFYNGL | CNRDRDGNTL | TYYRRPWNVA | SLIYETKGEK | NFRTEHYEEQ | IEAFKSIIQE | KTSNFNAAIS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LKFTPTETNK | AEQCCEETAS | SISLHGKGSF | RFSYSKNETY | QLFLSYSSKK | EKMFLHVKGE | IHLGRFVMRN | RDVVLTTTFV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DDIKALPTTY | EKGEYFAFLE | TYGTHYSSSG | SLGGLYELIY | VLDKASMKRK | GVELKDIKRC | LGYHLDVSLA | FSEISVGAEF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NKDDCVKRGE | GRAVNITSEN | LIDDVVSLIR | GGTRKYAFEL | KEKLLRGTVI | DVTDFVNWAS | SINDAPVLIS | QKLSPIYNLV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PVKMKNAHLK | KQNLERAIED | YINEFSVRKC | HTCQNGGTVI | LMDGKCLCAC | PFKFEGIACE | ISKQKISEGL | PALEFPNEK |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1664 | 1 | 626.5306 | -153.93 | 3 | 50.6 | 13.4 | 1 | 509-525 | R.KCHTCQNGGTVILMDGK.C | Carbamidomethyl: 2;<br>Oxidation: 14 |

# Detailed Protein Report

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## Protein 1210: cerebral cavernous malformations 2 protein-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|31542255 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| | | **Sequence Coverage [%]:** | 4.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578835776 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: cerebral cavernous malformations 2 protein-like isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEYEVKKGKK | GFVSPIRRLV | FPKAGRRAAC | RSSVSRRPLH | SMPLYPPDYL | IDPQILLCDY | LEKEVKFLGH | LTWVTSSLNP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SSRDELLQLL | DTARQLKELP | LKTTAEQDSI | LSLSARCLLL | TWRDNEELIL | RIPTHEIAAA | SYLQDDALHL | LVLKTGLGVD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PVPAGVDASP | GGAGRDPGPP | GGAPEKRRVG | TAERRHTICS | LDWRMGWGGG | AAEARAGGGG | GGSLERQRAG | ARASGSWERR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QTFSGSWERR | HGGGGGGGGA | GKPGGSWERR | QAGSGGGGSW | ERRHPGPNPL | DPQDPSPDAY | CNLVILAVAN | RDAAEESCAL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ICQVFQIIYG | DQSIECVDRA | GYHYTSTPER | PWLCSRIMAP | RTPLKHVTAA | RPHLLSMAPT | AAAATTAVWA | WSSYRITWSR |
| 410 | 420 | 430 | 440 | | | | |
| CGVSWGPSRS | SSLRCCCGST | GWGCPSRTIA | QAC | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2317 | 1 | 819.4008 | 25.39 | 2 | 57.3 | 13.4 | 0 | 251-269 | R.HGGGGGGGGAGKPGGSWER.R | |

# Detailed Protein Report

## Protein 1211: prickle-like protein 4 [Homo sapiens]

**Accession:** gi|118722347
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 13.4
**MW [kDa]:** 41.7
**pI:** 5.0
**Sequence Coverage [%]:** 4.9
**No. of unique Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSVQNSGWPH | QEDSPKPQDP | GPPANSDSDS | GHLPGEDPED | THAQGPAVLS | LGSLCLDTNQ | APNWTGLQTL | LQQLPPQDID |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ERYCLALGEE | ERAELQLFCA | RRKQEALGQG | VARLVLPKLE | GHTCEKCREL | LKPGEYGVFA | ARAGEQRCWH | QPCFACQACG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QALINLIYFY | HDGQLYCGRH | HAELLRPRCP | ACDQLIFSWR | CTEAEGQRWH | ENHFCCQDCA | GPLGGGRYAL | PGGSPCCPSC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FENRYSDAGS | SWAGALEGQA | FLGETGLDRT | EGRDQTSVNS | ATLSRTLLAA | AGGSSLQTQR | GLPGSSPQQE | NRPGDKAEAP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| KGQEQCRLET | IRDPKDTPFS | TCSSSSDSEP | EGFFLGERLP | QSWKTPGSLQ | AEDSNASKTH | CTMC | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1234 | 1 | 1136.1482 | 87.82 | 2 | 43.7 | 13.4 | 1 | 83-101 | R.YCLALGEEERAELQLFCAR.R | Carbamidomethyl: 2 |

# Detailed Protein Report

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## Protein 1212: malcavernin isoform 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|269308190 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.32 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MEEEGKKGKK PGIVSPFKRV FLKGEKSRDK KAHEKVTERR PLHTVVLSLP ERVEPDRLLS DYIEKEVKYL GQLTSIPGYL
        90        100        110        120        130        140        150        160
NPSSRTEILH FIDNAKRAHQ LPGHLTQEHD AVLSLSAYNV KLAWRDGEDI ILRVPIHDIA AVSYVRDDAA HLVVLKTDDS
       170        180        190        200        210        220        230        240
STKVDIKETY EVEASTFCFP ESVDVGGASP HSKTISESEL SASATELLQD YMLTLRTKLS SQEIQQFAAL LHEYRNGASI
       250        260        270        280        290        300        310        320
HEFCINLRQL YGDSRKFLLL GLRPFIPEKD SQHFENFLET IGVKDGRGII TDSFGRHRRA LSTTSSSTTN GNRATGSSDD
       330        340        350        360
RSAPSEGDEW DRMISDISSD IEALGCSMDQ DSA
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1332 | 1 | 698.9025 | 94.05 | 2 | 45.0 | 13.4 | 0 | 300-313 | R.ALSTTSSSTTNGNR.A | | QU:MU | 0.32 |

# Detailed Protein Report

## Protein 1213: UDP-glucuronosyltransferase 1-6 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|45827767 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 29.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPNMVFIGGI | NCKKRKDLSQ | EFEAYINASG | EHGIVVFSLG | SMVSEIPEKK | AMAIADALGK | IPQTVLWRYT | GTRPSNLANN |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| TILVKWLPQN | DLLGHPMTRA | FITHAGSHGV | YESICNGVPM | VMMPLFGDQM | DNAKRMETKG | AGVTLNVLEM | TSEDLENALK |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| AVINDKSYKE | NIMRLSSLHK | DRPVEPLDLA | VFWVEFVMRH | KGAPHLRPAA | HDLTWYQYHS | LDVIGFLLAV | VLTVAFITFK |
| **250** | **260** | **270** | | | | | |
| CCAYGYRKCL | GKKGRVKKAH | KSKTH | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1581 | 1 | 720.3513 | 7.56 | 2 | 49.5 | 13.4 | 0 | 1-13 | -.MPNMVFIGGINCK.K | Oxidation: 4 |

# Detailed Protein Report

## Protein 1214: probable G-protein coupled receptor 152 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|46243671 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 50.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.90 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDTTMEADLG | ATGHRPRTEL | DDEDSYPQGG | WDTVFLVALL | LLGLPANGLM | AWLAGSQARH | GAGTRLALLL | LSLALSDFLF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LAAAAFQILE | IRHGGHWPLG | TAACRFYYFL | WGVSYSSGLF | LLAALSLDRC | LLALCPHWYP | GHRPVRLPLW | VCAGVWVLAT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LFSVPWLVFP | EAAVWWYDLV | ICLDFWDSEE | LSLRMLEVLG | GFLPFLLLLV | CHVLTQATAC | RTCHRQQQPA | ACRGFARVAR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TILSAYVVLR | LPYQLAQLLY | LAFLWDVYSG | YLLWEALVYS | DYLILLNSCL | SPFLCLMASA | DLRTLLRSVL | SSFAAALCEE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RPGSFTPTEP | QTQLDSEGPT | LPEPMAEAQS | QMDPVAQPQV | NPTLQPRSDP | TAQPQLNPTA | QPQSDPTAQP | QLNLMAQPQS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DSVAQPQADT | NVQTPAPAAS | SVPSPCDEAS | PTPSSHPTPG | ALEDPATPPA | SEGESPSSTP | PEAAPGAGPT | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1794 | 1 | 872.3077 | -114.49 | 2 | 52.8 | 13.4 | 0 | 2-17 | M.DTTMEADLGATGHRPR.T | Oxidation: 4 | WUP:QUP 0.90 |

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# Detailed Protein Report

## Protein 1215: PREDICTED: C-type lectin domain family 18 member C isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530423816 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLHPETSPGR | GHLLAVLLAL | LGTAWAEVWP | PQLQEQAPMA | GALNRKESFL | LLSLHNRLRS | WVQPPAADMR | RLDWSDSLAQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LAQARAALCG | IPTPSLASGL | WRTLQVGWNM | QLLPAGLASF | VEVVSLWFAE | GQRYSHAAGE | CARNATCTHY | TQVSVLQLVW |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ATSSQLGCGR | HLCSAGQAAI | EAFVCAYSPR | GNWEVNGKTI | VPYKKGAWCS | LCTASVSGCF | KAWDHAGGLC | EVPRNPCRMS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CQNHGRLNIS | TCHCHCPPGY | TGRYCQVRCS | LQCVHGRFRE | EECSCVCDIG | YGGAQCATKV | HFPFHTCDLR | IDGDCFMVSS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EADTYYRARM | KCQRKGGVLA | QIKSQKVQDI | LAFYLGRLET | TNEVIDSDFE | TRNFWIAQGS | PTRPPRTPSA | GPQGSTRPSP |
| 410 | 420 | | | | | | |
| VLPLGSLTTT | DPPAIL | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2848 | 2 | 856.9527 | -9.97 | 2 | 66.0 | 13.4 | 0 | 86-102 | R.AALCGIPTPSLASGLWR.T | |

# Detailed Protein Report

## Protein 1216: PREDICTED: ubiquitin carboxyl-terminal hydrolase 21 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578800816 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 42.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 8.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPQASEHRLG | RTREPPVNIQ | PRVGSKLPFA | PRARSKERRN | PASGPNPMLR | PLPPRPGLPD | ERLKKLELGR | GRTSGPRPRG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PLRADHGVPL | PGSPPPTVAL | PLPSRTNLAR | SKSVSSGDLR | PMGIALGGHR | GTGELGAALS | RLALRPEPPT | LRRSTSLRRL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GGFPGPPTLF | SIRTEPPASH | GSFHMISARS | SEPFYSDDKM | AHHTLLLGSG | HVGLRNLGNT | CFLNAVLQCL | SSTRPLRDFC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LRRDFRQEVP | GGGRAQELTE | AFADVIGALW | HPDSCEAVNP | TRFRAVFQKY | VPSFSGYSQQ | DAQEFLKLLM | ERLHLEINRR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| GRRAPPILAN | GPVPSPPRRG | GALLEEPELS | DDDRANLMWK | RYLEREDSKI | VDLFVGQLKS | CLKCQA | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1329 | 1 | 1018.4526 | -81.05 | 3 | 46.2 | 13.4 | 2 | 111-141 | R.SKSVSSGDLRPMGIALGGHRGTGELGAALSR.L | Oxidation: 12 |

# Detailed Protein Report

## Protein 1217: PREDICTED: src kinase-associated phosphoprotein 1 isoform X2 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|530413029 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.2 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQAAALPEEI | RWLLEDAEEF | LAEGLRNENL | SAVARDHRDH | ILRGFQQIKA | RYYWDFQPQG | GDIGQDSSDD | NHSGTLGLSL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TSDAPFLSDY | QDEGMEDIVK | GAQELDNVIK | QGYLEKKSKD | HSFFGSEWQK | RWCVVSRGLF | YYYANEKSKQ | PKGTFLIKGY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GVRMAPHLRR | DSKKESCFEL | TSQDRRSYEF | TATSPAEARD | WVDQISFLLK | DLSSLTIPYE | EDEEEEEKEE | TYDDIDGFDS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PSCGSQCRPT | ILPGSVGIKE | PTEEKEEEDI | YEVLPDYASY | YQGLWDCHGD | QPDELSFQRG | DLIRILSKEY | NMYGWWVGEL |
| 330 | 340 | 350 |  |  |  |  |  |
| NSLVGIVPKE | YLTTAFEVEE | R |  |  |  |  |  |

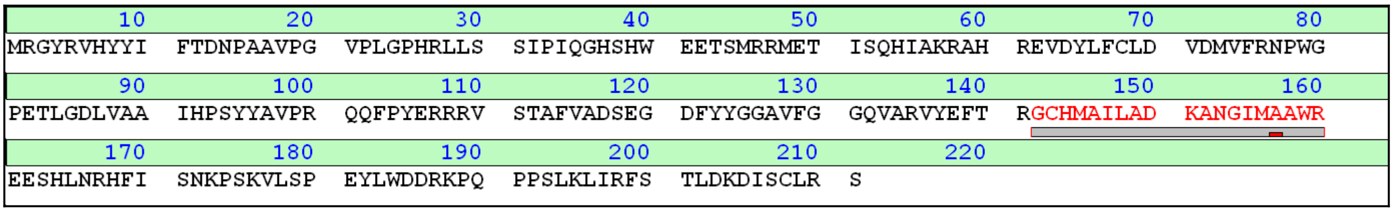
| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1055 | 1 | 622.8431 | 39.01 | 2 | 43.3 | 13.4 | 0 | 1-11 | -.MQAAALPEEIR.W | Oxidation: 1 |

# Detailed Protein Report

---

## Protein 1218: globoside alpha-1,3-N-acetylgalactosaminyltransferase 1 isoform 5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|568384828 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 9.0 |
| | | **No. of unique Peptides:** | 1 |



| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MRGYRVHYYI | FTDNPAAVPG | VPLGPHRLLS | SIPIQGHSHW | EETSMRRMET | ISQHIAKRAH | REVDYLFCLD | VDMVFRNPWG |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| PETLGDLVAA | IHPSYYAVPR | QQFPYERRRV | STAFVADSEG | DFYYGGAVFG | GQVARVYEFT | RGCHMAILAD | KANGIMAAWR |
| **170** | **180** | **190** | **200** | **210** | **220** | | |
| EESHLNRHFI | SNKPSKVLSP | EYLWDDRKPQ | PPSLKLIRFS | TLDKDISCLR | S | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2127 | 1 | 701.2657 | -107.81 | 3 | 57.0 | 13.4 | 1 | 142-160 | R.GCHMAILADKANGIMAAWR.E | Carbamidomethyl: 2;<br>Oxidation: 15 |

# Detailed Protein Report

## Protein 1219: PREDICTED: syntaxin-binding protein 5-like isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530375552 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 128.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKKFNFRKVL | DGLTASSPGS | GSSSGSNSGG | GAGSGSVHPA | GTAGVLREEI | QETLTSEYFQ | ICKTVRHGFP | HQPTALAFDP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VQKILAIGTR | TGAIRILGRP | GVDCYCQHES | GAAVLQLQFL | INEGALVSAS | SDDTLHLWNL | RQKRPAILHS | LKFNRERITY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CHLPFQSKWL | YVGTERGNTH | IVNIESFILS | GYVIMWNKAI | ELSTKTHPGP | VVHLSDSPRD | EGKLLIGYEN | GTVVFWDLKS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KRAELRVYYD | EAIHSIDWHH | EGKQFMCSHS | DGSLTLWNLK | SPSRPFQTTI | PHGKSQREGR | KSESCKPILK | VEYKTCKNSE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PFIIFSGGLS | YDKACRRPSL | TIMHGKAITV | LEMDHPIVEF | LTLCETPYPN | EFQEPYAVVV | LLEKDLIVVD | LTQSNFPIFE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NPYPMDIHES | PVTCTAYFAD | CPPDLILVLY | SIGVKHKKQG | YSNKEWPISG | GAWNLGAQTY | PEIIITGHAD | GSIKFWDASA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ITLQMLYKLK | TSKVFEKQKV | GEGKQTCEIV | EEDPFAIQMI | YWCPESRIFC | VSGVSAYVII | YKFSRHEITT | EIVSLEVRLQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YDVEDIITPE | PETSPPFPDL | SAQLPSSRSL | SGSTNTVASE | GVTKDSIPCL | NVKTRPVRMP | PGYQAELVIQ | LVWVDGEPPQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QITSLAVSSA | YGIVAFGNCN | GLAVVDFIQK | TVLLSMGTID | LYRSSDLYQR | QPRSPRKNKQ | FIAGLTELND | SPVPLELERC |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KSPTSDHVNG | HCTSPTSQSC | SSGKRLSSAD | VSKVNRWGPG | RPPFRKAQSA | ACMEISLPVT | TEENRENSYN | RSRSSSISSI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DKDSKEAITA | LYFMDSFARK | NDSTISPCLF | VGTSLGMVLI | ISLNLPLADE | QRFTEPVMVL | PSGTFLSLKG | AVLTFSCMDR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| MGGLMQPPYE | VWRDPNNIDE | NEKSWRRKVV | MNSSSASQEI | GDHQYTIICS | EKQAKVFSLP | SQTCLYVHNI | TETSFILQAN |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VVVMCSSACL | ACFCANGHIM | IMSLPSLRPM | LDVNYLPLTD | MRIARTFCFT | NEGQALYLVS | PTEIQRLTYS | QEMCDNLQDM |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LGDLFTPIET | PEAQNRGFLK | GLFGGSGQTF | DREELFGEAS | AGKASRSLAQ | HIPGPGSIEG | MKGAAGGVMG | ELTRARIALD |
| 1130 | 1140 | 1150 | 1160 | 1170 | | | |
| ERGQRLGELE | EKTAGMMTSA | EAFSKHAHEL | MLKYKDKKWY | QF | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2983 | 1 | 965.4581 | -8.88 | 2 | 66.1 | 13.4 | 2 | 786-802 | R.ENSYNRSRSSSISSIDK.D | |

# Detailed Protein Report

## Protein 1220: uncharacterized protein ARIH2OS [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|176866318 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 30.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 8.3 |
| | | **No. of unique Peptides:** | 1 |

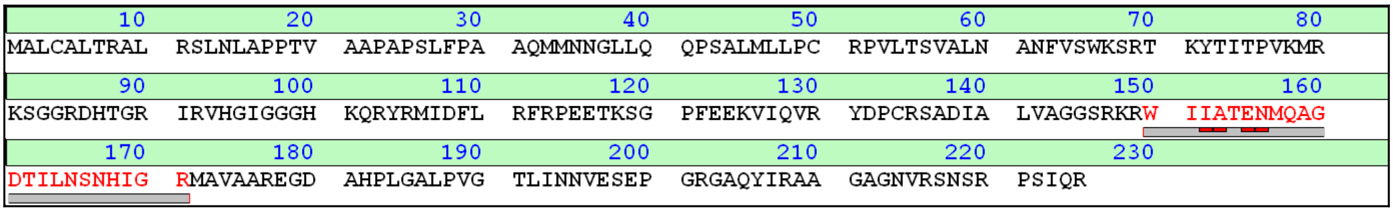
| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLGQRAGDGE | RPGLPGDGEG | GVPARPGRRA | ERPPQRPAKV | NKAVTCAAHL | PGAAASRPLS | PNKPDRVRPG | QRDRIGAKRQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RRRRADAGQA | RAASSRRVVP | TAPEVLGAVA | SLPDRGRPTV | ARVATGSRLE | GLFSAASLKL | SALTQSLTRV | RQAPTASGAT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IRLPASPVEM | FLTSAFLTGF | SFHCLYSGIG | HGEDILASVE | QITIVSRPLS | GQRGAGPGNS | AYTPRRSQGG | PRAATTPGFR |
| 250 | 260 | 270 | 280 | 290 | 300 | | |
| FPCRGLVRRA | VLRLTVTVQD | CILTALLAVS | FHSIGVVIMT | SSYLLGPVVK | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 573 | 1 | 819.8424 | 95.39 | 3 | 35.6 | 13.4 | 0 | 43-66 | K.AVTCAAHLPGAAASRPLSPNKPDR.V | Carbamidomethyl: 4 |

# Detailed Protein Report

## Protein 1221: PREDICTED: 39S ribosomal protein L2, mitochondrial isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530382111 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 9.8 |
| | | **No. of unique Peptides:** | 1 |



```
        10         20         30         40         50         60         70         80
MALCALTRAL RSLNLAPPTV AAPAPSLFPA AQMMNNGLLQ QPSALMLLPC RPVLTSVALN ANFVSWKSRT KYTITPVKMR
        90        100        110        120        130        140        150        160
KSGGRDHTGR IRVHGIGGGH KQRYRMIDFL RFRPEETKSG PFEEKVIQVR YDPCRSADIA LVAGGSRKRW IIATENMQAG
       170        180        190        200        210        220        230
DTILNSNHIG RMAVAAREGD AHPLGALPVG TLINNVESEP GRGAQYIRAA GAGNVRSNSR PSIQR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 767 | 1 | 824.1049 | 34.67 | 3 | 39.6 | 13.4 | 0 | 150-171 | R.WIIATENMQAGDTILNSNHIGR.M | Oxidation: 8 |

# Detailed Protein Report

## Protein 1222: PREDICTED: nuclear factor erythroid 2-related factor 1 isoform X6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530412326 | **Score:** | 13.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 80.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.4 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLSLKKYLTE | GLLQFTILLS | LIGVRVDVDT | YLTSQLPPLR | EIILGPSSAY | TQTQFHNLRN | TLDGYGIHPK | SIDLDNYFTA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RRLLSQVRAL | DRFQVPTTEV | NAWLVHRDPE | GSVSGSQPNS | GLALESSSGL | QDVTGPDNGV | RESETEQGFG | EDLEDLGAVA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PPVSGDLTKE | DIDLGAGREV | FDYSHRQKEQ | DVEKELRDGG | EQDTWAGEGA | EALARNLLVD | GETGESFPAQ | FPADISSITE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AVPSESEPPA | LQNNLLSPLL | TGTESPFDLE | QQWQDLMSIM | EMQAMEVNTS | ASEILYSAPP | GDPLSTNYSL | APNTPINQNV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SLHQASLGGC | SQDFLLFSPE | VESLPVASSS | TLLPLAPSNS | TSLNSTFGST | NLTGLFFPPQ | LNGTANDTAG | PELPDPLGGL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LDEAMLDEIS | LMDLAIEEGF | NPVQASQLEE | EFDSDSGLSL | DSSHSPSSLS | SSEGSSSSSS | SSSSSSSSAS | SSASSSFSEE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GAVGYSSDSE | TLDLEEAEGA | VGYQPEYSKF | CRMSYQDPAQ | LSCLPYLEHV | GHNHTYNMAP | SALDSADLPP | PSALKKGSKE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KQADFLDKQM | SRDEHRARAM | KIPFTNDKII | NLPVEEFNEL | LSKYQLSEAQ | LSLIRDIRRR | GKNKMAAQNC | RKRKLDTILN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LERDVEDLQR | DKARLLREKV | EFLRSLRQMK | QKVQSLYQEV | FGRLRDENGR | PYSPSQYALQ | YAGDGSVLLI | PRTMADQQAR |
| 730 | 740 | | | | | | |
| RQERKPKDRR | K | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 179 | 1 | 879.5102 | 25.46 | 2 | 32.0 | 13.4 | 0 | 589-603 | K.IINLPVEEFNELLSK.Y | |

# Detailed Protein Report

**Protein 1223:** **glucose-fructose oxidoreductase domain-containing protein 1 isoform 2 [Homo sapiens]**

**Accession:** gi|336285206
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 13.3
**MW [kDa]:** 31.8
**pI:** 5.7
**Sequence Coverage [%]:** 6.6
**No. of unique Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|336285213 | refseq_human (refseq_human_20140103.fasta) | glucose-fructose oxidoreductase domain-containing protein 1 isoform 2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTSAAHYYPK | LMSIMGNVLR | FLPAFVRMKQ | LIEEGYVGEP | LVCEVQVHGG | SLLGKKYNWS | CDDLMGGGGL | HSVGTYIIDL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LTFLTGQKAV | KVHGLLKTFV | KQTDHIKGIR | QITSDDFCTF | QMVLEGGVCC | TVTLNFNVPG | EFKQDVTVVG | SAGRLLAVGT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DLYGQRNSAP | EQELLVQDAT | PVSNSLLPEK | AFSDIPSPYL | RGTIKMMQAV | RQAFQDQDDR | RTWDGRPLTM | AATFDDCLYA |
| 250 | 260 | 270 | 280 | 290 | | | |
| LCVVDTIKRS | SQTGEWQNIA | IMTEEPELSP | AYLISEAMRR | SRMSLYC | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 348 | 1 | 752.5027 | 120.14 | 3 | 33.0 | 13.3 | 2 | 11-29 | K.LMSIMGNVLRFLPAFVRMK.Q | Oxidation: 5, 18 |

# Detailed Protein Report

## Protein 1224: mitochondrial fission 1 protein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|151108473 | **Score:** | 13.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 16.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 8.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MEAVLNELVS VEDLLKFEKK FQSEKAAGSV SKSTQFEYAW CLVRSKYNDD IRKGIVLLEE LLPKGSKEEQ RDYVFYLAVG
        90        100        110        120        130        140        150        160
NYRLKEYEKA LKYVRGLLQT EPQNNQAKEL ERLIDKAMKK DGLVGMAIVG GMALGVAGLA GLIGLAVSKS KS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1550 | 1 | 720.8827 | 9.68 | 2 | 49.6 | 13.3 | 0 | 96-108 | R.GLLQTEPQNNQAK.E | |

# Detailed Protein Report

## Protein 1225: coiled-coil domain-containing protein 67 [Homo sapiens]

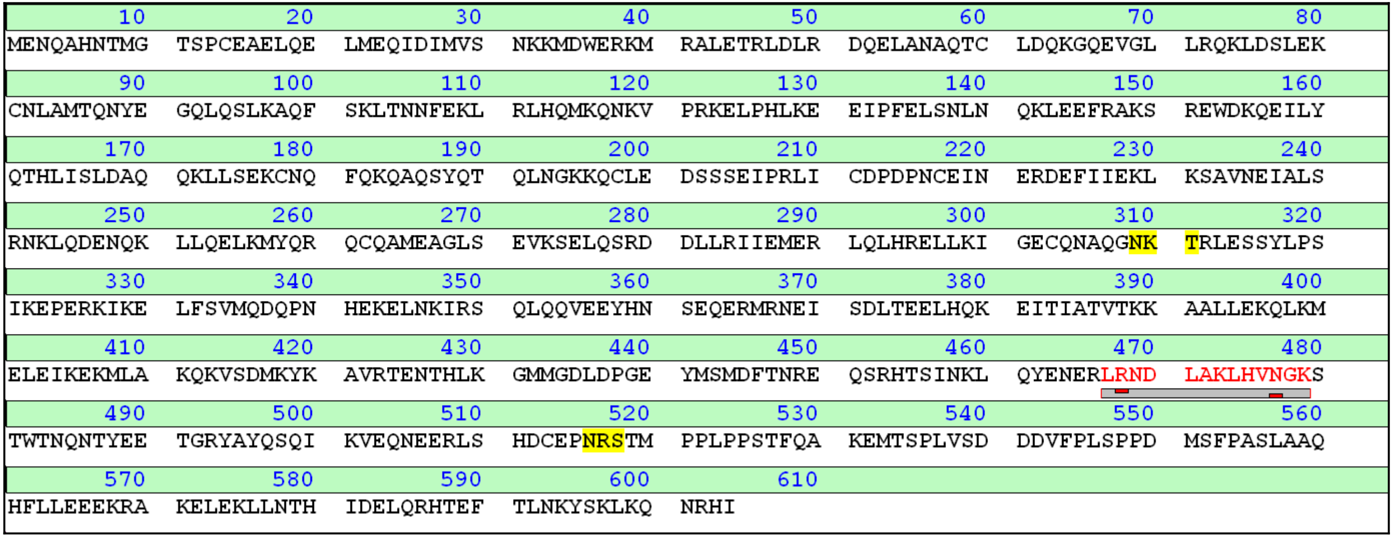
| | | | |
|---|---|---|---|
| **Accession:** | gi\|116812628 | **Score:** | 13.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 70.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***WUP:QUP*** | **Median:** | 1.43 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530396379 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: coiled-coil domain-containing protein 67 isoform X1 [Homo sapiens] |



| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MENQAHNTMG | TSPCEAELQE | LMEQIDIMVS | NKKMDWERKM | RALETRLDLR | DQELANAQTC | LDQKGQEVGL | LRQKLDSLEK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CNLAMTQNYE | GQLQSLKAQF | SKLTNNFEKL | RLHQMKQNKV | PRKELPHLKE | EIPFELSNLN | QKLEEFRAKS | REWDKQEILY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QTHLISLDAQ | QKLLSEKCNQ | FQKQAQSYQT | QLNGKKQCLE | DSSSEIPRLI | CDPDPNCEIN | ERDEFIIEKL | KSAVNEIALS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RNKLQDENQK | LLQELKMYQR | QCQAMEAGLS | EVKSELQSRD | DLLRIIEMER | LQLHRELLKI | GECQNAQGNK | TRLESSYLPS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IKEPERKIKE | LFSVMQDQPN | HEKELNKIRS | QLQQVEEYHN | SEQERMRNEI | SDLTEELHQK | EITIATVTKK | AALLEKQLKM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ELEIKEKMLA | KQKVSDMKYK | AVRTENTHLK | GMMGDLDPGE | YMSMDFTNRE | QSRHTSINKL | QYENERLRND | LAKLHVNGKS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TWTNQNTYEE | TGRYAYQSQI | KVEQNEERLS | HDCEPNRSTM | PPLPPSTFQA | KEMTSPLVSD | DDVFPLSPPD | MSFPASLAAQ |
| 570 | 580 | 590 | 600 | 610 | | | |
| HFLLEEEKRA | KELEKLLNTH | IDELQRHTEF | TLNKYSKLKQ | NRHI | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 233 | 1 | 493.3908 | 201.48 | 3 | 32.9 | 13.3 | 2 | 467-479 | R.LRNDLAKLHVNGK.S | | WUP:QUP 1.43 |

# Detailed Protein Report

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## Protein 1226: PREDICTED: group IIF secretory phospholipase A2 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578799581 | **Score:** | 13.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 12.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 8.2 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MADGAKANPK GFKKKVLDRC FSGWRGPRFG ASCPSRTSRS SLGMKKFFTV AILAGSVLST AHGSLLNLKA MVEAVTGRSA
        90        100        110        120        130
ILSFVGYGCY CGLGGRGQPK DEVDWKGPLT CSKTHMGEQS HS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1142 | 1 | 509.6230 | -255.01 | 2 | 43.9 | 13.3 | 1 | 1-10 | -.MADGAKANPK.G | Oxidation: 1 |

# Detailed Protein Report

## Protein 1227: molybdenum cofactor sulfurase [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|157388923 | **Score:** | 13.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 98.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAGAAAESGR | ELWTFAGSRD | PSAPRLAYGY | GPGSLRELRA | REFSRLAGTV | YLDHAGATLF | SQSQLESFTS | DLMENTYGNP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HSQNISSKLT | HDTVEQVRYR | ILAHFHTTAE | DYTVIFTAGS | TAALKLVAEA | FPWVSQGPES | SGSRFCYLTD | SHTSVVGMRN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VTMAINVIST | PVRPEDLWSA | EERSASASNP | DCQLPHLFCY | PAQSNFSGVR | YPLSWIEEVK | SGRLHPVSTP | GKWFVLLDAA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SYVSTSPLDL | SAHQADFVPI | SFYKIFGFPT | GLGALLVHNR | AAPLLRKTYF | GGGTASAYLA | GEDFYIPRQS | VAQRFEDGTI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SFLDVIALKH | GFDTLERLTG | GMENIKQHTF | TLAQYTYVAL | SSLQYPNGAP | VVRIYSDSEF | SSPEVQGPII | NFNVLDDKGN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IIGYSQVDKM | ASLYNIHLRT | GCFCNTGACQ | RHLGISNEMV | RKHFQAGHVC | GDNMDLIDGQ | PTGSVRISFG | YMSTLDDVQA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FLRFIIDTRL | HSSGDWPVPQ | AHADTGETGA | PSADSQADVI | PAVMGRRSLS | PQEDALTGSR | VWNNSSTVNA | VPVAPPVCDV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ARTQPTPSEK | AAGVLEGALG | PHVVTNLYLY | PIKSCAAFEV | TRWPVGNQGL | LYDRSWMVVN | HNGVCLSQKQ | EPRLCLIQPF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IDLRQRIMVI | KAKGMEPIEV | PLEENSERTQ | IRQSRVCADR | VSTYDCGEKI | SSWLSTFFGR | PCHLIKQSSN | SQRNAKKKHG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KDQLPGTMAT | LSLVNEAQYL | LINTSSILEL | HRQLNTSDEN | GKEELFSLKD | LSLRFRANII | INGKRAFEEE | KWDEISIGSL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RFQVLGPCHR | CQMICIDQQT | GQRNQHVFQK | LSESRETKVN | FGMYLMHASL | DLSSPCFLSV | GSQVLPVLKE | NVEGHDLPAS |
| 890 | | | | | | | |
| EKHQDVTS | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2428 | 1 | 856.6281 | 166.17 | 2 | 60.8 | 13.3 | 0 | 265-280 | K.IFGFPTGLGALLVHNR.A | |

# Detailed Protein Report

## Protein 1228: PREDICTED: proline-rich protein 16 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530379999 | **Score:** | 13.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 32.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 7.2 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSAKSKGNPS SSCPAEGPPA ASKTKVKEQI KIIVEDLELV LGDLKDVAKE LKEVVDQIDT LTSDLQLEDE MTDSSKTDTL
        90        100        110        120        130        140        150        160
NSSSSGTTAS SLEKIKVQAN APLIKPPAHP SAILTVLRKP NPPPPPPRLT PVKCEDPKRV VPTANPVKTN GTLLRNGGLP
       170        180        190        200        210        220        230        240
GGPNKIPNGD ICCIPNSNLD KAPVQLLMHR PEKDRCPQAG PRERVRFNEK VQYHGYCPDC DTRYNIKNRE VHLHSEPVHP
       250        260        270        280        290        300        310
PGKIPHQGPP LPPTPHLPPF PLENGGMGIS HSNSFPPIRP ATVPPPTAPK PQKTILRKST TTTV
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 111 | 1 | 1029.4480 | -50.18 | 2 | 31.3 | 13.3 | 2 | 2-23 | M.SAKSKGNPSSSCPAEGPPAASK.T | |

# Detailed Protein Report

## Protein 1229: alcohol dehydrogenase 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|71565152 | **Score:** | 13.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MGTKGKVIKC KAAIAWEAGK PLCIEEVEVA PPKAHEVRIQ IIATSLCHTD ATVIDSKFEG LAFPVIVGHE AAGIVESIGP
        90        100        110        120        130        140        150        160
GVTNVKPGDK VIPLYAPLCR KCKFCLSPLT NLCGKISNLK SPASDQQLME DKTSRFTCKG KPVYHFFGTS TFSQYTVVSD
       170        180        190        200        210        220        230        240
INLAKIDDDA NLERVCLLGC GFSTGYGAAI NNAKVTPGST CAVFGLGGVG LSAVMGCKAA GASRIIGIDI NSEKFVKAKA
       250        260        270        280        290        300        310        320
LGATDCLNPR DLHKPIQEVI IELTKGGVDF ALDCAGGSET MKAALDCTTA GWGSCTFIGV AAGSKGLTIF PEELIIGRTI
       330        340        350        360        370        380        390
NGTFFGGWKS VDSIPKLVTD YKNKKFNLDA LVTHTLPFDK ISEAFDLMNQ GKSVRTILIF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1369 | 1 | 676.8982 | 87.95 | 2 | 45.4 | 13.3 | 0 | 104-115 | K.FCLSPLTNLCGK.I | Carbamidomethyl: 10 |

# Detailed Protein Report

## Protein 1230: kanadaptin [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|155722990 | **Score:** | 13.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 88.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.93 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.47 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLAPLRNAPG | REGATSPSPP | TDATGSLGEW | DVDRNVKTEG | WVSKERISKL | HRLRMADILS | QSETLASQDL | SGDFKKPALP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VSPAARSKAP | ASSSSNPEEV | QKEGPTALQD | SNSGEPDIPP | PQPDCGDFRS | LQEEQSRPPT | AVSSPGGPAR | APPYQEPPWG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GPATAPYSLE | TLKGGTILGT | RSLKGTSYCL | FGRLSGCDVC | LEHPSVSRYH | AVLQHRASGP | DGECDSNGPG | FYLYDLGSTH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GTFLNKTRIP | PRTYCRVHVG | HVVRFGGSTR | LFILQGPEED | REAESELTVT | QLKELRKQQQ | ILLEKKMLGE | DSDEEEEMDT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SERKINAGSQ | DDEMGCTWGM | GEDAVEDDAE | ENPIVLEFQQ | EREAFYIKDP | KKALQGFFDR | EGEELEYEFD | EQGHSTWLCR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VRLPVDDSTG | KQLVAEAIHS | GKKKEAMIQC | SLEACRILDT | LGLLRQEAVS | RKRKAKNWED | EDFYDSDDDT | FLDRTGLIEK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KRLNRMKKAG | KIDEKPETFE | SLVAKLNDAE | RELSEISERL | KASSQVLSES | PSQDSLDAFM | SEMKSGSTLD | GVSRKKLHLR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TFELRKEQQR | LKGLIKIVKP | AEIPELKKTE | TQTTGAENKA | KKLTLPLFGA | MKGGSKFKLK | TGTVGKLPPK | RPELPPTLMR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| MKDEPEVEEE | EEEEEEEEKE | KEEHEKKKLE | DGSLSRPQPE | IEPEAAVQEM | RPPTDLTHFK | ETQTHENMSQ | LSEEEQNKDY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QDCSKTTSLC | AGPSASKNEY | EKSRGELKKK | KTPGPGKLPP | TLSSKYPEDD | PDYCVWVPPE | GQSGDGRTHL | NDKYGY |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2677 | 1 | 973.4892 | -48.43 | 2 | 61.8 | 13.3 | 2 | 249-264 | R.IPPRTYCRVHVGHVVR.F | Carbamidomethyl: 7 | WUP:QUP 1.47<br>QU:MU 0.93 |

# Detailed Protein Report

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## Protein 1231: PREDICTED: ankyrin repeat domain-containing protein SOWAHC-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|341914886 | **Score:** | 13.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 25.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.2 |
| | | **Sequence Coverage [%]:** | 4.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.16 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.93 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MRSAAFTIPS LKQWSPRCST GRAELGKGEP SPCTGRPEQR GRRKSSLAPP APTPDAGPQT SKDLEPPPHG CQEADRGGSW
        90        100        110        120        130        140        150        160
GATTSRPFRQ NLSDLGRHSV LPLKRNLCPG GSSLGAPPLR TPQRRVTLAA QRWLSRPQRR AVGLGELDQG AQLAALGLRW
       170        180        190        200        210        220        230        240
GVDSLGGCPR ASQPAGHSGL HHTLTCLRRH LALQAGASGH AGQLPQRASA AWEQQGQSYT ALHLAAMYLG DGEAASGNIG
       250
RRC
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1952 | 1 | 661.2554 | -170.97 | 2 | 54.3 | 13.3 | 1 | 1-12 | -.MRSAAFTIPSLK.Q | | WUP:QUP 0.93<br>QU:MU 1.16 |

# Detailed Protein Report

## Protein 1232: protein ECT2 isoform b [Homo sapiens]

**Accession:** gi|21735572
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 13.3
**MW [kDa]:** 100.0
**pI:** 7.9
**Sequence Coverage [%]:** 1.9
**No. of unique Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|385198081 | refseq_human (refseq_human_20140103.fasta) | protein ECT2 isoform b [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAENSVLTST | TGRTSLADSS | IFDSKVTEIS | KENLLIGSTS | YVEEEMPQIE | TRVILVQEAG | KQEELIKALK | DIKVGFVKME |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SVEEFEGLDS | PEFENVFVVT | DFQDSVFNDL | YKADCRVIGP | PVVLNCSQKG | EPLPFSCRPL | YCTSMMNLVL | CFTGFRKKEE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LVRLVTLVHH | MGGVIRKDFN | SKVTHLVANC | TQGEKFRVAV | SLGTPIMKPE | WIYKAWERRN | EQDFYAAVDD | FRNEFKVPPF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QDCILSFLGF | SDEEKTNMEE | MTEMQGGKYL | PLGDERCTHL | VVEENIVKDL | PFEPSKKLYV | VKQEWFWGSI | QMDARAGETM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YLYEKANTPE | LKKSVSMLSL | NTPNSNRKRR | RLKETLAQLS | RETDVSPFPP | RKRPSAEHSL | SIGSLLDISN | TPESSINYGD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TPKSCTKSSK | SSTPVPSKQS | ARWQVAKELY | QTESNYVNIL | ATIIQLFQVP | LEEEGQRGGP | ILAPEEIKTI | FGSIPDIFDV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HTKIKDDLED | LIVNWDESKS | IGDIFLKYSK | DLVKTYPPFV | NFFEMSKETI | IKCEKQKPRF | HAFLKINQAK | PECGRQSLVE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LLIRPVQRLP | SVALLLNDLK | KHTADENPDK | STLEKAIGSL | KEVMTHINED | KRKTEAQKQI | FDVVYEVDGC | PANLLSSHRS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LVQRVETISL | GEHPCDRGEQ | VTLFLFNDCL | EIARKRHKVI | GTFRSPHGQT | RPPASLKHIH | LMPLSQIKKV | LDIRETEDCH |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| NAFALLVRPP | TEQANVLLSF | QMTSDELPKE | NWLKMLCRHV | ANTICKADAE | NLIYTADPES | FEVNTKDMDS | TLSRASRAIK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KTSKKVTRAF | SFSKTPKRAL | RRALMTSHGS | VEGRSPSSND | KHVMSRLSST | SSLAGIPSPS | LVSLPSFFER | RSHTLSRSTT |
| 890 | | | | | | | |
| HLI | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2201 | 1 | 928.4175 | -66.81 | 2 | 55.9 | 13.3 | 1 | 113-129 | K.ADCRVIGPPVVLNCSQK.G | Carbamidomethyl: 14 |

# Detailed Protein Report

## Protein 1233: P2Y purinoceptor 8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|30023826 | **Score:** | 13.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.7 |
| | | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578838987 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: P2Y purinoceptor 8 isoform X6 [Homo sapiens] |
| gi\|578837768 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: P2Y purinoceptor 8 isoform X5 [Homo sapiens] |
| gi\|530423005 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: P2Y purinoceptor 8 isoform X4 [Homo sapiens] |
| gi\|530423003 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: P2Y purinoceptor 8 isoform X3 [Homo sapiens] |
| gi\|530420927 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: P2Y purinoceptor 8 isoform X2 [Homo sapiens] |
| gi\|530420925 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: P2Y purinoceptor 8 isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MQVPNSTGPD | NATLQMLRNP | AIAVALPVVY | SLVAAVSIPG | NLFSLWVLCR | RMGPRSPSVI | FMINLSVTDL | MLASVLPFQI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YYHCNRHHWV | FGVLLCNVVT | VAFYANMYSS | ILTMTCISVE | RFLGVLYPLS | SKRWRRRRYA | VAACAGTWLL | LLTALSPLAR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TDLTYPVHAL | GIITCFDVLK | WTMLPSVAMW | AVFLFTIFIL | LFLIPFVITV | ACYTATILKL | LRTEEAHGRE | QRRRAVGLAA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VVLLAFVTCF | APNNFVLLAH | IVSRLFYGKS | YYHVYKLTLC | LSCLNNCLDP | FVYYFASREF | QLRLREYLGC | RRVPRDTLDT |
| 330 | 340 | 350 | 360 | | | | |
| RRESLFSART | TSVRSEAGAH | PEGMEGATRP | GLQRQESVF | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 961 | 1 | 1025.8925 | -94.87 | 2 | 40.3 | 13.2 | 0 | 335-354 | R.SEAGAHPEGMEGATRPGLQR.Q | |

# Detailed Protein Report

## Protein 1234: syntaxin-7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|170932494 | **Score:** | 13.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 29.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 5.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSYTPGVGGD | PAQLAQRISS | NIQKITQCSV | EIQRTLNQLG | TPQDSPELRQ | QLQQKQQYTN | QLAKETDKYI | KEFGSLPTTP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SEQRQRKIQK | DRLVAEFTTS | LTNFQKVQRQ | AAEREKEFVA | RVRASSRVSG | SFPEDSSKER | NLVSWESQTQ | PQVQVQDEEI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TEDDLRLIHE | RESSIRQLEA | DIMDINEIFK | DLGMMIHEQG | DVIDSIEANV | ENAEVHVQQA | NQQLSRAADY | QRKSRKTLCI |
| 250 | 260 | 270 | | | | | |
| IILILVIGVA | IISLIIWGLN | H | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2771 | 1 | 616.3212 | -15.13 | 3 | 63.2 | 13.2 | 1 | 50-64 | R.QQLQQKQQYTNQLAK.E | |

BRUKER

# Detailed Protein Report

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## Protein 1235: sex-determining region Y protein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4507225 | **Score:** | 13.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 23.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 13.7 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MQSYASAMLS VFNSDDYSPA VQENIPALRR SSSFLCTESC NSKYQCETGE NSKGNVQDRV KRPMNAFIVW SRDQRRKMAL
        90        100        110        120        130        140        150        160
ENPRMRNSEI SKQLGYQWKM LTEAEKWPFF QEAQKLQAMH REKYPNYKYR PRRKAKMLPK NCSLLPADPA SVLCSEVQLD
       170        180        190        200        210
NRLYRDDCTK ATHSRMEHQL GHLPPINAAS SPQQRDRYSH WTKL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1830 | 2 | 1023.8975 | 40.66 | 3 | 52.7 | 13.2 | 2 | 135-162 | K.AKMLPKNCSLLPADPASVLCSEVQLDNR.L | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 1236: alpha-2-macroglobulin-like protein 1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|539846446 | **Score:** | 13.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 105.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLIGKGSLVM | EGQKHLNSKK | KGLKASFSLS | LTFTSRLAPD | PSLVIYAIFP | SGGVVADKIQ | FSVEMCFDNQ | VSLGFSPSQQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LPGAEVELQL | QAAPGSLCAL | RAVDESVLLL | RPDRELSNRS | VYGMFPFWYG | HYPYQVAEYD | QCPVSGPWDF | PQPLIDPMPQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GHSSQRSIIW | RPSFSEGTDL | FSFFRDVGLK | ILSNAKIKKP | VDCSHRSPEY | STAMGAGGGH | PEAFESSTPL | HQAEDSQVRQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YFPETWLWDL | FPIGNSGKEA | VHVTVPDAIT | EWKAMSFCTS | QSRGFGLSPT | VGLTAFKPFF | VDLTLPYSVV | RGESFRLTAT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IFNYLKDCIR | VQTDLAKSHE | YQLESWADSQ | TSSCLCADEA | KTHHWNITAV | KLGHINFTIS | TKILDSNEPC | GGQKGFVPQK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GRSDTLIKPV | LVKPEGVLVE | KTHSSLLCPK | GKVASESVSL | ELPVDIVPDS | TKAYVTVLGD | IMGTALQNLD | GLVQMPSGCG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EQNMVLFAPI | IYVLQYLEKA | GLLTEEIRSR | AVGFLEIGYQ | KELMYKHSNG | SYSAFGERDG | NGNTWLTAFV | TKCFGQAQKF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IFIDPKNIQD | ALKWMAGNQL | PSGCYANVGN | LLHTAMKGGV | DDEVSLTAYV | TAALLEMGKD | VDDPMVSQGL | RCLKNSATST |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TNLYTQALLA | YIFSLAGEMD | IRNILLKQLD | QQAIISGESI | YWSQKPTPSS | NASPWSEPAA | VDVELTAYAL | LAQLTKPSLT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QKEIAKATSI | VAWLAKQRNA | YGGFSSTQDT | VVALQALAKY | ATTAYMPSEE | INLVVKSTEN | FQRTFNIQSV | NRLVFQQDTL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PNVPGMYTLE | ASGQGCVYVQ | TVLRYNILPP | TNMKTFSLSV | EIGKARCEQP | TSPRSLTLTI | HTSYVGSRSS | SNMAIVEVKM |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LSGFSPMEGT | NQLLLQQPLV | KKVEFGTDTL | NIYLDELIKN | TQTYTFTISQ | SVLVTNLKPA | TIKVYDYYLP | DEQATIQYSD |
| 970 | | | | | | | |
| PCE | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2228 | 1 | 972.9750 | -10.10 | 2 | 56.2 | 13.2 | 0 | 760-776 | K.YATTAYMPSEEINLVVK.S | Oxidation: 7 |

## Protein 1237: absent in melanoma 1-like protein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|301069394 | **Score:** | 13.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 177.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530361198 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: absent in melanoma 1-like protein isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEEAGGPMAR | AKARVVSATL | TWRQRPPTQE | EIKHGFHKVS | LVSGAQMEAP | QKEMFEFSRR | EEVEVNGFAT | QEEETVNCQG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PRDTAGSKNF | QSHGPIFSKK | YIPPPKEKRP | EGRLKEAVDQ | SDGSRQAPRT | EPPCVGAMAR | TELLVPLPGP | REPSPHPGVG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LTSGSSRSLE | EYRVTRTVRT | TTVVGGHVDR | RMSSSVTVRP | VSSGEALPRG | RQVSRMVPPV | VVGSPPGSPS | RSQAVKVLSN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LVPAGHSPPA | SHLPRPTAGG | PRSTGLGSTV | GAALRQLPET | GTAELKDSSA | LASTGIPASA | HLPKNQDAPA | ACPDRDQGRA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PDARACELWQ | VLGAPSSTEL | PLQTSQGQAS | VPSSPRLETH | VPSPGLTHPA | KQPVVPTHPG | ARLTPLVLPP | KKKDGPVDPP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AATVLPMVRS | EHVTVPGQPP | APSTTRRKDV | PSPGGLSAPS | SPRNKFVQNS | ENVPVLPFTQ | REVVKGPGAP | AASSPTRKEV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VQGSSASAAS | SPTWKEVVKG | PGAPAASSPT | QKEVVQGSSA | PAALFPTWKE | VVKGPGAPDA | SFPTWKEVVK | GPGAPAASSP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TQKEVVQGSG | APAALSTTPK | EVVKGPGAPA | ASSPTQKEVV | KGPCAPAASS | PTQKEVVQGS | GAPAALSPKS | TEVVQGPKGS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SSIQKEAVQG | IAGSLAPPLT | KEETVQGPIA | PATSLPKQDK | GVQDSEGSPI | SSLTQKEVVQ | DPDALPAPSS | SVDRVSPSPG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GTPAPVPTGA | EASTESQLVS | DPTEGKTCTE | TSREEDEVAL | AADLEIFLDT | LRSMEPPEIL | RTHRLPRAPR | SSYLSMYATL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PAIEEDQLGP | WVLGPGPQEV | PSLEEKEEEE | EEEPENPYLS | DDEKLQRRQE | KAGPSPSRDL | HPARPTQVSC | SPLEMMKKHV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| AGTKGPHSEL | GLELQGGSRP | TSRLGGSLLF | GSLVPTAKEA | STPEPLGTKL | SALLPHGAPG | LRKVPGQLPL | LCSERSSPTE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KLACSLPLEG | WSPALKTQGK | LNTRPGKVIF | FSESGCQGSG | REVWGDIVDA | SGWAPVASIR | VVRGCWVLYE | EPEFRGQKLV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LPEGDMELRT | PGTKWSPQGI | GSLRRVVWDY | STPEISLFSE | EGLKGEQVKL | TEALKNSQGL | EKPLQVASAT | VSAGLWLLYP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KPLFEDTPYI | LEPGEYPTSE | AWGTSDPSVG | SLKPMRLGCP | SVEKPGEPRA | VVYEAPGFQG | RSWEVSRDIY | NLQQPEDSQS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PHLASVGSLR | VLGGCWVGYE | KEGFRGHQYL | LEEGEYPDWS | HWGGYDELLT | SLRVIRTDFG | DPAVVLFEAM | DFEGHGVEVS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KALPDVELVQ | HGPSTQAIHV | LSGVWVAYQE | VGFSGEQYVL | EKGVYRNCED | WGAGNSTLAS | LQPVLQVGEH | DLHFVSKIQL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| FSRPDFLGDH | FSFEDDQAAL | PASFRPQSCR | VHGGSWILFD | ETNFEGDQHI | LSEGEFPTLT | AMGCLASTVL | GSLQKVSLHF |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SEPSIFLYGL | ECFEGKEIEL | SREVRSLQAE | GFNNHVLSVR | IKGGIWVLCE | HSDFRGRQWL | VGSCEITNWL | TYSGTQRVGS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| LYPIKQRRVY | FRLWNAALGG | FLAVPDHVED | MKAGRVVVAD | PQAGGSCIWY | YEDGLLKNQM | APTMSLQVIG | PPSPGSKVVL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | |
| WAESRLPRQT | WSISESGHIC | SQMFEGQILD | VKGGRGYDRD | HVVLWEPDED | RASQIWTIHV | L | |

| Cmpd. | No. of | m/z meas. | Δ m/z | z | Rt | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| | Cmpds. | | [ppm] | | [min] | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 1638 | 1 | 745.8087 | -73.79 | 2 | 50.2 | 13.2 | 2 | 1-14 | -.MEEAGGPMARAKAR.V | Oxidation: 1 |

# Detailed Protein Report

**Protein 1238:** **PREDICTED: FYVE, RhoGEF and PH domain-containing protein 4 isoform X8 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578822755 | **Score:** | 13.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MVNKIFSNIS SINAFHSKFL LPELEKRMQE WETTPRIGDI LQKLAPFLKM YGEYVKGFDN AMELVKNMTE RIPQFKSVVE
        90        100        110        120        130        140        150        160
EIQKQKICGS LTLQHHMLEP VQRIPRYEML LKDYLRKLPP DSLDWNDAKK SLEIISTAAS HSNSAIRKME NLKKLLEIYE
       170        180        190        200        210        220        230        240
MLGEEEDIVN PSNELIKEGQ ILKLAARNTS AQERYLFLFN NMLLYCVPKF SLVGSKFTVR TRVGIDGMKI VETQNEEYPH
       250        260        270        280        290        300        310        320
TFQVSGKERT LELQASSAQD KEEWIKALQE TIDAFHQRHE TFRNAIAKDN DIHSEVSTAE LGKRAPRWIR DNEVTMCMKC
       330        340        350        360        370        380        390        400
KEPFNALTRR RHHCRACGYV VCWKCSDYKA QLEYDGGKLS KVCKDCYQII SGFTDSEEKK RKGILEIESA EVSGNSVVCS
       410        420        430        440        450        460        470        480
FLQYMEKSKP WQKAWCVIPK QDPLVLYMYG APQVSKPHLS EGTDALGGKG KRVDSGLKIC RTRVQAVSLF H
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 90 | 1 | 793.8780 | -69.04 | 2 | 30.1 | 13.2 | 2 | 459-471 | K.ICRTRVQAVSLFH.- | Carbamidomethyl: 2 |

# Detailed Protein Report

## Protein 1239: PREDICTED: PR domain zinc finger protein 5 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530377106 | **Score:** | 13.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 1.16 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLGMYVPDRF | SLKSSRVQDG | MGLYTARRVR | KGEKFGPFAG | EKRMPEDLDE | NMDYRLMWEV | RGSKGEVLYI | LDATNPRHSN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| WLRFVHEAPS | QEQKNLAAIQ | EGENIFYLAV | EDIETDTELL | IGYLDSDMEA | EEEEQQIMTV | IKEGEVENSR | RQSTAGRKDR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LGCKEDYACP | QCESSFTSED | ILAEHLQTLH | QKPTEEKEFK | CKNCGKKFPV | KQALQRHVLQ | CTAKSSLKES | SRSFQCSVCN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SSFSSASSFE | QHQETCRGDA | RFVCKADSCG | KRLKSKDALK | RHQENVHTGD | PKKKLICSVC | NKKCSSASSL | QEHRKIHEIF |
| 330 | 340 | 350 | | | | | |
| DCQECMKKFI | SANQLKRHMI | THSDPL | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1184 | 1 | 533.6372 | -216.94 | 2 | 44.4 | 13.2 | 0 | 338-346 | R.HMITHSDPL.- | Oxidation: 2 | WUP:QUP 1.16 |

# Detailed Protein Report

## Protein 1240: adenosine 3'-phospho 5'-phosphosulfate transporter 1 isoform f [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|557357687 | **Score:** | 13.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 32.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| | | **Sequence Coverage [%]:** | 4.7 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|557357693 | refseq_human(refseq_human_20140103.fasta) | adenosine 3'-phospho 5'-phosphosulfate transporter 1 isoform f [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTRSYGATAT | SPGERFTDSQ | FLVLMNRVLA | LIVAGLSCVL | CKQPRHGAPM | YRYSFASLSN | VLSSWCQYEA | LKFVSFPTQV |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| LAKASKVIPV | MLMGKLVSRR | SYEHWEYLTA | TLISIGVSMF | LLSSGPEPRS | SPATTLSGLI | LLAGYIAFDS | FTSNWQDALF |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| AYKMSSVQMM | FGVNFFSCLF | TVGSLLEQGA | LLEGTRFMGR | HSEFAAHALL | LSICSACGQL | FIFYTIGQFG | AAVFTIIMTL |
| **250** | **260** | **270** | **280** | **290** | **300** | | |
| RQAFAILLSC | LLYGHTVTVV | GGLGVAVVFA | ALLLRVYARG | RLKQRGKKAV | PVESPVQKV | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1312 | 1 | 727.2069 | -203.76 | 2 | 46.0 | 13.2 | 1 | 2-15 | M.TRSYGATATSPGER.F | |

# Detailed Protein Report

## Protein 1241: pentraxin-4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|61966763 | **Score:** | 13.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 51.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.8 |
| | | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.05 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.30 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MGSGNWEVTG PPCGSRCERP PGLPRGVHGQ FRSAVGLSGL RWFRRFQEVT WTHLQNIASN YNVSYNVDVR FRSLAEESQA
        90        100        110        120        130        140        150        160
VAQAVNRSQA SVQGELAQLK AWVRKLQRRG RKVDTRLRAL DLTLGERSQQ RARERKAHKA QRDALQDSLA RLEGLVHSQG
       170        180        190        200        210        220        230        240
ARLAALEGRL PVAHPGTAAL GPALVPTPTQ PEELGPTSLK LQRDRQELRA ASEHRGPPQD SSAPLQGRRE PPASGSHRVL
       250        260        270        280        290        300        310        320
SGTAPKDPRQ QAWSPQVPGE ICGVGPTLVF PNASTRNVVF LSPGFVTALR ALSFCSWVRT ASGRLGTLLS YATEDNDNKL
       330        340        350        360        370        380        390        400
VLHGRDSLLP GSIHFVIGDP AFRELPLQLL LDGQWHHICV IWTSTQGRYW LHVDRRLVAT GSRFREGYEI PPGGSLVLGQ
       410        420        430        440        450        460        470        480
EQDSVGGGFD SSEAFVGSMS GLAIWDRALV PGEVANLAIG KEFPTGAILT LANAALAGGF VQGANCTCLE RCP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 424 | 1 | 787.0347 | 168.04 | 2 | 33.8 | 13.2 | 0 | 73-87 | R.SLAEESQAVAQAVNR.S | | WUP:QUP 0.30<br>QU:MU 1.05 |

# Detailed Protein Report

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## Protein 1242: protein IWS1 homolog [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|217330641 | **Score:** | 13.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 91.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.4 |
| | | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.38 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.48 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDSEYYSGDQ | SDDGGATPVQ | DERDSGSDGE | DDVNEQHSGS | DTGSVERHSE | NETSDREDGL | PKGHHVTDSE | NDEPLNLNAS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DSESEELHRQ | KDSDSESEER | AEPPASDSEN | EDVNQHGSDS | ESEETRKLPG | SDSENEELLN | GHASDSENED | VGKHPASDSE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IEELQKSPAS | DSETEDALKP | QISDSESEEP | PRHQASDSEN | EEPPKPRMSD | SESEELPKPQ | VSDSESEEPP | RHQASDSENE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ELPKPRISDS | ESEDPPRHQA | SDSENEELPK | PRISDSESED | PPRNQASDSE | NEELPKPRVS | DSESEGPQKG | PASDSETEDA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SRHKQKPESD | DDSDRENKGE | DTEMQNDSFH | SDSHMDRKKF | HSSDSEEEEH | KKQKMDSDED | EKEGEEEKVA | KRKAAVLSDS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EDEEKASAKK | SRVVSDADDS | DSDAVSDKSG | KREKTIASDS | EEEAGKELSD | KKNEEKDLFG | SDSESGNEEE | NLIADIFGES |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GDEEEEEFTG | FNQEDLEEEK | GETQVKEAED | SDSDDNIKRG | KHMDFLSDFE | MMLQRKKSMS | GKRRRNRDGG | TFISDADDVV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SAMIVKMNEA | AEEDRQLNNQ | KKPALKKLTL | LPAVVMHLKK | QDLKETFIDS | GVMSAIKEWL | SPLPDRSLPA | LKIREELLKI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LQELPSVSQE | TLKHSGIGRA | VMYLYKHPKE | SRSNKDMAGK | LINEWSRPIF | GLTSNYKGMT | REEREQRDLE | QMPQRRRMNS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TGGQTPRRDL | EKVLTGEEKA | LRPGDPGFCA | RARVPMPSNK | DYVVRPKWNV | EMESSRFQAT | SKKGISRLDK | QMRKFTDIRK |
| 810 | 820 | | | | | | |
| KSRSAHAVKI | SIEGNKMPL | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1950 | 1 | 794.7765 | -89.11 | 2 | 54.8 | 13.2 | 1 | 359-371 | K.KFHSSDSEEEEHK.K | | WUP:QUP 0.48<br>QU:MU 1.38 |

# Detailed Protein Report

## Protein 1243: keratin-like protein KRT222 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|22748757 | **Score:** | 13.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MELSQLLNEI | RANYEKILTR | NQIETVLSTR | IQLEEDISKK | MDKDEEALKA | AQAELKEARR | QWHHLQVEIE | SLHAVERGLE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NSLHASEQHY | QMQLQDLETV | IEGLEKELQE | VRRGIEKQLQ | EHEMLLNTKM | RLEQEIATYR | HLLEKEEIRY | YGCIQGGKKD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KKPTTSRVGF | VLPSAIINEI | SFTTKVPQKY | ENENVETVTK | QAILNGSIVK | ESTEAHGTIQ | TEKVDEVIKE | WEGSFFKDNP |
| 250 | 260 | 270 | 280 | 290 | 300 | | |
| RLRKKSVSLR | FDLHLAATDE | GCLETKQDNL | PDIEVRLIMR | RSCSIPSIKP | PSTAN | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1053 | 1 | 530.7772 | -60.09 | 2 | 41.4 | 13.2 | 2 | 159-167 | K.KDKKPTTSR.V | |

# Detailed Protein Report

## Protein 1244: ATP-binding cassette sub-family B member 6, mitochondrial [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|9955963 | **Score:** | 13.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 93.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVTVGNYCEA | EGPVGPAWMQ | DGLSPCFFFT | LVPSTRMALG | TLALVLALPC | RRRERPAGAD | SLSWGAGPRI | SPYVLQLLLA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TLQAALPLAG | LAGRVGTARG | APLPSYLLLA | SVLESLAGAC | GLWLLVVERS | QARQRLAMGI | WIKFRHSPGL | LLLWTVAFAA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ENLALVSWNS | PQWWWARADL | GQQVQFSLWV | LRYVVSGGLF | VLGLWAPGLR | PQSYTLQVHE | EDQDVERSQV | RSAAQQSTWR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DFGRKLRLLS | GYLWPRGSPA | LQLVVLICLG | LMGLERALNV | LVPIFYRNIV | NLLTEKAPWN | SLAWTVTSYV | FLKFLQGGGT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GSTGFVSNLR | TFLWIRVQQF | TSRRVELLIF | SHLHELSLRW | HLGRRTGEVL | RIADRGTSSV | TGLLSYLVFN | VIPTLADIII |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GIIYFSMFFN | AWFGLIVFLC | MSLYLTLTIV | VTEWRTKFRR | AMNTQENATR | ARAVDSLLNF | ETVKYYNAES | YEVERYREAI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IKYQGLEWKS | SASLVLLNQT | QNLVIGLGLL | AGSLLCAYFV | TEQKLQVGDY | VLFGTYIIQL | YMPLNWFGTY | YRMIQTNFID |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MENMFDLLKE | ETEVKDLPGA | GPLRFQKGRI | EFENVHFSYA | DGRETLQDVS | FTVMPGQTLA | LVGPSGAGKS | TILRLLFRFY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DISSGCIRID | GQDISQVTQA | SLRSHIGVVP | QDTVLFNDTI | ADNIRYGRVT | AGNDEVEAAA | QAAGIHDAIM | AFPEGYRTQV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GERGLKLSGG | EKQRVAIART | ILKAPGIILL | DEATSALDTS | NERAIQASLA | KVCANRTTIV | VAHRLSTVVN | ADQILVIKDG |
| 810 | 820 | 830 | 840 | 850 | | | |
| CIVERGRHEA | LLSRGGVYAD | MWQLQQGQEE | TSEDTKPQTM | ER | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2525 | 1 | 841.5355 | 86.99 | 2 | 62.2 | 13.2 | 1 | 331-343 | R.TFLWIRVQQFTSR.R | |

# Detailed Protein Report

## Protein 1245: protein ARV1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|12232479 | **Score:** | 13.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGNGGRSGLQ | QGKGNVDGVA | ATPTAASASC | QYRCIECNQE | AKELYRDYNH | GVLKITICKS | CQKPVDKYIE | YDPVIILINA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ILCKAQAYRH | ILFNTQINIH | GKLCIFCLLC | EAYLRWWQLQ | DSNQNTAPDD | LIRYAKEWDF | YRMFAIAALE | QTAYFIGIFT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FLWVERPMTA | KKKPNFILLL | KALLLSSYGK | LLLIPAVIWE | HDYTSVCLKL | IKVFVLTSNF | QAIRVTLNIN | RKLSFLAVLS |
| 250 | 260 | 270 | 280 | | | | |
| GLLLESIMVY | FFQSMEWDVG | SDYAIFKSQD | F | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2796 | 1 | 639.3467 | 71.37 | 2 | 63.5 | 13.1 | 1 | 134-142 | R.YAKEWDFYR.M | |

# Detailed Protein Report

## Protein 1246: polyserase-2 isoform 3 precursor [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|385137135 | **Score:** | 13.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 80.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
|  |  | **Sequence Coverage [%]:** | 1.7 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MARHLLLPLV | MLVISPIPGA | FQDSALSPTQ | EEPEDLDCGR | PEPSARIVGG | SNAQPGTWPW | QVSLHHGGGH | ICGGSLIAPS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| WVLSAAHCFM | TNGTLEPAAE | WSVLLGVHSQ | DGPLDGAHTR | AVAAIVVPAN | YSQVELGADL | ALLRLASPAS | LGPAVWPVCL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PRASHRFVHG | TACWATGWGD | VQEADPLPLP | WVLQEVELRL | LGEATCQCLY | SQPGPFNLTL | QILPGMLCAG | YPEGRRDTCQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GDSGGPLVCE | EGGRWFQAGI | TSFGFGCGRR | NRPGVFTAVA | TYEAWIREQV | MGSEPGPAFP | TQPQKTQSDP | QEPREENCTI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ALPECGKAPR | PGAWPWEAQV | MVPGSRPCHG | ALVSESWVLA | PASCFLDPNS | SDSPPRDLDA | WRVLLPSRPR | AERVARLVQH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ENASWDNASD | LALLQLRTPV | NLSAASRPVC | LPHPEHYFLP | GSRCRLARWG | RGEPALGPGA | LLEAELLGGW | WCHCLYGRQG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AAVPLPGDPP | HALCPAYQEK | EEVGSCWNDS | RWSLLCQEEG | TWFLAGIRDF | PSGCLRPRAF | FPLQTHGPWI | SHVTRGAYLE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DQLAWDWGPD | GEETETQTCP | PHTEHGACGL | RLEAAPVGVL | WPWLAEVHVA | GDRVCTGILL | APGWVLAATH | CVLRPGSTTV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PYIEVYLGRA | GASSLPQGHQ | MTSAPPLLCQ | MTEGSWILVG | MAVQGSRELF | AAIGPEEAWI | SQTVGEANFL | PPSGSPHWPT |
| 730 | 740 | 750 | 760 |  |  |  |  |
| GGSNLCPPEL | AKASGSPHAV | YFLLLLTLLI | QS |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2023 | 3 | 703.7681 | -71.04 | 2 | 53.7 | 13.1 | 0 | 315-327 | R.EENCTIALPECGK.A |  |

# Detailed Protein Report

## Protein 1247: adenosylhomocysteinase isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|239937451 | **Score:** | 13.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 44.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530417912 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: adenosylhomocysteinase isoform X3 [Homo sapiens] |
| gi\|530417910 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: adenosylhomocysteinase isoform X2 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MPGLMRMRER YSASKPLKGA RIAGCLHMTV ETAVLIETLV TLGAEVQWSS CNIFSTQDHA AAAIAKAGIP VYAWKGETDE
        90        100        110        120        130        140        150        160
EYLWCIEQTL YFKDGPLNMI LDDGGDLTNL IHTKYPQLLP GIRGISEETT TGVHNLYKMM ANGILKVPAI NVNDSVTKSK
       170        180        190        200        210        220        230        240
FDNLYGCRES LIDGIKRATD VMIAGKVAVV AGYGDVGKGC AQALRGFGAR VIITEIDPIN ALQAAMEGYE VTTMDEACQE
       250        260        270        280        290        300        310        320
GNIFVTTTGC IDIILGRHFE QMKDDAIVCN IGHFDVEIDV KWLNENAVEK VNIKPQVDRY RLKNGRRIIL LAEGRLVNLG
       330        340        350        360        370        380        390        400
CAMGHPSFVM SNSFTNQVMA QIELWTHPDK YPVGVHFLPK KLDEAVAEAH LGKLNVKLTK LTEKQAQYLG MSCDGPFKPD
       410
HYRY
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1225 | 1 | 918.1238 | 109.95 | 2 | 45.5 | 13.1 | 2 | 361-377 | K.KLDEAVAEAHLGKLNVK.L | |

# Detailed Protein Report

## Protein 1248: CMT1A duplicated region transcript 1 protein isoform b [Homo sapiens]

**Accession:** gi|543173106
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 13.1
**MW [kDa]:** 82.0
**pI:** 10.1
**Sequence Coverage [%]:** 2.4
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MENLESRLKN | APYFRCEKGT | DSIPLCRKCE | TRVLAWKIFS | TKEWFCRIND | ISQRRFLVGI | LKQLNSLYLL | HYFQNILQTT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QGKDFIYNRS | RIDLSKKEGK | VVKSSLNQML | DKTVEQKMKE | ILYWFANSTQ | WTKANYTLLL | LQMCNPKLLL | TAANVIRVLF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LREENNISGL | NQDITDVCFS | PEKDHSSKSA | TSQVYWTAKT | QHTSLPLSKA | PENEHFLGAA | SNPEEPWRNS | LRCISEMNRL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FSGKADITKP | GYDPCNLLVD | LDDIRDLSSG | FSKYRDFIRY | LPIHLSKYIL | RMLDRHTLNK | CASVSQHWAA | MAQQVKMDLS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AHGFIQNQIT | FLQGSYTRGI | DPNYANKVSI | PVPKMVDDGK | SMRVKHPKWK | LRTKNEYNLW | TAYQNEETQQ | VLMEERNVFC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GTYNVRILSD | TWDQNRVIHY | SGGDLIAVSS | NRKIHLLDII | QVKAIPVEFR | GHAGSVRALF | LCEEENFLLS | GSYDLSIRYW |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DLKSGVCTRI | FGGHQGTITC | MDLCKNRLVS | GGRDCQVKVW | DVDTGKCLKT | FRHKDPILAT | RINDTYIVSS | CERGLVKVWH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IAMAQLVKTL | SGHEGAVKCL | FFDQWHLLSG | STDGLVMAWS | MVGKYERCLM | AFKHPKEVLD | VSLLFLRVIS | ACADGKIRIY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NFFNGNCMKV | IKANGRGDPV | LSFFIQGNSD | HLRKTYLPVE | WKTDGRRVRK | KAEKSAGMCC | NNPRKTDDGL | KLKH |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2576 | 1 | 913.4775 | 81.39 | 2 | 62.9 | 13.1 | 2 | 695-711 | K.SAGMCCNNPRKTDDGLK.L | Oxidation: 4 |

# Detailed Protein Report

## Protein 1249: GTPase IMAP family member 7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|23397516 | **Score:** | 13.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAESEDRSLR | IVLVGKTGSG | KSATANTILG | EEIFDSRIAA | QAVTKNCQKA | SREWQGRDLL | VVDTPGLFDT | KESLDTTCKE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ISRCIISSCP | GPHAIVLVLL | LGRYTEEEQK | TVALIKAVFG | KSAMKHMVIL | FTRKEELEGQ | SFHDFIADAD | VGLKSIVKEC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GNRCCAFSNS | KKTSKAEKES | QVQELVELIE | KMVQCNEGAY | FSDDIYKDTE | ERLKQREEVL | RKIYTDQLNE | EIKLVEEDKH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | |
| KSEEEKEKEI | KLLKLKYDEK | IKNIREEAER | NIFKDVFNRI | WKMLSEIWHR | FLSKCKFYSS | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 495 | 1 | 953.6899 | 278.40 | 1 | 36.2 | 13.1 | 0 | 72-79 | K.ESLDTTCK.E | Carbamidomethyl: 7 |

# Detailed Protein Report

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## Protein 1250: chitinase-3-like protein 2 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|68533260 | **Score:** | 13.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| | | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLYQTINSLK | TKNPKLKILL | SIGGYLFGSK | GFHPMVDSST | SRLEFINSII | LFLRNHNFDG | LDVSWIYPDQ | KENTHFTVLI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HELAEAFQKD | FTKSTKERLL | LTAGVSAGRQ | MIDNSYQVEK | LAKDLDFINL | LSFDFHGSWE | KPLITGHNSP | LSKGWQDRGP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SSYYNVEYAV | GYWIHKGMPS | EKVVMGIPTY | GHSFTLASAE | TTVGAPASGP | GAAGPITESS | GFLAYYEICQ | FLKGAKITRL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QDQQVPYAVK | GNQWVGYDDV | KSMETKVQFL | KNLNLGGAMI | WSIDMDDFTG | KSCNQGPYPL | VQAVKRSLGS | L |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2277 | 1 | 671.8603 | -49.68 | 2 | 58.9 | 13.1 | 1 | 97-109 | K.ERLLLTAGVSAGR.Q | |

# Detailed Protein Report

## Protein 1251: POTE ankyrin domain family member A isoform 1 [Homo sapiens]

**Accession:** gi|50897294
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl, Oxidation

**Score:** 13.1
**MW [kDa]:** 51.2
**pI:** 6.2
**Sequence Coverage [%]:** 2.9
**No. of unique Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MVAEVSPKLA | ASPMKKPFGF | RGKMGKWCCC | CFPCCRGSGK | NNMGAWRDHD | DSAFTEPRYH | VRREDLGKLH | RAAWWGEVPR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ADLIVMLRGP | GINKRDKKKR | TALHLACANG | NSEVVSLLLD | RQCQLHVFDS | KKRTALIKAV | QCQEDECALM | LLQHGTDPNL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PDMYGNTALH | YAVYNEDKLM | AKTLLLYGAD | IESKNKGGLT | PLLLAVHGQK | QRMVKFLIKK | KANLNALDRF | GRICQLLSDY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KENQMPNNSS | GNSNPEQDLK | LTSEEEPQRL | KGSENSQHEK | VTQEPDINKD | CDREVEEEMQ | KHGSNNVGLS | ENLTDGAAAG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NGDGGLVPQR | KSRKHENQQF | PNTEIEEYHR | PEKKSNEKNK | VKSQIHSVDN | LDDITWPSEI | ASEDYDLLFS | NYETFTLLIE |
| 410 | 420 | 430 | 440 | 450 | 460 | | |
| QLKMDFNDSA | SLSKIQDAVI | SEEHLLELKN | SHYEQLTVEV | EQMENMVHVL | QK | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2257 | 1 | 557.1115 | -149.12 | 3 | 58.1 | 13.1 | 1 | 24-36 | K.MGKWCCCCFPCCR.G | Carbamidomethyl: 5, 11;<br>Oxidation: 1 |

# Detailed Protein Report

## Protein 1252: UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21687139 | **Score:** | 13.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSLWKKTVYR SLCLALALLV AVTVFQRSLT PGQFLQEPPP PTLEPQKAQK PNGQLVNPNN FWKNPKDVAA PTPMASQGPQ
        90        100        110        120        130        140        150        160
AWDVTTTNCS ANINLTHQPW FQVLEPQFRQ FLFYRHCRYF PMLLNHPEKC RGDVYLLVVV KSVITQHDRR EAIRQTWGRE
       170        180        190        200        210        220        230        240
RQSAGGGRGA VRTLFLLGTA SKQEERTHYQ QLLAYEDRLY GDILQWGFLD TFFNLTLKEI HFLKWLDIYC PHVPFIFKGD
       250        260        270        280        290        300        310        320
DDVFVNPTNL LEFLADRQPQ ENLFVGDVLQ HARPIRRKDN KYYIPGALYG KASYPPYAGG GGFLMAGSLA RRLHHACDTL
       330        340        350        360        370        380        390        400
ELYPIDDVFL GMCLEVLGVQ PTAHEGFKTF GISRNRNSRM NKEPCFFRAM LVVHKLLPPE LLAMWGLVHS NLTCSRKLQV
       410
L
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2975 | 1 | 619.0047 | 20.87 | 3 | 66.0 | 13.1 | 0 | 48-63 | K.AQKPNGQLVNPNNFWK.N | |

# Detailed Protein Report

## Protein 1253: ankyrin repeat and SOCS box protein 2 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|18252778 | **Score:** | 13.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 65.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.5 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTRFSYAEYF | SLFHSCSAPS | RSTAPPESSP | ARAPMGLFQG | VMQKYSSSLF | KTSQLAPADP | LIKAIKDGDE | EALKTMIKEG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KNLAEPNKEG | WLPLHEAAYY | GQVGCLKVLQ | RAYPGTIDQR | TLQEETAVYL | ATCRGHLDCL | LSLLQAGAEP | DISNKSRETP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LYKACERKNA | EAVKILVQHN | ADTNHRCNRG | WTALHESVSR | NDLEVMQILV | SGGAKVESKN | AYGITPLFVA | AQSGQLEALR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FLAKYGADIN | TQASDNASAL | YEACKNEHEE | VVEFLLSQGA | DANKTNKDGL | LPLHIASKKG | NYRIVQMLLP | VTSRTRIRRS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GVSPLHLAAE | RNHDEVLEAL | LSARFDVNTP | LAPERARLYE | DRRSSALYFA | VVNNNVYATE | LLLQHGADPN | RDVISPLLVA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IRHGCLRTMQ | LLLDHGANID | AYIATHPTAF | PATIMFAMKC | LSLLKFLMDL | GCDGEPCFSC | LYGNGPHPPA | PQPSSRFNDA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PAADKEPSVV | QFCEFVSAPE | VSRWAGPIID | VLLDYVGNVQ | LCSRLKEHID | SFEDWAVIKE | KAEPPRPLAH | LCRLRVRKAI |
| 570 | 580 | 590 | | | | | |
| GKYRIKLLDT | LPLPGRLIRY | LKYENTQ | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 979 | 1 | 941.2165 | 136.71 | 2 | 42.3 | 13.1 | 2 | 567-582 | K.LLDTLPLPGRLIRYLK.Y | |

# Detailed Protein Report

## Protein 1254: small conductance calcium-activated potassium channel protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|25777643 | **Score:** | 13.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNSHSYNGSV | GRPLGSGPGA | LGRDPPDPEA | GHPPQPPHSP | GLQVVVAKSE | PARPSPGSPR | GQPQDQDDDE | DDEEDEAGRQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RASGKPSNVG | HRLGHRRALF | EKRKRLSDYA | LIFGMFGIVV | MVTETELSWG | VYTKESLYSF | ALKCLISLST | AILLGLVVLY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HAREIQLFMV | DNGADDWRIA | MTCERVFLIS | LELAVCAIHP | VPGHYRFTWT | ARLAFTYAPS | VAEADVDVLL | SIPMFLRLYL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LGRVMLLHSK | IFTDASSRSI | GALNKITFNT | RFVMKTLMTI | CPGTVLLVFS | ISSWIIAAWT | VRVCERYHDK | QEVTSNFLGA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MWLISITFLS | IGYGDMVPHT | YCGKGVCLLT | GIMGAGCTAL | VVAVVARKLE | LTKAEKHVHN | FMMDTQLTKR | VKNAAANVLR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ETWLIYKHTR | LVKKPDQARV | RKHQRKFLQA | IHQAQKLRSV | KIEQGKLNDQ | ANTLTDLAKT | QTVMYDLVSE | LHAQHEELEA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | |
| RLATLESRLD | ALGASLQALP | GLIAQAIRPP | PPPLPPRPGP | GPQDQAARSS | PCRWTPVAPS | DCG | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2958 | 1 | 724.8727 | -73.27 | 2 | 65.7 | 13.1 | 2 | 408-419 | K.HTRLVKKPDQAR.V | |

# Detailed Protein Report

## Protein 1255: PREDICTED: UPF0692 protein C19orf54 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530416253 | **Score:** | 13.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 33.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578834306 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: UPF0692 protein C19orf54 isoform X6 [Homo sapiens] |
| gi\|578834304 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: UPF0692 protein C19orf54 isoform X5 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MTSPCSPPLK PPISPPKTPV PQASSIPSPP LPPSPLDFSA LPSPPWSQQT PVPPPLPLPP PPAATGPAPR HVFGLEKSQL
        90        100        110        120        130        140        150        160
LKEAFDKAGP VPKGREDVKR LLKLHKDRFR GDLRWILFCA DLPSLIQEGP QCGLVALWMA GTLLSPPSGV PLERLIRVAT
       170        180        190        200        210        220        230        240
ERGYTAQGEM FSVADMGRLA QEVLGCQAKL LSGGLGGPNR DLVLQHLVTG HPLLIPYDED FNHEPCQRKG HKAHWAGSCW
       250        260        270        280        290        300        310
VFGLCPVSAT LRTLSCRACS TQCWARPANH HPCQRRAPRE LSTCCPSRAR VGTISCGTTT RSGRATCS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2691 | 1 | 690.3641 | 10.83 | 2 | 62.0 | 13.0 | 1 | 289-301 | R.ARVGTISCGTTTR.S | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 1256: PREDICTED: FYVE, RhoGEF and PH domain-containing protein 6 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530400569 | **Score:** | 13.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 155.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTSAAEIKKP | PVAPKPKFVV | ANNKPAPPPI | APKPDIVISS | VPQSTKKMKP | AIAPKPKVLK | TSPVREIGQS | PSRKIMLNLE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GHKQELAEST | DNFNCKYEGN | QSNDYISPMC | SCSSECIHKL | GHRENLCVKQ | LVLEPLEMNE | NLENSKIDET | LTIKTRSKCD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LYGEKAKNQG | GVVLKASVLE | EELKDALIHQ | MPPFISAQKH | RPTDSPEMNG | GCNSNGQFRI | EFADLSPSPS | SFEKVPDHHS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CHLQLPSDEC | EHFETCQDDS | EKSNNCFQSS | ELEALENGKR | STLISSDGVS | KKSEVKDLGP | LEIHLVPYTP | KFPTPKPRKT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RTARLLRQKC | VDTPSESTEE | PGNSDSSSSC | LTENSLKINK | ISVLHQNVLC | KQEQVDKMKL | GNKSELNMES | NSDAQDLVNS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QKAMCNETTS | FEKMAPSFDK | DSNLSSDSTT | VDGSSMSLAV | DEGTGFIRCT | VSMSLPKQLK | LTCNEHLQSG | RNLGVSAPQM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QKESVIKEEN | SLRIVPKKPQ | RHSLPATGVL | KKAASEELLE | KSSYPSSEEK | SSEKSLERNH | LQHLCAQNRG | VSSSFDMPKR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ASEKPVWKLP | HPILPFSGNP | EFLKSVTVSS | NSEPSTALTK | PRAKSLSAMD | VEKCTKPCKD | STKKNSFKKL | LSMKLSICFM |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KSDFQKFWSK | SSQLGDTTTG | HLSSGEQKGI | ESDWQGLLVG | EEKRSKPIKA | YSTENYSLES | QKKRKKSRGQ | TSAANGLRAE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SLDDQMLSRE | SSSQAPYKSV | TSLCAPEYEN | IRHYEEIPEY | ENLPFIMAIR | KTQELEWQNS | SSMEDADANV | YEVEEPYEAP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DGQLQLGPRH | QHSSSGASQE | EQNDLGLGDL | PSDEEEIINS | SDEDDVSSES | SKGEPDPLED | KQDEDNGMKS | KVHHIAKEIM |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SSEKVFVDVL | KLLHIDFRDA | VAHASRQLGK | PVIEDRILNQ | ILYYLPQLYE | LNRDLLKELE | ERMLHWTEQQ | RIADIFVKKG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PYLKMYSTYI | KEFDKNIALL | DEQCKKNPGF | AAVVREFEMS | PRCANLALKH | YLLKPVQRIP | QYRLLLTDYL | KNLIEDAGDY |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RDTQDALAVV | IEVANHANDT | MKQGDNFQKL | MQIQYSLNGH | HEIVQPGRVF | LKEGILMKLS | RKVMQPRMFF | LFNDALLYTT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PVQSGMYKLN | NMLSLAGMKV | RKPTQEAYQN | ELKIESVERS | FILSASSATE | RDEWLEAISR | AIEEYAKKRI | TFCPSRSLDE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ADSENKEEVS | PLGSKAPIWI | PDTRATMCMI | CTSEFTLTWR | RHHCRACGKI | VCQACSSNKY | GLDYLKNQPA | RVCEHCFQEL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| QKLDHQHSPR | IGSPGNHKSP | SSALSSVLHS | IPSGRKQKKI | PAALKEVSAN | TEDSSMSGYL | YRSKGNKKPW | KHFWFVIKNK |
| 1370 | 1380 | 1390 | | | | | |
| VLYTYAASEV | DRSISGRHNI | VAVLVSSLL | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 867 | 1 | 819.8514 | -51.08 | 2 | 40.4 | 13.0 | 0 | 739-752 | K.SVTSLCAPEYENIR.H | Carbamidomethyl: 6 |

# Detailed Protein Report

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**Protein 1257:** **PREDICTED: ERV-FRD provirus ancestral Env polyprotein-like isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530359463 | **Score:** | 13.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 36.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530436370 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: ERV-FRD provirus ancestral Env polyprotein-like isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSLMTRENLA | FRGSLMGCSE | LKPFQELTHQ | SAVSHSRADV | ADVWWYCGGP | LLDTLPSNWS | GTCTLVQFAI | PFALAFLQPE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KEKPQHRKIR | EAPYGSFDSQ | VYLDATGVPQ | GVPHKFKAQD | QIAAGFESIF | WWVTISKNID | WINYIYYNQQ | RFINYTRDAV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KGIAEQLGPT | SQMAWENRMA | LDMILAKKGG | VCVMIKTQCC | TFIPNNTAPS | GSITRALQGL | TALSNELAKN | SGVNDPFSGW |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LERWFGKWKG | IIASILTSLA | AVIGVVILFG | CCVTPCIRGL | VQRLIETVLT | KTSLSSPPPY | SDKLFLLEDQ | VEQQSQDLLK |
| 330 | | | | | | | |
| RFEEEGP | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1330 | 1 | 977.1505 | 129.70 | 2 | 46.8 | 13.0 | 2 | 179-196 | R.MALDMILAKKGGVCVMIK.T | Oxidation: 1, 16 |

# Detailed Protein Report

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## Protein 1258: transcription factor p65 isoform 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|345842445 | **Score:** | 13.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDELFPLIFP | AEPAQASGPY | VEIIEQPKQR | GMRFRYKCEG | RSAGSIPGER | STDTTKTHPT | IKINGYTGPG | TVRISLVTKD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PPHRPHPHEL | VGKDCRDGFY | EAELCPDRCI | HSFQNLGIQC | VKKRDLEQAI | SQRIQTNNNP | FQVPIEEQRG | DYDLNAVRLC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FQVTVRDPSG | RPLRLPPVLS | HPIFDNRAPN | TAELKICRVN | RNSGSCLGGD | EIFLLCDKVQ | KEDIEVYFTG | PGWEARGSFS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QADVHRQVAI | VFRTPPYADP | SLQAPVRVSM | QLRRPSDREL | SEPMEFQYLP | DTDDRHRIEE | KRKRTYETFK | SIMKKSPFSG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PTDPRPPPRR | IAVPSRSSAS | VPKPAPQPYP | FTSSLSTINY | DEFPTMVFPS | GQISQASALA | PAPPQVLPQA | PAPAPAPAMV |
| 410 | 420 | 430 | 440 | 450 | | | |
| SALAQRPPDP | APAPLGAPGL | PNGLLSGDED | FSSIADMDFS | ALLSQISS | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1871 | 1 | 1057.5041 | 3.81 | 3 | 51.7 | 13.0 | 2 | 97-123 | R.DGFYEAELCPDRCIHSFQNLGIQCVKK.R | Carbamidomethyl: 24 |

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# Detailed Protein Report

## Protein 1259: PREDICTED: transmembrane protein 50A isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530360988 | **Score:** | 13.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 14.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.8 |
| | | **Sequence Coverage [%]:** | 21.4 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSGFLEGLRC SECIDWGEKR NTIASIAAGV LFFTGWWIII DAAVIYPTMK DFNHSYHACG VIATIAFLMI NAVSNGQVRG
        90        100        110        120        130
DSYSEGCLGQ TEKDIVYPGI AVFFQNAFIF FGGLVFKFGR TEDLWQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1914 | 1 | 1023.9081 | 23.01 | 3 | 53.8 | 13.0 | 1 | 94-120 | K.DIVYPGIAVFFQNAFIFFGGLVFKFGR.T | |

# Detailed Protein Report

## Protein 1260: 6-phosphogluconate dehydrogenase, decarboxylating [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|40068518 | **Score:** | 13.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 53.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.0 |
| | | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAQADIALIG | LAVMGQNLIL | NMNDHGFVVC | AFNRTVSKVD | DFLANEAKGT | KVVGAQSLKE | MVSKLKKPRR | IILLVKAGQA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VDDFIEKLVP | LLDTGDIIID | GGNSEYRDTT | RRCRDLKAKG | ILFVGSGVSG | GEEGARYGPS | LMPGGNKEAW | PHIKTIFQGI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AAKVGTGEPC | CDWVGDEGAG | HFVKMVHNGI | EYGDMQLICE | AYHLMKDVLG | MAQDEMAQAF | EDWNKTELDS | FLIEITANIL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KFQDTDGKHL | LPKIRDSAGQ | KGTGKWTAIS | ALEYGVPVTL | IGEAVFARCL | SSLKDERIQA | SKKLKGPQKF | QFDGDKKSFL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EDIRKALYAS | KIISYAQGFM | LLRQAATEFG | WTLNYGGIAL | MWRGGCIIRS | VFLGKIKDAF | DRNPELQNLL | LDDFFKSAVE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NCQDSWRRAV | STGVQAGIPM | PCFTTALSFY | DGYRHEMLPA | SLIQAQRDYF | GAHTYELLAK | PGQFIHTNWT | GHGGTVSSSS |
| 490 | | | | | | | |
| YNA | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2781 | 1 | 1080.6827 | 110.97 | 2 | 65.2 | 13.0 | 0 | 88-107 | K.LVPLLDTGDIIIDGGNSEYR.D | |

# Detailed Protein Report

## Protein 1261: dynein heavy chain 6, axonemal [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|194353966 | **Score:** | 13.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 475.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 0.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578802753 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: dynein heavy chain 6, axonemal isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTFRATDSEF | DLTNIEEYAE | NSALSRLNNI | KAKQRVSYVT | STENESDTQI | LTFRHITKAQ | EKTRKRQQPI | KLEPLPVLKV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YQDHKQPEYI | HEQNRFQLMT | AGIIKRPVSI | AKKSFATSST | QFLEHQDAVK | KMQIHRPYVE | VFSPSPPKLP | HTGIGKRGLF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GTRSSAYPKY | TFHDREEVVK | ANIRDPLQII | KIIRENEHLG | FLYMIPAVPR | SSIEYDTYNL | KVVSYENINK | NDYYTISQRA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VTHIYNEDIE | FIEIDRWEQE | YLYHRELTKI | PIFSLFRKWK | AFSVWRKNVR | SKKITGCQKS | LQKNLFIVNP | HLRPALLKIN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ELCYHLSFMG | LCYIEKCHTY | TLQEFKAAQV | IRLAEVTERL | GEFRNEAKYV | VRRACRFALR | AAGFVPDDCA | FGPFEDYHKV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QSSGSFINTP | HELPTYGDSE | KMTYTEQASK | RHYCMRLTCF | IRLNDYLIEN | TMHILTVNAV | NSLLNHLTDK | LKRTPSADVI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QKWITEEKPE | VPDKKGTLMV | EKQEEDESLI | PMFLTELMLT | VQSLLFEPSL | EDFLDGILGA | VNHCQNTVLS | VPNLVPDSYF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DAFTSPYINN | KLEGKTCGTG | PSLAAVFEDD | KNFHTIISQI | KETIQAAFES | ARIYAATFEK | FQIFFKENES | LDLQALKLQE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PDINFFSEQL | EKYHKQHKDA | VALRPTRNVG | LLLIDTRLLR | EKLIPSPLRC | LEVLNFMLPR | QSKKKVDAII | FEAQDAEYKL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EFVPTTTTEY | VHSLLFLDEI | QERIESLEDE | GNIVTQMYKL | MEQYQVPTPP | EDFAVFATMK | PSIVAVRNAI | DKSVGDRESS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IKQFCVHLGS | DLEELNNEVN | EVKLQAQDPQ | ILDISADQDK | IRLILNNLQS | VLADLQKRAF | QYKSYQKNFK | VEVSKFEALE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EVSAELKLKQ | LLWDSFSEWD | KLQQEWLKSK | FDCLDPEVLN | GQVSKYAKFV | TQLEKGLPPN | SVVPQLKYKV | EKMKEKLPVI |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| IDLRNPTLKA | RHWAAIEQTV | DATLVDAEIP | LTLERLSQLH | VFDFGQEIQD | ISGQASGEAA | LEAILKKVED | SWKTTEFVIL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PHRDSKDVFI | LGGTDDIQVL | LDDSTINVAT | LASSRYLGPL | KTRVDEWQKQ | LALFNQTLEE | WLTCQRNWLY | LESIFNAPDI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QRQLPAEAKM | FLQVDKSWKE | IMRKVNRLPN | ALRAATQPGL | LETFQNNNAL | LDQIQKCLEA | YLESKRVIFP | RFYFLSNDEL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LEILAQTRNP | QAVQPHLRKC | FDSISKLEFA | LMPPAEGKIP | GIDGEPEKVY | TNDILAMLSP | EGERVSLGKG | LKARGNVEEW |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LGKVEEAMFT | SLRRLCKAAI | ADYQGKLRTD | WVVAGHPSQV | ILTVSQIMWC | RDLTECLETE | HSNHIQALKN | FEKVNFERLN |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ALAAIVQGSL | PKLHRNILTA | LITIDVHARD | IVTELVQSKV | ETVESFDWQR | QLRYYWDIDL | DNCVARMALS | QYTYGYEYLG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ACPRLVITPL | TDRCYLCLMG | ALQLDLGGAP | AGPAGTGKTE | TTKDLAKALA | IQCVVFNCSD | GLDYKMMGRF | FSGLAQSGAW |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| CCFDEFNRID | IEVLSVIAQQ | LITIRNAKAA | KLSRFMFEGR | EIKLVMTCAA | FITMNPGYAG | RTELPDNLKA | LFRPFAMMVP |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| NYALIAEVIL | YSEGFESSKI | LARKMTQMYK | LCSEQLSQQD | HYDFGMRAVK | SVLVMAGSLK | RENPDLNEDV | VLIRALQDSN |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LPKFLTDDAL | LFSGIISDLF | PGVQIPEHDY | GILQSTIVDV | MNRQNLQPEM | CMVRKVIQFY | ETMLVRHGVM | LVGPTGGGKT |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| TVYRILAETL | GNLQKLGIEN | SFYQAVKTYV | LNPKSITMGE | LYGEVNNLTL | EWKDGLMALS | VRAAVNDTSE | DHKWIISDGP |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| VDALWIENMN | TVLDDNKMLC | LANSERIKLT | PQIHMLFEVQ | DLRVASPATV | SRCGMVFVDP | EELKWMPYVK | TWMKGISKKL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| TEETQEYILN | LFQRYVDEGL | HFINKKCSQA | IPQVDISKVT | TLCCLLESLI | LGKDGVNLAM | EQTKLNTILC | QTFVFCYLWS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| LGGNLTENYY | DSFDTFIRTQ | FDDNPDARLP | NSGDLWSIHM | DFDTKRLDPW | ERIIPTFKYN | RDVPFFEMLV | PTTDTVRYGY |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| LMEKLLAVKH | SVLFTGITGV | GKSVIAKGLL | NKIQESAGYV | PVYLNFSAQT | SSARTQEIIE | SKLERKRKNI | LGAPGNKRIV |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |
| IFVDDLNMPR | LDRYGSQPPI | ELLRQYQDFG | GFYDRNKLFW | KEIQDVTIIS | ACAPPGGGRN | PVTPRFIRHF | SMLCLPMPSE |
| 2250 | 2260 | 2270 | 2280 | 2290 | 2300 | 2310 | 2320 |
| HSLKQIFQAI | LNGFLSDFPP | AVKQTASSIV | EASVEIYNKM | SVDLLPTPAK | SHYVFNLRDL | SKCVQGILQC | DPGTIREEIQ |
| 2330 | 2340 | 2350 | 2360 | 2370 | 2380 | 2390 | 2400 |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1872 | 1 | 973.5013 | -53.30 | 2 | 51.7 | 13.0 | 2 | 2694-2710 | K.NGLTKLLETNILVDKMK.L | Oxidation: 16 |

# Detailed Protein Report

## Protein 1262: gamma-glutamylcyclotransferase isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|315360620 | **Score:** | 13.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 12.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 14.0 |
| | | **No. of unique Peptides:** | 1 |

```
         10         20         30         40         50         60         70         80
MANSGCKDVT GPDEESFLYF AYGSNLLTER IHLRNPSAAF FCVARLQDFK LDFGNSQGKT SQTWHGGIAT IFQSPGDEVW
         90        100        110        120
GVVWKMNKSN LNSLDELFAW VQKKMVCRWS IKRS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2373 | 1 | 907.3649 | -100.81 | 2 | 57.9 | 13.0 | 1 | 35-50 | R.NPSAAFFCVARLQDFK.L | |

# Detailed Protein Report

## Protein 1263: myelin-oligodendrocyte glycoprotein isoform alpha5 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|300360476 | **Score:** | 13.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 15.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| | | **Sequence Coverage [%]:** | 9.9 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MASLSRPSLP SCLCSFLLLL LLQVSSSYAD PFYWVSPGVL VLLAVLPVLL LQITVGLIFL CLQYRLRGKL RAEIENLHRT
        90        100        110        120        130        140
FDPHFLRVPC WKITLFVIVP VLGPLVALII CYNWLHRRLA GQFLEELRNP F
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 425 | 1 | 767.5397 | 173.43 | 2 | 33.9 | 13.0 | 1 | 119-131 | R.LAGQFLEELRNPF.- | |

# Detailed Protein Report

## Protein 1264: myelin transcription factor 1 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|17975763 | **Score:** | 13.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 122.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
|  |  | **Sequence Coverage [%]:** | 0.9 |
|  |  | **No. of unique Peptides:** | 1 |

## Quantitation

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.46 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.06 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSLENEDKRA | RTRSKALRGP | PETTAADLSC | PTPGCTGSGH | VRGKYSRHRS | LQSCPLAKKR | KLEGAEAEHL | VSKRKSHPLK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LALDEGYGVD | SDGSEDTEVK | DASVSDESEG | TLEGAEAETS | GQDEIHRPET | AEGRSPVKSH | FGSNPIGSAT | ASSKGSYSSY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QGIIATSLLN | LGQIAEETLV | EEDLGQAAKP | GPGIVHLLQE | AAEGAASEEG | EKGLFIQPED | AEEVVEVTTE | RSQDLCPQSL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EDAASEESSK | QKGILSHEEE | DEEEEEEEEE | EEEDEEEEEE | EEEEEEEEEE | EEEEEEEEEE | EEEEEEAAPD | VIFQEDTSHT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SAQKAPELRG | PESPSPKPEY | SVIVEVRSDD | DKDEDTHSRK | STVTDESEMQ | DMMTRGNLGL | LEQAIALKAE | QVRTVCEPGC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PPAEQSQLGL | GEPGKAAKPL | DTVRKSYYSK | DPSRAEKREI | KCPTPGCDGT | GHVTGLYPHH | RSLSGCPHKD | RIPPEILAMH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ENVLKCPTPG | CTGQGHVNSN | RNTHRSLSGC | PIAAAEKLAK | SHEKQQPQTG | DPSKSSSNSD | RILRPMCFVK | QLEVPPYGSY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RPNVAPATPR | ANLAKELEKF | SKVTFDYASF | DAQVFGKRML | APKIQTSETS | PKAFQCFDYS | QDAEAAHMAA | TAILNLSTRC |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| WEMPENLSTK | PQDLPSKSVD | IEVDENGTLD | LSMHKHRKRE | NAFPSSSSCS | SSPGVKSPDA | SQRHSSTSAP | SSSMTSPQSS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QASRQDEWDR | PLDYTKPSRL | REEEPEESEP | AAHSFASSEA | DDQEVSEENF | EERKYPGEVT | LTNFKLKFLS | KDIKKELLTC |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PTPGCDGSGH | ITGNYASHRS | LSGCPLADKS | LRNLMAAHSA | DLKCPTPGCD | GSGHITGNYA | SHRSLSGCPR | AKKSGVKVAP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TKDDKEDPEL | MKCPVPGCVG | LGHISGKYAS | HRSASGCPLA | ARRQKEGSLN | GSSFSWKSLK | NEGPTCPTPG | CDGSGHANGS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FLTHRSLSGC | PRATFAGKKG | KLSGDEVLSP | KFKTSDVLEN | DEEIKQLNQE | IRDLNESNSE | MEAAMVQLQS | QISSMEKNLK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| NIEEENKLIE | EQNEALFLEL | SGLSQALIQS | LANIRLPHME | PICEQNFDAY | VSTLTDMYSN | QDPENKDLLE | SIKQAVRGIQ |
| 1130 |  |  |  |  |  |  |  |
| V |  |  |  |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 234 | 2 | 1074.6988 | 94.18 | 1 | 31.7 | 13.0 | 1 | 50-59 | R.SLQSCPLAKK.R |  | QU:MU 1.46<br>WUP:QUP 2.06 |

# Detailed Protein Report

## Protein 1265: PREDICTED: protein CDV3 homolog isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530374901 | **Score:** | 13.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 6.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAETEERSLD | NFFAKRDKKK | KKERSNRAAS | AAGAAGSAGG | SSGAAGAAGG | GAGAGTRPGD | GGTASAGAAG | PGAATKAVTK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DEDEWKELEQ | KEVDYSGLRV | QAMQISSEKE | EDDNEKRQDP | GDNWEEGGGG | GGGMEKSSGP | WNKTAPVQAP | PAPVIVTETP |
| 170 | 180 | 190 | 200 | 210 | 220 | | |
| EPAMTSGVYR | PPGARLTTTR | KTPQGPPEIY | SDTQFPSLQS | TAKHVESRKY | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1616 | 1 | 783.3508 | -55.03 | 2 | 50.4 | 13.0 | 1 | 87-99 | K.ELEQKEVDYSGLR.V | |

# Detailed Protein Report

## Protein 1266: GTPase NRas [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4505451 | **Score:** | 13.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 10.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTEYKLVVVG | AGGVGKSALT | IQLIQNHFVD | EYDPTIEDSY | RKQVVIDGET | CLLDILDTAG | QEEYSAMRDQ | YMRTGEGFLC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VFAINNSKSF | ADINLYREQI | KRVKDSDDVP | MVLVGNKCDL | PTRTVDTKQA | HELAKSYGIP | FIETSAKTRQ | GVEDAFYTLV |
| 170 | 180 | 190 | | | | | |
| REIRQYRMKK | LNSSDDGTQG | CMGLPCVVM | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2078 | 1 | 715.2762 | -46.00 | 3 | 56.4 | 13.0 | 1 | 170-189 | K.KLNSSDDGTQGCMGLPCVVM.- | Carbamidomethyl: 12;<br>Oxidation: 13, 20 |

# Detailed Protein Report

## Protein 1267: PREDICTED: centrosomal protein of 192 kDa isoform X12 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578832148 | **Score:** | 13.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 154.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 1.83 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEDFRGIAEE | SFPSFLTNSL | FGNSGILENV | TLSSNLGLPV | AVSTLARDRS | STDNRYPDIQ | ASYLVEGRFS | VPSGSSPGSQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SDAEPRERLQ | LSFQDDDSIS | RKKSYVESQR | LSNALSKQSA | LQMETAGPEE | EPAGATESLQ | GQDLFNRASP | LEQAQDSPID |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FHLQSWMNNK | EPKIVVLDAG | KHFEDKTLKS | DLSHTSLLEN | EKLILPTSLE | DSSDDDIDDE | MFYDDHLEAY | FEQLAIPGMI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YEDLEGPEPP | EKGFKLPTNG | LRQANENGSL | NCKFQSENNS | SLISLDSHSS | ETTHKESEES | QVICLPGTSN | SIGTGDSRRY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TDGMLPFSSG | TWGTEKEIEN | LKGIVPDLNS | ECASKDVLVK | TLRAIDVKLN | SDNFHDANAN | RGGFDLTDPV | KQGAECPHQN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KTVLHMDGCL | DTETPTVSIQ | ENVDVASLKP | ISDSGINFTD | AIWSPTCERR | TCECHESIEK | NKDKTDLPQS | VVYQNEEGRW |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VTDLAYYTSF | NSKQNLNVSL | SDEMNEDFRS | GSEAFDLIAQ | DEEEFNKEHQ | FIQEENIDAH | NTSVALGDTS | WGATINYSLL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RKSRSTSDLD | KDDASYLRLS | LGEFFAQRSE | ALGCLGGGNN | VKRPSFGYFI | RSPEKREPIA | LIRKSDVSRG | NLEKEMAHLN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HDLYSGDLNE | QSQAQLSEGS | ITLQVEAVES | TSQVDENDVT | LTADKGKTED | TFFMSNKPQR | YKDKLPDSGD | SMLRISTIAS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AIAEASVNTD | PSQLAAMIKA | LSNKTRDKTF | QEDEKQKDYS | HVRHFLPNDL | EKSNGSNALD | MEKYLKKTEV | SRYESALENF |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SRASMSDTWD | LSLPKEQTTQ | DIHPVDLSAT | SVSVRAPEEN | TAAIVYVENG | ESENQESFRT | INSSNSVTNR | ENNSAVVDVK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TCSIDNKLQD | VGNDEKATSI | STPSDSYSSV | RNPRITSLCL | LKDCEEIRDN | RENQRQNECV | SEISNSEKHV | TFENHRIVSP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KNSDLKNTSP | EHGGRGSEDE | QESFRPSTSP | LSHSSPSEIS | GTSSSGCALE | SFGSAAQQQQ | PPCEQELSPL | VCSPAGVSRL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TYVSEPESSY | PTTATDDALE | DRKSDITSEL | STTIIQGSPA | ALEERAMEKL | REKVPFQNRG | KGTLSSIIQN | NSDTRKATET |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TSLSSKPEYV | KPDFRWSKDP | SSKSGNLLET | SEVGWTSNPE | ELDPIRLALL | GKSGLSCQVG | SATSHPVSCQ | EPIDEDQRIS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PKDKSTAGRE | FSGQVSHQTT | SENQCTPIPS | STVHSSVADM | QNMPAAVHAL | LTQPSLSAAP | FAQRYLGTLP | STGSTTLPQC |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| HAGNATVCGF | SGGLPYPAVA | GEPVQNSVAV | GICLGSNIGS | GWMGTSSLCN | PYSNTLNQNL | LSTTKPFPVP | SVGTNCGIEP |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | | |
| WDSGVTSGLG | SVRVPEELKL | PHACCVGIAS | QTLLSVLNPT | DRWLQVSIGV | LSISVNGEK | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1517 | 1 | 993.4897 | -5.03 | 2 | 49.2 | 13.0 | 1 | 256-273 | K.LPTNGLRQANENGSLNCK.F | Carbamidomethyl: 17 | WUP:QUP 1.83 |

# Detailed Protein Report

## Protein 1268: gamma-aminobutyric acid receptor subunit delta precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|34734071 | **Score:** | 13.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 50.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| | | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.06 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDAPARLLAP | LLLLCAQQLR | GTRAMNDIGD | YVGSNLEISW | LPNLDGLIAG | YARNFRPGIG | GPPVNVALAL | EVASIDHISE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ANMEYTMTVF | LHQSWRDSRL | SYNHTNETLG | LDSRFVDKLW | LPDTFIVNAK | SAWFHDVTVE | NKLIRLQPDG | VILYSIRITS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TVACDMDLAK | YPMDEQECML | DLESYGYSSE | DIVYYWSESQ | EHIHGLDKLQ | LAQFTITSYR | FTTELMNFKS | AGQFPRLSLH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FHLRRNRGVY | IIQSYMPSVL | LVAMSWVSFW | ISQAAVPARV | SLGITTVLTM | TTLMVSARSS | LPRASAIKAL | DVYFWICYVF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VFAALVEYAF | AHFNADYRKK | QKAKVKVSRP | RAEMDVRNAI | VLFSLSAAGV | TQELAISRRQ | RRVPGNLMGS | YRSVGVETGE |
| 410 | 420 | 430 | 440 | 450 | 460 | | |
| TKKEGAARSG | GQGGIRARLR | PIDADTIDIY | ARAVFPAAFA | AVNVIYWAAY | AM | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1088 | 2 | 565.6602 | -213.89 | 2 | 41.9 | 13.0 | 0 | 221-229 | R.FTTELMNFK.S | | WUP:QUP 0.06 |

BRUKER

# Detailed Protein Report

## Protein 1269: protein-methionine sulfoxide oxidase MICAL2 isoform e [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|544063447 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 109.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGENEDEKQA | QAGQVFENFV | QASTCKGTLQ | AFNILTRHLD | LDPLDHRNFY | SKLKSKVTTW | KAKALWYKLD | KRGSHKEYKR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GKSCTNTKCL | IVGGGPCGLR | TAIELAYLGA | KVVVVEKRDS | FSRNNVLHLW | PFTIHDLRGL | GAKKFYGKFC | AGSIDHISIR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QLQLILFKVA | LMLGVEIHVN | VEFVKVLEPP | EDQENQKIGW | RAEFLPTDHS | LSEFEFDVII | GADGRRNTLE | GFRRKEFRGK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LAIAITANFI | NRNSTAEAKV | EEISGVAFIF | NQKFFQDLKE | ETGIDLENIV | YYKDCTHYFV | MTAKKQSLLD | KGVIINDYID |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TEMLLCAENV | NQDNLLSYAR | EAADFATNYQ | LPSLDFAMNH | YGQPDVAMFD | FTCMYASENA | ALVRERQAHQ | LLVALVGDSL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LEPFWPMGTG | CARGFLAAFD | TAWMVKSWNQ | GTPPLELLAE | RESLYRLLPQ | TTPENINKNF | EQYTLDPGTR | YPNLNSHCVR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PHQVKHLYIT | KELEHYPLER | LGSVRRSVNL | SRKESDIRPS | KLLTWCQQQT | EGYQHVNVTD | LTTSWRSGLA | LCAIIHRFRP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ELINFDSLNE | DDAVENNQLA | FDVAEREFGI | PPVTTGKEMA | SAQEPDKLSM | VMYLSKFYEL | FRGTPLRPVD | SWRKNYGENA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DLSLAKSSIS | NNYLNLTFPR | KRTPRVDGQT | GENDMNKRRR | KGFTNLDEPS | NFSSRSLGSN | QECGSSKEGG | NQNKVKSMAN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QLLAKFEEST | RNPSLMKQES | MRKSFPLNLG | GSDTCYFCKK | RVYVMERLSA | EGHFFHRECF | RCSICATTLR | LAAYTFDCDE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GKFYCKPHFI | HCKTNSKQRK | RRAELKQQRE | EEATWQEQEA | PRRDTPTESS | CAVAAIGTLE | GSPPGISTSF | FRKVLGWPLR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LPRDLCNWMQ | GLLQAAGLHI | RDNAYNYCYM | YELLSLGLPL | LWAFSEVLAA | MYRESEGSLE | SICNWVLRCF | PVKLR |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2161 | 1 | 1051.4053 | -76.44 | 2 | 56.9 | 12.9 | 2 | 726-742 | K.FEESTRNPSLMKQESMR.K | Oxidation: 11, 16 |

# Detailed Protein Report

## Protein 1270: cell cycle exit and neuronal differentiation protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|30795225 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 14.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| | | **Sequence Coverage [%]:** | 9.4 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MESRGKSASS | PKPDTKVPQV | TTEAKVPPAA | DGKAPLTKPS | KKEAPAEKQQ | PPAAPTTAPA | KKTSAKADPA | LLNNHSNLKP |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | |
| APTVPSSPDA | TPEPKGPGDG | AEEDEAASGG | PGGRGPWSCE | NFNPLLVAGG | VAVAAIALIL | GVAFLVRKK | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2135 | 2 | 703.2937 | -141.99 | 2 | 55.1 | 12.9 | 1 | 49-62 | K.QQPPAAPTTAPAKK.T | |

# Detailed Protein Report

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## Protein 1271: heparan-sulfate 6-O-sulfotransferase 3 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|45580707 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| | | **Sequence Coverage [%]:** | 5.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|397137664 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: heparan-sulfate 6-O-sulfotransferase 3 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDERFNKWLL | TPVLTLLFVV | IMYQYVSPSC | TSSCTNFGEQ | PRAGEAGPPA | VPGPARRAQA | PPEEWERRPQ | LPPPPRGPPE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GPRGAAAPEE | EDEEPGDPRE | GEEEEEEDEP | DPEAPENGSL | PRFVPRFNFS | LKDLTRFVDF | NIKGRDVIVF | LHIQKTGGTT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FGRHLVKNIR | LEQPCSCKAG | QKKCTCHRPG | KKETWLFSRF | STGWSCGLHA | DWTELTNCVP | AIMEKKDCPR | NHSHTRNFYY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ITMLRDPVSR | YLSEWKHVQR | GATWKTSLHM | CDGRSPTPDE | LPTCYPGDDW | SGVSLREFMD | CTYNLANNRQ | VRMLADLSLV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GCYNLTFMNE | SERNTILLQS | AKNNLKNMAF | FGLTEFQRKT | QFLFERTFNL | KFISPFTQFN | ITRASNVEIN | EGARQRIEDL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NFLDMQLYEY | AKDLFQQRYH | HTKQLEHQRD | RQKRREERRL | QREHRDHQWP | KEDGAAEGTV | TEDYNSQVVR | W |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2728 | 2 | 1006.4684 | 8.21 | 3 | 65.2 | 12.9 | 2 | 446-471 | R.DHQWPKEDGAAEGTVTEDYNSQVVRW.- | |

# Detailed Protein Report

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## Protein 1272: PREDICTED: zinc finger protein GLIS3 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578816405 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 60.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNGRSCSMSL | HRTSGTPQGP | RMVSGHHIPA | IRAHSGTPGP | SPCGSTSSPT | MASLANNLHL | KMPSGGGMAP | QNNVAESRIH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LPALSPRRQM | LTNGKPRFQV | TQAGGMSGSH | TLKPKQQEFG | SPFPPNPGKG | ALGFGPQCKS | IGKGSCNNLV | VTSSPMMVQR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LGLISPPASQ | VSTACNQISP | SLQRAMNAAN | LNIPPSDTRS | LISRESLAST | TLSLTESQSA | SSMKQEWSQG | YRALPSLSNH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GSQNGLDLGD | LLSLPPGTSM | SSNSVSNSLP | SYLFGTESSH | SPYPSPRHSS | TRSHSARSKK | RALSLSPLSD | GIGIDFNTII |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RTSPTSLVAY | INGSRASPAN | LSPQPEVYGH | FLGVRGSCIP | QPRPVPGSQK | GVLVAPGGLA | LPAYGEDGAL | EHERMQQLEH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GGLQPGLVNH | MVVQHGLPGP | DSQSAGLFKT | ERLEEFPGST | VDLPPAPPLP | PLPPPPGPPP | PYHAHAHLHH | PELGPHAQQL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ALPQATLDDD | GEMDGIGGKH | CCRWIDCSAL | YDQQEELVRH | IEKVHIDQRK | GEDFTCFWAG | CPRRYKPFNA | RYKLLIHMRV |
| 570 | 580 | | | | | | |
| HSGEKPNKCT | AA | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1615 | 1 | 1011.0568 | -79.57 | 3 | 50.4 | 12.9 | 2 | 500-523 | K.HCCRWIDCSALYDQQEELVRHIEK.V | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 1273: kiSS-1 receptor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|62865887 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 42.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MHTVATSGPN | ASWGAPANAS | GCPGCGANAS | DGPVPSPRAV | DAWLVPLFFA | ALMLLGLVGN | SLVIYVICRH | KPMRTVTNFY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IANLAATDVT | FLLCCVPFTA | LLYPLPGWVL | GDFMCKFVNY | IQQVSVQATC | ATLTAMSVDR | WYVTVFPLRA | LHRRTPRLAL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AVSLSIWVGS | AAVSAPVLAL | HRLSPGPRAY | CSEAFPSRAL | ERAFALYNLL | ALYLLPLLAT | CACYAAMLRH | LGRVAVRPAP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ADSALQGQVL | AERAGAVRAK | VSRLVAAVVL | LFAACWGPIQ | LFLVLQALGP | AGSWHPRSYA | AYALKTWAHC | MSYSNSALNP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LLYAFLGSHF | RQAFRRVCPC | APRRPRRPRR | PGPSDPAAPH | AELLRLGSHP | APARAQKPGS | SGLAARGLCV | LGEDNAPL |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1840 | 1 | 897.8543 | -87.85 | 2 | 52.9 | 12.9 | 1 | 183-198 | R.LSPGPRAYCSEAFPSR.A | Carbamidomethyl: 9 |

# Detailed Protein Report

## Protein 1274: PREDICTED: lysophospholipid acyltransferase LPCAT4 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578826781 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.9 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.90 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSQGSPGDWA | PLDPTPGPPA | SPNPFVHELH | LSRLQRVKFC | LLGALLAPIR | VLLAFIVLFL | LWPFAWLQVA | GLSEEQLQEP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ITGWRKTVCH | NGVLGLSRLL | FFLLGFLRIR | VRGQRASRLQ | APVLVAAPHS | TFFDPIVLLP | CDLPKVVSRA | ENLSVPVIGA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLRFNQAILV | SRHDPASRRR | VVEEVRRRAT | SGGKWPQVLF | FPEGTCSNKK | ALLKFKPGAF | IAGVPVQPVL | IRYPNSLDTT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SWAWRGPGVL | KVLWLTASQP | CSIVDVEFLP | VYHPSPEESR | DPTLYANNVQ | RVMAQALGIP | ATECEFVGSL | PVIVVGRLKV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ALEPQLWELG | KVLRKAGLSA | GYVDAGAEPG | RSRMISQEEF | ARQLQLSDPQ | TVAGAFGYFQ | QASSALKSNV | IIMRRNKGEI |
| 410 | | | | | | | |
| IMVPRSFLI | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 431 | 1 | 643.7993 | -135.15 | 2 | 35.4 | 12.9 | 0 | 39-50 | K.FCLLGALLAPIR.V | | QU:MU | 0.90 |

# Detailed Protein Report

## Protein 1275: protein FAM71C [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|23503301 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| | | **Sequence Coverage [%]:** | 10.8 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MEDCCMLPYY TAQSSPAMGM FNTSMGKLQR QLYKGEYTIF RYAPMFESDF IQISKRGEVI DVHNRARMVT MGIVRTSPCL
        90        100        110        120        130        140        150        160
TLPDVMLLAR PAAVCDNARC GPATQKRESP PAEILELTRL LPLMFVKITI HNSVKKQLHL KLATGRSFYL QLCPPSDASE
       170        180        190        200        210        220        230        240
DLFVHWENLV YILRPPVEAY SDTRAILAGN TLDSSVLEEV QRSPVGYAMK FCEEKEQFRI SRLHMNAEMF GSTYCDYTIE
       250
I
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1606 | 1 | 1052.1622 | 9.14 | 3 | 49.8 | 12.9 | 2 | 216-241 | K.EQFRISRLHMNAEMFGSTYCDYTIEI.- | |

# Detailed Protein Report

## Protein 1276: PREDICTED: uncharacterized protein C1orf173 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578798370 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 145.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.5 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 1.03 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLAKGKKAVM | KFRNSIGNSQ | RMNSYQLPNI | NSYMMPIPPP | LPPTGKITRE | NRSETWRRRR | FRPTTAPNGL | EPLLTKDSRR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IHKTSLHSNA | AITMIYLGKN | VHLSSDNPDF | RDEIKVYQQH | CGGENLCVYK | GKLLEKETFQ | FISKRHHGFP | FSLTFFLNGM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QVNRLSSCCE | YKHRKGSRLG | GKRGYFGFVC | VERSSPCYKC | IIAMGLDKKP | SLPKSRKEKS | TEKGEELKKA | EGKVRKEREY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VIPKRNEIKE | NKTSVSAKFS | AQEIKTGLKE | VVTAVEEMTS | KGKPGQEVLE | DDQENTLKYE | YEEDFEVDEE | KQGEKSNEEG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QADVQMNGIP | QSPLDDKKDN | LDPEKESETS | SQKAPDARDN | VKDENDGCSE | SELEEDKQDM | KTASSTSSRS | HPYSSDSEDE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SAVGDREAHT | DSSTDESARR | SSSQELSEND | KPRKSHLPIE | ESLEIEIEDQ | EITKADVETK | PMPIDESFEN | VLKEGTEKGT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QEIAEGLSEK | SGKHVSAEEK | EKDKSKLWEE | STAQVKDKKA | GLPGLEEGGK | DSLPLAYVLA | LGAPTMNFMV | DETAAINSNK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ESQQLVQKTY | TLEKKEAMEE | DEAPQHRDAD | IVQGKGEAAL | WGEAGAVHEA | PLRAWKPTAE | QPELAEEFTE | KREIPPGIER |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GAEGAAEAEG | VRRLGEGGSD | PIGQAAAKDA | VGLSKDEAPE | KQALMLTVLE | TDKAASEGEQ | GLEKAVLANE | AAALNLEHLH |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EVAALREAAT | SEEGEAEGGV | AVSDVGESEE | EASIDLEDTG | PMEDTASKRE | DGSEEAILGG | EEPAKERKEV | MRTETRLSPF |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TGEAEASRMQ | VSEGSPEEGS | LAKEAFLCKE | DVEGEEMVTE | AEANREDDRK | EILPKELDLA | RERRKAERPK | TSLRKTDSER |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EEVTRANALK | DEDAFKEEQK | LKAEEGETET | EVRAEEETKA | PPNEMGSDAE | NEAPVEASEL | SDNPGLLGED | SLKETVVPIF |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| EATPGFEKSL | ENITALRKEG | GGERLSEARD | TEHKDREELS | SRENRALKEG | HRQDGEGALA | APEAEPAGKV | QAPEGLIPAT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GQAEELAAKD | HDSCAGLEGR | AEGQGGVDVV | LRTQEAVAEE | DPIMAEKFRE | EAVDEDPEEE | EDKECTLETE | AMQDRNSEGD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GDMEGEGNTQ | KNEGMGGGRV | VAVEVLHGGG | ETAETAAEER | EVLAGSETAE | EKTIANKASS | FSDVAEEETW | HQQDELVGKT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| AAAGKVVVEE | LARSGEEVPA | AEEMTVTYTT | EAGVGTPGAL | ERKTSGLGQE | QEEGSEGQEA | ATGSGDGRQE | TGAAEKFRLG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | | |
| LSREGERELS | PESLQAMATL | PVKPDFTETR | EKQQHMVQGE | SETADVSPNN | VQV | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 26 | 1 | 803.7029 | -57.88 | 3 | 30.0 | 12.9 | 2 | 194-214 | R.SSPCYKCIIAMGLDKKPSLPK.S | Carbamidomethyl: 4, 7; Oxidation: 11 | WUP:QUP 1.03 |

# Detailed Protein Report

## Protein 1277: ras GTPase-activating protein 1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|12545406 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 100.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKGWYHGKLD | RTIAEERLRQ | AGKSGSYLIR | ESDRRPGSFV | LSFLSQMNVV | NHFRIIAMCG | DYYIGGRRFS | SLSDLIGYYS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HVSCLLKGEK | LLYPVAPPEP | VEDRRRVRAI | LPYTKVPDTD | EISFLKGDMF | IVHNELEDGW | MWVTNLRTDE | QGLIVEDLVE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EVGREEDPHE | GKIWFHGKIS | KQEAYNLLMT | VGQVCSFLVR | PSDNTPGDYS | LYFRTNENIQ | RFKICPTPNN | QFMMGGRYYN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SIGDIIDHYR | KEQIVEGYYL | KEPVPMQDQE | QVLNDTVDGK | EIYNTIRRKT | KDAFYKNIVK | KGYLLKKGKG | KRWKNLYFIL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EGSDAQLIYF | ESEKRATKPK | GLIDLSVCSV | YVVHDSLFGR | PNCFQIVVQH | FSEEHYIFYF | AGETPEQAED | WMKGLQAFCN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LRKSSPGTSN | KRLRQVSSLV | LHIEEAHKLP | VKHFTNPYCN | IYLNSVQVAK | THAREGQNPV | WSEEFVFDDL | PPDINRFEIT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LSNKTKKSKD | PDILFMRCQL | SRLQKGHATD | EWFLLSSHIP | LKGIEPGSLR | VRARYSMEKI | MPEEEYSEFK | ELILQKELHV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VYALSHVCGQ | DRTLLASILL | RIFLHEKLES | LLLCTLNDRE | ISMEDEATTL | FRATTLASTL | MEQYMKATAT | QFVHHALKDS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ILKIMESKQS | CELSPSKLEK | NEDVNTNLTH | LLNILSELVE | KIFMASEILP | PTLRYIYGCL | QKSVQHKWPT | NTTMRTRVVS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GFVFLRLICP | AILNPRMFNI | ISDSPSPIAA | RTLILVAKSV | QNLANLVEFG | AKEPYMEGVN | PFIKSNKHRM | IMFLDELGNV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PELPDTTEHS | RTDLSRDLAA | LHEICVAHSD | ELRTLSNERG | AQQHVLKKLL | AITELLQQKQ | NQYTKTNDVR | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 82 | 1 | 951.7644 | -30.51 | 3 | 30.7 | 12.9 | 1 | 788-811 | K.HRMIMFLDELGNVPELPDTTEHSR.T | Oxidation: 5 |

# Detailed Protein Report

## Protein 1278: disks large-associated protein 5 isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|226371667 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 95.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSSHFASRH | RKDISTEMIR | TKIAHRKSLS | QKENRHKEYE | RNRHFGLKDV | NIPTLEGRIL | VELDETSQGL | VPEKTNVKPR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AMKTILGDQR | KQMLQKYKEE | KQLQKLKEQR | EKAKRGIFKV | GRYRPDMPCF | LLSNQNAVKA | EPKKAIPSSV | RITRSKAKDQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MEQTKIDNES | DVRAIRPGPR | QTSEKKVSDK | EKKVVQPVMP | TSLRMTRSAT | QAAKQVPRTV | SSTTARKPVT | RAANENEPEG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KVPSKGRPAK | NVETKPDKGI | SCKVDSEENT | LNSQTNATSG | MNPDGVLSKM | ENLPEINTAK | IKGKNSFAPK | DFMFQPLDGL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KTYQVTPMTP | RSANAFLTPS | YTWTPLKTEV | DESQATKEIL | AQKCKTYSTK | TIQQDSNKLP | CPLGPLTVWH | EEHVLNKNEA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TTKNLNGLPI | KEVPSLERNE | GRIAQPHHGV | PYFRNILQSE | TEKLTSHCFE | WDRKLELDIP | DDAKDLIRTA | VGQTRLLMKE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RFKQFEGLVD | DCEYKRGIKE | TTCTDLDGFW | DMVSFQIEDV | IHKFNNLIKL | EESGWQVNNN | MNHNMNKNVF | RKKVVSGIAS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KPKQDDAGRI | AARNRLAAIK | NAMRERIRQE | ECAETAVSVI | PKEVDKIVFD | AGFFRVESPV | KLFSGLSVSS | EGPSQRLGTP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KSVNKAVSQS | RNEMGIPQQT | TSPENAGPQN | TKSEHVKKTL | FLSIPESRSS | IEDAQCPGLP | DLIEENHVVN | KTDLKVDCLS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SERMSLPLLA | GGVADDINTN | KKEGISDVVE | GMELNSSITS | QDVLMSSPEK | NTASQNSILE | EGETKISQSE | LFDNKSLTTE |
| 810 | 820 | 830 | 840 | 850 | | | |
| CHLLDSPGLN | CSNPFTQLER | RHQEHARHIS | FGGNLITFSP | LQPGEF | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2694 | 1 | 963.8006 | 12.70 | 3 | 64.8 | 12.9 | 0 | 796-820 | K.SLTTECHLLDSPGLNCSNPFTQLER.R | Carbamidomethyl: 6, 16 |

# Detailed Protein Report

## Protein 1279: vesicular, overexpressed in cancer, prosurvival protein 1 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|546231038 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 18.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 11.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLSETLGYLS | SVLLQCTEAK | KHCWYFEGLY | PTYYICRSYE | DCCGSRCCVR | ALSIQRLWYF | WFLLMMGVLF | CCGAGFFIRR |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| RMYPPPLIEE | PAFNVSYTRQ | PPNPGPGAQQ | PGPPYYTDPG | GPGMNPVGNS | MAMAFQVPPN | SPQGSVACPP | PPAYCNTPPP |
| **170** | | | | | | | |
| PYEQVVKAK | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1673 | 1 | 1101.4440 | -101.03 | 2 | 50.7 | 12.9 | 0 | 1-20 | -.MLSETLGYLSSVLLQCTEAK.K | Oxidation: 1 |

# Detailed Protein Report

## Protein 1280: PREDICTED: protein FAM219B isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530406238 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 10.2 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MATAEPSGRA LRLSTPGPRP SGARDRAPGA AGPPSGQIGN RALRLGERTP AAVEKRGPYM VTRAPSIQAK LQKHRDLAKA
        90        100        110        120        130        140        150        160
VLRRKGMLGA SPNRPDSSGK RSVKFNKGYT ALSQSPDENL VSLDSDSDGE LGSRYSSGYS SAEVNQDVSR QLLQDGYHLD
       170        180        190        200
EIPDDEDLDL IPPKPMASST CSCCWCCLGD SSSCTLQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1458 | 1 | 980.9236 | -103.15 | 2 | 48.4 | 12.9 | 2 | 25-44 | R.DRAPGAAGPPSGQIGNRALR.L | |

# Detailed Protein Report

## Protein 1281: activating signal cointegrator 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|32189376 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 66.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAVAGAVSGE | PLVHWCTQQL | RKTFGLDVSE | EIIQYVLSIE | SAEEIREYVT | DLLQGNEGKK | GQFIEELITK | WQKNDQELIS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DPLQQCFKKD | EILDGQKSGD | HLKRGRKKGR | NRQEVPAFTE | PDTTAEVKTP | FDLAKAQENS | NSVKKKTKFV | NLYTREGQDR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LAVLLPGRHP | CDCLGQKHKL | INNCLICGRI | VCEQEGSGPC | LFCGTLVCTH | EEQDILQRDS | NKSQKLLKKL | MSGVENSGKV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DISTKDLLPH | QELRIKSGLE | KAIKHKDKLL | EFDRTSIRRT | QVIDDESDYF | ASDSNQWLSK | LERETLQKRE | EELRELRHAS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RLSKKVTIDF | AGRKILEEEN | SLAEYHSRLD | ETIQAIANGT | LNQPLTKLDR | SSEEPLGVLV | NPNMYQSPPQ | WVDHTGAASQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KKAFRSSGFG | LEFNSFQHQL | RIQDQEFQEG | FDGGWCLSVH | QPWASLLVRG | IKRVEGRSWY | TPHRGRLWIA | ATAKKPSPQE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VSELQATYRL | LRGKDVEFPN | DYPSGCLLGC | VDLIDCLSQK | QFKEQFPDIS | QESDSPFVFI | CKNPQEMVVK | FPIKGNPKIW |
| 570 | 580 | 590 | | | | | |
| KLDSKIHQGA | KKGLMKQNKA | V | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 397 | 1 | 1294.0084 | 69.60 | 3 | 35.0 | 12.9 | 1 | 190-222 | R.IVCEQEGSGPCLFCGTLVCTHEEQDILQRDSNK.S | Carbamidomethyl: 3, 11, 14, 19 |

# Detailed Protein Report

## Protein 1282: PREDICTED: run domain Beclin-1 interacting and cysteine-rich containing protein isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578807915 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 93.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578807917 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: run domain Beclin-1 interacting and cysteine-rich containing protein isoform X6 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLQCLEAVEQ | NNPRLLAQID | ASMFARKHES | PLLVTKSQSL | TALPSSTYTP | PNSYAQHSYF | GSFSSLHQSV | PNNGSERRST |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SFPLSGPPRK | PQESRGHVSP | AEDQTIQAPP | VSVSALARDS | PLTPNEMSSS | TLTSPIEASW | VSSQNDSPGD | ASEGPEYLAI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GNLDPRGRTA | SCQSHSSNAE | SSSSNLFSSS | SSQKPDSAAS | SLGDQEGGGE | SQLSSVLRRS | SFSEGQTLTV | TSGAKKSHIR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SHSDTSIASR | GAPGGPRNIT | IIVEDPIAES | CNDKAKLRGP | LPYSGQSSEV | STPSSLYMEY | EGGRYLCSGE | GMFRRPSEGQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SLISYLSEQD | FGSCADLEKE | NAHFSISESL | IAAIELMKCN | MMSQCLEEEE | VEEEDSDREI | QELKQKIRLR | RQQIRTKNLL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PMYQEAEHGS | FRVTSSSSQF | SSRDSAQLSD | SGSADEVDEF | EIQDGSEGSN | LTHISKNGLS | VSLASMFSDA | DIRRNTASSS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KSFVSSQSFS | HCFLHSTSAE | AVAMGLLKQF | EGMQLPAASE | LEWLVPEHDA | PQKLLPIPDS | LPISPDDGQH | ADIYKLRIRV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RGNLEWAPPR | PQIIFNVHPA | PTRKIAVAKQ | NYRCAGCGIR | TDPDYIKRLR | YCEYLGKYFC | QCCHENAQMA | IPSRVLRKWD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FSKYYVSNFS | KDLLIKIWND | PLFNVQDINS | ALYRKVKLLN | QVRLLRVQLC | HMKNMFKTCR | LAKELLDSFD | TVPGHLTEDL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HLYSLNDLTA | TRKGELGPRL | AELTRAGATH | VERCMLCQAK | GFICEFCQNE | DDIIFPFELH | KCRTCEECKA | CYHKACFKSG |
| 810 | 820 | 830 | 840 | 850 | | | |
| SCPRCERLQA | RREALARQSL | ESYLSDYEEE | PAEALALEAA | VLEAT | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1246 | 1 | 660.7639 | 71.36 | 3 | 45.2 | 12.9 | 2 | 678-693 | K.LLNQVRLLRVQLCHMK.N | Oxidation: 15 |

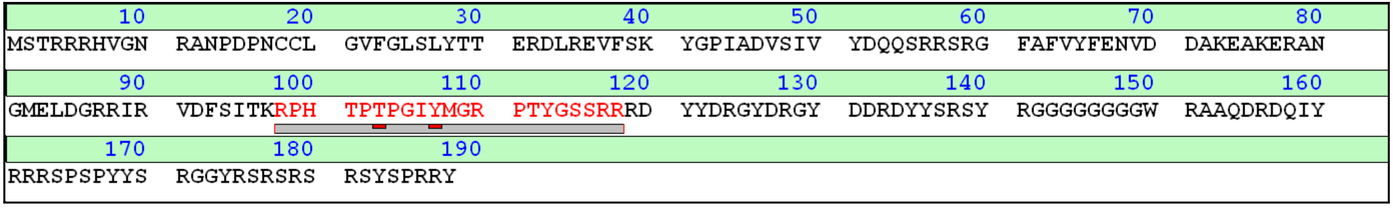
# Detailed Protein Report

## Protein 1283: transformer-2 protein homolog beta isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|345197228 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 11.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578807655 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: transformer-2 protein homolog beta isoform X2 [Homo sapiens] |
| gi\|530375128 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: transformer-2 protein homolog beta isoform X1 [Homo sapiens] |



```
        10         20         30         40         50         60         70         80
MSTRRRHVGN RANPDPNCCL GVFGLSLYTT ERDLREVFSK YGPIADVSIV YDQQSRRSRG FAFVYFENVD DAKEAKERAN
        90        100        110        120        130        140        150        160
GMELDGRRIR VDFSITKRPH TPTPGIYMGR PTYGSSRRRD YYDRGYDRGY DDRDYYSRSY RGGGGGGGGW RAAQDRDQIY
       170        180        190
RRRSPSPYYS RGGYRSRSRS RSYSPRRY
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 237 | 1 | 1202.1810 | 60.23 | 2 | 32.7 | 12.9 | 1 | 98-118 | K.RPHTPTPGIYMGRPTYGSSRR.R | Oxidation: 11 |

# Detailed Protein Report

## Protein 1284: lipid phosphate phosphatase-related protein type 2 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|282400942 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 36.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.0 |
| | | **Sequence Coverage [%]:** | 6.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAGGRPHLKR | SFSIIPCFVF | VESVLLGIVI | LLAYRLEFTD | TFPVHTQGFF | CYDSTYAKPY | PGPEAASRVP | PALVYALVTA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GPTLTILLGE | LARAFFPAPP | SAVPVIGEST | IVSGACCRFS | PPVRRLVRFL | GVYSFGLFTT | TIFANAGQVV | TGNPTPHFLS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VCRPNYTALG | CLPPSPDRPG | PDRFVTDQGA | CAGSPSLVAA | ARRAFPCKDA | ALCAYAVTYT | AMYVTLVFRV | KGSRLVKPSL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CLALLCPAFL | VGVVRVAEYR | NHWSDVLAGF | LTGAAIATFL | VTCVVHNFQS | RPPSGRRLSP | WEDLGQAPTM | DSPLEKNPRS |
| 330 | 340 | 350 | | | | | |
| AGRIRHRHGS | PHPSRRTAPA | VAT | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 805 | 1 | 1106.2552 | 86.41 | 2 | 40.1 | 12.9 | 0 | 235-255 | R.LVKPSLCLALLCPAFLVGVVR.V | |

# Detailed Protein Report

## Protein 1285: PREDICTED: glucocorticoid-induced transcript 1 protein isoform X4 [Homo sapiens]

**Accession:** gi|578813292
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 12.9
**MW [kDa]:** 38.3
**pI:** 8.8
**Sequence Coverage [%]:** 6.0
**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MKDKATQTPS CWAEEGAEKR SHQRSASWGS ADQLKEQIAK LRQQLQRSKQ SSRHSKEKDR QSPLHGNHIT ISHTQATGSR
        90        100        110        120        130        140        150        160
SVPMPLSNIS VPKSSVSRVP CNVEGISPEL EKVFIKENNG KEEVSKPLDI PDGRRAPLPA HYRSSSTRSI DTQTPSVQER
       170        180        190        200        210        220        230        240
SSSCSSHSPC VSPFCPPESQ DGSPCSTEDL LYDRDKDSGS SSPLPKYASS PKPNNSYMFK REPPEGCERV KVFEEMASRQ
       250        260        270        280        290        300        310        320
PISAPLFSCP DKNKVNFIPT GSAFCPVKLL GPLLPASDLM LKNSPNSGQS SALATLTVEQ LSSRVSFTSL SDDTSTAGSM
       330        340        350        360
EASVQQPSQQ QQLLQELQGE DHISAQNYVI I
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 10 | 1 | 1205.0326 | -41.44 | 2 | 29.6 | 12.9 | 1 | 232-252 | K.VFEEMASRQPISAPLFSCPDK.N | Carbamidomethyl: 18 |

# Detailed Protein Report

## Protein 1286: PREDICTED: solute carrier family 35 member B1 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578830240 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 43.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRPLPPVGDV | RLELSPPPPL | LPVPVVSGSP | VGSSGRLMAS | SSSLVPDRLR | LPLCFLGVFV | CYFYYGILQE | KMTRVGPLLV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LPDACKQPIR | PRPWCHSRNT | VSSCLGTRGK | YGEGAKQETF | TFALTLVFIQ | CVINAVFAKI | LIQFFDTARV | DRTRSWLYAA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CSISYLGAMV | SSNSALQFVN | YPTQVLGKSC | KPIPVMLLGV | TLLKKKYPLA | KYLCVLLIVA | GVALFMYKPK | KVVGIEEHTV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GYGELLLLLS | LTLDGLTGVS | QDHMRAHYQT | GSNHMMLNIN | LWSTLLLGMG | ILFTGELWEF | LSFAERYPAI | IYNILLFGLT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SALGQSFIFM | TVVYFGPLTC | SIITTTRKFF | TILASVILFA | NPISPMQWVG | TVLVFLGLGL | DAKFGKGAKK | TSH |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2847 | 1 | 1080.8719 | -36.05 | 3 | 66.0 | 12.9 | 2 | 72-98 | K.MTRVGPLLVLPDACKQPIRPRPWCHSR.N | Carbamidomethyl: 14, 24 |

# Detailed Protein Report

## Protein 1287: tudor domain-containing protein 5 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|312283653 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 60.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| | | **Sequence Coverage [%]:** | 5.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MANHDIPPDA | VPNKKLCRLP | PLDTSSLIGV | FVEYIISPSQ | FYIRIYSRDS | SELLEDMMIE | MRRCYSNQLV | SDRYVMPECF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IQPGHLCCVR | ISEDKWWYRV | IIHRVLEKQE | VEVFYPDFGN | IGIVQKSSLR | FLKCCYTKLP | AQAIPCSLAW | VRPVEEHWTS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KAILQFQKLC | GLKPLVGVVD | EYVDGILNIF | LCDTSSNEDV | YFHHVLRTEG | HAIVCRENIS | SKGFSELNPL | ALYTTSSGGP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EDIVLTELGY | PSQQHYFNED | RKISPQSKES | ELRILDEIPT | GMPCLESVTI | GDDIWDENWL | PLQAKMGKGG | DAASHLFTAS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LGGKNQYSSC | KEMPQKDWCF | STPKDTWDDS | WQPSGLVNGT | KVEVHKPEVL | GAQEKNTGTN | RTQKQLDING | SSDSSTLPKL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EEFCTSLTQS | EQSADGSQSE | PNNSQTQPKQ | IQLSTAAPCS | TTAVDDSAEK | PSGSVESSPE | ILKNEDFSSS | RAITLYKDKR |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| QESVDQLSLI | LSYECQISQK | LYIPRSTATA | ALGAAARLAT | SRSLLHWYPS | VKRMEA | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 673 | 1 | 1106.2391 | 51.93 | 3 | 38.0 | 12.9 | 2 | 63-90 | R.RCYSNQLVSDRYVMPECFIQPGHLCCVR.I | |

# Detailed Protein Report

## Protein 1288: PREDICTED: E3 ubiquitin-protein ligase MIB2 isoform X7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578798430 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 111.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.75 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAGALRRGRA | LGSRPSGPTV | SSRRSPQCPV | AQEGLGARSR | PRVAPRSLAR | CGPSSRLMGW | KPSEARGQSQ | SFQASGLQPR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SLKAARRATG | RPDRSRAARP | TMDPSAHRSR | AAPPNMDPDP | QAGVQVGMRV | VRGVDWKWGQ | QDGGEGGVGT | VVELGRHGSP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| STPDRTVVVQ | WDQGTRTNYR | AGYQGAHDLL | LYDNAQIGVR | HPNIICDCCK | KHGLRGMRWK | CRVCLDYDLC | TQCYMHNKHE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LAHAFDRYET | AHSRPVTLSP | RQGLPRIPLR | GIFQGAKVVR | GPDWEWGSQD | GGEGKPGRVV | DIRGWDVETG | RSVASVTWAD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GTTNVYRVGH | KGKVDLKCVG | EAAGGFYYKD | HLPRLGKPAE | LQRRVSADSQ | PFQHGDKVKC | LLDTDVLREM | QEGHGGWNPR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MAEHHSFWVG | DVVRVIGDLD | TVKRLQAGHG | EWTDDMAPAL | GRVGKVVKVF | GDGNLRVAVA | GQRWTFSPSC | LVAYRPEEDA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NLDVAERARE | NKSSLSVALD | KLRAQKSDPE | HPGRLVVEVA | LGNAARALDL | LRRRPEQVDT | KNQGRTALQV | AAYLGQVELI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RLLLQARAGV | DLPDDEGNTA | LHYAALGNQP | EATRVLLSAG | CRADAINSTQ | STALHVAVQR | GFLEVVRALC | ERGCDVNLPD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AHSDTPLHSA | ISAGTGASGI | VEVLTEVPNI | DVTATNSQGF | TLLHHASLKG | HALAVRKILA | RARQLVDAKK | EDGFTALHLA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ALNNHREVAQ | ILIREGRCDV | NVRNRKLQSP | LHLAVQQAHV | GLVPLLVDAG | CSVNAEDEEG | DTALHVALQR | HQLLPLVADG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AGGDPGPLQL | LSRLQASGLP | GSAELTVGAA | VACFLALEGA | DVSYTNHRGR | SPLDLAAEGR | VLKALQGCAQ | RFRERQAGGG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| AAPGPRQTLG | TPNTVTNLHV | GAAPGPEAAE | CLVCSELALL | VLFSPCQHRT | VCEECARRMK | KCIRCQVVVS | KKLRPDGSEV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ASAAPAPGPP | RQLVEELQSR | YRQMEERITC | PICIDSHIRL | VFQCGHGACA | PCGSALSACP | ICRQPIRDRI | QIFV |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2600 | 1 | 835.4660 | 80.35 | 2 | 63.2 | 12.9 | 0 | 401-414 | R.MAEHHSFWVGDVVR.V | | WUP:QUP 0.75 |

# Detailed Protein Report

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## Protein 1289: relaxin receptor 2 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|18677729 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 86.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MIVFLVFKHL | FSLRLITMFF | LLHFIVLINV | KDFALTQGSM | ITPSCQKGYF | PCGNLTKCLP | RAFHCDGKDD | CGNGADEENC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GDTSGWATIF | GTVHGNANSV | ALTQECFLKQ | YPQCCDCKET | ELECVNGDLK | SVPMISNNVT | LLSLKKNKIH | SLPDKVFIKY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TKLKKIFLQH | NCIRHISRKA | FFGLCNLQIL | YLNHNCITTL | RPGIFKDLHQ | LTWLILDDNP | ITRISQRLFT | GLNSLFFLSM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VNNYLEALPK | QMCAQMPQLN | WVDLEGNRIK | YLTNSTFLSC | DSLTVLFLPR | NQIGFVPEKT | FSSLKNLGEL | DLSSNTITEL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SPHLFKDLKL | LQKLNLSSNP | LMYLHKNQFE | SLKQLQSLDL | ERIEIPNINT | RMFQPMKNLS | HIYFKNFRYC | SYAPHVRICM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PLTDGISSFE | DLLANNILRI | FVWVIAFITC | FGNLFVIGMR | SFIKAENTTH | AMSIKILCCA | DCLMGVYLFF | VGIFDIKYRG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QYQKYALLWM | ESVQCRLMGF | LAMLSTEVSV | LLLTYLTLEK | FLVIVFPFSN | IRPGKRQTSV | ILICIWMAGF | LIAVIPFWNK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DYFGNFYGKN | GVCFPLYYDQ | TEDIGSKGYS | LGIFLGVNLL | AFLIIVFSYI | TMFCSIQKTA | LQTTEVRNCF | GREVAVANRF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FFIVFSDAIC | WIPVFVVKIL | SLFRVEIPDT | MTSWIVIFFL | PVNSALNPIL | YTLTTNFFKD | KLKQLLHKHQ | RKSIFKIKKK |
| 730 | 740 | 750 | 760 | | | | |
| SLSTSIVWIE | DSSSLKLGVL | NKITLGDSIM | KPVS | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 869 | 1 | 764.0295 | -45.76 | 3 | 39.3 | 12.9 | 0 | 271-290 | K.YLTNSTFLSCDSLTVLFLPR.N | |

# Detailed Protein Report

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## Protein 1290: RNA-binding protein 47 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|148833511 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530376680 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: RNA-binding protein 47 isoform X9 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTAEDSTAAM | SSDSAAGSSA | KVPEGVAGAP | NEAALLALME | RTGYSMVQEN | GQRKYGGPPP | GWEGPHPQRG | CEVFVGKIPR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DVYEDELVPV | FEAVGRIYEL | RLMMDFDGKN | RGYAFVMYCH | KHEAKRAVRE | LNNYEIRPGR | LLGVCCSVDN | CRLFIGGIPK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MKKREEILEE | IAKVTEGVLD | VIVYASAADK | MKNRGFAFVE | YESHRAAAMA | RRKLMPGRIQ | LWGHQIAVDW | AEPEIDVDED |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VMETVKILYV | RNLMIETTED | TIKKSFGQFN | PGCVERVKKI | RDYAFVHFTS | REDAVHAMNN | LNGTELEGSC | LEVTLAKPVD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KEQYSRYQKA | ARGGGAAEAA | QQPSYVYSCD | PYTLAYYGYP | YNALIGPNRD | YFVKVAIPAI | GAQYSMFPAA | PAPKMIEDGK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IHTVEHMISP | IAVQPDPASA | AAAAAAAAAA | AAAVIPTVST | PPPFQGRPIT | PVYTVAPNVQ | RIPTAGIYGA | SYVPFAAPAT |
| 490 | 500 | 510 | 520 | 530 | | | |
| ATIATLQKNA | AAAAAMYGGY | AGYIPQAFPA | AAIQVPIPDV | YQTY | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1602 | 1 | 781.3841 | 36.49 | 2 | 49.8 | 12.9 | 1 | 110-121 | K.NRGYAFVMYCHK.H | Carbamidomethyl: 10;<br>Oxidation: 8 |

# Detailed Protein Report

## Protein 1291: ataxin-3 isoform o [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|258614025 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 17.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| | | **Sequence Coverage [%]:** | 14.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MESIFHEKQE | GSLCAQHCLN | NLLQGEYFSP | VELSSIAHQL | DEEERMRMAE | GGVTSEDYRT | FLQQPSGNMD | DSGFFSIQVI |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| SNALKVWGLE | LILFNSPEYQ | RLRIDPINER | SFICNYKEHW | FTVRKLGKQT | AAKAATAAAA | AAAGGPIRTE | FTSM |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1220 | 1 | 1019.1330 | 50.19 | 2 | 44.8 | 12.9 | 2 | 126-148 | K.LGKQTAAKAATAAAAAAAGGPIR.T | |

# Detailed Protein Report

## Protein 1292: PREDICTED: lamin-B receptor isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530366190 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 65.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPSRKFADGE | VVRGRWPGSS | LYYEVEILSH | DSTSQLYTVK | YKDGTELELK | ENDIKPLTSF | RQRKGGSTSS | SPSRRRGSRS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RSRSRSPGRP | PKSARRSASA | SHQADIKEAR | REVEVKLTPL | ILKPFGNSIS | RYNGEPEHIE | RNDAPHKNTQ | EKFSLSQESS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YIATQYSLRP | RREEVKLKEI | DSKEEKYVAK | ELAVRTFEVT | PIRAKDLEFG | GVPGVFLIMF | GLPVFLFLLL | LMCKQKDPSL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LNFPPPLPAL | YELWETRVFG | VYLLWFLIQV | LFYLLPIGKV | VEGTPLIDGR | RLKYRLNGFY | AFILTSAVIG | TSLFQGVEFH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YVYSHFLQFA | LAATVFCVVL | SVYLYMRSLK | APRNDLSPAS | SGNAVYDFFI | GRELNPRIGT | FDLKYFCELR | PGLIGWEALL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TTMDIIHDGF | GFMLAFGDLV | WVPFIYSFQA | FYLVSHPNEV | SWPMASLIIV | LKLCGYVIFR | GANSQKNAFR | KNPSDPKLAH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LKTIHTSTGK | NLLVSGWWGF | VRHPNYLGDL | IMALAWSLPC | GFNHILPYFY | IIYFTMLLVH | REARDEYHCK | KKYGVAWEKY |
| 570 | 580 | | | | | | |
| CQRVPYRIFP | YIY | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1479 | 1 | 682.3534 | -33.25 | 3 | 48.7 | 12.9 | 2 | 472-490 | K.NPSDPKLAHLKTIHTSTGK.N | |

# Detailed Protein Report

## Protein 1293: myogenic factor 6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4505299 | **Score:** | 12.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 26.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 1.78 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMMDLFETGS | YFFYLDGENV | TLQPLEVAEG | SPLYPGSDGT | LSPCQDQMPP | EAGSDSSGEE | HVLAPPGLQP | PHCPGQCLIW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ACKTCKRKSA | PTDRRKAATL | RERRRLKKIN | EAFEALKRRT | VANPNQRLPK | VEILRSAISY | IERLQDLLHR | LDQQEKMQEL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GVDPFSYRPK | QENLEGADFL | RTCSSQWPSV | SDHSRGLVIT | AKEGGASIDS | SASSSLRCLS | SIVDSISSEE | RKLPCVEEVV |
| 250 | | | | | | | |
| EK | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2534 | 1 | 841.8750 | -46.34 | 2 | 61.7 | 12.9 | 0 | 157-170 | K.MQELGVDPFSYRPK.Q | Oxidation: 1 | QU:MU | 1.78 |

# Detailed Protein Report

## Protein 1294: keratin, type I cuticular Ha2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|116488398 | **Score:** | 12.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 50.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTSSCCVTNN | LQASLKSCPR | PASVCSSGVN | CRPELCLGYV | CQPMACLPSV | CLPTTFRPAS | CLSKTYLSSS | CQAASGISGS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MGPGSWYSEG | AFNGNEKETM | QFLNDRLASY | LTRVRQLEQE | NAELESRIQE | ASHSQVLTMT | PDYQSHFRTI | EELQQKILCT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KAENARMVVN | IDNAKLAADD | FRAKYEAELA | MRQLVEADIN | GLRRILDDLT | LCKADLEAQV | ESLKEELMCL | KKNHEEEVGS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LRCQLGDRLN | IEVDAAPPVD | LTRVLEEMRC | QYEAMVEANR | RDVEEWFNMQ | MEELNQQVAT | SSEQLQNYQS | DIIDLRRTVN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TLEIELQAQH | SLRDSLENTL | TESEARYSSQ | LAQMQCMITN | VEAQLAEIRA | DLERQNQEYQ | VLLDVRARLE | GEINTYRSLL |
| 410 | 420 | 430 | 440 | 450 | | | |
| ENEDCKLPCN | PCSTPSCTTC | VPSPCVPRTV | CVPRTVGMPC | SPCPQGRY | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2221 | 1 | 1051.4304 | -58.38 | 2 | 57.6 | 12.8 | 1 | 429-447 | R.TVCVPRTVGMPCSPCPQGR.Y | Carbamidomethyl: 3, 15 |

# Detailed Protein Report

## Protein 1295: insulin gene enhancer protein ISL-1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|115387114 | **Score:** | 12.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 6.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGDMGDPPKK | KRLISLCVGC | GNQIHDQYIL | RVSPDLEWHA | ACLKCAECNQ | YLDESCTCFV | RDGKTYCKRD | YIRLYGIKCA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KCSIGFSKND | FVMRARSKVY | HIECFRCVAC | SRQLIPGDEF | ALREDGLFCR | ADHDVVERAS | LGAGDPLSPL | HPARPLQMAA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EPISARQPAL | RPHVHKQPEK | TTRVRTVLNE | KQLHTLRTCY | AANPRPDALM | KEQLVEMTGL | SPRVIRVWFQ | NKRCKDKKRS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IMMKQLQQQQ | PNDKTNIQGM | TGTPMVAASP | ERHDGGLQAN | PVEVQSYQPP | WKVLSDFALQ | SDIDQPAFQQ | LVNFSEGGPG |
| 330 | 340 | 350 | | | | | |
| SNSTGSEVAS | MSSQLPDTPN | SMVASPIEA | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2453 | 1 | 900.1989 | 108.21 | 3 | 58.9 | 12.8 | 2 | 107-130 | R.CVACSRQLIPGDEFALREDGLFCR.A | |

# Detailed Protein Report

## Protein 1296: PREDICTED: cip1-interacting zinc finger protein isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578817288 | **Score:** | 12.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 94.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPRGMADPSG | RQTDLGLRAS | PSRCGGRGTE | ATMFSQQQQQ | QLQQQQQQLQ | QLQQQQLQQQ | QLQQQQLLQL | QQLLQQSPPQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| APLPMAVSRG | LPPQQPQQPL | LNLQGTNSAS | LLNGSMLQRA | LLLQQLQGNL | RGYGMASPGL | AAPSLTPPQL | ATPNLQQFFP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QATRQSLLGP | PPVGVPMNPS | QFNLSGRNPQ | KQARTSSSTT | PNRKDSSSQT | MPVEDKSDPP | EGSEEAAEPR | MDTPEDQDLP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PCPEDIAKEK | RTPAPEPEPC | EASELPAKRL | RSSEEPTEKE | PPGQLQVKAQ | PQARMTVPKQ | TQTPDLLPEA | LEAQVLPRFQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PRVLQVQAQV | QSQTQPRIPS | TDTQVQPKLQ | KQAQTQTSPE | HLVLQQKQVQ | PQLQQEAEPQ | KQVQPQVHTQ | AQPSVQPQEH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PPAQVSVQPP | EQTHEQPHTQ | PQVSLLAPEQ | TPVVVHVCGL | EMPPDAVEAG | GGMEKTLPEP | VGTQVSMEEI | QNESACGLDV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GECENRAREM | PGVWGAGGSL | KVTILQSSDS | RAFSTVPLTP | VPRPSDSVSS | TPAATSTPSK | QALQFFCYIC | KASCSSQQEF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QDHMSEPQHQ | QRLGEIQHMS | QACLLSLLPV | PRDVLETEDE | EPPPRRWCNT | CQLYYMGDLI | QHRRTQDHKI | AKQSLRPFCT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VCNRYFKTPR | KFVEHVKSQG | HKDKAKELKS | LEKEIAGQDE | DHFITVDAVG | CFEGDEEEEE | DDEDEEEIEV | EEELCKQVRS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RDISREEWKG | SETYSPNTAY | GVDFLVPVMG | YICRICHKFY | HSNSGAQLSH | CKSLGHFENL | QKYKAAKNPS | PTTRPVSRRC |
| 810 | 820 | 830 | 840 | 850 | 860 | | |
| AINARNALTA | LFTSSGRPPS | QPNTQDKTPS | KVTARPSQPP | LPRRSTRLKT | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 38 | 2 | 837.3492 | -94.93 | 2 | 29.4 | 12.8 | 2 | 12-27 | R.QTDLGLRASPSRCGGR.G | |

# Detailed Protein Report

## Protein 1297: cytoplasmic FMR1-interacting protein 1 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|74271907 | **Score:** | 12.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 94.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| | | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAESLGSAEL | LRQLKSLGME | RLLHAVNTFL | RQSCTYLPLL | TFGGKTSFVS | LDVYGTEANC | SATSCSFPKA | AATWPRRQAP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GPLGELVRGP | PDQGVAEQSF | SHGLFEFGIT | NVPCIFSPPQ | MFPWIIQLYM | VRTMLESLIA | DKSGSKKTLR | SSLEGPTILD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IEKFHRESFF | YTHLINFSET | LQQCCDLSQL | WFREFFLELT | MGRRIQFPIE | MSMPWILTDH | ILETKEASMM | EYVLYSLDLY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NDSAHYALTR | FNKQFLYDEI | EAEVNLCFDQ | FVYKLADQIF | AYYKVMAGSL | LLDKRLRSEC | KNQGATIHLP | PSNRYETLLK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QRHVQLLGRS | IDLNRLITQR | VSAAMYKSLE | LAIGRFESED | LTSIVELDGL | LEINRMTHKL | LSRYLTLDGF | DAMFREANHN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VSAPYGRITL | HVFWELNYDF | LPNYCYNGST | NRFVRTVLPF | SQEFQRDKQP | NAQPQYLHGS | KALNLAYSSI | YGSYRNFVGP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PHFQVICRLL | GYQGIAVVME | ELLKVVKSLL | QGTILQYVKT | LMEVMPKICR | LPRHEYGSPG | ILEFFHHQLK | DIVEYAELKT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VCFQNLREVG | NAILFCLLIE | QSLSLEEVCD | LLHAAPFQNI | LPRVHVKEGE | RLDAKMKRLE | SKYAPLHLVP | LIERLGTPQQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IAIAREGDLL | TKERLCCGLS | MFEVILTRIR | SFLDDPIWRG | PLPSNGVMHV | DECVEFHRLW | SAMQFVYCIP | VGTHEFTVEQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CFGDGLHWAG | CMIIVLLGQQ | RRFAVLDFCY | HLLKVQKHDG | KDEIIKNVPL | KKMVERIRKF | QILNDEIITI | LDKYLKSGDG |
| 810 | 820 | 830 | | | | | |
| EGTPVEHVRC | FQPPIHQSLA | SS | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 199 | 1 | 797.8837 | -38.98 | 2 | 32.2 | 12.8 | 1 | 436-448 | R.TVLPFSQEFQRDK.Q | |

# Detailed Protein Report

## Protein 1298: UDP-glucuronosyltransferase 2A3 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|193211427 | **Score:** | 12.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 60.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MRSDKSALVF LLLQLFCVGC GFCGKVLVWP CDMSHWLNVK VILEELIVRG HEVTVLTHSK PSLIDYRKPS ALKFEVVHMP
        90        100        110        120        130        140        150        160
QDRTEENEIF VDLALNVLPG LSTWQSVIKL NDFFVEIRGT LKMMCESFIY NQTLMKKLQE TNYDVMLIDP VIPCGDLMAE
       170        180        190        200        210        220        230        240
LLAVPFVLTL RISVGGNMER SCGKLPAPLS YVPVPMTGLT DRMTFLERVK NSMLSVLFHF WIQDYDYHFW EEFYSKALGR
       250        260        270        280        290        300        310        320
PTTLCETVGK AEIWLIRTYW DFEFPQPYQP NFEFVGGLHC KPAKALPKEM ENFVQSSGED GIVVFSLGSL FQNVTEEKAN
       330        340        350        360        370        380        390        400
IIASALAQIP QKVLWRYKGK KPSTLGANTR LYDWIPQNDL LGHPKTKAFI THGGMNGIYE AIYHGVPMVG VPIFGDQLDN
       410        420        430        440        450        460        470        480
IAHMKAKGAA VEINFKTMTS EDLLRALRTV ITDSSYKENA MRLSRIHHDQ PVKPLDRAVF WIEFVMRHKG AKHLRSAAHD
       490        500        510        520        530
LTWFQHYSID VIGFLLACVA TAIFLFTKCF LFSCQKFNKT RKIEKRE
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1155 | 1 | 652.5392 | -138.06 | 3 | 42.7 | 12.8 | 1 | 123-137 | K.MMCESFIYNQTLMKK.L | Carbamidomethyl: 3;<br>Oxidation: 1, 13 |

# Detailed Protein Report

## Protein 1299: chorionic somatomammotropin hormone-like 1 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|38201628 | **Score:** | 12.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 14.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 10.9 |
| | | **No. of unique Peptides:** | 1 |

```
         10         20         30         40         50         60         70         80
MEETQQKSNL ELLHISLLLI ESRLEPVRFL RSTFTNNLVY DTSDSDDYHL LKDLEEGIQM LMGRLEDGSH LTGQTLKQTY
         90        100        110        120        130
SKFDTNSHNH DALLKNYGLL HCFRKDMDKV ETFLRMVQCR SVEGSCGF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1804 | 1 | 898.8338 | -109.46 | 2 | 52.4 | 12.8 | 2 | 96-109 | K.NYGLLHCFRKDMDK.V | Carbamidomethyl: 7 |

# Detailed Protein Report

## Protein 1300: blood group Rh(CE) polypeptide isoform 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|301129229 | **Score:** | 12.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 28.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 10.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSKYPRSVR | RCLPLWALTL | EAALILLFYF | FTHYDASLED | QKGLVASYQV | GQDLTVMAAL | GLGFLTSNFR | RHSWSSVAFN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LFMLALGVQW | AILLDGFLSQ | FPPGKVVITL | FSIRLATMSA | MSVLISAGAV | LGKVNLAQLV | VMVLVEVTAL | GTLRMVISNI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FNTYVHSAVL | AGGVAVGTSC | HLIPSPWLAM | VLGLVAGLIS | IGGAKCLPVC | CNRVLGIHHI | SVMHSIFSLL | GLLGEITYIV |
| 250 | 260 | 270 | | | | | |
| LLVLHTVWNG | NGMFAPKSQN | MESTSCG | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1121 | 1 | 955.6361 | 90.17 | 3 | 44.1 | 12.8 | 1 | 106-133 | K.VVITLFSIRLATMSAMSVLISAGAVLGK.V | Oxidation: 13 |

# Detailed Protein Report

## Protein 1301: phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|40254823 | **Score:** | 12.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 133.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVPCWNHGNI | TRSKAEELLS | RTGKDGSFLV | RASESISRAY | ALCVLYRNCV | YTYRILPNED | DKFTVQASEG | VSMRFFTKLD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QLIEFYKKEN | MGLVTHLQYP | VPLEEEDTGD | DPEEDTESVV | SPPELPPRNI | PLTASSCEAK | EVPFSNENPR | ATETSRPSLS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ETLFQRLQSM | DTSGLPEEHL | KAIQDYLSTQ | LAQDSEFVKT | GSSSLPHLKK | LTTLLCKELY | GEVIRTLPSL | ESLQRLFDQQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LSPGLRPRPQ | VPGEANPINM | VSKLSQLTSL | LSSIEDKVKA | LLHEGPESPH | RPSLIPPVTF | EVKAESLGIP | QKMQLKVDVE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SGKLIIKKSK | DGSEDKFYSH | KKILQLIKSQ | KFLNKLVILV | ETEKEKILRK | EYVFADSKKR | EGFCQLLQQM | KNKHSEQPEP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DMITIFIGTW | NMGNAPPPKK | ITSWFLSKGQ | GKTRDDSADY | IPHDIYVIGT | QEDPLSEKEW | LEILKHSLQE | ITSVTFKTVA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IHTLWNIRIV | VLAKPEHENR | ISHICTDNVK | TGIANTLGNK | GAVGVSFMFN | GTSLGFVNSH | LTSGSEKKLR | RNQNYMNILR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FLALGDKKLS | PFNITHRFTH | LFWFGDLNYR | VDLPTWEAET | IIQKIKQQQY | ADLLSHDQLL | TERREQKVFL | HFEEEEITFA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PTYRFERLTR | DKYAYTKQKA | TGMKYNLPSW | CDRVLWKSYP | LVHVVCQSYG | STSDIMTSDH | SPVFATFEAG | VTSQFVSKNG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PGTVDSQGQI | EFLRCYATLK | TKSQTKFYLE | FHSSCLESFV | KSQEGENEEG | SEGELVVKFG | ETLPKLKPII | SDPEYLLDQH |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ILISIKSSDS | DESYGEGCIA | LRLEATETQL | PIYTPLTHHG | ELTGHFQGEI | KLQTSQGKTR | EKLYDFVKTE | RDESSGPKTL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KSLTSHDPMK | QWEVTSRAPP | CSGSSITEII | NPNYMGVGPF | GPPMPLHVKQ | TLSPDQQPTA | WSYDQPPKDS | PLGPCRGESP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PTPPGQPPIS | PKKFLPSTAN | RGLPPRTQES | RPSDLGKNAG | DTLPQEDLPL | TKPEMFENPL | YGSLSSFPKP | APRKDQESPK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| MPRKEPPPCP | EPGILSPSIV | LTKAQEADRG | EGPGKQVPAP | RLRSFTCSSS | AEGRAAGGDK | SQGKPKTPVS | SQAPVPAKRP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | |
| IKPSRSEINQ | QTPPTPTPRP | PLPVKSPAVL | HLQHSKGRDY | RDNTELPHHG | KHRPEEGPPG | PLGRTAMQ | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 234 | 1 | 850.8764 | -41.35 | 2 | 32.6 | 12.8 | 0 | 167-181 | R.LQSMDTSGLPEEHLK.A | Oxidation: 4 |

## Protein 1302: uncharacterized protein C21orf62 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|254911037 | **Score:** | 12.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|254911043 | refseq_huma (refseq_human_20140103.fasta) | uncharacterized protein C21orf62 precursor [Homo sapiens] |
| gi\|254911041 | refseq_huma (refseq_human_20140103.fasta) | uncharacterized protein C21orf62 precursor [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAPPSRHCLL | LISTLGVFAL | NCFTKGQKNS | TLIFTRENTI | RNCSCSADIR | DCDYSLANLM | CNCKTVLPLA | VERTSYNGHL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TIWFTDTSAL | GHLLNFTLVQ | DLKLSLCSTN | TLPTEYLAIC | GLKRLRINME | AKHPFPEQSL | LIHSGGDSDS | REKPMWLHKG |
| 170 | 180 | 190 | 200 | 210 | 220 | | |
| WQPCMYISFL | DMALFNRDSA | LKSYSIENVT | SIANNFPDFS | YFRTFPMPSN | KSYVVTFIY | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1513 | 1 | 513.1408 | -136.07 | 2 | 47.3 | 12.8 | 0 | 42-50 | R.NCSCSADIR.D | Carbamidomethyl: 4 |

# Detailed Protein Report

## Protein 1303: hypoxia-inducible factor 1-alpha isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|31077211 | **Score:** | 12.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 82.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEGAGGANDK | KKISSERRKE | KSRDAARSRR | SKESEVFYEL | AHQLPLPHNV | SSHLDKASVM | RLTISYLRVR | KLLDAGDLDI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EDDMKAQMNC | FYLKALDGFV | MVLTDDGDMI | YISDNVNKYM | GLTQFELTGH | SVFDFTHPCD | HEEMREMLTH | RNGLVKKGKE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QNTQRSFFLR | MKCTLTSRGR | TMNIKSATWK | VLHCTGHIHV | YDTNSNQPQC | GYKKPPMTCL | VLICEPIPHP | SNIEIPLDSK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TFLSRHSLDM | KFSYCDERIT | ELMGYEPEEL | LGRSIYEYYH | ALDSDHLTKT | HHDMFTKGQV | TTGQYRMLAK | RGGYVWVETQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ATVIYNTKNS | QPQCIVCVNY | VVSGIIQHDL | IFSLQQTECV | LKPVESSDMK | MTQLFTKVES | EDTSSLFDKL | KKEPDALTLL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| APAAGDTIIS | LDFGSNDTET | DDQQLEEVPL | YNDVMLPSPN | EKLQNINLAM | SPLPTAETPK | PLRSSADPAL | NQEVALKLEP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NPESLELSFT | MPQIQDQTPS | PSDGSTRQSS | PEPNSPSEYC | FYVDSDMVNE | FKLELVEKLF | AEDTEAKNPF | STQDTDLDLE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MLAPYIPMDD | DFQLRSFDQL | SPLESSSASP | ESASPQSTVT | VFQQTQIQEP | TANATTTTAT | TDELKTVTKD | RMEDIKILIA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SPSPTHIHKE | TTSATSSPYR | DTQSRTASPN | RAGKGVIEQT | EKSHPRSPNV | LSVALSQRTT | VPEEELNPKI | LALQNAQRKR |
| 730 | 740 | | | | | | |
| KMEHDGSLFQ | AVGII | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2689 | 2 | 616.8502 | 77.22 | 2 | 62.0 | 12.8 | 1 | 661-671 | R.DTQSRTASPNR.A | |

# Detailed Protein Report

## Protein 1304: PREDICTED: protein crumbs homolog 2 isoform X1 [Homo sapiens]

**Accession:** gi|530391003
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 12.8
**MW [kDa]:** 99.8
**pI:** 5.8
**Sequence Coverage [%]:** 1.5
**No. of unique Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAMEPGALWT | FLGHLWLLAG | PTCEEDVDEC | LSDPCLHGGT | CSDTVAGYIC | RCPETWGGRD | CSVQLTGCQG | HTCPLAATCI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PIFESGVHSY | VCHCPPGTHG | PFCGQNTTFS | VMAGSPIQAS | VPAGGPLGLA | LRFRTTLPAG | TLATRNDTKE | SLELALVAAT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LQATLWSYST | TVLVLRLPDL | ALNDGHWHQV | EVVLHLATLE | LRLWHEGCPA | RLCVASGPVA | LASTASATPL | PAGISSAQLG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DATFAGCLQD | VRVDGHLLLP | EDLGENVLLG | CERREQCRPL | PCVHGGSCVD | LWTHFRCDCA | RPHRGPTCAD | EIPAATFGLG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GAPSSASFLL | QELPGPNLTV | SFLLRTRESA | GLLLQFANDS | AAGLTVFLSE | GRIRAEVPGS | PAVVLPGRWD | DGLRHLVMLS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FGPDQLQDLG | QHVHVGGRLL | AADSQPWGGP | FRGCLQDLRL | DGCHLPFFPL | PLDNSSQPSE | LGGRQSWNLT | AGCVSEDMCS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PDPCFNGGTC | LVTWNDFHCT | CPANFTGPTC | AQQLWCPGQP | CLPPATCEEV | PDGFVCVAEA | TFREGPPAAF | SGHNASSGRL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LGGLSLAFRT | RDSEAWLLRA | AAGALEGVWL | AVRNGSLAGG | VRGGHGLPGA | VLPIPGPRVA | DGAWHRVRLA | MERPAATTSR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| WLLWLDGAAT | PVALRGLASD | LGFLQGPGAV | RILLAENFTG | CLGRVALGGL | PLPLARPRPG | AAPGAREHFA | SWPGTPAPIL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GCRGAPVCAP | SPCLHDGACR | DLFDAFACAC | GPGWEGPRCE | AHVDPCHSAP | CARGRCHTHP | DGRFECRCPP | GFGGPRCRLP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VPSKECSLNV | TCLDGSPCEG | GSPAANCSCL | EGLAGQRCQV | PTLPCEANPC | LNGGTCRAAG | GVSECICNAR | FSGQFCEVAK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GLPLPLPFPL | LEVAVPAACA | CLLLLLLGLL | SGILAARKRR | QSEGTYSPSQ | QEVAGARLEM | DSVLKVPPEE | RLI |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 47 | 1 | 829.3877 | -47.23 | 2 | 29.5 | 12.8 | 1 | 938-951 | R.LEMDSVLKVPPEER.L | Oxidation: 3 |

# Detailed Protein Report

## Protein 1305: rho-associated protein kinase 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4885583 | **Score:** | 12.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 158.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSTGDSFETR | FEKMDNLLRD | PKSEVNSDCL | LDGLDALVYD | LDFPALRKNK | NIDNFLSRYK | DTINKIRDLR | MKAEDYEVVK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VIGRGAFGEV | QLVRHKSTRK | VYAMKLLSKF | EMIKRSDSAF | FWEERDIMAF | ANSPWVVQLF | YAFQDDRYLY | MVMEYMPGGD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LVNLMSNYDV | PEKWARFYTA | EVVLALDAIH | SMGFIHRDVK | PDNMLLDKSG | HLKLADFGTC | MKMNKEGMVR | CDTAVGTPDY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ISPEVLKSQG | GDGYYGRECD | WWSVGVFLYE | MLVGDTPFYA | DSLVGTYSKI | MNHKNSLTFP | DDNDISKEAK | NLICAFLTDR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EVRLGRNGVE | EIKRHLFFKN | DQWAWETLRD | TVAPVVPDLS | SDIDTSNFDD | LEEDKGEEET | FPIPKAFVGN | QLPFVGFTYY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SNRRYLSSAN | PNDNRTSSNA | DKSLQESLQK | TIYKLEEQLH | NEMQLKDEME | QKCRTSNIKL | DKIMKELDEE | GNQRRNLEST |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VSQIEKEKML | LQHRINEYQR | KAEQENEKRR | NVENEVSTLK | DQLEDLKKVS | QNSQLANEKL | SQLQKQLEEA | NDLLRTESDT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AVRLRKSHTE | MSKSISQLES | LNRELQERNR | ILENSKSQTD | KDYYQLQAIL | EAERRDRGHD | SEMIGDLQAR | ITSLQEEVKH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LKHNLEKVEG | ERKEAQDMLN | HSEKEKNNLE | IDLNYKLKSL | QQRLEQEVNE | HKVTKARLTD | KHQSIEEAKS | VAMCEMEKKL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KEEREAREKA | ENRVVQIEKQ | CSMLDVDLKQ | SQQKLEHLTG | NKERMEDEVK | NLTLQLEQES | NKRLLLQNEL | KTQAFEADNL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KGLEKQMKQE | INTLLEAKRL | LEFELAQLTK | QYRGNEGQMR | ELQDQLEAEQ | YFSTLYKTQV | KELKEEIEEK | NRENLKKIQE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LQNEKETLAT | QLDLAETKAE | SEQLARGLLE | EQYFELTQES | KKAASRNRQE | ITDKDHTVSR | LEEANSMLTK | DIEILRRENE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ELTEKMKKAE | EEYKLEKEEE | ISNLKAAFEK | NINTERTLKT | QAVNKLAEIM | NRKDFKIDRK | KANTQDLRKK | EKENRKLQLE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LNQEREKFNQ | MVVKHQKELN | DMQAQLVEEC | AHRNELQMQL | ASKESDIEQL | RAKLLDLSDS | TSVASFPSAD | ETDGNLPESR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| IEGWLSVPNR | GNIKRYGWKK | QYVVVSSKKI | LFYNDEQDKE | QSNPSMVLDI | DKLFHVRPVT | QGDVYRAETE | EIPKIFQILY |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ANEGECRKDV | EMEPVQQAEK | TNFQNHKGHE | FIPTLYHFPA | NCDACAKPLW | HVFKPPPALE | CRRCHVKCHR | DHLDKKEDLI |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| CPCKVSYDVT | SARDMLLLAC | SQDEQKKWVT | HLVKKIPKNP | PSGFVRASPR | TLSTRSTANQ | SFRKVVKNTS | GKTS |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1917 | 1 | 696.9347 | -101.57 | 3 | 52.3 | 12.8 | 1 | 290-307 | K.IMNHKNSLTFPDDNDISK.E | |

# Detailed Protein Report

## Protein 1306: glutamate receptor ionotropic, kainate 4 isoform 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|541862236 | **Score:** | 12.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 85.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.72 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.63 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPRVSAPLVL | LPAWLVMVAC | SPHSLRIAAI | LDDPMECSRG | ERLSITLAKN | RINRAPERLG | KAKVEVDIFE | LLRDSEYETA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ETMCQILPKG | VVAVLGPSSS | PASSSIISNI | CGEKEVPHFK | VAPEEFVKFQ | FQRFTTLNLH | PSNTDISVAV | AGILNFFNCT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TACLICAKAE | CLLNLEKLLR | QFLISKDTLS | VRMLDDTRDP | TPLLKEIRDD | KTATIIIHAN | ASMSHTILLK | AAELGMVSAY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YTYIFTNLEF | SLQRMDSLVD | DRVNILGFSI | FNQSHAFFQE | FAQSLNQSWQ | ENCDHVPFTG | PALSSALLFD | AVYAVVTAVQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ELNRSQEIGV | KPLSCGSAQI | WQHGTSLMNY | LRMVELEGLT | GHIEFNSKGQ | RSNYALKILQ | FTRNGFRQIG | QWHVAEGLSM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DSHLYASNIS | DTLFNTTLVV | TTILENPYLM | LKGNHQEMEG | NDRYEGFCVD | MLKELAEILR | FNYKIRLVGD | GVYGVPEANG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TWTGMVGELI | ARKADLAVAG | LTITAEREKV | IDFSKPFMTL | GISILYRVHM | GRKPGYFSFL | DPFSPGVWLF | MLLAYLAVSC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VLFLVARLTP | YEWYSPHPCA | QGRCNLLVNQ | YSLGNSLWFP | VGGFMQQGST | IAPRALSTRC | VSGVWWAFTL | IIISSYTANL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AAFLTVQRMD | VPIESVDDLA | DQTAIEYGTI | HGGSSMTFFQ | NSRYQTYQRM | WNYMYSKQPS | VFVKSTEEGI | ARVLNSNYAF |
| 730 | 740 | 750 | 760 | 770 | | | |
| LLESTMNEYY | RQRNCNLTQI | GGLLDTKGYG | IGMPVGMRER | NSLFG | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2176 | 1 | 937.3251 | -94.18 | 2 | 57.6 | 12.8 | 0 | 74-89 | R.DSEYETAETMCQILPK.G | Oxidation: 10 | WUP:QUP 1.63<br>QU:MU 0.72 |

# Detailed Protein Report

## Protein 1307: 39S ribosomal protein L52, mitochondrial isoform e [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|31083085 | **Score:** | 12.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 9.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 17.2 |
| | | **No. of unique Peptides:** | 1 |

```
         10         20         30         40         50         60         70         80
MAALGTVLFT GVRRLHCSVA AWAGGQWRLQ QGLAANPSGY GPLTELPDWS YAETSCTAVT GNGRWITSMA AQAAEVAGRT
         90
KEAGKCS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2712 | 1 | 878.0523 | 131.96 | 2 | 62.4 | 12.8 | 1 | 14-28 | R.RLHCSVAAWAGGQWR.L | Carbamidomethyl: 4 |

# Detailed Protein Report

## Protein 1308: PREDICTED: protein FAM189A2 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530391776 | **Score:** | 12.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 32.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.0 |
| | | **Sequence Coverage [%]:** | 4.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MERMVGPDVI | PLPHIYGARI | KGVEVFCPLD | PPPPYEAVVS | QMDQEQGSSF | QMSEGSEAAV | IPLDLGCTQV | TQDGDIPNIP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AEENASTSTP | SSTLVRPIRS | RRALPPLRTR | SKSDPVLHPS | EERAAPVLSC | EAATQTERRL | DLAAVTLRRG | LRSRASRCRP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RSLIDYKSYM | DTKLLVARFL | EQSSCTMTPD | IHELVENIKS | VLKSDEEHME | EAITSASFLE | QIMAPLQPST | SRAHKLPSRR |
| 250 | 260 | 270 | 280 | 290 | | | |
| QPGLLHLQSC | GDLHTFTPAG | RPRAERRPRR | VEAERPHSLI | GVIRETVL | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2134 | 1 | 788.3187 | -168.98 | 2 | 56.6 | 12.8 | 0 | 271-284 | R.VEAERPHSLIGVIR.E | |

# Detailed Protein Report

## Protein 1309: T-cell surface glycoprotein CD3 zeta chain isoform 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4557431 | **Score:** | 12.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 18.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 7.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.99 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.43 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MKWKALFTAA ILQAQLPITE AQSFGLLDPK LCYLLDGILF IYGVILTALF LRVKFSRSAD APAYQQGQNQ LYNELNLGRR
        90        100        110        120        130        140        150        160
EEYDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE RRRGKGHDGL YQGLSTATKD TYDALHMQAL
       170
PPR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 477 | 1 | 686.3590 | 14.33 | 2 | 35.9 | 12.7 | 2 | 90-101 | R.RGRDPEMGGKPR.R | Oxidation: 7 | WUP:QUP 0.43<br>QU:MU 1.99 |

BRUKER

# Detailed Protein Report

## Protein 1310: PREDICTED: neuroblastoma breakpoint family member 20 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530429910 | **Score:** | 12.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 136.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.5 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530433897 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: neuroblastoma breakpoint family member 20 isoform X5 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVVSAGHWSS | EKAEMNILEI | NETLRPQLPE | NKQQLRNLKE | KCFLTQLAGF | LANRQKKYKY | EECKDLIKFM | LRNERQFKEE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KLAEQLKQAE | ELRQYKVLVH | SQERELTQLK | EKLREGRDAS | RSLNEHLQAL | LTPDEPDKSQ | GQDLQEQLAE | GCRLAQHLVQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KLSPENDEDE | DEDVQVEEDE | KVLESSAPRE | VQKTEESKVP | EDSLEECAIT | CSNSHGPCDS | NQPHKNIKIT | FEEDEVNSTL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VVDRESSHDE | CQDALNILPV | PGPTSSATNV | SMVVSAGPLS | GEKAAINILE | INEKLRPQLA | EKKQQFRNLK | EKCFLTQLAG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FLANQQNKYK | YEECKDLIKS | MLRNERQFKE | EKLAEQLKQA | EELRQYKVLV | HAQERELTQL | REKLREGRDA | SRSLNEHLQA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LLTPDEPDKS | QGQDLQEQLA | EGCRLAQHLV | QKLSPENDND | DDEDVQVEVA | EKVQKSSAPR | EMQKAEEKEV | PEDSLEECAI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TCSNSHGPYD | CNQPHRKTKI | TFEEDKVDST | LIGSSSHVEW | EDAVHIIPEN | ESDDEEEEEK | GPVSPRNLQE | SEEEEVPQES |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| WDEGYSTLSI | PPEMLASYKS | YSSTFHSLEE | QQVCMAVDIG | RHRWDQVKKE | DHEATGPRLS | RELLDEKGPE | VLQDSLDRCY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| STPSGCLELT | DSCQPYRSAF | YVLEQQRVGL | AVDMDEIEKY | QEVEEDQDPS | CPRLSRELLD | EKEPEVLQDS | LGRCYSTPSG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YLELPDLGQP | YSSAVYSLEE | QYLGLALDVD | RIKKDQEEEE | DQGPPCPRLS | RELLEVVEPE | VLQDSLDRCY | STPSSCLEQP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DSCQPYGSSF | YALEEKHVGF | SLDVGEIEKK | GKGKKRRGRR | SKKERRRGRK | EGEEDQNPPC | PRLSRELLDE | KGPEVLQDSL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DRCYSTPSGC | LELTDSCQPY | RSAFYILEQQ | RVGLAVDMDE | IEKYQEVEED | QDPSCPRLSR | ELLDEKEPEV | LQDSLGRCYS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TPSGYLELPD | LGQPYSSAVY | SLEEQYLGLA | LDVDRIKKDQ | EEEEDQGPPC | PRLSRELLEV | VEPEVLQDSL | DRCYSTPSSC |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LEQPDSCQPY | GSSFYALEEK | HVGFSLDVGE | IEKKGKGKKR | RGRRSKKERR | RGRKEGEEDQ | NPPCPRLNSM | LMEVEEPEVL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | |
| QDSLDICYST | PSMYFELPDS | FQHYRSVFYS | FEEEHISFAL | YVDNRFFTLT | VTSLHLVFQM | GVIFPQ | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2087 | 1 | 958.8549 | -151.09 | 2 | 56.0 | 12.7 | 2 | 182-198 | K.VLESSAPREVQKTEESK.V | |

# Detailed Protein Report

## Protein 1311: protein KRI1 homolog [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|145580615 | **Score:** | 12.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 83.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGHRTAMPEP | RGSSQLRVNA | AFAARYNRYR | EREELQRLKD | RYGDRDSSSD | SSSESDSSDE | RVEFDPQQER | DFYKTLSLLK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KKDPRIYQKD | ATFYNRTASS | SDSEEDPEAL | EKQKKVRPMY | LKDYERKVIL | EKAGKYVDEE | NSDGETSNHR | LQETSSQSYV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EEQKQLKESF | RAFVEDSEDE | DGAGEGGSSL | LQKRAKTRQE | KAQEEADYIE | WLKGQKEIRN | PDSLKELTHL | KEYWNDPELD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EGERFLRDYI | LNKRYEEEEE | EEEDEEEMEE | EEGVHGPPVQ | LAVDDSSDEG | ELFLKKQEDF | EQKYNFRFEE | PDSASVKTYP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RSIASSVRRK | DERRKEKREE | TRERKKREKA | KKQEELKQLK | NLKRKEILAK | LEKLRKVTGN | EMLGLEEGDL | EDDFDPAQHD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QLMQKCFGDE | YYGAVEEEKP | QFEEEEGLED | DWNWDTWDGP | EQEGDWSQQE | LHCEDPNFNM | DADYDPSQPR | KKKREAPLTG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KKKRKSPFAA | AVGQEKPVFE | PGDKTFEEYL | DEYYRLDYED | IIDDLPCRFK | YRTVVPCDFG | LSTEEILAAD | DKELNRWCSL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KKTCMYRSEQ | EELRDKRAYS | QKAQNSWKKR | QVFKSLCREE | AETPAEATGK | PQRDEAGPQR | QLPALDGSLM | GPESPPAQEE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | |
| EAPVSPHKKP | APQKRRRAKK | ARLLGPTVML | GGCEFSRQRL | QAFGLNPKRL | HFRQLGRQRR | KQQGPKNSS | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1620 | 1 | 932.4928 | 11.55 | 2 | 50.5 | 12.7 | 1 | 661-677 | K.ARLLGPTVMLGGCEFSR.Q | Carbamidomethyl: 13 |

# Detailed Protein Report

## Protein 1312: TRAF-type zinc finger domain-containing protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5729828 | **Score:** | 12.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 64.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|219879806 | refseq_human (refseq_human_20140103.fasta) | TRAF-type zinc finger domain-containing protein 1 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MAEFLDDQET RLCDNCKKEI PVFNFTIHEI HCQRNIGMCP TCKEPFPKSD METHMAAEHC QVTCKCNKKL EKRLLKKHEE
        90        100        110        120        130        140        150        160
TECPLRLAVC QHCDLELSIL KLKEHEDYCG ARTELCGNCG RNVLVKDLKT HPEVCGREGE EKRNEVAIPP NAYDESWGQD
       170        180        190        200        210        220        230        240
GIWIASQLLR QIEALDPPMR LPRRPLRAFE SDVFHNRTTN QRNITAQVSI QNNLFEEQER QERNRGQQPP KEGGEESANL
       250        260        270        280        290        300        310        320
DFMLALSLQN EGQASSVAEQ DFWRAVCEAD QSHGGPRSLS DIKGAADEIM LPCEFCEELY PEELLIDHQT SCNPSRALPS
       330        340        350        360        370        380        390        400
LNTGSSSPRG VEEPDVIFQN FLQQAASNQL DSLMGLSNSH PVEESIIIPC EFCGVQLEEE VLFHHQDQCD QRPATATNHV
       410        420        430        440        450        460        470        480
TEGIPRLDSQ PQETSPELPR RRVRHQGDLS SGYLDDTKQE TANGPTSCLP PSRPINNMTA TYNQLSRSTS GPRPGCQPSS
       490        500        510        520        530        540        550        560
PCVPKLSNSD SQDIQGRNRD SQNGAIAPGH VSVIRPPQNL YPENIVPSFS PGPSGRYGAS GRSEGGRNSR VTPAAANYRS
       570        580        590
RTAKAKPSKQ QGAGDAEEEE EE
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2095 | 1 | 1052.4843 | 39.57 | 2 | 56.6 | 12.7 | 1 | 1-17 | -.MAEFLDDQETRLCDNCK.K | Carbamidomethyl: 13;<br>Oxidation: 1 |

# Detailed Protein Report

## Protein 1313: patatin-like phospholipase domain-containing protein 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|17196626 | **Score:** | 12.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 52.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MYDAERGWSL | SFAGCGFLGF | YHVGATRCLS | EHAPHLLRDA | RMLFGASAGA | LHCVGVLSGI | PLEQTLQVLS | DLVRKARSRN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IGIFHPSFNL | SKFLRQGLCK | CLPANVHQLI | SGKIGISLTR | VSDGENVLVS | DFRSKDEVVD | ALVCSCFIPF | YSGLIPPSFR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GVRYVDGGVS | DNVPFIDAKT | TITVSPFYGE | YDICPKVKST | NFLHVDITKL | SLRLCTGNLY | LLSRAFVPPD | LKVLGEICLR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GYLDAFRFLE | EKGICNRPQP | GLKSSSEGMD | PEVAMPSWAN | MSLDSSPESA | ALAVRLEGDE | LLDHLRLSIL | PWDESILDTL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SPRLATALSE | EMKDKGGYMS | KICNLLPIRI | MSYVMLPCTL | PVESAIAIVQ | RLVTWLPDMP | DDVLWLQWVT | SQVFTRVLMC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LLPASRSQMP | VSSQQASPCT | PEQDWPCWTP | CSPKGCPAET | KAEATPRSIL | RSSLNFFLGN | KVPAGAEGLS | TFPSFSLEKS |
| 490 | | | | | | | |
| L | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2856 | 1 | 655.3750 | 51.86 | 2 | 66.1 | 12.7 | 0 | 296-306 | R.LEGDELLDHLR.L | |

# Detailed Protein Report

## Protein 1314: PREDICTED: apoptosis-enhancing nuclease isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578827297 | **Score:** | 12.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGPGRDDRRS | VSLPFSLKFP | ASMAGSQHEL | RPLQESLPFC | SRPPPRCQAG | STNQKRSWAG | AAVQRANRRA | VGAGLARACG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SCRLSGRHVQ | TGRDTRGFRL | LPHWKITPQA | SLAPSSELTG | MVPREAPESA | QCLCPSLTIP | NAKDVLRKRH | KRRSRQHQRF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MARKALLQEQ | GLLSMPPEPG | SSPLPTPFGA | ATATEAASSG | KQCLRAGSGS | APCSRRPAPG | KASGPLPSKC | VAIDCEMVGT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GPRGRVSELA | RCSIVSYHGN | VLYDKYIRPE | MPIADYRTRW | SGITRQHMRK | AVPFQVAQKE | ILKLLKGKVV | VGHALHNDFQ |
| 330 | 340 | 350 | 360 | 370 | | | |
| ALKYVHPRSQ | TRDTTYVPNF | LSEPGLHTRA | RVSLKDLALQ | LLHKKIQ | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 677 | 1 | 752.8492 | -44.65 | 2 | 38.0 | 12.7 | 2 | 69-83 | R.RAVGAGLARACGSCR.L | Carbamidomethyl: 11 |

# Detailed Protein Report

## Protein 1315: PREDICTED: NACHT, LRR and PYD domains-containing protein 11 isoform X1 [Homo sapiens]

**Accession:** gi|530415954
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 12.7
**MW [kDa]:** 105.8
**pI:** 9.0
**Sequence Coverage [%]:** 1.6
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRRKFMLQWE | SHTFGKFHYK | FFRDVSSDVF | YILQLAYDST | SYYSANNLNV | FLMGERASGK | TIVINLAVLR | WIKGEMWQNM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ISYVVHLTAH | EINQMTNSSL | AELIAKDWPD | GQAPIADILS | DPKKLLFILE | DLDNIRFELN | VNESALCSNS | TQKVPIPVLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VSLLKRKMAP | GCWFLISSRP | TRGNNVKTFL | KEVDCCTTLQ | LSNGKREIYF | NSFFKDRQRA | SAALQLVHED | EILVGLCRVA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ILCWITCTVL | KRQMDKGRDF | QLCCQTPTDL | HAHFLADALT | SEAGLTANQY | HLGLLKRLCL | LAAGGLFLST | LNFSGEDLRC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VGFTEADVSV | LQAANILLPS | NTHKDRYKFI | HLNVQEFCTA | IAFLMAVPNY | LIPSGSREYK | EKREQYSDFN | QVFTFIFGLL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NANRRKILET | SFGYQLPMVD | SFKWYSVGYM | KHLDRDPEKL | THHMPLFYCL | YENREEEFVK | TIVDALMEVT | VYLQSDKDMM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VSLYCLDYCC | HLRTLKLSVQ | RIFQNKEPLI | RPTASQMKSL | VYWREICSLF | YTMESLRELH | IFDNDLNGIS | ERILSKALEH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SSCKLRTLKL | SYVSTASGFE | DLLKALARNR | SLTYLSINCT | SISLNMFSLL | HDILHEPTCQ | ISHLSLMKCD | LRASECEEIA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SLLISGGSLR | KLTLSSNPLR | SDGMNILCDA | LLHPNCTLIS | LVLVFCCLTE | NCCSALGRVL | LFSPTLRQLD | LCVNRLKNYG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VLHVTFPLLF | PTCQLEELHL | SGCFFSSDIC | QYIAIVIATN | EKLRSLEIGS | NKIEDAGMQL | LCGGLRHPNC | MLVNIGLEEC |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| MLTSACCRSL | ASVLTTNKTL | ERLNLLQNHL | GNDGVAKLLE | SLISPDCVLK | VVGLPLTGLN | TQTQQLLMTV | KERKPSLIFL |
| 890 | 900 | 910 | 920 | 930 | 940 | | |
| SETWSLKEGR | EIGVTPASQP | GSIIPNSNLD | YMFFKFPRMS | AAMRTSNTAS | RQPL | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2048 | 2 | 862.2843 | -144.29 | 2 | 55.5 | 12.7 | 1 | 192-206 | K.EVDCCTTLQLSNGKR.E | Carbamidomethyl: 4 |

# Detailed Protein Report

## Protein 1316: kelch-like protein 14 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|55741643 | **Score:** | 12.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 70.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSRSGDRTST | FDPSHSDNLL | HGLNLLWRKQ | LFCDVTLTAQ | GQQFHCHKAV | LASCSQYFRS | LFSSHPPLGG | GVGGQDGLGA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PKDQQQPPQQ | QPSQQQQPPP | QEEPGTPSSS | PDDKLLTSPR | AINNLVLQGC | SSIGLRLVLE | YLYTANVTLS | LDTVEEVLSV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SKILHIPQVT | KLCVQFLNDQ | ISVQNYKQVC | KIAALHGLEE | TKKLANKYLV | EDVLLLNFEE | MRALLDSLPP | PVESELALFQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MSVLWLEHDR | ETRMQYAPDL | MKRLRFALIP | APELVERVQS | VDFMRTDPVC | QKLLLDAMNY | HLMPFRQHCR | QSLASRIRSN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KKMLLLVGGL | PPGPDRLPSN | LVQYYDDEKK | TWKILTIMPY | NSAHHCVVEV | ENFLFVLGGE | DQWNPNGKHS | TNFVSRYDPR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FNSWIQLPPM | QERRASFYAC | RLDKHLYVIG | GRNETGYLSS | VECYNLETNE | WRYVSSLPQP | LAAHAGAVHN | GKIYISGGVH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NGEYVPWLYC | YDPVMDVWAR | KQDMNTKRAI | HTLAVMNDRL | YAIGGNHLKG | FSHLDVMLVE | CYDPKGDQWN | ILQTPILEGR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| SGPGCAVLDD | SIYLVGGYSW | SMGAYKSSTI | CYCPEKGTWT | ELEGDVAEPL | AGPACVTVIL | PSCVPYNK | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2525 | 1 | 1155.0426 | -61.91 | 2 | 61.5 | 12.7 | 1 | 204-222 | K.LANKYLVEDVLLLNFEEMR.A | |

# Detailed Protein Report

## Protein 1317: protein RRNAD1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|216548564 | **Score:** | 12.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 29.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 5.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPGISARGLS | HEGRKQLAVN | LTRVLALYRS | ILDAYIIEFF | TDNLWDTLPC | SWQEALDGLK | PPQLATMLLG | MPGEGEVVRY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RSVWPLTLLA | LKSTACALAF | TRMPGFQTPS | EFLENPSQSS | RLTAPFRKHV | RPKKQHEIRR | LGELVKKLSD | FTGCTQVVDV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GSGQGHLSRF | MALGLGLMVK | SIEGDQRLVE | RAQRLDQELL | QALEKEEKRN | PQICAAGATA | SGARSPAATE | SGCPSGPRGP |
| 250 | 260 | 270 | 280 | | | | |
| GEPCGGLLQP | GSTACPTGGD | AYSTGPAAVP | SGTGFPC | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2066 | 1 | 734.3148 | -85.92 | 2 | 54.2 | 12.7 | 1 | 1-14 | -.MPGISARGLSHEGR.K | |

# Detailed Protein Report

## Protein 1318: PREDICTED: unconventional myosin-XVIIIb isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578837445 | **Score:** | 12.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 272.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| | | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTSINGEKAQ | ELGSSATPTK | KTVPFKRGVR | RGDVLLMVAK | LDPDSAKPEK | THPHDAPPCK | TSPPATDTGK | EKKGETSRTP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CGSQASTEIL | APKAEKTRTG | GLGDPGQGTV | ALKKGEEGQS | IVGKGLGTPK | TTELKEAEPQ | GKDRQGTRPQ | AQGPGEGVRP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GKAEKEGAEP | TNTVEKGNVS | KDVGSEGKHV | RPQIPGRKWG | GFLGRRSKWD | GPQNKKDKEG | VLLSKAEKTG | EPQTQMEKTS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QVQGELGDDL | RMGEKAGELR | STTGKAGESW | DKKEKMGQPQ | GKSGNAGEAR | SQTEKGCEAP | KEVSTMVESP | AAPGKGGWPG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SRGQEAEEPC | SRAGDGAGAL | ETELEGPSQP | ALEKDAERPR | IRKENQDGPA | PQEEGKGGQS | RDSDQAPEDR | WYEAEKVWLA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QKDGFTLATV | LKPDEGTADL | PAGRVRLWID | ADKTITEVDE | EHVHRANPPE | LDQVEDLASL | ISVNESSVLN | TLLQRYKAQL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LHTCTGPDLI | VLQPRGPSVP | SAGKVPKGRR | DGLPAHIGSM | AQRAYWALLN | QRRDQSIVAL | GWSGAGKTTC | CEQVLEHLVG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MAGSVDGRVS | VEKIRATFTV | LRAFGSVSMA | HSRSATRFSM | VMSLDFNATG | RITAAQLQTM | LLEKSRVARQ | PEGESNFLVF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SQMLAGLDLD | LRTELNLHQM | ADSSSFGMGV | WSKPEDKQKA | AAAFAQLQGA | MEMLGISESE | QRAVWRVLAA | IYHLGAAGAC |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KVGRKQFMRF | EWANYAAEAL | GCEYEELNTA | TFKHHLRQII | QQMTFGPSRW | GLEDEETSSG | LKMTGVDCVE | GMASGLYQEL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FAAVVSLINR | SFSSHHLSMA | SIMVVDSPGF | QNPRHQGKDR | AATFEELCHN | YAHERLQLLF | YQRTFVSTLQ | RYQEEGVPVQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| FDLPDPSPGT | TVAVVDQNPS | QQVRLPAGGG | AQDARGLFWV | LDEEVHVEGS | SDSVVLERLC | AAFEKKGAGT | EGSSALRTCE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QPLQCEIFHQ | LGWDPVRYDL | TGWLHRAKPN | LSALDAPQVL | HQSKREELRS | LFQARAKLPP | VCRAVAGLEG | TSQQALQRSR |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| MVRRTFASSL | AAVRRKAPCS | QIKLQMDALT | SMIKRSRLHF | IHCLVPNPVV | ESRSGQESPP | PPQPGRDKPG | AGGPLALDIP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ALRVQLAGFH | ILEALRLHRT | GYADHMGLTR | FRRQFQVLDA | PLLKKLMSTS | EGIDERKAVE | ELLETLDLEK | KAVAVGHSQV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| FLKAGVISRL | EKQREKLVSQ | SIVLFQAACK | GFLSRQEFKK | LKIRRLAAQC | IQKNVAVFLA | VKDWPWWQLL | GSLQPLLSAT |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| IGTEQLRAKE | EELTTLRRKL | EKSEKLRNEL | RQNTDLLESK | IADLTSDLAD | ERFKGDVACQ | VLESERAERL | QAFREVQELK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| SKHEQVQKKL | GDVNKQLEEA | QQKIQLNDLE | RNPTGGADEW | QMRFDCAQME | NEFLRKRLQQ | CEERLDSELT | ARKELEQKLG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ELQSAYDGAK | KMAHQLKRKC | HHLTCDLEDT | CVLLENQQSR | NHELEKKQKK | FDLQLAQALG | ESVFEKGLRE | KVTQENTSVR |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| WELGQLQQQL | KQKEQEASQL | KQQVEMLQDH | KRELLGSPSL | GENCVAGLKE | RLWKLESSAL | EQQKIQSQQE | NTIKQLEQLR |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QRFELEIERM | KQMHQKDRED | QEEELEDVRQ | SCQKRLHQLE | MQLEQEYEEK | QMVLHEKQDL | EGLIGTLCDQ | IGHRDFDVEK |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| RLRRDLRRTH | ALLSDVQLLL | GTMEDGKTSV | SKEELEKVHS | QLEQSEAKCE | EALKTQKVLT | ADLESMHSEL | ENMTRNKSLV |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| DEQLYRLQFE | KADLLKRIDE | DQDDLNELMQ | KHKDLIAQSA | ADIGQIQELQ | LQLEEAKKEK | HKLQEQLQVA | QMRIEYLEQS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| TVDRAIVSRQ | EAVICDLENK | TEFQKVQIKR | FEVLVIRLRD | SLIKMGEELS | QAATSESQQR | ESSQYYQRRL | EELKADMEEL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| VQREAEASRR | CMELEKYVEE | LAAVRQTLQT | DLETSIRRIA | DLQAALEEVA | SSDSDTESVQ | TAVDCGSSGR | KEMDNVSILS |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| SQPEGSLQSW | LSCTLSLATD | TMRTPSRQSA | TSSRILSPRI | NEEAGDTERT | QSALALSRAR | STNVHSKTSG | DKPVSPHFVR |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| RQKYCHFGDG | EVLAVQRKST | ERLEPASSPL | ASRSTNTSPL | SREKLPSPSA | ALSEFVEGLR | RKRAQRGQGS | TLGLEDWPTL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 731 | 1 | 698.3535 | -16.01 | 3 | 39.1 | 12.7 | 1 | 2205-2225 | R.STSLKCISSDGVGGTTLLPEK.S | |

# Detailed Protein Report

**Protein 1319:** **PREDICTED: U3 small nucleolar RNA-associated protein 6 homolog isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530411102 | **Score:** | 12.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 55.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| | | **Sequence Coverage [%]:** | 3.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MRLRILLYTG | YKVFSSVPQQ | NGKTMFNFGS | PMWLFVRSGL | LKLDLARYSL | PCWRFIPTNQ | YFRMELMHAE | KLRKEKEEFE |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| KASMDVENPD | YSEEILKGEL | AWIIYKNSVS | IIKGAEFHVS | LLSIAQLFDF | AKDLQKEIYD | DLQALHTDDP | LTWDYVARRE |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| LEIESQTEEQ | PTTKQAKAVE | VGRKEERCCA | VYEEAVKTLP | TEAMWKCYIT | FCLERFTKKS | NSGFLRGKRL | ERTMTVFRKA |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| HELKLLSECQ | YKQLSVSLLC | YNFLREALEV | AVAGTELFRD | SGTMWQLKLQ | VLIESKSPDI | AMLFEEAFVH | LKPQVCLPLW |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| ISWAEWSEGA | KSQEDTEAVF | KKALLAVIGA | DSVTLKNKYL | DWAYRSGGYK | KARAVFKSLQ | ESRPFSVDFF | RKMIQFEKEQ |
| **410** | **420** | **430** | **440** | **450** | **460** | **470** | **480** |
| ESCNMANIRE | YYERALREFG | SADSDLWMDY | MKEELNHPLG | RPENCGQIYW | RAMKMLQGES | AEAFVAKHAM | HQTGHL |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2485 | 1 | 1045.1567 | 132.37 | 2 | 61.0 | 12.6 | 1 | 160-177 | R.ELEIESQTEEQPTTKQAK.A | |

## Protein 1320: protein fem-1 homolog C [Homo sapiens]

**Accession:** gi|17864094
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 12.6
**MW [kDa]:** 68.6
**pI:** 8.5
**Sequence Coverage [%]:** 1.9
**No. of unique Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530380049 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein fem-1 homolog C isoform X1 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MDLKTAVFNA ARDGKLRLLT KLLASKSKEE VSSLISEKTN GATPLLMAAR YGHLDMVEFL LEQCSASIEV GGSVNFDGET
        90        100        110        120        130        140        150        160
IEGAPPLWAA SAAGHLKVVQ SLLNHGASVN NTTLTNSTPL RAACFDGHLE IVKYLVEHKA DLEVSNRHGH TCLMISCYKG
       170        180        190        200        210        220        230        240
HKEIAQYLLE KGADVNRKSV KGNTALHDCA ESGSLDIMKM LLMYCAKMEK DGYGMTPLLS ASVTGHTNIV DFLTHHAQTS
       250        260        270        280        290        300        310        320
KTERINALEL LGATFVDKKR DLLGALKYWK KAMNMRYSDR TNIISKPVPQ TLIMAYDYAK EVNSAEELEG LIADPDEMRM
       330        340        350        360        370        380        390        400
QALLIRERIL GPSHPDTSYY IRYRGAVYAD SGNFKRCINL WKYALDMQQS NLDPLSPMTA SSLLSFAELF SFMLQDRAKG
       410        420        430        440        450        460        470        480
LLGTTVTFDD LMGILCKSVL EIERAIKQTQ CPADPLQLNK ALSIILHLIC LLEKVPCTLE QDHFKKQTIY RFLKLHPRGK
       490        500        510        520        530        540        550        560
NNFSPLHLAV DKNTTCVGRY PVCKFPSLQV TAILIECGAD VNVRDSDDNS PLHIAALNNH PDIMNLLIKS GAHFDATNLH
       570        580        590        600        610        620
KQTASDLLDE KEIAKNLIQP INHTTLQCLA ARVIVNHRIY YKGHIPEKLE TFVSLHR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2809 | 1 | 676.8768 | 34.84 | 2 | 63.7 | 12.6 | 1 | 1-12 | -.MDLKTAVFNAAR.D | Oxidation: 1 |

# Detailed Protein Report

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## Protein 1321: uncharacterized protein LOC388780 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|567315929 | **Score:** | 12.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 14.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.7 |
| | | **Sequence Coverage [%]:** | 7.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 1.60 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MATAGSQHRR | RENEDRSRVT | ALAFEQPRES | LCVLQPPLPF | MSEVLSPQRS | PQRAFPDAYE | TGSAWAQVEE | GPAWPPPRSP |
| **90** | **100** | **110** | **120** | **130** | | | |
| WGPCPFRRFS | RVLHHGNSGV | GSVGCEPSGW | GSRRALSASP | REVTQEHH | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2121 | 1 | 557.8753 | 170.20 | 2 | 54.9 | 12.6 | 1 | 1-10 | -.MATAGSQHRR.R | | WUP:QUP 1.60 |

# Detailed Protein Report

## Protein 1322: transcription factor AP-2-delta [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|151301211 | **Score:** | 12.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 2.63 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSTTFPGLVH | DAEIRHDGSN | SYRLMQLGCL | ESVANSTVAY | SSSSPLTYST | TGTEFASPYF | STNHQYTPLH | HQSFHYEFQH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SHPAVTPDAY | SLNSLHHSQQ | YYQQIHHGEP | TDFINLHNAR | ALKSSCLDEQ | RRELGCLDAY | RRHDLSLMSH | GSQYGMHPDQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RLLPGPSLGL | AAAGADDLQG | SVEAQCGLVL | NGQGGVIRRG | GTCVVNPTDL | FCSVPGRLSL | LSSTSKYKVT | IAEVKRRLSP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PECLNASLLG | GILRRAKSKN | GGRCLREKLD | RLGLNLPAGR | RKAANVTLLT | SLVEGEALHL | ARDFGYTCET | EFPAKAVGEH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LARQHMEQKE | QTARKKMILA | TKQICKEFQD | LLSQDRSPLG | SSRPTPILDL | DIQRHLTHFS | LITHGFGTPA | ICAALSTFQT |
| 410 | 420 | 430 | 440 | 450 | 460 | | |
| VLSEMLNYLE | KHTTHKNGGA | ADSGQGHANS | EKAPLRKTSE | AAVKEGKTEK | TD | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 607 | 1 | 689.3448 | -28.75 | 2 | 37.6 | 12.6 | 2 | 438-450 | K.TSEAAVKEGKTEK.T | | WUP:QUP 2.63 |

# Detailed Protein Report

## Protein 1323: anion exchange protein 4 isoform 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|385862233 | **Score:** | 12.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 98.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 1.51 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEMKLPGQEG | FEASSAPRNI | PSGELDSNPD | PGTGPSPDGP | SDTESKELGV | PKDPLLFIQL | NELLGWPQAL | EWRETGRWVL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FEEKLEVAAG | RWSAPHVPTL | ALPSLQKLRS | LLAEGLVLLD | CPAQSLLELV | EQVTRVESLS | PELRGQLQAL | LLQRPQHYNQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TTGTRPCWGS | THPRKASDNE | EAPLREQCQN | PLRQKLPPGA | EAGTVLAGEL | GFLAQPLGAF | VRLRNPVVLG | SLTEVSLPSR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FFCLLLGPCM | LGKGYHEMGR | AAAVLLSDPQ | FQWSVRRASN | LHDLLAALDA | FLEEVTVLPP | GRWDPTARIP | PPKCLPSQHK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RLPSQQREIR | GPAVPRLTSA | EDRHRHGPHA | HSPELQRTGR | LFGGLIQDVR | RKVPWYPSDF | LDALHLQCFS | AVLYIYLATV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TNAITFGGLL | GDATDGAQGV | LESFLGTAVA | GAAFCLMAGQ | PLTILSSTGP | VLVFERLLFS | FSRDYSLDYL | PFRLWVGIWV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ATFCLVLVAT | EASVLVRYFT | RFTEEGFCAL | ISLIFIYDAV | GKMLNLTHTY | PIQKPGSSAY | GCLCQYPGPG | GNESQWIRTR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PKDRDDIVSM | VRKGLSDFSS | VLAILLGCGL | DAFLGLATPK | LMVPREFKPT | LPGRGWLVSP | FGANPWWWSV | AAALPALLLS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ILIFMDQQIT | AVILNRMEYR | LQKGAGFHLD | LFCVAVLMLL | TSALGLPWYV | SATVISLAHM | DSLRRESRAC | APGERPNFLG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| IREQRLTGLV | VFILTGASIF | LAPVLKFIPM | PVLYGIFLYM | GVAALSSIQF | TNRVKLLLMP | AKHQPDLLLL | RHVPLTRVHL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FTAIQLACLG | LLWIIKSTPA | AIIFPLMLLG | LVGVRKALER | VFSPQELLWL | DELMPEEERS | IPEKGLEPEH | SFSGSDSEDS |
| 890 | 900 | | | | | | |
| ELMYQPKAPE | INISVN | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2782 | 1 | 729.3683 | -4.13 | 2 | 65.9 | 12.6 | 0 | 241-253 | R.FFCLLLGPCMLGK.G | Oxidation: 10 | WUP:QUP 1.51 |

# Detailed Protein Report

## Protein 1324: U3 small nucleolar RNA-associated protein 15 homolog isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|548923952 | **Score:** | 12.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAGYKPVAIQ | TYPILGEKIT | QDTLYWNNYK | PPYNYAVTAS | SRIHIYGRYS | QEPIKTFSRF | KDTAYCATFR | QDGRLLVAGS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EDGGVQLFDI | SGRAPLRQFE | GHTKAVHTVD | FTADKYHVVS | GADDYTVKLW | DIPNSKEILT | FKEHSDYVRC | GCASKLNPDL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FITGSYDHTV | KMFDARTSES | VLSVEHGQPV | ESVLLFPSGG | LLVSAGGRYV | KVWDMLKGGQ | LLVSLKNHHK | TVTCLCLSSS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GQRLLSGSLD | RKVKVYSTTS | YKVVHSFDYA | ASILSLALAH | EDETIVVGMT | NGILSVKHRK | SEAKKESLPR | RRRPAYRTFI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KGKNYMKQRD | DILINRPAKK | HLELYDRDLK | HFRISKALDR | VLDPTCTIKT | PEITVSIIKE | LNRRGVLANA | LAGRDEKEIS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HVLNFLIRNL | SQPRFAPVLI | NAAEIIIDIY | LPVIGQSPVV | DKKFLLLQGL | VEKEIDYQRE | LLETLGMMDM | LFATMRRKEG |
| 490 | 500 | | | | | | |
| TSVLEHTSDG | FPENKKIES | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 609 | 1 | 661.9075 | 142.03 | 2 | 37.2 | 12.6 | 1 | 60-70 | R.FKDTAYCATFR.Q | |

# Detailed Protein Report

## Protein 1325: melanoma-associated antigen B17 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|472235301 | **Score:** | 12.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 37.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

```
        10          20          30          40          50          60          70          80
MPRGQASKRR  AREKRRQARG  EDQCLGGAQA  TAAEKEKLPS  SSSPACQSPP  QSFPNAGIPQ  ESQRASYPSS  PASAVSLTSS
        90         100         110         120         130         140         150         160
DEGAKGQKGE  SPNSFHGPSS  SESTGRDLLN  TKTGELVQFL  LNKYIRKEPI  TREAMLKVIN  RKYKQHFPEI  LRRSTENVEV
       170         180         190         200         210         220         230         240
VFGLYLKEMD  PSRQSYVLVG  KLDFPNQGSL  SDGGGFPLSG  LLMVLLSTIF  MHGNRATEEE  MWECLNALGM  YKGRKHFIYG
       250         260         270         280         290         300         310         320
EPQELVTKDL  VREGYLEYQQ  VPSSDPPRYE  FLWGPRARAE  TSKMKVLEFV  AKLNDTVAST  YKSRYEEALR  EEEEQARARA
       330         340
VARDSARARA  SRSFQP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1134 | 1 | 510.1594 | -222.02 | 2 | 42.4 | 12.6 | 2 | 328-336 | R.ARASRSFQP.- | |

# Detailed Protein Report

## Protein 1326: fas-activated serine/threonine kinase isoform 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|39995107 | **Score:** | 12.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 1.18 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MRRPRGEPGP | RAPRPTEGAT | CAGPGESCFP | SDGPLVCALE | QERRLRLPPK | PPPPLQPLLR | GGQGLEAALS | CPRFLRYPRQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HLISSLAEAR | PEELTPHVMV | LLAQHLARHR | LREPQLLEAI | AHFLVVQETQ | LSSKVVQKLV | LPFGRLNYLP | LEQQFMPCLE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RILAREAGVA | PLATVNILMS | LCQLRCLPFR | ALHFVFSPGF | INYISGTPHA | LIVRRYLSLL | DTAVELELPG | YRGPRLPRRQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QVPIFPQPLI | TDRARCKYSH | KDIVAEGLRQ | LLGEEKYRQD | LTVPPGYCTD | FLLCASSSGA | VLPVRTQDPF | LPYPPRSCPQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GQAASSATTR | DPAQRVVLVL | RERWHFCRDG | RVLLGSRALR | ERHLGLMGYQ | LLPLPFEELE | SQRGLPQLKS | YLRQKLQALG |
| 410 | | | | | | | |
| LRWGPEGG | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 889 | 1 | 711.1759 | -210.31 | 2 | 41.2 | 12.6 | 0 | 317-330 | R.SCPQGQAASSATTR.D | Carbamidomethyl: 2 | WUP:QUP 1.18 |

# Detailed Protein Report

## Protein 1327: PREDICTED: zinc finger protein 688 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530407669 | **Score:** | 12.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 26.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 8.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAPPPAPLLA | PRPGETRPGC | RKPGTVSFAD | VAVYFSPEEW | GCLRPAQRAL | YRDVMQETYG | HLGALGDVPN | RKEEEPEEVP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RAKGPRKAPV | KESPEVLVER | NPDPAISVAP | ARAQPPKNAA | WDPTTGAQPP | APIPSMDAQA | GQRRHVCTDC | GRRFTYPSLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VSHRRMHSGE | RPFPCPECGM | RFKRKFAVEA | HQWIHRSCSG | GRRGRRPGIR | AVPRAPVRGD | RDPPVLFRHY | PDIFEECG |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2232 | 1 | 1129.1831 | 83.97 | 2 | 57.8 | 12.5 | 0 | 1-21 | -.MAPPPAPLLAPRPGETRPGCR.K | Carbamidomethyl: 20;<br>Oxidation: 1 |

# Detailed Protein Report

## Protein 1328: thyrotropin receptor isoform 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|64085121 | **Score:** | 12.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 86.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530404564 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: thyrotropin receptor isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRPADLLQLV | LLLDLPRDLG | GMGCSSPPCE | CHQEEDFRVT | CKDIQRIPSL | PPSTQTLKLI | ETHLRTIPSH | AFSNLPNISR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IYVSIDVTLQ | QLESHSFYNL | SKVTHIEIRN | TRNLTYIDPD | ALKELPLLKF | LGIFNTGLKM | FPDLTKVYST | DIFFILEITD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NPYMTSIPVN | AFQGLCNETL | TLKLYNNGFT | SVQGYAFNGT | KLDAVYLNKN | KYLTVIDKDA | FGGVYSGPSL | LDVSQTSVTA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LPSKGLEHLK | ELIARNTWTL | KKLPLSLSFL | HLTRADLSYP | SHCCAFKNQK | KIRGILESLM | CNESSMQSLR | QRKSVNALNS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PLHQEYEENL | GDSIVGYKEK | SKFQDTHNNA | HYYVFFEEQE | DEIIGFGQEL | KNPQEETLQA | FDSHYDYTIC | GDSEDMVCTP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KSDEFNPCED | IMGYKFLRIV | VWFVSLLALL | GNVFVLLILL | TSHYKLNVPR | FLMCNLAFAD | FCMGMYLLLI | ASVDLYTHSE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YYNHAIDWQT | GPGCNTAGFF | TVFASELSVY | TLTVITLERW | YAITFAMRLD | RKIRLRHACA | IMVGGWVCCF | LLALLPLVGI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SSYAKVSICL | PMDTETPLAL | AYIVFVLTLN | IVAFVIVCCC | YVKIYITVRN | PQYNPGDKDT | KIAKRMAVLI | FTDFICMAPI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SFYALSAILN | KPLITVSNSK | ILLVLFYPLN | SCANPFLYAI | FTKAFQRDVF | ILLSKFGICK | RQAQAYRGQR | VPPKNSTDIQ |
| 730 | 740 | 750 | 760 | 770 | | | |
| VQKVTHEMRQ | GLHNMEDVYE | LIENSHLTPK | KQGQISEEYM | QTVL | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2272 | 1 | 820.1172 | 175.07 | 2 | 58.8 | 12.5 | 2 | 688-701 | R.DVFILLSKFGICKR.Q | |

# Detailed Protein Report

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## Protein 1329: epithelial cell adhesion molecule precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|218505670 | **Score:** | 12.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| | | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAPPQVLAFG | LLLAAATATF | AAAQEECVCE | NYKLAVNCFV | NNNRQCQCTS | VGAQNTVICS | KLAAKCLVMK | AEMNGSKLGR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RAKPEGALQN | NDGLYDPDCD | ESGLFKAKQC | NGTSMCWCVN | TAGVRRTDKD | TEITCSERVR | TYWIIIELKH | KAREKPYDSK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SLRTALQKEI | TTRYQLDPKF | ITSILYENNV | ITIDLVQNSS | QKTQNDVDIA | DVAYYFEKDV | KGESLFHSKK | MDLTVNGEQL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DLDPGQTLIY | YVDEKAPEFS | MQGLKAGVIA | VIVVVVIAVV | AGIVVLVISR | KKRMAKYEKA | EIKEMGEMHR | ELNA |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 98 | 1 | 850.1495 | 168.44 | 2 | 30.2 | 12.5 | 2 | 139-151 | R.VRTYWIIIELKHK.A | |

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# Detailed Protein Report

## Protein 1330: spermatogenesis-associated protein 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|31543825 | **Score:** | 12.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| | | **Sequence Coverage [%]:** | 6.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAAGQEKGY | LTQTAAALDK | SPSLSPQLAA | PIRGRPKKCL | VYPHAPKSSR | LSRSVLRWLQ | GLDLSFFPRN | INRDFSNGFL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IAEIFCIYYP | WELELSSFEN | GTSLKVKLDN | WAQLEKFLAR | KKFKLPKELI | HGTIHCKAGV | PEILIEEVYT | LLTHREIKSI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QDDFVNFTDY | SYQMRLPLVS | RSTVSKSIKD | NIRLSELLSN | PNMLTNELKA | EFLILLHMLQ | RKLGRKLNPE | WFDVKPTVGE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | |
| VTLNHLPAQA | SGRRYNLKVK | RGRVVPVLPN | IGSGGSSHRE | IHVKQAGQHS | YYSAMKPIRN | MDKKP | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2620 | 1 | 973.0041 | -42.64 | 2 | 62.8 | 12.5 | 2 | 261-279 | K.RGRVVPVLPNIGSGGSSHR.E | |

# Detailed Protein Report

## Protein 1331: E3 ubiquitin-protein ligase SMURF1 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|315434204 | **Score:** | 12.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 83.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.9 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSNPGTRRNG | SSIKIRLTVL | CAKNLAKKDF | FRLPDPFAKI | VVDGSGQCHS | TDTVKNTLDP | KWNQHYDLYV | GKTDSITISV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| WNHKKIHKKQ | GAGFLGCVRL | LSNAISRLKD | TGYQRLDLCK | LNPSDTDAVR | GQIVVSLQTR | DRIGTGGSVV | DCRGLLENEG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TVYEDSGPGR | PLSCFMEEPA | PYTDSTGAAA | GGGNCRFVES | PSQDQRLQAQ | RLRNPDVRGS | LQTPQNRPHG | HQSPELPEGY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EQRTTVQGQV | YFLHTQTGVS | TWHDPRIPRD | LNSVNCDELG | PLPPGWEVRS | TVSGRIYFVD | HNNRTTQFTD | PRLHHIMNHQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CQLKEPSQPL | PLPSEGSLED | EELPAQRYER | DLVQKLKVLR | HELSLQQPQA | GHCRIEVSRE | EIFEESYRQI | MKMRPKDLKK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RLMVKFRGEE | GLDYGGVARE | WLYLLCHEML | NPYYGLFQYS | TDNIYMLQIN | PDSSINPDHL | SYFHFVGRIM | GLAVFHGHYI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NGGFTVPFYK | QLLGKPIQLS | DLESVDPELH | KSLVWILEND | ITPVLDHTFC | VEHNAFGRIL | QHELKPNGRN | VPVTEENKKE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YVRLYVNWRF | MRGIEAQFLA | LQKGFNELIP | QHLLKPFDQK | ELELIIGGLD | KIDLNDWKSN | TRLKHCVADS | NIVRWFWQAV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ETFDEERRAR | LLQFVTGSTR | VPLQGFKALQ | GAAGPRLFTI | HLIDANTDNL | PKAHTCFNRI | DIPPYESYEK | LYEKLLTAVE |
| 730 | | | | | | | |
| ETCGFAVE | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 760 | 1 | 918.1508 | 152.98 | 2 | 39.5 | 12.5 | 2 | 100-115 | R.LLSNAISRLKDTGYQR.L | |

# Detailed Protein Report

## Protein 1332: kelch domain-containing protein 9 isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|55956888 | **Score:** | 12.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 37.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAVAVPPGRA | AGSGWAWRPV | ARDALLARAF | HSCTELRGRF | YLVGGLLAGG | AREPSSDTVV | FDPARGQAVR | LGARGSPPRS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HHDAAPVDGR | WLCVVGGWDG | SRRLATVTAL | DTERGVWEAW | TGTPGDCPPA | GLSSHTCTRI | SDRELQVAGR | EGGIHTQRRY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GSIYTLRLDP | SARTYCYKQE | GCHTASRSGH | CAALLQTPGP | HPGHQLLLFG | GCNLAEPEVA | GHWSHGKIKE | EPPVAPHLME |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QLARLVSSGQ | GSQKGPHGLR | HHSCSVVGPF | AVLFGGETLT | RARDTICNDL | YIYDTRTSPP | LWFHFPCADR | GMKRMGHRTC |
| 330 | 340 | 350 | | | | | |
| LWNDQLYLVG | GFGEDGRTAS | PQVCILDFI | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1017 | 1 | 946.5067 | 59.74 | 3 | 42.8 | 12.5 | 2 | 314-337 | K.RMGHRTCLWNDQLYLVGGFGEDGR.T | Carbamidomethyl: 7 |

# Detailed Protein Report

## Protein 1333: olfactory receptor 13J1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|52218862 | **Score:** | 12.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 0.29 | **CV:** 0.00 % | **No. of Peptides:** 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEPLNRTEVS | EFFLKGFSGY | PALEHLLFPL | CSAMYLVTLL | GNTAIMAVSV | LDIHLHTPVY | FFLGNLSTLD | ICYTPTFVPL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MLVHLLSSRK | TISFAVCAIQ | MCLSLSTGST | ECLLLAITAY | DRYLAICQPL | RYHVLMSHRL | CVLLMGAAWV | LCLLKSVTEM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VISMRLPFCG | HHVVSHFTCK | ILAVLKLACG | NTSVSEDFLL | AGSILLLPVP | LAFICLSYLL | ILATILRVPS | AARCCKAFST |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CLAHLAVVLL | FYGTIIFMYL | KPKSKEAHIS | DEVFTVLYAM | VTTMLNPTIY | SLRNKEVKEA | ARKVWGRSRA | SR |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2253 | 1 | 524.7006 | -103.56 | 2 | 56.5 | 12.5 | 1 | 228-236 | R.VPSAARCCK.A | Carbamidomethyl: 7, 8 | QU:MU 0.29 |

# Detailed Protein Report

## Protein 1334: PREDICTED: uncharacterized protein C1orf194 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578798360 | **Score:** | 12.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 8.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.44 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVSSQHFSAE | AQECNSKSRA | RSAERSLCSP | RSFLPRGLPW | SAARWRPPLR | EFLCHRWLGS | CLATETSAPN | NWDPGSYASE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AVLRLSGPPI | PLKRVRHLAM | PPTRDPFQQP | TLDNDDSYLG | ELRASKKLPY | KNPTHLAQQQ | EPWSRLNSTP | TITSMRRDAY |
| 170 | 180 | 190 | | | | | |
| YFDPENQDPI | PWRIFNPSHS | THHFPG | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1672 | 1 | 881.8269 | -144.73 | 2 | 50.7 | 12.5 | 2 | 22-36 | R.SAERSLCSPRSFLPR.G | Carbamidomethyl: 7 | WUP:QUP 0.44 |

# Detailed Protein Report

## Protein 1335: PREDICTED: solute carrier family 23 member 1 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578810697 | **Score:** | 12.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 4.8 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MLLWIWDRVL HLVLYACCVV WVELSVHGAV SAGGRAWSPQ HPGEFWEEKL ERKVLGSCRG FKLVQQLWKL GAVAKRERRG
        90        100        110        120        130        140        150        160
QADRGTVWTP AGGRTQCCGM KLLPSWRAVL PLGPSGRAWP WAQRPRRTAQ TCAPKMRAQE DLEGRTQHET TRDPSTPLPT
       170        180        190        200        210        220        230        240
EPKFDMLYKI EDVPPWYLCI LLGFQHYLTC FSGTIAVPFL LAEALCVGHD QHMVSQLIGT IFTCVGITTL IQTTVGIRLP
       250        260        270        280        290        300        310        320
LFQASAFAFL VPAKAILALE RWKCPPEEEI YGNWSLPLNT SHIWHPRIRE VGLHVQGAIM VSSVVEVVIG LLGLPGALLN
       330        340        350        360
YIGPLTVTPT VSLIGLSVFQ AAGDRAGSHW GISA
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2549 | 3 | 913.4434 | 35.71 | 2 | 61.8 | 12.5 | 1 | 85-101 | R.GTVWTPAGGRTQCCGMK.L | Carbamidomethyl: 14;<br>Oxidation: 16 |

# Detailed Protein Report

## Protein 1336: PREDICTED: protein angel homolog 2 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530366645 | **Score:** | 12.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530366649 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein angel homolog 2 isoform X3 [Homo sapiens] |
| gi\|530366647 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: protein angel homolog 2 isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFPHHSRSLG | RDWTTPWENL | QRCCWNRHIS | SCMRWPGHYS | RAPYPYFSSR | HFSLNWRPPC | LFESRTQFQY | CNWRPDNLSQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TSLIHLSSYV | MNAEGDEPSS | KRRKHQGVIK | RNWEYICSHD | KEKTKILGDK | NVDPKCEDSE | NKFDFSVMSY | NILSQDLLED |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NSHLYRHCRR | PVLHWSFRFP | NILKEIKHFD | ADVLCLQEVQ | EDHYGAEIRP | SLESLGYHCE | YKMRTGRKPD | GCAICFKHSK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FSLLSVNPVE | FFRPDISLLD | RDNVGLVLLL | QPKIPYAACP | AICVANTHLL | YNPRRGDIKL | TQLAMLLAEI | SSVAHQKDGS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FCPIVMCGDF | NSVPGSPLYS | FIKEGKLNYE | GLPIGKVSGQ | EQSSRGQRIL | SIPIWPPNLG | ISQNCVYEVQ | QVPKVEKTDS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DLTQTQLKQT | EVLVTAEKLS | SNLQHHFSLS | SVYSHYFPDT | GIPEVTTCHS | RSAITVDYIF | YSAEKEDVAG | HPGAEVALVG |
| 490 | 500 | 510 | 520 | 530 | | | |
| GLKLLARLSL | LTEQDLWTVN | GLPNENNSSD | HLPLLAKFRL | EL | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 910 | 1 | 866.9745 | 93.61 | 2 | 41.4 | 12.5 | 1 | 28-41 | R.HISSCMRWPGHYSR.A | Oxidation: 6 |

# Detailed Protein Report

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## Protein 1337: PREDICTED: integrator complex subunit 8 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578816078 | **Score:** | 12.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 107.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.92 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSAEAADREA | ATSSRPCTPP | QTCWFEFLLE | ESLLEKHLRK | PCPDPAPVQL | IVQFLEQASK | PSVNEQNQVQ | PPPDNKRNRI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LKLLALKVAA | HLKWDLDILE | KSLSVPVLNM | LLNELLCISK | VPPGTKHVDM | DLATLPPTTA | MAVLLYNRWA | IRTIVQSSFP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VKQAKPGPPQ | LSVMNQMQQE | KELTENILKV | LKEQAADSIL | VLEAALKLNK | DLYVHTMRTL | DLLAMEPGMV | NGETESSTAG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LKVKTEEMQC | QVCYDLGAAY | FQQGSTNSAV | YENAREKFFR | TKELIAEEVI | QIFIEDNLTL | SLPVQFRQSV | LRELFKKAQQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GNEALDEICF | KVCACNTVRD | ILEGRTISVQ | FNQLFLRPNK | EKIDFLLEVC | SRSVNLEKAS | ESLKGNMAAF | LKNVCLGLED |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LQYVFMISSH | ELFITLLKDE | ERKLLVDQMR | KRSPRVNLCI | KPVTSFYDIP | ASASVNIGQL | EHQLILSVDP | WRIRQILIEL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HGMTSERQFW | TVSNKWEVPS | VYSGVILGIK | DNLTRDLVYI | LMAKGLHCST | VKDFSHAKQL | FAACLELVTE | FSPKLRQVML |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NEMLLLDIHT | HEAGTGQAGE | RPPSDLISRV | RGYLEMRLPD | IPLRQVIAEE | CVAFMLNWRE | NEYLTLQVPA | FLLQSNPYVK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LGQLLAATCK | ELPGPKESRR | TAKDLWEVVV | QICSVSSQHK | RGNDGRVSLI | KQRESTLGIM | YRSELLSFIK | KLREPLVLTI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ILSLFVKLHN | VREDIVNDIT | AEHISIWPSS | IPNLQSVDFE | AVAITVKELV | RYTLSINPNN | HSWLIIQADI | YFATNQYSAA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LHYYLQAGAV | CSDFFNKAVP | PDVYTDQVIK | RMIKCCSLLN | CHTQVAILCQ | FLREIDYKTA | FKSLQEQNSH | DAMDSYYDYI |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | |
| WDVTILEYLT | YLHHKRGETD | KRQIAIKAIG | QTELNASNPE | EVLQLAAQRR | KKKFLQAMAK | LYF | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2583 | 1 | 701.3615 | -42.72 | 3 | 60.6 | 12.5 | 0 | 102-120 | K.SLSVPVLNMLLNELLCISK.V | Oxidation: 9 | QU:MU 0.92 |

# Detailed Protein Report

## Protein 1338: transmembrane protein 63C [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|190341095 | **Score:** | 12.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 93.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSASPDDLST | GGRLQNMTVD | ECFQSRNTVL | QGQPFGGVPT | VLCLNIALWV | LVLVVYSFLR | KAAWDYGRLA | LLIHNDSLTS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LIYGEQSEKT | SPSETSLEME | RRDKGFCSWF | FNSITMKDED | LINKCGDDAR | IYIVFQYHLI | IFVLIICIPS | LGIILPINYT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GSVLDWSSHF | ARTTIVNVST | ESKLLWLHSL | LSFFYFITNF | MFMAHHCLGF | APRNSQKVTR | TLMITYVPKD | IEDPELIIKH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FHEAYPGSVV | TRVHFCYDVR | NLIDLDDQRR | HAMRGRLFYT | AKAKKTGKVM | IRIHPCARLC | FCKCWTCFKE | VDAEQYYSEL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EEQLTDEFNA | ELNRVPLKRL | DLIFVTFQDS | RMAKRVRKDY | KYVQCGVQPQ | QSSVTTIVKS | YYWRVTMAPH | PKDIIWKHLS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VRRFFWWARF | IAINTFLFFL | FFFLTTPAII | MNTIDMYNVT | RPIEKLQNPI | VTQFFPSVML | WGFTVILPLI | VYFSAFLEAH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| WTRSSQNLVM | VHKCYIFLVF | MVVILPSMGL | TSLDVFLRWL | FDIYYLEQAS | IRFQCVFLPD | NGAFFVNYVI | TAALLGTGME |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LLRLGSLFCY | STRLFFSRSE | PERVNIRKNQ | AIDFQFGREY | AWMMNVFSVV | MAYSITCPII | VPFGLLYLCM | KHLTDRYNMY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| YSFAPTKLNE | QIHMAAVSQA | IFAPLLGLFW | MLFFSILRLG | SLHAITIFSL | STLLIAMVIA | FVGIFLGKLR | MVADYEPEEE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EIQTVFDMEP | SSTSSTPTSL | LYVATVLQEP | ELNLTPASSP | ARHTYGTMNN | QPEEGEEESG | LRGFARELDS | AQFQEGLELE |
| 810 | | | | | | | |
| GQNQYH | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2846 | 1 | 626.8511 | 14.67 | 2 | 64.3 | 12.5 | 1 | 289-298 | K.VMIRIHPCAR.L | Carbamidomethyl: 8 |

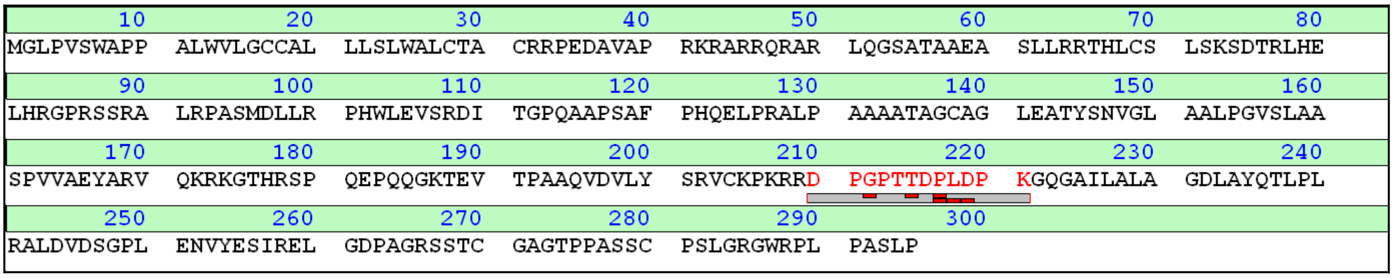
# Detailed Protein Report

## Protein 1339: lck-interacting transmembrane adapter 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|157388906 | **Score:** | 12.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.1 |
| | | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.61 | **CV:** | 0.00 % | **No. of Peptides:** | 1 | |



| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGLPVSWAPP | ALWVLGCCAL | LLSLWALCTA | CRRPEDAVAP | RKRARRQRAR | LQGSATAAEA | SLLRRTHLCS | LSKSDTRLHE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LHRGPRSSRA | LRPASMDLLR | PHWLEVSRDI | TGPQAAPSAF | PHQELPRALP | AAAATAGCAG | LEATYSNVGL | AALPGVSLAA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SPVVAEYARV | QKRKGTHRSP | QEPQQGKTEV | TPAAQVDVLY | SRVCKPKRRD | PGPTTDPLDP | KGQGAILALA | GDLAYQTLPL |
| 250 | 260 | 270 | 280 | 290 | 300 | | |
| RALDVDSGPL | ENVYESIREL | GDPAGRSSTC | GAGTPPASSC | PSLGRGWRPL | PASLP | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2206 | 1 | 626.6775 | -205.72 | 2 | 55.9 | 12.4 | 0 | 210-221 | R.DPGPTTDPLDPK.G | | QU:MU 0.61 |

# Detailed Protein Report

## Protein 1340: PREDICTED: N-glycosylase/DNA lyase isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530372567 | **Score:** | 12.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 35.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 8.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPARALLPRR | MGHRTLASTP | ALWASIPCPR | SELRLDLVLP | SGQSFRWREQ | SPAHWSGVLA | DQVWTLTQTE | EQLHCTVYRG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DKSQASRPTP | DELEAVRKYF | QLDVTLAQLY | HHWGSVDSHF | QEVAQKFQGV | RLLRQDPIEC | LFSFICSSNN | NIARITGMVE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RLCQAFGPRL | IQLDDVTYHG | FPSLQALAGP | EVEAHLRKLG | LGYRARYVSA | SARAILEEQG | GLAWLQQLRE | SSYEEAHKAL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CILPGVGTKV | ADCICLMALD | KPQAVPVDVH | MWHIAQRDYS | WHPTTSQAKG | PSPQTNKELG | NFFRSLWGPY | AGWAQAINF |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1563 | 1 | 1059.1172 | -72.43 | 3 | 47.9 | 12.4 | 0 | 250-277 | K.VADCICLMALDKPQAVPVDVHMWHIAQR.D | Oxidation: 8 |

# Detailed Protein Report

## Protein 1341: ATP-binding cassette sub-family D member 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|9945308 | **Score:** | 12.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 83.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTHMLNAAAD | RVKWTRSSAA | KRAACLVAAA | YALKTLYPII | GKRLKQSGHG | KKKAAAYPAA | ENTEILHCTE | TICEKPSPGV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NADFFKQLLE | LRKILFPKLV | TTETGWLCLH | SVALISRTFL | SIYVAGLDGK | IVKSIVEKKP | RTFIIKLIKW | LMIAIPATFV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NSAIRYLECK | LALAFRTRLV | DHAYETYFTN | QTYYKVINMD | GRLANPDQSL | TEDIMMFSQS | VAHLYSNLTK | PILDVMLTSY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TLIQTATSRG | ASPIGPTLLA | GLVVYATAKV | LKACSPKFGK | LVAEEAHRKG | YLRYVHSRII | ANVEEIAFYR | GHKVEMKQLQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KSYKALADQM | NLILSKRLWY | IMIEQFLMKY | VWSSSGLIMV | AIPIITATGF | ADGEDGQKQV | MVSERTEAFT | TARNLLASGA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DAIERIMSSY | KEVTELAGYT | ARVYNMFWVF | DEVKRGIYKR | TAVIQESESH | SKNGAKVELP | LSDTLAIKGK | VIDVDHGIIC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ENVPIITPAG | EVVASRLNFK | VEEGMHLLIT | GPNGCGKSSL | FRILSGLWPV | YEGVLYKPPP | QHMFYIPQRP | YMSLGSLRDQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VIYPDSVDDM | HDKGYTDQDL | ERILHNVHLY | HIVQREGGWD | AVMDWKDVLS | GGEKQRMGMA | RMFYHKPKYA | LLDECTSAVS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IDVEGKIFQA | AKGAGISLLS | ITHRPSLWKY | HTHLLQFDGE | GGWRFEQLDT | AIRLTLSEEK | QKLESQLAGI | PKMQQRLNEL |
| 730 | 740 | 750 | | | | | |
| CKILGEDSVL | KTIKNEDETS | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1413 | 1 | 1132.0559 | -86.14 | 2 | 47.8 | 12.4 | 2 | 23-43 | R.AACLVAAAYALKTLYPIIGKR.L | Carbamidomethyl: 3 |

# Detailed Protein Report

## Protein 1342: troponin T, slow skeletal muscle isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|187173292 | **Score:** | 12.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 30.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.4 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSDTEEQEYE EEQPEEEAAE EEEEEEERPK PSRPVVPPLI PPKIPEGERV DFDDIHRKRM EKDLLELQTL IDVHFEQRKK
        90        100        110        120        130        140        150        160
EEEELVALKE RIERRRSERA EQQRFRTEKE RERQAKLAEE KMRKEEEEAK KRAEDDAKKK KVLSNMGAHF GGYLVKAEQK
       170        180        190        200        210        220        230        240
RGKRQTGREM KVRILSERKK PLDIDYMGEE QLREKAQELS DWIHQLESEK FDLMAKLKQQ KYEINVLYNR ISHAQKFRKG
       250        260
AGKGRVGGRW K
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2290 | 1 | 869.0717 | 127.16 | 2 | 59.1 | 12.4 | 1 | 141-156 | K.KVLSNMGAHFGGYLVK.A | Oxidation: 6 |

# Detailed Protein Report

## Protein 1343: PREDICTED: uncharacterized protein LOC100996412 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530355840 | **Score:** | 12.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 22.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.0 |
| | | **Sequence Coverage [%]:** | 6.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

*QU:MU* **Median:** 1.55 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MALQLRWFKH | RRPFFLLLIA | QLCVHWPPHL | PPDQRGFCLP | QHCQPGVFLD | SSPGPPSAPL | PPSALTSRPP | SLLLGNLAWV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GLPSQPSRLF | FLSLAACLAH | HCGQVSLSEN | TISSHHGPVY | KAVSHLPITS | DQIRTLRLWI | EADATVPGKP | HCPPIPALAS |
| 170 | 180 | 190 | 200 | 210 | | | |
| VPVRSCTMLL | SAILPSPALP | ACWSCIALHL | TDSYSTALAS | PKHTWPS | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 348 | 1 | 718.8478 | -67.63 | 2 | 34.0 | 12.4 | 0 | 122-134 | K.AVSHLPITSDQIR.T | | QU:MU 1.55 |

# Detailed Protein Report

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**Protein 1344:** **PREDICTED: FH1/FH2 domain-containing protein 3 isoform X11 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530413969 | **Score:** | 12.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 156.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| | | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MATLACRVQF | LDDTDPFNST | NFPEPSRPPL | FTFREDLALG | TQLAGVHRLL | QAPHKLDDCT | LQLSHNGAYL | DLEATLAEQR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DELEGFQDDA | GRGKKHSIIL | RTQLSVRVHA | CIEKLYNSSG | RDLRRALFSL | KQIFQDDKDL | VHEFVVAEGL | TCLIKVGAEA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DQNYQNYILR | ALGQIMLYVD | GMNGVINRNE | TIQWLYTLIG | SKFRLVVKTA | LKLLLVFVEY | SESNAPLLIQ | AVTAVDTKRG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VKPWSNIMEI | LEEKDGVDTE | LLVYAMTLVN | KTLSGLPDQD | TFYDVVDCLE | ELGIAAVSQR | HLNKKGTDLD | LVEQLNIYEV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ALRHEDGDET | TEPPPSGCRD | RRRASVCSSG | GGEHRGLDRR | RSRRHSVQSI | KSTLSAPTSP | CSQSAPSFKP | NQVRDLREKS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SPSGLLTSSF | RQHQESLAAE | RERRRQEREE | RLQRIEREER | NKFSRDYLDK | REEQRQAREE | RYKYLEQLAA | EEHEKELRSR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SVSRGRADLS | LDLTSPAAPA | CLAPLSHSPS | SSDSQEALTV | SASSPGTPHH | PQASAGDPEP | ESEAEPEAEA | GAGQVADEAG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QDIASAHEGA | ETEVEQALEQ | EPEERASLSE | KERQNEGVNE | RDNCSASSVS | SSSSTLEREE | KEDKLSRDRT | TGLWPAGVQD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AGVNGQCGDI | LTNKRFMLDM | LYAHNRKSPD | DEEKGDGEAG | RTQQEAEAVA | SLATRISTLQ | ANSQTQDESV | RRVDVGCLDN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RGSVKAFAEK | FNSGDLGRGS | ISPDAEPNDK | VPETAPVQPK | TESDYIWDQL | MANPRELRIQ | DMDFTDLGEE | DDIDVLDVDL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GHREAPGPPP | PPPPTFLGLP | PPPPPPLLDS | IPPPPVPGNL | LVPPPPVFNA | PQGLGWSQVP | RGQPTFTKKK | KTIRLFWNEV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RPFDWPCKNN | RRCREFLWSK | LEPIKVDTSR | LEHLFESKSK | ELSVSKKTAA | DGKRQEIIVL | DSKRSNAINI | GLTVLPPPRT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| IKIAILNFDE | YALNKEGIEK | ILTMIPTDEE | KQKIQEAQLA | NPEIPLGSAE | QFLLTLSSIS | ELSARLHLWA | FKMDYETTEK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| EVAEPLLDLK | EGIDQLENNK | TLGFILSTLL | AIGNFLNGTN | AKAFELSYLE | KVPEVKDTVH | KQSLLHHVCT | MVVENFPDSS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DLYSEIGAIT | RSAKVDFDQL | QDNLCQMERR | CKASWDHLKA | IAKHEMKPVL | KQRMSEFLKD | CAERIIILKI | VHRRIINRFH |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SFLLFMGHPP | YAIREVNINK | FCRIISEFAL | EYRTTRERVL | QQKQKRANHR | ERNKTRGKMI | TDSGKFSGSS | PAPPSQPQGL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SYAEDAAEHE | NMKAVLKTSS | PSVEDATPAL | GVRTRSRASR | GSTSSWTMGT | DDSPNVTDDA | ADEIMDRIVK | SATQVPSQRV |
| 1370 | 1380 | 1390 | 1400 | 1410 | | | |
| VPRERKRSRA | NRKSLRRTLK | SGLTPEEARA | LGLVGTSELQ | L | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1388 | 1 | 940.5630 | 69.95 | 2 | 47.5 | 12.4 | 2 | 395-411 | R.DLREKSSPSGLLTSSFR.Q | |

# Detailed Protein Report

## Protein 1345: PREDICTED: rap1 GTPase-activating protein 2 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578829776 | **Score:** | 12.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 77.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLASLKVKKQ | ELANSSDATL | PDRPLSPPLT | APPTMKSSEF | FEMLEKMQGI | KLEEQKPGPQ | KNKDDYIPYP | SIDEVVEKGG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PYPQVILPQF | GGYWIEDPEN | VGTPTSLGSS | ICEEEEEDNL | SPNTFGYKLE | CKGEARAYRR | HFLGKDHLNF | YCTGSSLGNL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ILSVKCEEAE | GIEYLRVILR | SKLKTVHERI | PLAGLSKLPS | VPQIAKAFCD | DAVGLRFNPV | LYPKASQMIV | SYDEHEVNNT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FKFGVIYQKA | RQTLEEELFG | NNEESPAFKE | FLDLLGDTIT | LQDFKGFRGG | LDVTHGQTGV | ESVYTTFRDR | EIMFHVSTKL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PFTDGDAQQL | QRKRHIGNDI | VAIIFQEENT | PFVPDMIASN | FLHAYIVVQV | ETPGTETPSY | KVSVTAREDV | PTFGPPLPSP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PVFQKGPEFR | EFLLTKLTNA | ENACCKSDKF | AKLEDRTRAA | LLDNLHDELH | AHTQAMLGLG | PEEDKFENGG | HGGFLESFKR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AIRVRSHSME | TMVGGQKKSH | SGGIPGSLSG | GISHNSMEVT | KTTFSPPVVA | ATVKNQSRSP | IKRRSGLFPR | LHTGSEGQGD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SRARCDSTSS | TPKTPDGGHS | SQEIKSETSS | NPSSPEICPN | KEKPFMKLKE | NGRAISRSSS | STSSVSSTAG | EGEAMEEGDS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GGSQPSTTSP | FKQEVFVYSP | SPSSESPSLG | AAATPIIMSR | SPTDAKSRNS | PRSNLKFRFD | KLSHASSGAG | H |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1079 | 1 | 622.3300 | 69.53 | 2 | 43.6 | 12.4 | 0 | 551-562 | R.LHTGSEGQGDSR.A | |

# Detailed Protein Report

## Protein 1346: PREDICTED: glycerol-3-phosphate acyltransferase 2, mitochondrial isoform X7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530368526 | **Score:** | 12.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 73.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578803790 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: glycerol-3-phosphate acyltransferase 2, mitochondrial isoform X21 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MATMLEGRCQ TQPRSSPSGR EASLWSSGFG MKLEAVTPFL GKYRPFVGRC CQTCTPKSWE SLFHRSITDL GFCNVILVKE
        90        100        110        120        130        140        150        160
ENTRFRGWLV RRLCYFLWSL EQHIPPCQDV PQKIMESTGV QNLLSGRVPG GTGEGQVPDL VKKEVQRILG HIQAPPRPFL
       170        180        190        200        210        220        230        240
VRLFSWALLR FLNCLFLNVQ LHKGQMKMVQ KAAQAGLPLV LLSTHKTLLD GILLPFMLLS QGLGVLRVAW DSRACSPALR
       250        260        270        280        290        300        310        320
ALLRKLGGLF LPPEASLSLD SSEGLLARAV VQAVIEQLLV SGQPLLIFLE EPPGALGPRL SALGQAWVGF VVQAVQVGIV
       330        340        350        360        370        380        390        400
PDALLVPVAV TYDLVPDAPC DIDHASAPLG LWTGALAVLR SLWSRWGCSH RICSRVHLAQ PFSLQEYIVS ARSCWGGRQT
       410        420        430        440        450        460        470        480
LEQLLQPIVL GQCTAVPDTE KEQEWTPITG PLLALKEEDQ LLVRRLSCHV LSASVGSSAV MSTAIMATLL LFKHQKLLGE
       490        500        510        520        530        540        550        560
FSWLTEEILL RGFDVGFSGQ LRSLLQHSLS LLRAHVALLR IRQGDLLVVP QPGPGLTHLA QLSAELLPVF LSEAVGACAV
       570        580        590        600        610        620        630        640
RGLLAGRVPP QGPWELQGIL LLSQNELYRQ ILLLMHLLPQ DLLLLKPCQS SYCYCQEVLD RLIQCGLLVA EESWATQSSC
       650        660        670        680
SSSCRPPPRK KGSSSVRTQS SPSVLSGPSE T
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 637 | 1 | 824.1210 | -2.68 | 3 | 37.5 | 12.4 | 1 | 245-268 | R.KLGGLFLPPEASLSLDSSEGLLAR.A | |

## Protein 1347: AT-rich interactive domain-containing protein 1A isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21264575 | **Score:** | 12.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 218.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAQVAPAAA | SSLGNPPPPP | PSELKKAEQQ | QREEAGGEAA | AAAAAERGEM | KAAAGQESEG | PAVGPPQPLG | KELQDGAESN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GGGGGGGAGS | GGGPGAEPDL | KNSNGNAGPR | PALNNNLTEP | PGGGGGGSSD | GVGAPPHSAA | AALPPPAYGF | GQPYGRSPSA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VAAAAAAVFH | QQHGGQQSPG | LAALQSGGGG | GLEPYAGPQQ | NSHDHGFPNH | QYNSYYPNRS | AYPPPAPAYA | LSSPRGGTPG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SGAAAAAGSK | PPPSSSASAS | SSSSSFAQQR | FGAMGGGGPS | AAGGGTPQPT | ATPTLNQLLT | SPSSARGYQG | YPGGDYSGGP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QDGGAGKGPA | DMASQCWGAA | AAAAAAAAAS | GGAQQRSHHA | PMSPGSSGGG | GQPLARTPQP | SSPMDQMGKM | RPQPYGGTNP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YSQQQGPPSG | PQQGHGYPGQ | PYGSQTPQRY | PMTMQGRAQS | AMGGLSYTQQ | IPPYGQQGPS | GYGQQGQTPY | YNQQSPHPQQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QQPPYSQQPP | SQTPHAQPSY | QQQPQSQPPQ | LQSSQPPYSQ | QPSQPPHQQS | PAPYPSQQST | TQQHPQSQPP | YSQPQAQSPY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QQQQPQQPAP | STLSQQAAYP | QPQSQQSQQT | AYSQQRFPPP | QELSQDSFGS | QASSAPSMTS | SKGGQEDMNL | SLQSRPSSLP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DLSGSIDDLP | MGTEGALSPG | VSTSGISSSQ | GEQSNPAQSP | FSPHTSPHLP | GIRGPSPSPV | GSPASVAQSR | SGPLSPAAVP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GNQMPPRPPS | GQSDSIMHPS | MNQSSIAQDR | GYMQRNPQMP | QYSSPQPGSA | LSPRQPSGGQ | IHTGMGSYQQ | NSMGSYGPQG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GQYGPQGGYP | RQPNYNALPN | ANYPSAGMAG | GINPMGAGGQ | MHGQPGIPPY | GTLPPGRMSH | ASMGNRPYGP | NMANMPPQVG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SGMCPPPGGM | NRKTQETAVA | MHVAANSIQN | RPPGYPNMNQ | GGMMGTGPPY | GQGINSMAGM | INPQGPPYSM | GGTMANNSAG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| MAASPEMMGL | GDVKLTPATK | MNNKADGTPK | TESKSKKSSS | STTTNEKITK | LYELGGEPER | KMWVDRYLAF | TEEKAMGMTN |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LPAVGRKPLD | LYRLYVSVKE | IGGLTQVNKN | KKWRELATNL | NVGTSSSAAS | SLKKQYIQCL | YAFECKIERG | EDPPPDIFAA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| ADSKKSQPKI | QPPSPAGSGS | MQGPQTPQST | SSSMAEGGDL | KPPTPASTPH | SQIPPLPGMS | RSNSVGIQDA | FNDGSDSTFQ |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KRNSMTPNPG | YQPSMNTSDM | MGRMSYEPNK | DPYGSMRKAP | GSDPFMSSGQ | GPNGGMGDPY | SRAAGPGLGN | VAMGPRQHYP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| YGGPYDRVRT | EPGIGPEGNM | STGAPQPNLM | PSNPDSGMYS | PSRYPPQQQQ | QQQQRHDSYG | NQFSTQGTPS | GSPFPSQQTT |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| MYQQQQQVSS | PAPLPRPMEN | RTSPSKSPFL | HSGMKMQKAG | PPVPASHIAP | APVQPPMIRR | DITFPPGSVE | ATQPVLKQRR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| RLTMKDIGTP | EAWRVMMSLK | SGLLAESTWA | LDTINILLYD | DNSIMTFNLS | QLPGLLELLV | EYFRRCLIEI | FGILKEYEVG |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| DPGQRTLLDP | GRFSKVSSPA | PMEGGEEEEE | LLGPKLEEEE | EEEVVENDEE | IAFSGKDKPA | SENSEEKLIS | KFDKLPVKIV |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QKNDPFVVDC | SDKLGRVQEF | DSGLLHWRIG | GGDTTEHIQT | HFESKTELLP | SRPHAPCPPA | PRKHVTTAEG | TPGTTDQEGP |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| PPDGPPEKRI | TATMDDMLST | RSSTLTEDGA | KSSEAIKESS | KFPFGISPAQ | SHRNIKILED | EPHSKDETPL | CTLLDWQDSL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| AKRCVCVSNT | IRSLSFVPGN | DFEMSKHPGL | LLILGKLILL | HHKHPERKQA | PLTYEKEEEQ | DQGVSCNKVE | WWWDCLEMLR |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| ENTLVTLANI | SGQLDLSPYP | ESICLPVLDG | LLHWAVCPSA | EAQDPFSTLG | PNAVLSPQRL | VLETLSKLSI | QDNNVDLILA |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| TPPFSRLEKL | YSTMVRFLSD | RKNPVCREMA | VVLLANLAQG | DSLAARAIAV | QKGSIGNLLG | FLEDSLAATQ | FQQSQASLLH |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | |
| MQNPPFEPTS | VDMMRRAARA | LLALAKVDEN | HSEFTLYESR | LLDISVSPLM | NSLVSQVICD | VLFLIGQS | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2386 | 1 | 1023.7784 | 0.96 | 3 | 59.7 | 12.3 | 1 | 1817-1840 | K.EEEQDQGVSCNKVEWWWDCLEMLR.E | Carbamidomethyl: 19 |

# Detailed Protein Report

## Protein 1348: tensin-like C1 domain-containing phosphatase isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|38787970 | **Score:** | 12.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 138.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.1 |
| | | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MERRWDLDLT | YVTERILAAA | FPARPDEQRH | RGHLRELAHV | LQSKHRDKYL | LFNLSEKRHD | LTRLNPKVQD | FGWPELHAPP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LDKLCSICKA | METWLSADPQ | HVVVLYCKGN | KGKLGVIVSA | YMHYSKISAG | ADQALATLTM | RKFCEDKVAT | ELQPSQRRYI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SYFSGLLSGS | IRMNSSPLFL | HYVLIPMLPA | FEPGTGFQPF | LKIYQSMQLV | YTSGVYHIAG | PGPQQLCISL | EPALLLKGDV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MVTCYHKGGR | GTDRTLVFRV | QFHTCTIHGP | QLTFPKDQLD | EAWTDERFPF | QASVEFVFSS | SPEKIKGSTP | RNDPSVSVDY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NTTEPAVRWD | SYENFNQHHE | DSVDGSLTHT | RGPLDGSPYA | QVQRPPRQTP | PAPSPEPPPP | PMLSVSSDSG | HSSTLTTEPA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AESPGRPPPT | AAERQELDRL | LGGCGVASGG | RGAGRETAIL | DDEEQPTVGG | GPHLGVYPGH | RPGLSRHCSC | RQGYREPCGV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PNGGYYRPEG | TLERRRLAYG | GYEGSPQGYA | EASMEKRRLC | RSLSEGLYPY | PPEMGKPATG | DFGYRAPGYR | EVVILEDPGL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PALYPCPACE | EKLALPTAAL | YGLRLEREAG | EGWASEAGKP | LLHPVRPGHP | LPLLLPACGH | HHAPMPDYSC | LKPPKAGEEG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HEGCSYTMCP | EGRYGHPGYP | ALVTYSYGGA | VPSYCPAYGR | VPHSCGSPGE | GRGYPSPGAH | SPRAGSISPG | SPPYPQSRKL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SYEIPTEEGG | DRYPLPGHLA | SAGPLASAES | LEPVSWREGP | SGHSTLPRSP | RDAPCSASSE | LSGPSTPLHT | SSPVQGKEST |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RRQDTRSPTS | APTQRLSPGE | ALPPVSQAGT | GKAPELPSGS | GPEPLAPSPV | SPTFPPSSPS | DWPQERSPGG | HSDGASPRSP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VPTTLPGLRH | APWQGPRGPP | DSPDGSPLTP | VPSQMPWLVA | SPEPPQSSPT | PAFPLAASYD | TNGLSQPPLP | EKRHLPGPGQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QPGPWGPEQA | SSPARGISHH | VTFAPLLSDN | VPQTPEPPTQ | ESQSNVKFVQ | DTSKFWYKPH | LSRDQAIALL | KDKDPGAFLI |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RDSHSFQGAY | GLALKVATPP | PSAQPWKGDP | VEQLVRHFLI | ETGPKGVKIK | GCPSEPYFGS | LSALVSQHSI | SPISLPCCLR |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| IPSKDPLEET | PEAPVPTNMS | TAADLLRQGA | ACSVLYLTSV | ETESLTGPQA | VARASSAALS | CSPRPTPAVV | HFKVSAQGIT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LTDNQRKLFF | RRHYPVNSIT | FSSTDPQDRR | WTNPDGTTSK | IFGFVAKKPG | SPWENVCHLF | AELDPDQPAG | AIVTFITKVL |
| 1290 | | | | | | | |
| LGQRK | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2463 | 1 | 701.7422 | -179.06 | 2 | 60.7 | 12.3 | 0 | 1194-1206 | K.VSAQGITLTDNQR.K | |

# Detailed Protein Report

## Protein 1349: PREDICTED: pericentriolar material 1 protein isoform X28 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578815347 | **Score:** | 12.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 180.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MATGGGPFED | GMNDQDLPNW | SNENVDDRLN | NMDWGAQQKK | ANRSSEKNKK | KFGVESDKRV | TNDISPESSP | GVGRRRTKTP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HTFPHSRYMS | QMSVPEQAEL | EKLKQRINFS | DLDQRSIGSD | SQGRATAANN | KRQLSENRKP | FNFLPMQINT | NKSKDASTNP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PNRETIGSAQ | CKELFASALS | NDLLQNCQVS | EEDGRGEPAM | ESSQIVSRLV | QIRDYITKAS | SMREDLVEKN | ERSANVERLT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HLIDHLKEQE | KSYMKFLKKI | LARENEEEDV | RTIDSAVGSG | SVAESTSLNI | DVQSEASDTT | EEASFSLRIR | PCIEDKLGNS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ASQEQVSDID | VTTSPKGKGD | RPQNDRELRP | NRKYSQKRGF | PSKARDPQQE | PMEEIENLKK | QHDLLKRMLQ | QQEQLRALQG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RQAALLALQH | KAEQAIAVMD | DSVVAETAGS | LSGVSITSEL | NEELNDLIQR | FHNQLRDSQP | PAVPDNRRQA | ESLSLTREVS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QSRKPSASER | LPDEKVELFS | KMRVLQEKKQ | KMDKLLGELH | TLRDQHLNNS | SSSPQRSVDQ | RSTSAPSASV | GLAPVVNGES |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NSLTSSVPYP | TASLVSQNES | ENEGHLNPSE | KLQKLNEVRK | RLNELRELVH | YYEQTSDMMT | DAVNENRKDE | ETEESEYDSE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HENSEPVTNI | RNPQVASTWN | EVNSHSNAQC | VSNNRDGRTV | NSNCEINNRS | AANIRALNMP | PSLADCRYNR | EGEQEIHVAQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GEDDEEEEEE | AEEEGVSGAS | LSSHRSSLVD | EHPEDAEFEQ | KINRLMAAKQ | KLRQLQDLVA | MVQDDDAAQG | VISASASNLD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DFYPAEEDTK | QNSNNTRGNA | NKTQKDTGVN | EKAREKFYEA | KLQQQQRELK | QLQEERKKLI | DIQEKIQALQ | TACPDLQLSA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ASVGNCPTKK | YMPAVTSTPT | VNQHETSTSK | SVFEPEDSSI | VDNELWSEMR | RHEMLREELR | QRRKQLEALM | AEHQRRQGLA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ETASPVAVSL | RSDGSENLCT | PQQSRTEKTM | ATWGGSTQCA | LDEEGDEDGY | LSEGIVRTDE | EEEEEQDASS | NDNFSVCPSN |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SVNHNSYNGK | ETKNRWKNNC | PFSADENYRP | LAKTRQQNIS | MQRQENLRWV | SELSYVEEKE | QWQEQINQLK | KQLDFSVSIC |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QTLMQDQQTL | SCLLQTLLTG | PYSVMPSNVA | SPQVHFIMHQ | LNQCYTQLTW | QQNNVQRLKQ | MLNELMRQQN | QHPEKPGGKE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| RGSSASHPPS | PSLFCPFSFP | TQPVNLFNIP | GFTNFSSFAP | GMNFSPLFPS | NFGDFSQNIS | TPSEQQQPLA | QNSSGKTEYM |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| AFPKPFESSS | SIGAEKPRNK | KLPEEEVESS | RTPWLYEQEG | EVEKPFIKTG | FSVSVEKSTS | SNRKNQLDTN | GRRRQFDEES |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LESFSSMPDP | VDPTTVTKTF | KTRKASAQAS | LASKDKTPKS | KSKKRNSTQL | KSRVKNIRYE | SASMSSTCEP | CKSRNRHSAQ |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| TEEPVQAKVF | SRKNHEQLEK | IIKCNRSTEI | SSAHARRILQ | QSNRNACNEA | PETGSDFSMF | EALRDTIYSE | VATLISQNES |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| RPHFLIELFH | ELQLLNTDYL | RQRALYALQD | IVSRHISESH | EKGENVKSVN | SGTWIASNSE | LTPSESLATT | DDVFIQEK |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 86 | 1 | 809.3666 | -141.33 | 2 | 30.8 | 12.3 | 1 | 397-411 | R.ALQGRQAALLALQHK.A | |

# Detailed Protein Report

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## Protein 1350: zinc finger and BTB domain-containing protein 11 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|166235167 | **Score:** | 12.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 119.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSEESYRAI | LRYLTNEREP | YAPGTEGNVK | RKIRKAAACY | VVRGGTLYYQ | RRQRHRKTFA | ELEVVLQPER | RRDLIEAAHL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GPGGTHHTRH | QTWHYLSKTY | WWRGILKQVK | DYIKQCSKCQ | EKLDRSRPIS | DVSEMLEELG | LDLESGEESN | ESEDDLSNFT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SSPTTASKPA | KKKPVSKHEL | VFVDTKGVVK | RSSPKHCQAV | LKQLNEQRLS | NQFCDVTLLI | EGEEYKAHKS | VLSANSEYFR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DLFIEKGAVS | SHEAVVDLSG | FCKASFLPLL | EFAYTSVLSF | DFCSMADVAI | LARHLFMSEV | LEICESVHKL | MEEKQLTVYK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KGEVQTVAST | QDLRVQNGGT | APPVASSEGT | TTSLPTELGD | CEIVLLVNGE | LPEAEQNGEV | GRQPEPQVSS | EAESALSSVG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CIADSHPEME | SVDLITKNNQ | TELETSNNRE | NNTVSNIHPK | LSKENVISSS | PEDSGMGNDI | SAEDICAEDI | PKHRQKVDQP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LKDQENLVAS | TAKTDFGPDD | DTYRSRLRQR | SVNEGAYIRL | HKGMEKKLQK | RKAVPKSAVQ | QVAQKLVQRG | KKMKQPKRDA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KENTEEASHK | CGECGMVFQR | RYALIMHKLK | HERARDYKCP | LCKKQFQYSA | SLRAHLIRHT | RKDAPSSSSS | NSTSNEASGT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SSEKGRTKRE | FICSICGRTL | PKLYSLRIHM | LKHTGVKPHA | CQVCGKTFIY | KHGLKLHQSL | HQSQKQFQCE | LCVKSFVTKR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SLQEHMSIHT | GESKYLCSVC | GKSFHRGSGL | SKHFKKHQPK | PEVRGYHCTQ | CEKSFFEARD | LRQHMNKHLG | VKPFQCQFCD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KCYSWKKDWY | SHVKSHSVTE | PYRCNICGKE | FYEKALFRRH | VKKATHGKKG | RAKQNLERVC | EKCGRKFTQL | REYRRHMNNH |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EGVKPFECLT | CGVAWADARS | LKRHVRTHTG | ERPYVCPVCS | EAYIDARTLR | KHMTKFHRDY | VPCKIMLEKD | TLQFHNQGTQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VAHAVSILTA | GMQEQESSGP | QELETVVVTG | ETMEALEAVA | ATEEYPSVST | LSDQSIMQVV | NYVLAQQQGQ | KLSEVAEAIQ |
| 1050 | 1060 | | | | | | |
| TVKVEVAHIS | GGE | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1488 | 1 | 627.2947 | -24.52 | 2 | 48.8 | 12.3 | 2 | 594-603 | R.ARDYKCPLCK.K | Carbamidomethyl: 6 |

# Detailed Protein Report

## Protein 1351: ankyrin repeat and fibronectin type-III domain-containing protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|114842396 | **Score:** | 12.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 87.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEASLTRRLL | FKDRHFTCSK | IIGRRFACFA | QRLSHRRKQS | QCDLLNESTG | QLPTTCSSAA | SNSINWNCRV | KMTQQMQNLH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LCQSKKHSAP | SSPNAAKRLY | RNLSEKLKGS | HSSFDEAYFR | TRTDRLSLRK | TSVNFQGNEA | MFEAVEQQDM | DAVQILLYQY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TPEELDLNTP | NSEGLTPLDI | AIMTNNVPIA | RILLRTGARE | SPHFVSLESR | AMHLNTLVQE | AQERVSELSA | QVENEGFTLD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NTEKEKQLKA | WEWRYRLYRR | MKTGFEHARA | PEMPTNVCLM | VTSSTSLTVS | FQEPLSVNAA | VVTRYKVEWS | MSEDFSPLAG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EIIMDNLQTL | RCTITGLTMG | QQYFVQVSAY | NMKGWGPAQT | TTPACASPSN | WKDYDDREPR | HKGQSEVLEG | LLQQVRALHQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HYSCRESTKL | QTTGRKQSVS | RSLKHLFHSS | NKFVKTLKRG | LYIAVIFYYK | DNILVTNEDQ | VPIVEIDDSH | TSSITQDFLW |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FTKLSCMWED | IRWLRQSIPI | SSSSSTVLQT | RQKMLAATAQ | LQNLLGTHNL | GRVYYEPIKD | RHGNILIVTI | REVEMLYSFF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NGKWMQISKL | QSQRKSLSTP | EEPTALDILL | ITIQDILSYH | KRSHQRLFPG | LYLGYLKLCS | SVDQIKVLVT | QKLPNILCHV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KIRENNNISR | EEWEWIQKLS | GSESMESVDH | TSDCPMQLFF | YELQMAVKAL | LQQINIPLHQ | ARNFRLYTQE | VLEMGHNVSF |
| 730 | 740 | 750 | 760 | 770 | | | |
| LLLLPASDDV | CTAPGQNNPY | TPHSGFLNLP | LQMFELGIVA | CFT | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2705 | 1 | 716.0445 | -19.86 | 3 | 62.3 | 12.3 | 1 | 493-511 | R.WLRQSIPISSSSSTVLQTR.Q | |

# Detailed Protein Report

## Protein 1352: transmembrane protein 171 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|239735594 | **Score:** | 12.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSPAAAAEPD | GDQQDRHVSK | LIFCFFVFGA | VLLCVGVLLS | IFGFQACQYK | PLPDCPMVLK | VAGPACAVVG | LGAVILARSR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AQLQLRAGLQ | RGQQMDPDRA | FICGESRQFA | QCLIFGFLFL | TSGMLISVLG | IWVPGCGSNW | AQEPLNETDT | GDSEPRMCGF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LSLQIMGPLI | VLVGLCFFVV | AHVKKRNTLN | AGQDASEREE | GQIQIMEPVQ | VTVGDSVIIF | PPPPPPYFPE | SSASAVAESP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GTNSLLPNEN | PPSYYSIFNY | GTPTSEGAAS | ERDCESIYTI | SGTNSSSEAS | HTPHLPSELP | PRYEEKENAA | ATFLPLSSEP |
| 330 | | | | | | | |
| SPP | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 640 | 1 | 565.2589 | -127.39 | 3 | 38.0 | 12.3 | 0 | 61-78 | K.VAGPACAVVGLGAVILAR.S | Carbamidomethyl: 6 |

# Detailed Protein Report

## Protein 1353: 28S ribosomal protein S35, mitochondrial isoform 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|300068923 | **Score:** | 12.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 9.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAAAALPAWL | SLQSRARTLR | AFSTAVYSAT | PVPTPSLPER | TPGNERPPRR | KALPPRTEKM | AVDQDWPSVY | PVAAPFKPSA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VPLPVRMGYP | VKKGVPMAKE | GNLELLKIPN | FLHLTPVAIK | KHCEALKDFC | TEWPAALDSD | EKCEKHFPIE | IDSTDYVSSG |
| 170 | 180 | 190 | 200 | | | | |
| PSVRNPRARV | VVLRVPFKEA | ELRLCSVSTN | SVIP | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2090 | 2 | 715.2693 | -47.17 | 3 | 56.5 | 12.3 | 1 | 128-145 | K.DFCTEWPAALDSDEKCEK.H | Carbamidomethyl: 16 |

# Detailed Protein Report

## Protein 1354: sphingosine 1-phosphate receptor 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|13027636 | **Score:** | 12.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 42.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.8 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578798500 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: sphingosine 1-phosphate receptor 1 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGPTSVPLVK | AHRSSVSDYV | NYDIIVRHYN | YTGKLNISAD | KENSIKLTSV | VFILICCFII | LENIFVLLTI | WKTKKFHRPM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YYFIGNLALS | DLLAGVAYTA | NLLLSGATTY | KLTPAQWFLR | EGSMFVALSA | SVFSLLAIAI | ERYITMLKMK | LHNGSNNFRL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FLLISACWVI | SLILGGLPIM | GWNCISALSS | CSTVLPLYHK | HYILFCTTVF | TLLLLSIVIL | YCRIYSLVRT | RSRRLTFRKN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ISKASRSSEK | SLALLKTVII | VLSVFIACWA | PLFILLLLDV | GCKVKTCDIL | FRAEYFLVLA | VLNSGTNPII | YTLTNKEMRR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| AFIRIMSCCK | CPSGDSAGKF | KRPIIAGMEF | SRSKSDNSSH | PQKDEGDNPE | TIMSSGNVNS | SS | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 133 | 1 | 830.0488 | -41.86 | 3 | 31.6 | 12.3 | 2 | 342-363 | K.RPIIAGMEFSRSKSDNSSHPQK.D | Oxidation: 7 |

# Detailed Protein Report

## Protein 1355: PREDICTED: schlafen-like protein 1 isoform X6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530362078 | **Score:** | 12.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 8.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530362080 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: schlafen-like protein 1 isoform X7 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTPMKRSVQT | QVSEPFMESW | GEESLPELPA | EQSLTEYSDL | EEAPSAHTLY | VGHLNPQFSV | PVLACLLRDT | LERLEMPVAR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EHIEVVRRPR | KAYALVQVTV | HRDTLASLPW | RLQTALEEHL | ILKELAARGK | DLLLSEAQGP | FSHREQIVGK | DQLFQGAFLG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SETRNMEFKR | GSGEYLSLAF | KHHVRRYVCA | FLNSEGGSLL | VGVEDSGLVQ | GIRCSHRDED | RARLLVDSIL | QGFKPQIFPD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AYTLTFIPVI | STSETSVPLK | VIRLTVHTPK | AQSQPQLYQT | DQGEVFLRRD | GSIQGPLSAS | AIQEWCRQRW | LVELGKLEEK |
| 330 | 340 | 350 | | | | | |
| MKALMMEKEQ | LQQQLQQHGP | VSCTCCVL | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2423 | 1 | 1131.2820 | 75.37 | 3 | 58.6 | 12.3 | 2 | 321-348 | K.MKALMMEKEQLQQQLQQHGPVSCTCCVL.- | Carbamidomethyl: 23, 25, 26; Oxidation: 1 |

# Detailed Protein Report

## Protein 1356: PREDICTED: neurogenic locus notch homolog protein 2-like isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578801920 | **Score:** | 12.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 48.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578842780 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: neurogenic locus notch homolog protein 2-like isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRTGPVTRSR | SLRAELGPAL | LPAGNPWVPK | AAGPRPRRQW | GGACGGRRRL | RRKDTRGCFA | AHPRKFQPNF | GRLRRRPRSG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GLRARGVEAF | APGLRSVAPG | PEPLKQEEGR | REWGSSIGTP | SPCGSAQAAA | AEEATEKMPA | LRPALLWALL | ALWLCCATPA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HVILLPTSPI | MVEKNSVSWL | HQNLLGWILD | SAPRDSDKCR | DGYEPCVNEG | MCVTYHNGTG | YCKCPEGFLG | EYCQHRDPCE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KNRCQNGGTC | VAQAMLGKAT | CRCASGFTGE | DCQYSTSHPC | FVSRPCLNGG | TCHMLSRDTY | ECTCQVGFTG | KECQWTDACL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SHPCANGSTC | TTVANQFSCK | CLTGFTGQKC | ETDVNECDIP | GHCQHGGICL | NLPGSYQCQC | LQGFTGQYCD | SLYVPCAPSP |
| 410 | 420 | 430 | 440 | 450 | | | |
| CVNGGTCRQT | GDFTFECNCL | PETVRRGTEL | WERDREVWNG | KEHDEN | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2463 | 1 | 864.4574 | -42.61 | 3 | 59.1 | 12.3 | 2 | 14-38 | R.AELGPALLPAGNPWVPKAAGPRPRR.Q | |

# Detailed Protein Report

## Protein 1357: PREDICTED: tetratricopeptide repeat protein 7A isoform X2 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|530367852 | **Score:** | 12.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 82.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
|  |  | **Sequence Coverage [%]:** | 2.4 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPSACTHGPG | LMTCPWRTSP | CIRCGCCRRL | LSSKHASGFL | GEHSPGGQRS | CRGGLSLERL | PNSIASRFRL | TEREEEVITC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FERASWIAQV | FLQELEKTTN | NSTSRHLKGC | HPLDYELTYF | LEAALQSAYV | KNLKKGNIVK | GMRELREVLR | TVETKATQNF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KVMAAKHLAG | VLLHSLSEEC | YWSPLSHPLP | EFMGKEESSF | ATQALRKPHL | YEGDNLYCPK | DNIEEALLLL | LISESMATRD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VVLSRVPEQE | EDRTVSLQNA | AAIYDLLSIT | LGRRGQYVML | SECLERAMKF | AFGEFHLWYQ | VALSMVACGK | SAYAVSLLRE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CVKLRPSDPT | VPLMAAKVCI | GSLRWLEEAE | HFAMMVISLG | EEAGEFLPKG | YLALGLTYSL | QATDATLKSK | QDELHRKALQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TLERAQQLAP | SDPQVILYVS | LQLALVRQIS | SAMEQLQEAL | KVRKDDAHAL | HLLALLFSAQ | KHHQHALDVV | NMAITEHPEN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FNLMFTKVKL | EQVLKGPEEA | LVTCRQVLRL | WQTLYSFSQL | GGLEKDGSFG | EGLTMKKQSG | MHLTLPDAHD | ADSGSRRASS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IAASRLEEAM | SELTMPSSVL | KQGPMQLWTT | LEQIWLQAAE | LFMEQQHLKE | AGFCIQEAAG | LFPTSHSVLY | MRGRLAEVKG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NLEEAKQLYK | EALTVNPDGV | RIMHSLGLML | SRLGHKSLAQ | KVLRDAVERQ | STCHEAWQGL | GEVLQAQGQN | EAAVDCFLTA |
| 730 | 740 |  |  |  |  |  |  |
| LELEASSPVL | PFSIIPREL |  |  |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2755 | 1 | 941.9676 | 29.42 | 2 | 62.9 | 12.2 | 1 | 35-52 | K.HASGFLGEHSPGGQRSCR.G |  |

# Detailed Protein Report

## Protein 1358: small nuclear protein PRAC2 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|533112475 | **Score:** | 12.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 10.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.6 |
| | | **Sequence Coverage [%]:** | 11.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578830849 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: small nuclear protein PRAC2 isoform X1 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MDRRRMALRP GSRRPTAFFF HSRWLVPNLL AFFLGLSGAG PIHLPMPWPN GRRHRVLDPH TQLSTHEAPG RWKPVAPRTM
        90        100
KACPQVLLEW
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 915 | 1 | 600.3484 | -0.60 | 2 | 41.5 | 12.2 | 2 | 4-13 | R.RRMALRPGSR.R | |

# Detailed Protein Report

## Protein 1359: deleted in autism protein 1 isoform a precursor [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|27734895 | **Score:** | 12.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.6 |
|  |  | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MWRLVPPKLG | RLSRSLKLAA | LGSLLVLMVL | HSPSLLASWQ | RNELTDRRFL | QLNKCPACFG | TSWCRRFLNG | QVVFEAWGRL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RLLDFLNVKN | VYFAQYGEPR | EGGRRRVVLK | RLGSQRELAQ | LDQSICKRAT | GRPRCDLLQA | MPRTEFARLN | GDVRLLTPEA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VEGWSDLVHC | PSQRLLDRLV | RRYAETKDSG | SFLLRNLKDS | ERMQLLLTLA | FNPEPLVLQS | FPSDEGWPFA | KYLGACGRMV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AVNYVGEELW | SYFNAPWEKR | VDLAWQLMEI | AEQLTNNDFE | FALYLLDVSF | DNFAVGPRDG | KVIIVDAENV | LVADKRLIRQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NKPENWDVWY | ESKFDDCDKE | ACLSFSKEIL | CARATVDHNY | YAVCQNLLSR | HATWRGTSGG | LLHDPPSEIA | KDGRLEALLD |
| 410 | 420 | 430 | 440 |  |  |  |  |
| ECANPKKRYG | RFQAAKELRE | YLAQLSNNVR |  |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2880 | 1 | 644.3218 | 100.55 | 2 | 64.7 | 12.2 | 0 | 55-65 | K.CPACFGTSWCR.R | Carbamidomethyl: 10 |

# Detailed Protein Report

## Protein 1360: PREDICTED: TNF receptor-associated factor 5 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578801456 | **Score:** | 12.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 67.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTVSASSRPL | PARPLFPCAR | PRPSARAPAP | PQASPPLRRR | RRPQPGAAAA | PADRPRGARA | PSPTMAYSEE | HKGMPCGFIR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QNSGNSISLD | FEPSIEYQFV | ERLEERYKCA | FCHSVLHNPH | QTGCGHRFCQ | HCILSLRELN | TVPICPVDKE | VIKSQEVFKD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NCCKREVLNL | YVYCSNAPGC | NAKVILGRYQ | DHLQQCLFQP | VQCSNEKCRE | PVLRKDLKEH | LSASCQFRKE | KCLYCKKDVV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VINLQNHEEN | LCPEYPVFCP | NNCAKIILKT | EVDEHLAVCP | EAEQDCPFKH | YGCAVTISDL | HKSLEQKESK | IQQLAETIKK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LEKEFKQFAQ | LFGKNGSFLP | NIQVFASHID | KSAWLEAQVH | QLLQMVNQQQ | NKFDLRPLME | AVDTVKQKIT | LLENNDQRLA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VLEEETNKHD | THINIHKAQL | SKNEERFKLL | EGTCYNGKLI | WKVTDYKMKK | REAVDGHTVS | IFSQSFYTSR | CGYRLCARAY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LNGDGSGRGS | HLSLYFVVMR | GEFDSLLQWP | FRQRVTLMLL | DQSGKKNIME | TFKPDPNSSS | FKRPDGEMNI | ASGCPRFVAH |
| 570 | 580 | 590 | 600 | | | | |
| SVLENAKNAY | IKDDTLFLKV | AVDLTDLEDL | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1679 | 1 | 865.0347 | -46.70 | 3 | 49.3 | 12.2 | 2 | 57-80 | R.GARAPSPTMAYSEEHKGMPCGFIR.Q | |

# Detailed Protein Report

## Protein 1361: RNA pseudouridylate synthase domain-containing protein 2 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|556695367 | **Score:** | 12.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWLDRRGWLR | VLGHWRYDLR | RPSFTRTWSG | DKGPMAETVS | TQVGTEGGLR | ASHQQNGDAG | GDAKVELSPG | PPKPAGREVE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PAPVGGEHPS | AAAPGPGKHK | KRRGATRERV | VPPPKKRRTG | VSFGDEHFAE | TSYYFEGGLR | KDNDFLRNTV | HRHEPPVTAE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PIRLLAENED | VVVVDKPSSI | PVHPCGRFRH | NTVIFILGKE | HQLKELHPLH | RLDRLTSGVL | MFAKTAAVSE | RIHEQVRDRQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LEKEYVCRVE | GEFPTEEVTC | KEPILVVSYK | VGVCRVDPRG | KPCETVFQRL | SYNGQSSVVR | CRPLTGRTHQ | IRVHLQFLGH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PILNDPIYNS | VAWGPSRGRG | GYIPKTNEEL | LRDLVAEHQA | KQSLDVLDLC | EGDLSPGLTD | STAPSSELGK | DDLEELAAAA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QKMEEVAEAA | PQELDTIALA | SEKAVETDVM | NQETDPLCAE | CRLVRQDPLP | QDLVMFLHAL | RYKGPGFEYF | SPMPAWAQDD |
| 490 | | | | | | | |
| WQKD | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 534 | 1 | 895.4431 | 2.30 | 2 | 36.7 | 12.2 | 0 | 33-50 | K.GPMAETVSTQVGTEGGLR.A | |

# Detailed Protein Report

**Protein 1362:** **tumor necrosis factor receptor superfamily member 25 isoform 12 precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|89142745 | **Score:** | 12.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 19.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 8.8 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MEQRPRGCAA VAAALLLVLL GARAQGGTRS PRCDCAGDFH KKIGLFCCRG CPAGHYLKAP CTEPCGNSTC LVCPQDTFLA
        90        100        110        120        130        140        150        160
WENHHNSECA RCQACDEQAS QVALENCSAV ADTRCGCKPG WFVECQVSQC VSSSPFYCQP CLDCGALHRH TRLLCSRRDT
       170        180        190
DCGTCLPGFY EHGDGCVSCP T
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1768 | 1 | 897.9818 | 53.60 | 2 | 51.9 | 12.2 | 1 | 43-58 | K.IGLFCCRGCPAGHYLK.A | Carbamidomethyl: 9 |

# Detailed Protein Report

## Protein 1363: PREDICTED: cytokine receptor-like factor 1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578833719 | **Score:** | 12.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 36.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 7.1 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MKDLTCRWTP GAHGETFLHT NYSLKYKLRW YGQDNTCEEY HTVGPHSCHI PKDLALFTPY EIWVEATNRL GSARSDVLTL
        90        100        110        120        130        140        150        160
DILDVVRSPQ KQPGYPHSTE NTWPGHHPLG SPVTTDPPPD VHVSRVGGLE DQLSVRWVSP PALKDFLFQA KYQIRYRVED
       170        180        190        200        210        220        230        240
SVDWKVVDDV SNQTSCRLAG LKPGTVYFVQ VRCNPFGIYG SKKAGIWSEW SHPTAASTPR SERPGPGGGA CEPRGGEPSS
       250        260        270        280        290        300        310        320
GPVRRELKQF LGWLKKHAYC SNLSFRLYDQ WRAWMQKSHK TRNQHRTRGS CPRADGARRE PKNIQCPENV RSGISSEMNE
       330
HTHPS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2740 | 1 | 920.1462 | 89.37 | 3 | 65.4 | 12.2 | 0 | 30-52 | R.WYGQDNTCEEYHTVGPHSCHIPK.D | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 1364: calpain-15 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5032105 | **Score:** | 12.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 117.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530408968 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: calpain-15 isoform X6 [Homo sapiens] |
| gi\|530408966 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: calpain-15 isoform X5 [Homo sapiens] |
| gi\|530408964 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: calpain-15 isoform X4 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MATVGEWSCV | RCTFLNPAGQ | RQCSICEAPR | HKPDLNHILR | LSVEEQKWPC | ARCTFRNFLG | KEACEVCGFT | PEPAPGAAFL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PVLNGVLPKP | PAILGEPKGS | CQEEAGPVRT | AGLVATEPAR | GQCEDKDEEE | KEEQEEEEGA | AEPRGGWACP | RCTLHNTPVA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SSCSVCGGPR | RLSLPRIPPE | ALVVPEVVAP | AGFHVVPAAP | PPGLPGEGAE | ANPPATSQGP | AAEPEPPRVP | PFSPFSSTLQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NNPVPRSRRE | VPPQLQPPVP | EAAQPSPSAG | CRGAPQGSGW | AGASRLAELL | SGKRLSVLEE | EATEGGTSRV | EAGSSTSGSD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IIDLAGDTVR | YTPASPSSPD | FTTWSCAKCT | LRNPTVAPRC | SACGCSKLHG | FQEHGEPPTH | CPDCGADKPS | PCGRSCGRVS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SAQKAARVLP | ERPGQWACPA | CTLLNALRAK | HCAACHTPQL | LVAQRRGAAP | LRRRESMHVE | QRRQTDEGEA | KALWENIVAF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CRENNVSFVD | DSFPPGPESV | GFPAGDSVQQ | RVRQWLRPQE | INCSVFRDHR | ATWSVFHTLR | PSDILQGLLG | NCWFLSALAV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LAERPDLVER | VMVTRSLCAE | GAYQVRLCKD | GTWTTVLVDD | MLPCDEAGCL | LFSQAQRKQL | WVALIEKALA | KLHGSYFALQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AGRAIEGLAT | LTGAPCESLA | LQLSSTNPRE | EPVDTDLIWA | KMLSSKEAGF | LMGASCGGGN | MKVDDSAYES | LGLRPRHAYS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ILDVRDVQGT | RLLRLRNPWG | RFSWNGSWSD | EWPHWPGHLR | GELMPHGSSE | GVFWMEYGDF | VRYFDSVDIC | KVHSDWQEAR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VQGCFPSSAS | APVGVTALTV | LERASLEFAL | FQEGSRRSDA | VDSHLLDLCI | LVFRATFGSG | GHLSLGRLLA | HSKRAVKKFV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SCDVMLEPGE | YAVVCCAFNH | WGPPLPGTPA | PQASSPSAGV | PRASPEPPGH | VLAVYSSRLV | MVEPVEAQPT | TLADAIILLT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ESRGERHEGR | EGMTCYYLTH | GWAGLIVVVE | NRHPKAYLHV | QCDCTDSFNV | VSTRGSLRTQ | DSVPPLHRQV | LVILSQLEGN |
| 1050 | 1060 | 1070 | 1080 | 1090 | | | |
| AGFSITHRLA | HRKAAQAFLS | DWTASKGTHS | PPLTPEVAGL | HGPRPL | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2419 | 1 | 973.4005 | -38.04 | 2 | 60.7 | 12.2 | 0 | 152-170 | R.CTLHNTPVASSCSVCGGPR.R | Carbamidomethyl: 12 |

# Detailed Protein Report

## Protein 1365: vacuolar protein sorting-associated protein 41 homolog isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|114199473 | **Score:** | 12.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 95.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAEAEEQETG | SLEESTDESE | EEESEEEPKL | KYERLSNGVT | EILQKDAASC | MTVHDKFLAL | GTHYGKVYLL | DVQGNITQKF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DVVQVFGLYS | GEEFHETFDC | PIKIIAVHPH | FVRSSCKQFV | TGGKKLLLFE | RSWMNRWKSA | VLHEGEGNIR | SVKWRGHLIA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WANNMGVKIF | DIISKQRITN | VPRDDISLRP | DMYPCSLCWK | DNVTLIIGWG | TSVKVCSVKE | RHASEMRDLP | SRYVEIVSQF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ETEFYISGLA | PLCDQLVVLS | YVKEISEKTE | REYCARPRLD | IIQPLSETCE | EISSDALTVR | GFQENECRDY | HLEYSEGESL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FYIVSPRDVV | VAKERDQDDH | IDWLLEKKKY | EEALMAAEIS | QKNIKRHKIL | DIGLAYINHL | VERGDYDIAA | RKCQKILGKN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AALWEYEVYK | FKEIGQLKAI | SPYLPRGDPV | LKPLIYEMIL | HEFLESDYEG | FATLIREWPG | DLYNNSVIVQ | AVRDHLKKDS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QNKTLLKTLA | ELYTYDKNYG | NALEIYLTLR | HKDVFQLIHK | HNLFSSIKDK | IVLLMDFDSE | KAVDMLLDNE | DKISIKKVVE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ELEDRPELQH | VYLHKLFKRD | HHKGQRYHEK | QISLYAEYDR | PNLLPFLRDS | THCPLEKALE | ICQQRNFVEE | TVYLLSRMGN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SRSALKMIME | ELHDVDKAIE | FAKEQDDGEL | WEDLILYSID | KPPFITGLLN | NIGTHVDPIL | LIHRIKEGME | IPNLRDSLVK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ILQDYNLQIL | LREGCKKILV | ADSLSLLKKM | HRTQMKGVLV | DEENICESCL | SPILPSDAAK | PFSVVVFHCR | HMFHKECLPM |
| 810 | 820 | 830 | | | | | |
| PSMNSAAQFC | NICSAKNRGP | GSAILEMKK | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1452 | 1 | 927.0219 | -102.54 | 3 | 48.3 | 12.2 | 1 | 178-200 | R.ITNVPRDDISLRPDMYPCSLCWK.D | Carbamidomethyl: 18 |

# Detailed Protein Report

## Protein 1366: PREDICTED: sodium/iodide cotransporter isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530415091 | **Score:** | 12.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 43.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDFNPDPRSR | YTFWTFVVGG | TLVWLSMYGV | NQAQVQRYVA | CRTEKQAKLA | LLINQVGLFL | IVSSAACCGI | VMFVFYTDCD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PLLLGRISAP | DQYMPLLVLD | IFEDLPGVPG | LFLACAYSGT | LSTASTSINA | MAAVTVEDLI | KPRLRSLAPR | KLVIISKGLS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LIYGSACLTV | AALSSLLGGG | VLQGSFTVMG | VISGPLLGAF | ILGMFLPACN | TPGVLAGLGA | GLALSLWVAL | GATLYPPSEQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TMRVLPSSAA | RCVALSVNAS | GLLDPALLPA | NDSSRAPSSG | MDASRPALAD | SFYAISYLYY | GALGTLTTVL | CGALISCLTG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PTKRSTLAPG | LLWWDLARQT | ASVAPKEEVA | ILDDNLVKGP | EELPTGNKKP | PGFLPTNEDR | LFFLGQKELE | GAGSWTPCVG |
| 410 | 420 | | | | | | |
| HDGGRDQQET | NL | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1609 | 1 | 685.7648 | -134.19 | 2 | 49.8 | 12.2 | 0 | 369-380 | K.KPPGFLPTNEDR.L | |

# Detailed Protein Report

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## Protein 1367: PREDICTED: LOW QUALITY PROTEIN: spermatogenesis-associated protein 31D1, partial [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530436439 | **Score:** | 12.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 176.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 0.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| NFICLSGLGL | FILYLFYMVL | TLYSSPTEKN | NDTQKHQGRA | RRKRKSVTFK | GFPDRKSLQK | EAEEERKLHS | FLKSFGPPVS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CSPLGQHHDT | TLFRRLLCPD | PVCRVCNRAT | ADIQRLLSWE | SLKDAAPSVS | PLASSASGAE | IVHSGFSSFT | LASTPSATTP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EDLILSSRPK | PSPPPPLILS | PDLITTLXLI | FTLTIADLFS | PSPLRDPLPP | QPTPLDSKFP | IDHSPPQQLP | FPLLPPHHIE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RVEPSLQPEA | SLSLNTIFSF | GSTLCQDISQ | AVNRTDSCAR | HHGPPTPSAL | PPEDCTVTQS | KSNLTVLKTF | PEMLSLGGSG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GSSTSAPTTK | GIDHSCPASS | EFSWWQPHAK | DSFSSNFVPS | DFMEELLTLH | SSEASLGGHS | VANIIQPVNI | SFLSHDIPAL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LERQVKRRGD | FLMWKENGKK | PGSFPTQLRP | NYQLNSSRNM | LTSTAVKHDL | AESFPFWASK | GKLEWQHIHQ | QPPYSKCFED |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HLEQKYVQLF | WGLPSLHSES | LHPTVFVQHG | RSSMFVFFNG | ITNTSMSHES | PVLPPPQPLF | LPSTQPLPLP | QTLPRGQSLH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LTQVKSLAQP | QSPFPALPPS | PLFLIRVCGV | CFHRPQNEAR | SLMPSEINHL | EWNVLQKVQE | SVWGLPSVVQ | KSQEDFCPPA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PNPVLVRKSF | KVHVPISIIP | GDFPLSSEVR | KKLEQHIRKR | LIQRRWGLPR | RIHESLSLLR | PQNKISELSV | SESIHGPLNI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SLVEGQRCNV | LKKSASSFPR | SFHERSSNML | SMENVGNYQG | CSQETAPKNH | LLHDPETSSE | EDLRSNSERD | LGTHMMHLSG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NDSGVRLGQK | QLENALTVHL | SKKFEEINEG | RMPGTVHSSW | HSVKQTICLP | EKSHSQIKHR | NLAALVSEDH | RVDTSQEMSF |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LSSNKQKMLS | PYXIFPYEAH | IKSFHMRMLW | GLPRKIREPT | EIFKSEEDIS | NSFSHFYLPS | SASFISQGDS | KDGVSKSCRR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| STFQGEKLGT | TSSVPVLNHP | QPVSSPIGKE | GQGTLRRQFS | DTDHDLIETD | AKDGASTPLR | RGTTYFQGEK | LETTSSFSIL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GHPHLVTSPV | DQEKQGTLRR | EFADTDEDLT | ESVWTTEDGR | QTFLPPTHSI | IDEVSQKQTV | LASRCSAELP | ILQAGVGRDS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RDKRESASNN | VNRLQGSRKT | FPVTNGSKEM | FKEEEICTLQ | SQTRNNLTTS | KSGSCLVTNV | KRSTSHETEI | FPPRISVPQT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PKSSYLKNQM | LSQLKLVQRK | HSQPQSHFTG | MSLALDNLSS | KDLLTHAQGI | SNQDLGTSQV | LHVHLEVRGI | RVAQQQEPRV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PTHVLQKCQV | KNFSPATKRV | SPLRPNGGEL | GGGDAGLGTS | QLRRKSHAIH | NKTSRESLGS | KSSPTLKTQP | PPENLFGTLM |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KTFLQQSNKP | IITYGKQESS | XEKGSSLSSS | VQNRGRVKSR | AVFTGTIEAQ | KIRKDTGEFI | EEKLGHRHXI | DITCPQEPLS |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| SPVQLGKSQN | VPELQVRAEP | VQGYPCNYMA | PSCKVTCTKS | CSQQAIFVGQ | NYPAMIRQII | DKDRXPQEVX | TFKGKILCQR |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | |
| HPQSMPHRKP | VPQPNPTCSX | EVNLVPPVIL | TSAKNTVFSD | VPLLTGQKIL | PKHLQGGKFP | PKK | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 149 | 1 | 636.2737 | -54.29 | 3 | 30.8 | 12.2 | 1 | 0-0 | .QESSPEKGSSLSSSVQNR. | |

# Detailed Protein Report

## Protein 1368: PREDICTED: 1-acyl-sn-glycerol-3-phosphate acyltransferase delta isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530383876 | **Score:** | 12.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578812839 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: 1-acyl-sn-glycerol-3-phosphate acyltransferase delta isoform X8 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDLAGLLKSQ | FLCHLVFCYV | FIASGLIINT | IQLFTLLLWP | INKQLFRKIN | CRLSYCISSQ | LVMLLEWWSG | TECTIFTDPR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AYLKYGKENA | IVVLNHKFEI | DFLCGWSLSE | RFGLLGGSKV | LAKKELAYVP | IIGWMWYFTE | MVFCSRKWEQ | DRKTVATSLQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HLRDYPEKYF | FLIHCEGTRF | TEKKHEISMQ | VARAKGLPRL | KHHLLPRTKG | FAITVRSLRN | VEIMKIQHCW | ES |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 40 | 1 | 845.3297 | -71.12 | 2 | 29.5 | 12.2 | 1 | 220-232 | R.NVEIMKIQHCWES.- | Carbamidomethyl: 10;<br>Oxidation: 5 |

# Detailed Protein Report

## Protein 1369: dexamethasone-induced Ras-related protein 1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|317008582 | **Score:** | 12.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 13.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.16 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MKLAAMIKKM CPSDSELSIP AKNCYRMVIL GSSKVGKTAI VSRFLTGRFE DAYTPTIEDF HRKFYSIRGE VYQLDILDTS
        90        100        110        120        130
GNHPFPAMRR LSILTDPRHQ VLPQEQNQGE RGRAPGHLRQ QG
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 574 | 1 | 469.1205 | -305.92 | 2 | 36.8 | 12.1 | 1 | 1-8 | -.MKLAAMIK.K | Oxidation: 1, 6 | WUP:QUP 0.16 |

# Detailed Protein Report

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## Protein 1370: PREDICTED: kinesin-like protein KIF21A isoform X9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530400550 | **Score:** | 12.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 179.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 0.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLGAPDESSV | RVAVRIRPQL | AKEKIEGCHI | CTSVTPGEPQ | VFLGKDKAFT | FDYVFDIDSQ | QEQIYIQCIE | KLIEGCFEGY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NATVFAYGQT | GAGKTYTMGT | GFDVNIVEEE | LGIISRAVKH | LFKSIEEKKH | IAIKNGLPAP | DFKVNAQFLE | LYNEEVLDLF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DTTRDIDAKS | KKSNIRIHED | STGGIYTVGV | TTRTVNTESE | MMQCLKLGAL | SRTTASTQMN | VQSSRSHAIF | TIHVCQTRVC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PQIDADNATD | NKIISESAQM | NEFETLTAKF | HFVDLAGSER | LKRTGATGER | AKEGISINCG | LLALGNVISA | LGDKSKRATH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VPYRDSKLTR | LLQDSLGGNS | QTIMIACVSP | SDRDFMETLN | TLKYANRARN | IKNKVMVNQD | RASQQINALR | SEITRLQMEL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MEYKTGKRII | DEEGVESIND | MFHENAMLQT | ENNNLRVRIK | AMQETVDALR | SRITQLVSDQ | ANHVLARAGE | GNEEISNMIH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SYIKEIEDLR | AKLLESEAVN | ENLRKNLTRA | TARAPYFSGS | STFSPTILSS | DKETIEIIDL | AKKDLEKLKR | KEKRKKKRLQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KLEESNREER | SVAGKEDNTD | TDQEKKEEKG | VSERENNELE | VEESQEVSDH | EDEEEEEEEE | EDDIDGGESS | DESDSESDEK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ANYQADLANI | TCEIAIKQKL | IDELENSQKR | LQTLKKQYEE | KLMMLQHKIR | DTQLERDQVL | QNLGSVESYS | EEKAKKVRSE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YEKKLQAMNK | ELQRLQAAQK | EHARLLKNQS | QYEKQLKKLQ | QDVMEMKKTK | VRLMKQMKEE | QEKARLTESR | RNREIAQLKK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DQRKRDHQLR | LLEAQKRNQE | VVLRRKTEEV | TALRRQVRPM | SDKVAGKVTR | KLSSSDAPAQ | DTGSSAAAVE | TDASRTGAQQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KMRIPVARVQ | ALPTPATNGN | RKKYQRKGLT | GRVFISKTAR | MKWQLLERRV | TDIIMQKMTI | SNMEADMNRL | LKQREELTKR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| REKLSKRREK | IVKENGEGDK | NVANINEEME | SLTANIDYIN | DSISDCQANI | MQMEEAKEEG | ETLDVTAVIN | ACTLTEARYL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LDHFLSMGIN | KGLQAAQKEA | QIKVLEGRLK | QTEITSATQN | QLLFHMLKEK | AELNPELDAL | LGHALQENVE | DSTDEDAPLN |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SPGSEGSTLS | SDLMKLCGEV | KPKNKARRRT | TTQMELLYAD | SSELASDTST | GDASLPGPLT | PVAEGQEIGM | NTETSGTSAR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EKELSPPPGL | PSKIGSISRQ | SSLSEKKIPE | PSPVTRRKAY | EKAEKSKAKE | QKQGIINPFP | ASKGIRAFPL | QCIHIAEGHT |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KAVLCVDSTD | DLLFTGSKDR | TCKVWNLVTG | QEIMSLGGHP | NNVVSVKYCN | YTSLVFTVST | SYIKVWDIRD | SAKCIRTLTS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| SGQVTLGDAC | SASTSRTVAI | PSGENQINQI | ALNPTGTFLY | AASGNAVRMW | DLKRFQSTGK | LTGHLGPVMC | LTVDQISSGQ |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DLIITGSKDH | YIKMFDVTEG | ALGTVSPTHN | FEPPHYDGIE | ALTIQGDNLF | SGSRDNGIKK | WDLTQKDLLQ | QVPNAHKDWV |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| CALGVVPDHP | VLLSGCRGGI | LKVWNMDTFM | PVGEMKGHDS | PINAICVNST | HIFTAADDRT | VRIWKARNLQ | DGQISDTGDL |
| 1610 | | | | | | | |
| GEDIASN | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 383 | 2 | 625.4008 | 133.02 | 2 | 34.4 | 12.1 | 1 | 759-768 | K.LQQDVMEMKK.T | |

# Detailed Protein Report

## Protein 1371: PREDICTED: SH2B adapter protein 2 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530431159 | **Score:** | 12.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 72.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 4.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDPSYCPAHG | FPSQDPLWPL | SSQQWSSAHY | SEPAAGGCDG | TEAMNGAGPG | PAAAAPVPVP | VPVPDWRQFC | ELHAQAAAVD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FAHKFCRFLR | DNPAYDTPDA | GASFSRHFAA | NFLDVFGEEV | RRVLVAGPTT | RGAAVSAEAM | EPELADTSAL | KAAPYGHSRS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SEDVSTHAAT | KARVRKGFSL | RNMSLCVVDG | VRDMWHRRAS | PEPDAAAAPR | TAEPRDKWTR | RLRLSRTLAA | KVELVDIQRE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GALRFMVADD | AAAGSGGSAQ | WQKCRLLLRR | AVAEERFRLE | FFVPPKASRP | KVSIPLSAII | EVRTTMPLEM | PEKDNTFVLK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VENGAEYILE | TIDSLQKHSW | VADIQGCVDP | GDSEEDTELS | CTRGGCLASR | VASCSCELLT | DVDLPRPPET | TAVGAVVTAP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HSRGRDAVRE | SLIHVPLETF | LQTLESPGGS | GSDSNNTGEQ | GAETDPEAEP | ELELSDYPWF | HGTLSRVKAA | QLVLAGGPRN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HGLFVIRQSE | TRPGEYVLTF | NFQGKAKHLR | LSLNGHGQCH | VQHLWFQSVL | DMLRHFHTHP | IPLESGGSAD | ITLRSYVRAQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DPPPEPGPTP | PAAPASPACW | SDSPGQHYFS | SLAAAACPPA | SPSDAAGASS | SSASSSSAAS | GPAPPRPVEG | QLSARSRSNS |
| 650 | 660 | 670 | 680 | | | | |
| AERLLEAVAA | TAAEEPPEAA | PGRARAVENQ | YSFY | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2484 | 1 | 1131.1716 | -58.41 | 3 | 59.3 | 12.1 | 0 | 371-403 | R.VASCSCELLTDVDLPRPPETTAVGAVVTAPHSR.G | |

# Detailed Protein Report

## Protein 1372: TPR and ankyrin repeat-containing protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|257467636 | **Score:** | 12.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 336.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 0.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | |
|---|---|---|---|
| ***WUP:QUP*** | **Median:** 1.13 | **CV:** 0.00 % | **No. of Peptides:** 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWDPRAARVP | PRDLAVLLCN | KSNAFFSLGK | WNEAFVAAKE | CLQWDPTYVK | GYYRAGYSLL | RLHQPYEAAR | MFFEGLRLVQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RSQDQAPVAD | FLVGVFTTMS | SDSIVLQSFL | PCFDHIFTTG | FPTEVWQSVI | EKLAKKGLWH | SFLLLSAKKD | RLPRNIHVPE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LSLKSLFEKY | VFIGLYEKME | QVPKLVQWLI | SIGASVETIG | PYPLHALMRL | CIQARENHLF | RWLMDHKPEW | KGRINQKDGD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GCTVLHVVAA | HSPGYLVKRQ | TEDVQMLLRF | GADPTLLDRQ | SRSVVDVLKR | NKNFKAIEKI | NSHLEKLATC | SKDLSGFSNG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DGPTSENDIF | RKVLEQLVKY | MNSGNRLLHK | NFLKQEVVQR | FLRLLSTLQE | IPPDLVCDIN | QDCATTVFKF | LLEKQRWPEV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LLLLTRKVSG | EPPLGDCLIK | DCNFSDLDIC | TIIPHLSTWD | QRKKQLLGCL | IDSGALPDGL | QESQERPVVT | CLKHEDFELA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FLLLTKGADP | RAISLTEGDT | PLHAALHIFL | EIKADIGFSF | LSHLLDLFWS | NPTEFDYLNP | NVQDSNGNTL | MHILFQKGML |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KRVKKLLDLL | VKFDINFNLK | NKEGKDARHR | IKKNDSLLLA | WNKALMENRR | RSRQDSAAHL | GKLSKSTAPG | HTSQLKSQGS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FKSVPCGATA | RTLPEGSAVP | DSWETLPGTQ | VTRKEPGALR | PCSLRDCLMQ | DITVLIQQVE | VDPSFPEDCL | QSSEPLEAGA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GKEGKKDDKP | TLGAGAPDCS | EVGEGHAQVG | LGALQLVPDD | NRGKEGNDDQ | DDWSTQEIEA | CLQDFDNMTW | EIECTSEMLK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KLSSKVMTKV | IKKKIILAIQ | QLGNGEWTQG | LQKRLKHLKG | SIQLFEAKLD | KGARMLWELA | IDFSPRCSEN | PEKIIATEQN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TCAMEKSGRI | YTEIIRIWDI | VLDHCKLADS | IKAICNAYNR | GLSCVLRKKL | KGINKGQVSA | NMKIQKRIPR | CYVEDTEAEK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GREHVNPEYF | PPASAVETEY | NIMKFHSFST | NMAFNILNDT | TATVEYPFRV | GELEYAVIDL | NPRPLEPIIL | IGRSGTGKTT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| CCLYRLWKKF | HVYWEKAEQA | GSPLLAKQVW | LKRRLEVEPG | KESPGGEEEE | EEEDEEEEDS | IEVETVESID | EQEYEACAGG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| AGVEPAGDGQ | AAEVCAPEHP | HQLEHLHQIF | VTKNHVLCQE | VQRNFIELSK | STKATSHYKP | LDPNIHKLQD | LRDENFPLFV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| TSKQLLLLLD | ASLPKPFFLR | NEDGSLKRTI | IGWSAQEEST | IPSWQEDEEE | AEVDGDYSEE | DKAVEMRTGD | SDPRVYVTFE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VFKNEIWPKM | TKGRTAYNPA | LIWKEIKSFL | KGSFEALSCP | HGRLTEEVYK | KLGRKRCPNF | KEDRSEIYSL | FSLYQQIRSQ |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KGYFDEEDVL | YNISRRLSKL | RVLPWSIHEL | YGDEIQDFTQ | AELALLMKCI | NDPNSMFLTG | DTAQSIMKGV | AFRFSDLRSL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| FHYASRNTID | KQCAVRKPKK | IHQLYQNYRS | HSGILNLASG | VVDLLQFYFP | ESFDRLPRDS | GLFDGPKPTV | LESCSVSDLA |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ILLRGNKRKT | QPIEFGAHQV | ILVANETAKE | KIPEELGLAL | VLTIYEAKGL | EFDDVLLYNF | FTDSEAYKEW | KIISSFTPTS |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| TDSREENRPL | VEVPLDKPGS | SQGRSLMVNP | EMYKLLNGEL | KQLYTAITRA | RVNLWIFDEN | REKRAPAFKY | FIRRDFVQVV |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| KTDENKDFDD | SMFVKTSTPA | EWIAQGDYYA | KHQCWKVAAK | CYQKGGAFEK | EKLALAHDTA | LSMKSKKVSP | KEKQLEYLEL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| AKTYLECKEP | TLSLKCLSYA | KEFQLSAQLC | ERLGKIRDAA | YFYKRSQCYK | DAFRCFEQIQ | EFDLALKMYC | QEELFEEAAI |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| AVEKYEEMLK | TKTLPISKLS | YSASQFYLEA | AAKYLSANKM | KEMMAVLSKL | DIEDQLVFLK | SRKRLAEAAD | LLNREGRREE |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| AALLMKQHGC | LLEAARLTAD | KDFQASCLLG | AARLNVARDS | DIEHTKDILR | EALDICYQTG | QLSGIAEAHF | LQGVILRDFQ |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| KLRDAFFKFD | TLNHSAGVVE | ALYEAASQCE | AEPEKILGLA | PGGLEILLSL | VRALKRVTNN | AEKEMVKSCF | EFFGISQVDA |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| KYCQIAQNDP | GPILRIIFDL | DLNLREKKTK | DHFLIMTDQV | KLALNKHLLG | RLCQITRSLL | GKTYRGVCMR | FIVGLKCEDE |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 825 | 1 | 575.2745 | -105.17 | 2 | 40.3 | 12.1 | 0 | 155-164 | R.NIHVPELSLK.S |  | WUP:QUP 1.13 |

# Detailed Protein Report

## Protein 1373: PREDICTED: NADH-cytochrome b5 reductase 2 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530395471 | **Score:** | 12.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 28.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 7.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MNERRSARST | RLQLGDAPAS | APPRKHPPRT | RPRVGAHEDP | SLLLTITVTG | VTVLVLVLKS | MNSRRREPIT | LQDPEAKYPL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PLIEKEKISH | NTRRFRFGLP | SPDHVLGLPV | GNYVQLLAKI | DNELVVRAYT | PVSSDDDRGF | VDLIIKIYFK | NVHPQYPEGG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KMTQYLENMK | IGETIFFRGP | RGRLFYHGPG | NLGIRPDQTS | EPKKTLADHL | GMIAGGTGIT | PMLQLIRHIT | KDPSDRTRMS |
| 250 | 260 | | | | | | |
| LIFANQAGST | AQASLLPT | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 13 | 1 | 1018.9359 | -82.25 | 2 | 29.7 | 12.1 | 0 | 239-258 | R.MSLIFANQAGSTAQASLLPT.- | Oxidation: 1 |

# Detailed Protein Report

## Protein 1374: PREDICTED: disco-interacting protein 2 homolog C isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530392112 | **Score:** | 12.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 154.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MEHWISQAIH GSTTSTTSSS STQSGGSGAA HRLADVMAQT HIENHSAPPD VTTYTSEHSI QVERPQGSTG SRTAPKYGNA

        90        100        110        120        130        140        150        160
ELMETGDGVP VSSRVSAKIQ QLVNTLKRPK RPPLREFFVD DFEELLEVQQ PDPNQPKPEG AQMLAMRGEQ LGVVTNWPPS

       170        180        190        200        210        220        230        240
LEAALQRWGT ISPKAPCLTT MDTNGKPLYI LTYGKLWTRS MKVAYSILHK LGTKQEPMVR PGDRVALVFP NNDPAAFMAA

       250        260        270        280        290        300        310        320
FYGCLLAEVV PVPIEVPLTR KDAGSQQIGF LLGSCGVTVA LTSDACHKGL PKSPTGEIPQ FKGWPKLLWF VTESKHLSKP

       330        340        350        360        370        380        390        400
PRDWFPHIKD ANNDTAYIEY KTCKDGSVLG VTVTRTALLT HCQALTQACG YTEAETIVNV LDFKKDVGLW HGILTSVMNM

       410        420        430        440        450        460        470        480
MHVISIPYSL MKVNPLSWIQ KVCQYKAKVA CVKSRDMHWA LVAHRDQRDI NLSSLRMLIV ADGANPWSIS SCDAFLNVFQ

       490        500        510        520        530        540        550        560
SKGLRQEVIC PCASSPEALT VAIRRPTDDS NQPPGRGVLS MHGLTYGVIR VDSEEKLSVL TVQDVGLVMP GAIMCSVKPD

       570        580        590        600        610        620        630        640
GVPQLCRTDE IGELCVCAVA TGTSYYGLSG MTKNTFEVFP MTSSGAPISE YPFIRTGLLG FVGPGGLVFV VGKMDGLMVV

       650        660        670        680        690        700        710        720
SGRRHNADDI VATALAVEPM KFVYRGRIAV FSVTVLHDER IVIVAEQRPD STEEDSFQWM SRVLQAIDSI HQVGVYCLAL

       730        740        750        760        770        780        790        800
VPANTLPKTP LGGIHLSETK QLFLEGSLHP CNVLMCPHTC VTNLPKPRQK QPEIGPASVM VGNLVSGKRI AQASGRDLGQ

       810        820        830        840        850        860        870        880
IEDNDQARKF LFLSEVLQWR AQTTPDHILY TLLNCRGAIA NSLTCVQLHK RAEKIAVMLM ERGHLQDGDH VALVYPPGID

       890        900        910        920        930        940        950        960
LIAAFYGCLY AGCVPITVRP PHPQNIATTL PTVKMIVEVS RSACLMTTQL ICKLLRSREA AAAVDVRTWP LILDTDDLPK

       970        980        990       1000       1010       1020       1030       1040
KRPAQICKPC NPDTLAYLDF SVSTTGMLAG VKMSHAATSA FCRSIKLQCE LYPSREVAIC LDPYCGLGFV LWCLCSVYSG

      1050       1060       1070       1080       1090       1100       1110       1120
HQSILIPPSE LETNPALWLL AVSQYKVRDT FCSYSVMELC TKGLGSQTES LKARGLDLSR VRTCVVVAEE RPRIALTQSF

      1130       1140       1150       1160       1170       1180       1190       1200
SKLFKDLGLH PRAVSTSFGC RVNLAICLQP HRLWTLAEQG TSGPDPTTVY VDMRALRHDR VRLVERGSPH SLPLMESGKI

      1210       1220       1230       1240       1250       1260       1270       1280
LPGVRIIIAN PETKGPLGDS HLGEIWVHSA HNASGYFTIY GDESLQSDHF NSRLSFGDTQ TIWARTGYLG FLRRTELTDA

      1290       1300       1310       1320       1330       1340       1350       1360
NGERHDALYV VGALDEAMEL RGMRYHPIDI ETSVIRAHKS VTECAVFTWT NLLVVVVELD GSEQEALDLV PLVTNVVLEE

      1370       1380       1390       1400       1410
HYLIVGVVVV VDIGVIPINS RGEKQRMHLR DGFLADQLDP IYVAYNM
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1464 | 1 | 682.1037 | 135.03 | 3 | 48.5 | 12.1 | 0 | 486-504 | R.QEVICPCASSPEALTVAIR.R | Carbamidomethyl: 5 |

# Detailed Protein Report

## Protein 1375: PREDICTED: WASH complex subunit FAM21A isoform X6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530393647 | **Score:** | 12.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 81.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSVHYPHPTQ | GHKSGSLNPI | LFVGPGSSHT | PYLAFRNAFS | APDTSYLLLF | PKLSVKFCVW | KVIHTFIRSQ | KKLYTHKKKL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SQKKTQRVSL | LFEDDVDSGG | SLFGSPPTSV | PPATKKKETV | SEAPPLLFSD | EEEKEAQLGV | KSVDKKVESA | KESLKFGRTD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VAESEKEGLL | TRSAQETVKH | SDLFSSSSPW | DKGTKPRTKT | VLSLFDEEED | KMEDQNIIQA | PQKEVGKGRD | PDAHPKSTGV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FQDEELLFSH | KLQKDNDPDV | DLFAGTKKTK | LLEPSVGSLF | GDDEDDDLFS | SAKSQPLVQE | KKRVVKKDHS | VDSFKNQKHP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ESIQGSKEKG | IWKPETPQDS | SGLAPFKTKE | PSTRIGKIQA | NLAINPAALL | PTAASQISEV | KPVLPELAFP | SSEHRRSHGL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ESVPVLPGSG | EAGVSFDLPA | QADTLHSANK | SRVKMRGKRR | PQTRAARRLA | AQESSETEDM | SVPRGPIAQW | ADGAISPNGH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RPQLRAASGE | DSTEEALAAA | AAPWEGGPVP | GVDRSPFAKS | LGHSRGEADL | FDSGDIFSTG | TGSQSVERTK | PKAKIAENPA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NPPVGGKAKS | PMFPALGEAS | SDDDLFQSAK | PKPAKKTNPF | PLLEDEDDLF | TDQKVKKNET | KSNSQQDVIL | TTQDIFEDDI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FATEAIKPSQ | KTREKEKTLE | SNLFDDNIDI | FADLTVKPKE | KSKKKVEAKS | IFDDDMDDIF | SSGIQAKTTK | PKSRSAQAAP |
| 730 | 740 | 750 | | | | | |
| EPRFEHKVSN | IFDDPLNAFG | GQ | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2876 | 1 | 703.3637 | 1.39 | 2 | 66.6 | 12.1 | 2 | 224-236 | K.EVGKGRDPDAHPK.S | |

# Detailed Protein Report

## Protein 1376: alpha/beta hydrolase domain-containing protein 17C [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|151301175 | **Score:** | 12.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 35.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPEPGPRMNG | FSLGELCWLF | CCPPCPSRIA | AKLAFLPPEP | TYTVLAPEQR | GAGASAPAPA | QATAAAAAAQ | PAPQQPEEGA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GAGPGACSLH | LSERADWQYS | QRELDAVEVF | FSRTARDNRL | GCMFVRCAPS | SRYTLLFSHG | NAVDLGQMCS | FYIGLGSRIN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CNIFSYDYSG | YGVSSGKPSE | KNLYADIDAA | WQALRTRYGV | SPENIILYGQ | SIGTVPTVDL | ASRYECAAVI | LHSPLMSGLR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VAFPDTRKTY | CFDAFPSIDK | ISKVTSPVLV | IHGTEDEVID | FSHGLAMYER | CPRAVEPLWV | EGAGHNDIEL | YAQYLERLKQ |
| 330 | | | | | | | |
| FISHELPNS | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1764 | 1 | 798.3011 | -121.75 | 2 | 52.4 | 12.1 | 2 | 114-126 | R.TARDNRLGCMFVR.C | Carbamidomethyl: 9 |

# Detailed Protein Report

## Protein 1377: mastermind-like domain-containing protein 1 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|294489308 | **Score:** | 12.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 106.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDDWKSRLVI | KSMLPHFAMV | GNRQEPRKLQ | ESGTVKRRQE | EDHFQFPDMA | DGGYPNKIKR | PCLEDVTLAM | GPGAHPSTAC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AELQVPPLTI | NPSPAAMGVA | GQSLLLENNP | MNGNIMGSPF | VVPQTTEVGL | KGPTVPYYEK | INSVPAVDQE | LQELLEELTK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IQDPSPNELD | LEKILGTKPE | EPLVLDHPQA | TLSTTPKPSV | QMSHLESLAS | SKEFASSCSQ | VTGMSLQIPS | SSTGISYSIP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| STSKQIVSPS | SSMAQSKSQV | QAMLPVALPP | LPVPQWHHAH | QLKALAASKQ | GSATKQQGPT | PSWSGLPPPG | LSPPYRPVPS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PHPPPLPLPP | PPPPFSPQSL | MVSCMSSNTL | SGSTLRGSPN | ALLSSMTSSS | NAALGPAMPY | APEKLPSPAL | TQQPQFGPQS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SILANLMSST | IKTPQGHLMS | ALPASNPGPS | PPYRPEKLSS | PGLPQQSFTP | QCSLIRSLTP | TSNLLSQQQQ | QQQQQQQANV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IFKPISSNSS | KTLSMIMQQG | MASSSPGATE | PFTFGNTKPL | SHFVSEPGPQ | KMPSMPTTSR | QPSLLHYLQQ | PTPTQASSAT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ASSTATATLQ | LQQQQQQQQQ | QPDHSSFLLQ | QMMQQPQRFQ | RSVASDSMPA | LPRQQEEQRS | GLMAMTPERQ | NAYISQQMSP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FEAVQEQVTS | KCSRIKASPP | SSKHLMPPRT | GLLQNNLSPG | MIPLTRHQSC | EGMGVISPTL | GKRQGIFTSS | PQCPILSHSG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QTPLGRLDSV | CQHMQSPKAT | PPEVPLPGFC | PSSLGTQSLS | PHQLRRPSVP | RMPTAFNNAA | WVTAAAAVTT | AVSGKTPLSQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VDNSVQQHSP | SGQACLQRPS | DWEAQVPAAM | GTQVPLANNP | SFSLLGSQSL | RQSPVQGPVP | VANTTKFLQQ | GMASFSPLSP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| IQGIEPPSYV | AAAATAAAAS | AVAASQFPGP | FDRTDIPPEL | PPADFLRQPQ | PPLNDLISSP | DCNEVDFIEA | LLKGSCVSPD |
| 970 | 980 | 990 | 1000 | | | | |
| EDWVCNLRLI | DDILEQHAAA | QNATAQNSGQ | VTQDAGAL | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2352 | 1 | 682.2315 | -142.50 | 3 | 59.9 | 12.1 | 1 | 602-619 | R.SVASDSMPALPRQQEEQR.S | Oxidation: 7 |

# Detailed Protein Report

## Protein 1378: glutamate receptor ionotropic, NMDA 2A isoform 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|197313638 | **Score:** | 12.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 144.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGRVGYWTLL | VLPALLVWRG | PAPSAAAEKG | PPALNIAVML | GHSHDVTERE | LRTLWGPEQA | AGLPLDVNVV | ALLMNRTDPK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SLITHVCDLM | SGARIHGLVF | GDDTDQEAVA | QMLDFISSHT | FVPILGIHGG | ASMIMADKDP | TSTFFQFGAS | IQQQATVMLK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IMQDYDWHVF | SLVTTIFPGY | REFISFVKTT | VDNSFVGWDM | QNVITLDTSF | EDAKTQVQLK | KIHSSVILLY | CSKDEAVLIL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SEARSLGLTG | YDFFWIVPSL | VSGNTELIPK | EFPSGLISVS | YDDWDYSLEA | RVRDGIGILT | TAASSMLEKF | SYIPEAKASC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YGQMERPEVP | MHTLHPFMVN | VTWDGKDLSF | TEEGYQVHPR | LVVIVLNKDR | EWEKVGKWEN | HTLSLRHAVW | PRYKSFSDCE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PDDNHLSIVT | LEEAPFVIVE | DIDPLTETCV | RNTVPCRKFV | KINNSTNEGM | NVKKCCKGFC | IDILKKLSRT | VKFTYDLYLV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TNGKHGKKVN | NVWNGMIGEV | VYQRAVMAVG | SLTINEERSE | VVDFSVPFVE | TGISVMVSRS | NGTVSPSAFL | EPFSASVWVM |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MFVMLLIVSA | IAVFVFEYFS | PVGYNRNLAK | GKAPHGPSFT | IGKAIWLLWG | LVFNNSVPVQ | NPKGTTSKIM | VSVWAFFAVI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FLASYTANLA | AFMIQEEFVD | QVTGLSDKKF | QRPHDYSPPF | RFGTVPNGST | ERNIRNNYPY | MHQYMTKFNQ | KGVEDALVSL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KTGKLDAFIY | DAAVLNYKAG | RDEGCKLVTI | GSGYIFATTG | YGIALQKGSP | WKRQIDLALL | QFVGDGEMEE | LETLWLTGIC |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| HNEKNEVMSS | QLDIDNMAGV | FYMLAAAMAL | SLITFIWEHL | FYWKLRFCFT | GVCSDRPGLL | FSISRGIYSC | IHGVHIEEKK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KSPDFNLTGS | QSNMLKLLRS | AKNISSMSNM | NSSRMDSPKR | AADFIQRGSL | IMDMVSDKGN | LMYSDNRSFQ | GKESIFGDNM |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NELQTFVANR | QKDNLNNYVF | QGQHPLTLNE | SNPNTVEVAV | STESKANSRP | RQLWKKSVDS | IRQDSLSQNP | VSQRDEATAE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| NRTHSLKSPR | YLPEEMAHSD | ISETSNRATC | HREPDNSKNH | KTKDNFKRSV | ASKYPKDCSE | VERTYLKTKS | SSPRDKIYTI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DGEKEPGFHL | DPPQFVENVT | LPENVDFPDP | YQDPSENFRK | GDSTLPMNRN | PLHNEEGLSN | NDQYKLYSKH | FTLKDKGSPH |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SETSERYRQN | STHCRSCLSN | MPTYSGHFTM | RSPFKCDACL | RMGNLYDIDE | DQMLQETGMT | NAWLLGDAPR | TLTNTRCHPR |
| 1290 | | | | | | | |
| R | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2193 | 1 | 952.8178 | -94.66 | 2 | 57.3 | 12.1 | 0 | 1216-1231 | R.SCLSNMPTYSGHFTMR.S | Carbamidomethyl: 2; Oxidation: 6 |

# Detailed Protein Report

**Protein 1379:** **nucleolar protein 58 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|7706254 | **Score:** | 12.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLVLFETSVG | YAIFKVLNEK | KLQEVDSLWK | EFETPEKANK | IVKLKHFEKF | QDTAEALAAF | TALMEGKINK | QLKKVLKKIV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KEAHEPLAVA | DAKLGGVIKE | KLNLSCIHSP | VVNELMRGIR | SQMDGLIPGV | EPREMAAMCL | GLAHSLSRYR | LKFSADKVDT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MIVQAISLLD | DLDKELNNYI | MRCREWYGWH | FPELGKIISD | NLTYCKCLQK | VGDRKNYASA | KLSELLPEEV | EAEVKAAAEI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SMGTEVSEED | ICNILHLCTQ | VIEISEYRTQ | LYEYLQNRMM | AIAPNVTVMV | GELVGARLIA | HAGSLLNLAK | HAASTVQILG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AEKALFRALK | SRRDTPKYGL | IYHASLVGQT | SPKHKGKISR | MLAAKTVLAI | RYDAFGEDSS | SAMGVENRAK | LEARLRTLED |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RGIRKISGTG | KALAKTEKYE | HKSEVKTYDP | SGDSTLPTCS | KKRKIEQVDK | EDEITEKKAK | KAKIKVKVEE | EEEEKVAEEE |
| 490 | 500 | 510 | 520 | 530 | | | |
| ETSVKKKKKR | GKKKHIKEEP | LSEEEPCTST | AIASPEKKKK | KKKKRENED | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1433 | 1 | 991.5926 | 119.73 | 2 | 48.1 | 12.0 | 1 | 134-150 | R.EMAAMCLGLAHSLSRYR.L | Carbamidomethyl: 6;<br>Oxidation: 2 |

# Detailed Protein Report

## Protein 1380: PREDICTED: tripartite motif-containing protein 2 isoform X2 [Homo sapiens]

**Accession:** gi|578808962

**Database:** refseq_human(refseq_human_20140103.fasta)

**Database Date:** 2015-11-30

**Score:** 12.0

**MW [kDa]:** 84.7

**pI:** 7.3

**Sequence Coverage [%]:** 1.4

**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MHRSGRYGTQ | QRAGSKTAGP | PCQWSRMASE | GTNIPSPVVR | QIDKQFLICS | ICLERYKNPK | VLPCLHTFCE | RCLQNYIPAH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SLTLSCPVCR | QTSILPEKGV | AALQNNFFIT | NLMDVLQRTP | GSNAEESSIL | ETVTAVAAGK | PLSCPNHDGN | VMEFYCQSCE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TAMCRECTEG | EHAEHPTVPL | KDVVEQHKAS | LQVQLDAVNK | RLPEIDSALQ | FISEIIHQLT | NQKASIVDDI | HSTFDELQKT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LNVRKSVLLM | ELEVNYGLKH | KVLQSQLDTL | LQGQESIKSC | SNFTAQALNH | GTETEVLLVK | KQMSEKLNEL | ADQDFPLHPR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ENDQLDFIVE | TEGLKKSIHN | LGTILTTNAV | ASETVATGEG | LRQTIIGQPM | SVTITTKDKD | GELCKTGNAY | LTAELSTPDG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SVADGEILDN | KNGTYEFLYT | VQKEGDFTLS | LRLYDQHIRG | SPFKLKVIRS | ADVSPTTEGV | KRRVKSPGSG | HVKQKAVKRP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ASMYSTGKRK | ENPIEDDLIF | RVGTKGRNKG | EFTNLQGVAA | STNGKILIAD | SNNQCVQIFS | NDGQFKSRFG | IRGRSPGQLQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RPTGVAVHPS | GDIIIADYDN | KWVSIFSSDG | KFKTKIGSGK | LMGPKGVSVD | RNGHIIVVDN | KACCVFIFQP | NGKIVTRFGS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RGNGDRQFAG | TLDGPHFAAV | NSNNEIIITD | FHNHSVKVFN | QEGEFMLKFG | SNGEGNGQFN | APTGVAVDSN | GNIIVADWGN |
| 730 | 740 | 750 | 760 | 770 | 780 | | |
| SRIQVFDGSG | SFLSYINTSA | DPLYGPQGLA | LTSDGHVVVA | DSGNHCFKVY | RYLQ | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2668 | 1 | 673.3612 | 23.64 | 2 | 63.5 | 12.0 | 2 | 2-12 | M.HRSGRYGTQQR.A | |

# Detailed Protein Report

## Protein 1381: EVI5-like protein isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21687020 | **Score:** | 12.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 91.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASPTLSPDS | SSQEALSAPT | CSPTSDSENL | SPDELELLAK | LEEQNRLLEA | DSKSMRSMNG | SRRNSGSSLV | SSSSASSNLS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HLEEDTWILW | GRIANEWEEW | RRRKEKLLKE | LIRKGIPHHF | RAIVWQLLCS | ATDMPVKNQY | SELLKMSSPC | EKLIRRDIAR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TYPEHEFFKG | QDSLGQEVLF | NVMKAYSLVD | REVGYCQGSA | FIVGLLLMQM | PEEEAFCVFV | RLMQEYRLRE | LFKPSMAELG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LCIYQFEYML | QEQLPDLNTH | FRSQSFHTSM | YASSWFLTLF | LTTFPLPVAT | RVFDIFMYEG | LEIVFRVGLA | LLQVNQAELM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QLDMEGMSQY | FQRVIPHQFD | SCPDKLVLKA | YQVKYNPKKM | KRLEKEYAAM | KSKEMEEQIE | IKRLRTENRL | LKQRIETLEK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GQVTRAQEAE | ENYVIKRELA | VVRQQCSSAA | EDLQKAQSTI | RQLQEQQENP | RLTEDFVSHL | ETELEQSRLR | ETETLGALRE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| MQDKVLDMEK | RNSSLPDENN | VAQLQEELKA | LKVREGQAVA | STRELKLQLQ | ELSDTWQAHL | ARGGRWKESP | RKLVVGELQD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ELMSVRLREA | QALAEGRELR | QRVVELETQD | HIHRNLLNRV | EAERAALQEK | LQYLAAQNKG | LQTQLSESRR | KQAEAECKSK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EEVMAVRLRE | ADSMAAVAEM | RQRIAELEIQ | REEGRIQGQL | NHSDSSQYIR | ELKDQIEELK | AEVRLLKGPP | PFEDPLAFDG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LSLARHLDED | SLPSSDEELL | GVGVGAALQD | ALYPLSPRDA | RFFRRLERPA | KDSEGSSDSD | ADELAAPYSQ | GLDN |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1090 | 1 | 775.2584 | -152.54 | 2 | 43.7 | 12.0 | 1 | 648-661 | R.LREADSMAAVAEMR.Q | |

# Detailed Protein Report

## Protein 1382: proline-rich nuclear receptor coactivator 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5802982 | **Score:** | 12.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 35.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTVVSVPQRE | PLVLGGRLAP | LGFSSRGYFG | ALPMVTTAPP | PLPRIPDPRA | LPPTLFLPHF | LGGDGPCLTP | QPRAPAALPN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RSLAVAGGTP | RAAPKKRRKK | KVRASPAGQL | PSRFHQYQQH | RPSLEGGRSP | ATGPSGAQEV | PGPAAALAPS | PAAAAGTEGA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SPDLAPLRPA | APGQTPLRKE | VLKSKMGKSE | KIALPHGQLV | HGIHLYEQPK | INRQKSKYNL | PLTKITSAKR | NENNFWQDSV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SSDRIQKQEK | KPFKNTENIK | NSHLKKSAFL | TEVSQKENYA | GAKFSDPPSP | SVLPKPPSHW | MGSTVENSNQ | NRELMAVHLK |
| 330 | | | | | | | |
| TLLKVQT | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2381 | 1 | 951.1462 | 150.40 | 2 | 58.0 | 12.0 | 0 | 27-44 | R.GYFGALPMVTTAPPPLPR.I | Oxidation: 8 |

# Detailed Protein Report

## Protein 1383: probable ATP-dependent RNA helicase DDX49 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|31542656 | **Score:** | 12.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 4.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAGFAELGLS | SWLVEQCRQL | GLKQPTPVQL | GCIPAILEGR | DCLGCAKTGS | GKTAAFVLPI | LQKLSEDPYG | IFCLVLTPTR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ELAYQIAEQF | RVLGKPLGLK | DCIIVGGMDM | VAQALELSRK | PHVVIATPGR | LADHLRSSNT | FSIKKIRFLV | MDEADRLLEQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GCTDFTVDLE | AILAAVPARR | QTLLFSATLT | DTLRELQGLA | TNQPFFWEAQ | APVSTVEQLD | QRYLLVPEKV | KDAYLVHLIQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RFQDEHEDWS | IIIFTNTCKT | CQILCMMLRK | FSFPTVALHS | MMKQKERFAA | LAKFKSSIYR | ILIATDVASR | GLDIPTVQVV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| INHNTPGLPK | IYIHRVGRTA | RAGRQGQAIT | LVTQYDIHLV | HAIEEQIKKK | LEEFSVEEAE | VLQILTQVNV | VRRECEIKLE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AAHFDEKKEI | NKRKQLILEG | KDPDLEAKRK | AELAKIKQKN | RRFKEKVEET | LKRQKAGRAG | HKGRPPRTPS | GSHSGPVPSQ |
| 490 | | | | | | | |
| GLV | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2337 | 1 | 848.8320 | 49.46 | 3 | 59.7 | 12.0 | 0 | 371-392 | K.LEEFSVEEAEVLQILTQVNVVR.R | |

# Detailed Protein Report

## Protein 1384: PREDICTED: multidrug resistance-associated protein 1 isoform X6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578828091 | **Score:** | 12.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 156.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| | | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MALRGFCSAD | GSDPLWDWNV | TWNTSNPDFT | KCFQNTVLVW | VPCFYLWACF | PFYFLYLSRH | DRGYIQMTPL | NKTKTNPCPE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SSASFLSRIT | FWWITGLIVR | GYRQPLEGSD | LWSLNKEDTS | EQVVPVLVKN | WKKECAKTRK | QPVKVVYSSK | DPAQPKESSK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VDANEEVEAL | IVKSPQKEWN | PSLFKVLYKT | FGPYFLMSFF | FKAIHDLMMF | SGPQILKLLI | KFVNDTKAPD | WQGYFYTVLL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FVTACLQTLV | LHQYFHICFV | SGMRIKTAVI | GAVYRKALVI | TNSARKSSTV | GEIVNLMSVD | AQRFMDLATY | INMIWSAPLQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VILALYLLWL | NLGPSVLAGV | AVMVLMVPVN | AVMAMKTKTY | QVAHMKSKDN | RIKLMNEILN | GIKVLKLYAW | ELAFKDKVLA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IRQEELKVLK | KSAYLSAVGT | FTWVCTPFLV | ALCTFAVYVT | IDENNILDAQ | TAFVSLALFN | ILRFPLNILP | MVISSIVQAS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VSLKRLRIFL | SHEELEPDSI | ERRPVKDGGG | TNSITVRNAT | FTWARSDPPT | LNGITFSIPE | GALVAVVGQV | GCGKSSLLSA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LLAEMDKVEG | HVAIKGSVAY | VPQQAWIQND | SLRENILFGC | QLEEPYYRSV | IQACALLPDL | EILPSGDRTE | IGEKGVNLSG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GQKQRVSLAR | AVYSNADIYL | FDDPLSAVDA | HVGKHIFENV | IGPKGMLKNK | TRILVTHSMS | YLPQVDVIIV | MSGGKISEMG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SYQELLARDG | AFAEFLRTYA | STEQEQDAEE | NGVTGVSGPG | KEAKQMENGM | LVTDSAGKQL | QRQLSSSSSY | SGDISRHHNS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TAELQKAEAK | KEETWKLMEA | DKAQTGQVKL | SVYWDYMKAI | GLFISFLSIF | LFMCNHVSAL | ASNYWLSLWT | DDPIVNGTQE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| HTKVRLSVYG | ALGISQGIAV | FGYSMAVSIG | GILASRCLHV | DLLHSILRSP | MSFFERTPSG | NLVNRFSKEL | DTVDSMIPEV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| IKMFMGSLFN | VIGACIVILL | ATPIAAIIIP | PLGLIYFFVQ | RFYVASSRQL | KRLESVSRSP | VYSHFNETLL | GVSVIRAFEE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QERFIHQSDL | KVDENQKAYY | PSIVANRWLA | VRLECVGNCI | VLFAALFAVI | SRHSLSAGLV | GLSVSYSLQV | TTYLNWLVRM |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SSEMETNIVA | VERLKEYSET | EKEAPWQIQE | TAPPSSWPQV | GRVEFRNYCL | RYREDLDFVL | RHINVTINGG | EKVGIVGRTG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| AGKSSLTLGL | FRINESAEGE | IIIDGINIAK | IGLHDLRFKI | TIIPQDPVLF | SGSLRMNLDP | FSQYSDEEVW | TSLELAHLKD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| FVSALPDKLD | HECAEGGENL | SVGQRQLVCL | ARALLRKTKI | LVLDEATAAV | DLETDDLIQS | TIRTQFEDCT | VLTIAHRLNT |
| 1370 | 1380 | 1390 | 1400 | 1410 | | | |
| IMDYTRVIVL | DKGEIQEYGA | PSDLLQQRGL | FYSMAKDAGL | V | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1249 | 1 | 863.6787 | 164.53 | 2 | 45.2 | 12.0 | 2 | 372-386 | R.IKLMNEILNGIKVLK.L | |

# Detailed Protein Report

## Protein 1385: PREDICTED: zinc finger CCCH domain-containing protein 14 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530404628 | **Score:** | 12.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 80.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEIGTEISRK | IRSAIKGKLQ | ELGAYVDEEL | PDYIMVMVAN | KKSQDQMTED | LSLFLGNNTI | RFTVWLHGVL | DKLRSVTTEP |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| SSLKSSDTNI | FDSNVPSNKS | NFSRGDERRH | EAAVPPLAIP | SARPEKRDSR | VSTSSQESKT | TNVRQTYDDG | AATRLMSTVK |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| PLREPAPSED | VIDIKPEPDD | LIDEDLNFVQ | ENPLSQKKPT | VTLTYGSSRP | SIEIYRPPAS | RNADSGVHLN | RLQFQQQQNS |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| IHAAKQLDMQ | SSWVYETGRL | CEPEVLNSLE | ETYSPFFRNN | SEKMSMEDEN | FRKRKLPVVS | SVVKVKKFNH | DGEEEEEDDD |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| YGSRTGSISS | SVSVPAKPER | RPSLPPSKQA | NKNLILKAIS | EAQESVTKTT | NYSTVPQKQT | LPVAPRTRTS | QEELLAEVVQ |
| **410** | **420** | **430** | **440** | **450** | **460** | **470** | **480** |
| GQSRTPRISP | PIKEEETKGD | SVEKNQDYYD | MESMVHADTR | SFILKKPKLS | EEVVVAPNQE | SGMKTADSLR | VLSGHLMQTR |
| **490** | **500** | **510** | **520** | **530** | **540** | **550** | **560** |
| DLVQPDKPAS | PKFIVTLDGV | PSPPGYMSDQ | EEDMCFEGMK | PVNQTAASNK | GLRGLLHPQQ | LHLLSRQLED | PNGSFSNAEM |
| **570** | **580** | **590** | **600** | **610** | **620** | **630** | **640** |
| SELSVAQKPE | KLLERCKYWP | ACKNGDECAY | HHPISPCKAF | PNCKFAEKCL | FVHPNCKYDA | KCTKPDCPFT | HVSRRIPVLS |
| **650** | **660** | **670** | **680** | **690** | **700** | **710** | **720** |
| PKPAVAPPAP | PSSSQLCRYF | PACKKMECPF | YHPKHCRFNT | QCTRPDCTFY | HPTINVPPRH | ALKWIRPQTS | E |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1725 | 1 | 1003.7849 | -111.00 | 2 | 51.4 | 12.0 | 0 | 425-440 | K.NQDYYDMESMVHADTR.S | Oxidation: 7, 10 |

# Detailed Protein Report

## Protein 1386: RNA-binding protein 14 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5454064 | **Score:** | 12.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKIFVGNVDG | ADTTPEELAA | LFAPYGTVMS | CAVMKQFAFV | HMRENAGALR | AIEALHGHEL | RPGRALVVEM | SRPRPLNTWK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IFVGNVSAAC | TSQELRSLFE | RRGRVIECDV | VKDYAFVHME | KEADAKAAIA | QLNGKEVKGK | RINVELSTKG | QKKGPGLAVQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SGDKTKKPGA | GDTAFPGTGG | FSATFDYQQA | FGNSTGGFDG | QARQPTPPFF | GRDRSPLRRS | PPRASYVAPL | TAQPATYRAQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PSVSLGAAYR | AQPSASLGVG | YRTQPMTAQA | ASYRAQPSVS | LGAPYRGQLA | SPSSQSAAAS | SLGPYGGAQP | SASALSSYGG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QAAAASSLNS | YGAQGSSLAS | YGNQPSSYGA | QAASSYGVRA | AASSYNTQGA | ASSLGSYGAQ | AASYGAQSAA | SSLAYGAQAA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SYNAQPSASY | NAQSAPYAAQ | QAASYSSQPA | AYVAQPATAA | AYASQPAAYA | AQATTPMAGS | YGAQPVVQTQ | LNSYGAQASM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GLSGSYGAQS | AAAATGSYGA | AAAYGAQPSA | TLAAPYRTQS | SASLAASYAA | QQHPQAAASY | RGQPGNAYDG | AGQPSAAYLS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MSQGAVANAN | STPPPYERTR | LSPPRASYDD | PYKKAVAMSK | RYGSDRRLAE | LSDYRRLSES | QLSFRRSPTK | SSLDYRRLPD |
| 650 | 660 | 670 | | | | | |
| AHSDYARYSG | SYNDYLRAAQ | MHSGYQRRM | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 349 | 1 | 639.8896 | 62.99 | 2 | 33.0 | 12.0 | 2 | 607-616 | R.RLAELSDYRR.L | |

# Detailed Protein Report

## Protein 1387: thioredoxin domain-containing protein 16 isoform 2 precursor [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|237648961 | **Score:** | 12.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 93.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
|  |  | **Sequence Coverage [%]:** | 1.5 |
|  |  | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.35 **CV:** 0.00 % **No. of Peptides:** 1

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFSGFNVFRV | GISFVIMCIF | YMPTVNSLPE | LSPQKYFSTL | QPGKASLAYF | CQADSPRTSV | FLEELNEAVR | PLQDYGISVA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KVNCVKEEIS | RYCGKEKDLM | KAYLFKGNIL | LREFPTDTLF | DVNAIVAHVL | FEVKYITNLE | DLQNIENALK | GKANIIFSYV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RAIGIPEHRA | VMEAAFVYGT | TYQFVLTTEI | ALLESIGSED | VEYAHLYFFH | CKLVLDLTQQ | CRRTLMEQPL | TTLNIHLFIK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TMKAPLLTEV | AEDPQQVSTV | HLQLGLPLVF | IVSQQATYEA | DRRTAEWVAW | RLLGKAGVLL | LLRDSLEVNI | PQDANVVFKR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AEEGVPVEFL | VLHDVDLIIS | HVENNMHIEE | IQEDEDNDME | GPDIDVQDDE | VAETVFRDRK | RKLPLELTVE | LTEETFNATV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MASDSIVLFY | AGWQAVSMAF | LQSYIDVAVK | LKGTSTMLLT | RINCADWSDV | CTKQNVTEFP | IIKMYKKGEN | PVSYAGMLGT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EDLLKFIQLN | RISYPVNITS | IQEAEEYLSG | ELYKDLILYS | SVSVLGLFSP | TMKTAKEDFS | EAGNYLKGYV | ITGIYSEEDV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LLLSTKYAAS | LPALLLARHT | EGKIESIPLA | STHAQDIVQI | ITDALLEMFP | EITVENLPSY | FRLQKPLLIL | FSDGTVNPQY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KKAILTLVKQ | KYLDSFTPCW | LNLKNTPVGR | GILRAYFDPL | PPLPLLVLVN | LHSGGQVFAF | PSDQAIIEEN | LVLWLKKLEA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GLENHITILP | AQEWKPPLPA | YDFLSMIDAA | TSQRGTRKVP | KCMKETDVQE | NDKEQHEDKS | AVRKEPIETL | RIKHWNRSNW |
| 810 | 820 | 830 |  |  |  |  |  |
| FKEAEKSFRR | DKELGCSKVN |  |  |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1399 | 1 | 720.3692 | 81.20 | 2 | 47.1 | 12.0 | 1 | 762-773 | K.CMKETDVQENDK.E |  | WUP:QUP 0.35 |

# Detailed Protein Report

## Protein 1388: carbohydrate sulfotransferase 11 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|291219907 | **Score:** | 12.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKPALLEVMR | MNRICRMVLA | TCLGSFILVI | FYFQIMRRNP | FGVDICCRKG | SRSPLQELYN | PIQLELSNTA | VLHQMRRDQV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TDTCRANSAT | SRKRRVLTPN | DLKHLVVDED | HELIYCYVPK | VACTNWKRLM | MVLTGRGKYS | DPMEIPANEA | HVSANLKTLN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QYSIPEINHR | LKSYMKFLFV | REPFERLVSA | YRNKFTQKYN | ISFHKRYGTK | IIKRQRKNAT | QEALRKGDDV | KFEEFVAYLI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DPHTQREEPF | NEHWQTVYSL | CHPCHIHYDL | VGKYETLEED | SNYVLQLAGV | GSYLKFPTYA | KSTRTTDEMT | TEFFQNISSE |
| 330 | 340 | 350 | | | | | |
| HQTQLYEVYK | LDFLMFNYSV | PSYLKLE | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2642 | 1 | 784.3526 | -74.09 | 3 | 61.3 | 12.0 | 2 | 158-176 | K.TLNQYSIPEINHRLKSYMK.F | Oxidation: 18 |

# Detailed Protein Report

## Protein 1389: PREDICTED: actin cytoskeleton-regulatory complex protein PAN1-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578844820 | **Score:** | 12.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MERHSTQARP | EEALKLEQPP | MCKDREPTTA | SQSTGMATPR | SHPPLDTDAA | TSSQGPEDRP | ENVVAKPASA | EVEGPDGALS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QLPLAKFFPP | DNPTHQLQML | ERSLREEELR | AQHQAALLRL | REMALQEKTL | AELAWLEHRR | GCLDSKRDRA | VLAALVEKQQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QALSRFEKEQ | REIQYLRHTQ | LFRHRDRKLL | LQHQRDVVSM | PGPVDILPIP | GPTDVVPAHE | LQAQAKLQQG | SSPKVKAAWE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GGSETSQQPE | ASLCPLTPCR | PSSSTSHRPQ | SSPASSKATR | PPTEQQDVTP | PQTTSDADGH | QQPPRPAWGE | DTHDPQGPLV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ESGSHVSQEP | GEQPRAPLLG | LQHVSPPDGQ | RLGPAFPAEE | AEGRLPTAQC | RSREVKEPPP | GKHPGNTAWA | STALDTSPTS |
| 410 | 420 | 430 | 440 | 450 | | | |
| SRACPRLELS | HWTRTESKED | GPWWPPTLAS | DPFTARRVAG | SISYRR | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1202 | 1 | 863.1498 | 168.34 | 2 | 44.6 | 12.0 | 1 | 150-165 | R.AVLAALVEKQQQALSR.F | |

# Detailed Protein Report

## Protein 1390: uncharacterized protein C2orf74 isoform 2 [Homo sapiens]

**Accession:** gi|221139896

**Database:** refseq_human(refseq_human_20140103.fasta)

**Database Date:** 2015-11-30

**Modification(s):** Oxidation

**Score:** 12.0

**MW [kDa]:** 13.2

**pI:** 5.2

**Sequence Coverage [%]:** 11.3

**No. of unique Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530367535 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: uncharacterized protein C2orf74 isoform X4 [Homo sapiens] |
| gi\|530367533 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: uncharacterized protein C2orf74 isoform X3 [Homo sapiens] |
| gi\|530367531 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: uncharacterized protein C2orf74 isoform X2 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MQVMNLNVPM RPGILVQRQS KEVLATPLEN RRDMEAEEEN QINEKQEPEN AGETGQEEDD GLQKIHTSVT RTPSVVESQK
        90        100        110        120
RPLKGVTFSR EVIVVDLGNE YPTPRSYTRE HKERK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 209 | 1 | 797.8984 | 85.12 | 2 | 32.3 | 12.0 | 0 | 33-45 | R.DMEAEEENQINEK.Q | Oxidation: 2 |

# Detailed Protein Report

## Protein 1391: GMP reductase 2 isoform 5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|545688070 | **Score:** | 12.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPHIDNDVKL | DFKDVLLRPK | RSTLKSRSEV | DLTRSFSFRN | SKQTYSGVPI | IAANMDTVGT | FEMAKVLCKH | LAASSGTGSS |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| DFEQLEQILE | AIPQVKYICL | DVANGYSEHF | VEFVKDVRKR | FPQHTIMAGN | VVTGEMVEEL | ILSGADIIKV | GIGPGSVCTT |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| RKKTGVGYPQ | LSAVMECADA | AHGLKGHIIS | DGGCSCPGDV | AKAFGAGADF | VMLGGMLAGH | SESGGELIER | DGKKYKLFYG |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| MSSEMAMKKY | AGGVAEYRAS | EGKTVEVPFK | GDVEHTIRDI | LGGIRSTCTY | VGAAKLKELS | RRTTFIRVTQ | QVNPIFSEAC |
| **330** | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1956 | 1 | 785.7909 | -76.62 | 2 | 54.8 | 12.0 | 1 | 237-249 | K.LFYGMSSEMAMKK.Y | Oxidation: 5, 9, 11 |

# Detailed Protein Report

## Protein 1392: angiogenin precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4557313 | **Score:** | 11.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 16.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.9 |
| | | **Sequence Coverage [%]:** | 6.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|148277046 | refseq_human (refseq_human_20140103.fasta) | angiogenin precursor [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MVMGLGVLLL | VFVLGLGLTP | PTLAQDNSRY | THFLTQHYDA | KPQGRDDRYC | ESIMRRRGLT | SPCKDINTFI | HGNKRSIKAI |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | |
| CENKNGNPHR | ENLRISKSSF | QVTTCKLHGG | SPWPPCQYRA | TAGFRNVVVA | CENGLPVHLD | QSIFRRP | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2690 | 3 | 607.3377 | 61.93 | 2 | 62.0 | 11.9 | 2 | 49-57 | R.YCESIMRRR.G | |

# Detailed Protein Report

## Protein 1393: engulfment and cell motility protein 1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|18765702 | **Score:** | 11.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 28.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 4.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.44 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.36 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|86788140 | refseq_human (refseq_human_20140103.fasta) | engulfment and cell motility protein 1 isoform 2 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MQVVKEQVMR ALTTKPSSLD QFKSKLQNLS YTEILKIRQS ERMNQEDFQS RPILELKEKI QPEILELIKQ QRLNRLVEGT
        90        100        110        120        130        140        150        160
CFRKLNARRR QDKFWYCRLS PNHKVLHYGD LEESPQGEVP HDSLQDKLPV ADIKAVVTGK DCPHMKEKGA LKQNKEVLEL
       170        180        190        200        210        220        230        240
AFSILYDSNC QLNFIAPDKH EYCIWTDGLN ALLGKDMMSD LTRNDLDTLL SMEIKLRLLD LENIQIPDAP PPIPKEPSNY
       250
DFVYDCN
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1995 | 1 | 678.8162 | -37.70 | 2 | 55.3 | 11.9 | 2 | 141-152 | K.DCPHMKEKGALK.Q | | QU:MU<br>WUP:QUP | 0.44<br>2.36 |

# Detailed Protein Report

## Protein 1394: spindle assembly abnormal protein 6 homolog [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|35038601 | **Score:** | 11.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 74.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.9 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSQVLFHQLV | PLQVKCKDCE | ERRVSIRMSI | ELQSVSNPVH | RKDLVIRLTD | DTDPFFLYNL | VISEEDFQSL | KFQQGLLVDF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LAFPQKFIDL | LQQCTQEHAK | EIPRFLLQLV | SPAAILDNSP | AFLNVVETNP | FKHLTHLSLK | LLPGNDVEIK | KFLAGCLKCS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KEEKLSLMQS | LDDATKQLDF | TRKTLAEKKQ | ELDKLRNEWA | SHTAALTNKH | SQELTNEKEK | ALQAQVQYQQ | QHEQQKKDLE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ILHQQNIHQL | QNRLSELEAA | NKDLTERKYK | GDSTIRELKA | KLSGVEEELQ | RTKQEVLSLR | RENSTLDVEC | HEKEKHVNQL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QTKVAVLEQE | IKDKDQLVLR | TKEAFDTIQE | QKVVLEENGE | KNQVQLGKLE | ATIKSLSAEL | LKANEIIKKL | QGDLKTLMGK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LKLKNTVTIQ | QEKLLAEKEE | KLQKEQKELQ | DVGQSLRIKE | QEVCKLQEQL | EATVKKLEES | KQLLKNNEKL | ITWLNKELNE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NQLVRKQDVL | GPSTTPPAHS | SSNTIRSGIS | PNLNVVDGRL | TYPTCGIGYP | VSSAFAFQNT | FPHSISAKNT | SHPGSGTKVQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FNLQFTKPNA | SLGDVQSGAT | ISMPCSTDKE | NGENVGLESK | YLKKREDSIP | LRGLSQNLFS | NSDHQRDGTL | GALHTSSKPT |
| 650 | 660 | | | | | | |
| ALPSASSAYF | PGQLPNS | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 239 | 1 | 801.7845 | -124.85 | 2 | 32.7 | 11.9 | 0 | 613-626 | R.GLSQNLFSNSDHQR.D | |

# Detailed Protein Report

## Protein 1395: PREDICTED: sodium/hydrogen exchanger 7 isoform X6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578838129 | **Score:** | 11.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 77.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MEPGDAARPG SGRATGAPPP RLLLLPLLLG WGLRVAAAAS ASSSGAAAED SSAMEELATE KEAEESHRQD SVSLLTFILL
        90        100        110        120        130        140        150        160
LTLTILTIWL FKHRRVRFLH ETGLAMIYGL IVGVILRYGT PATSGRDKSL SCTQEDRAFS TLLVNVSGKF FEYTLKGEIS
       170        180        190        200        210        220        230        240
PGKINSVEQN DMLRKVTFDP EVFFNILLPP IIFHAGYSLK KRHFFRNLGS ILAYAFLGTA VSCFIIGNLM YGVVKLMKIM
       250        260        270        280        290        300        310        320
GQLSDKFYYT DCLFFGAIIS ATDPVTVLAI FNELHADVDL YALLFGESVL NDAVAIVLSS SIVAYQPAGL NTHAFDAAAF
       330        340        350        360        370        380        390        400
FKSVGIFLGI FSGSFTMGAV TGVVTALVTK FTKLHCFPLL ETALFFLMSW STFLLAEACG FTGVVAVLFC GITQAHYTYN
       410        420        430        440        450        460        470        480
NLSVESRSRT KQLFEVLHFL AENFIFSYMG LALFTFQKHV FSPIFIIGAF VAIFLGRAAH IYPLSFFLNL GRRHKIGWNF
       490        500        510        520        530        540        550        560
QHMMMFSGLR GAMAFALAIR DTASYARQMM FTTTLLIVFF TVWIIGGGTT PMLSWLNIRV GVDPDQDPPP NNDSFQVLQG
       570        580        590        600        610        620        630        640
DGPDSARGNR TKQESAWIFR LWYSFDHNYL KPILTHSGPP LTTTLPAWCG LLARCLTSPQ VYDNQEPLRE EDSDFILTEG
       650        660        670        680        690        700        710
DLTLTYGDST VTANGSSSSH TASTSLEGSR RTKSSSEEVL ERDLGMGDQK VSSRGTRLVF PLEDNA
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 843 | 1 | 937.9669 | -59.83 | 2 | 38.9 | 11.9 | 1 | 458-473 | R.AAHIYPLSFFLNLGRR.H | |

# Detailed Protein Report

## Protein 1396: PREDICTED: DNA-(apurinic or apyrimidinic site) lyase isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530403617 | **Score:** | 11.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 33.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 6.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MYEPEAKKSK | TAAKKNDKEA | AGEGPALYED | PPDQKTSPSG | KPATLKICSW | NVDGLRAWIK | KKGLDWVKEE | APDILCLQET |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KCSENKLPAE | LQELPGLSHQ | YWSAPSDKEG | YSGVGLLSRQ | CPLKVSYGIG | DEEHDQEGRV | IVAEFDSFVL | VTAYVPNAGR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GLVRLEYRQR | WDEAFRKFLK | GLASRKPLVL | CGDLNVAHEE | IDLRNPKGNK | KNAGFTPQER | QGFGELLQAV | PLADSFRHLY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | |
| PNTPYAYTFW | TYMMNARSKN | VGWRLDYFLL | SHSLLPALCD | SKIRSKALGS | DHCPITLYLA | L | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1621 | 1 | 1130.4868 | -28.13 | 2 | 48.6 | 11.9 | 1 | 120-139 | R.QCPLKVSYGIGDEEHDQEGR.V | |

# Detailed Protein Report

## Protein 1397: helicase SRCAP [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|146219843 | **Score:** | 11.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 343.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 0.5 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQSSPSPAHP | QLPVLQTQMV | SDGMTGSNPV | SPASSSSPAS | SGAGGISPQH | IAQDSSLDGP | PGPPDGATVP | LEGFSLSQAA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DLANKGPKWE | KSHAEIAEQA | KHEAEIETRI | AELRKEGFWS | LKRLPKVPEP | PRPKGHWDYL | CEEMQWLSAD | FAQERRWKRG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VARKVVRMVI | RHHEEQRQKE | ERARREEQAK | LRRIASTMAK | DVRQFWSNVE | KVVQFKQQSR | LEEKRKKALD | LHLDFIVGQT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EKYSDLLSQS | LNQPLTSSKA | GSSPCLGSSS | AASSPPPPAS | RLDDEDGDFQ | PQEDEEEDDE | ETIEVEEQQE | GNDAEAQRRE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IELLRREGEL | PLEELLRSLP | PQLLEGPSSP | SQTPSSHDSD | TRDGPEEGAE | EEPPQVLEIK | PPPSAVTQRN | KQPWHPDEDD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EEFTANEEEA | EDEEDTIAAE | EQLEGEVDHA | MELSELAREG | ELSMEELLQQ | YAGAYAPGSG | SSEDEDEDEV | DANSSDCEPE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GPVEAEEPPQ | EDSSSQSDSV | EDRSEDEEDE | HSEEEETSGS | SASEESESEE | SEDAQSQSQA | DEEEEDDDFG | VEYLLARDEE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QSEADAGSGP | PTPGPTTLGP | KKEITDIAAA | AESLQPKGYT | LATTQVKTPI | PLLLRGQLRE | YQHIGLDWLV | TMYEKKLNGI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LADEMGLGKT | IQTISLLAHL | ACEKGNWGPH | LIIVPTSVML | NWEMELKRWC | PSFKILTYYG | AQKERKLKRQ | GWTKPNAFHV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CITSYKLVLQ | DHQAFRRKNW | RYLILDEAQN | IKNFKSQRWQ | SLLNFNSQRR | LLLTGTPLQN | SLMELWSLMH | FLMPHVFQSH |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| REFKEWFSNP | LTGMIEGSQE | YNEGLVKRLH | KVLRPFLLRR | VKVDVEKQMP | KKYEHVIRCR | LSKRQRCLYD | DFMAQTTTKE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TLATGHFMSV | INILMQLRKV | CNHPNLFDPR | PVTSPFITPG | ICFSTASLVL | RATDVHPLQR | IDMGRFDLIG | LEGRVSRYEA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DTFLPRHRLS | RRVLLEVATA | PDPPPRPKPV | KMKVNRMLQP | VPKQEGRTVV | VVNNPRAPLG | PVPVRPPPGP | ELSAQPTPGP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VPQVLPASLM | VSASPAGPPL | IPASRPPGPV | LLPPLQPNSG | SLPQVLPSPL | GVLSGTSRPP | TPTLSLKPTP | PAPVRLSPAP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PPGSSSLLKP | LTVPPGYTFP | PAAATTTSTT | TATATTTAVP | APTPAPQRLI | LSPDMQARLP | SGEVVSIGQL | ASLAQRPVAN |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| AGGSKPLTFQ | IQGNKLTLTG | AQVRQLAVGQ | PRPLQRNVVH | LVSAGGQHHL | ISQPAHVALI | QAVAPTPGPT | PVSVLPSSTP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| STTPAPTGLS | LPLAANQVPP | TMVNNTGVVK | IVVRQAPRDG | LTPVPPLAPA | PRPPSSGLPA | VLNPRPTLTP | GRLPTPTLGT |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ARAPMPTPTL | VRPLLKLVHS | PSPEVSASAP | GAAPLTISSP | LHVPSSLPGP | ASSPMPIPNS | SPLASPVSST | VSVPLSSSLP |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ISVPTTLPAP | ASAPLTIPIS | APLTVSASGP | ALLTSVTPPL | APVVPAAPGP | PSLAPSGASP | SASALTLGLA | TAPSLSSSQT |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| PGHPLLLAPT | SSHVPGLNST | VAPACSPVLV | PASALASPFP | SAPNPAPAQA | SLLAPASSAS | QALATPLAPM | AAPQTAILAP |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| SPAPPLAPLP | VLAPSPGAAP | VLASSQTPVP | VMAPSSTPGT | SLASASPVPA | PTPVLAPSST | QTMLPAPVPS | PLPSPASTQT |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LALAPALAPT | LGGSSPSQTL | SLGTGNPQGP | FPTQTLSLTP | ASSLVPTPAQ | TLSLAPGPPL | GPTQTLSLAP | APPLAPASPV |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| GPAPAHTLTL | APASSSASLL | APASVQTLTL | SPAPVPTLGP | AAAQTLALAP | ASTQSPASQA | SSLVVSASGA | APLPVTMVSR |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| LPVSKDEPDT | LTLRSGPPSP | PSTATSFGGP | RPRRQPPPPP | RSPFYLDSLE | EKRKRQRSER | LERIFQLSEA | HGALAPVYGT |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| EVLDFCTLPQ | PVASPIGPRS | PGPSHPTFWT | YTEAAHRAVL | FPQQRLDQLS | EIIERFIFVM | PPVEAPPPSL | HACHPPPWLA |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| PRQAAFQEQL | ASELWPRARP | LHRIVCNMRT | QFPDLRLIQY | DCGKLQTLAV | LLRQLKAEGH | RVLIFTQMTR | MLDVLEQFLT |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| YHGHLYLRLD | GSTRVEQRQA | LMERFNADKR | IFCFILSTRS | GGVGVNLTGA | DTVVFYDSDW | NPTMDAQAQD | RCHRIGQTRD |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1273 | 1 | 863.9281 | -68.36 | 2 | 45.5 | 11.9 | 2 | 3195-3209 | R.RLVGTTNQGDQRILR.S | |

# Detailed Protein Report

## Protein 1398: PREDICTED: uncharacterized protein LOC102724905 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578835678 | **Score:** | 11.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 22.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| | | **Sequence Coverage [%]:** | 8.4 |
| | | **No. of unique Peptides:** | 1 |

```
         10         20         30         40         50         60         70         80
MKCSTSNCII SIKDYTSIRI NVAEVDKVTS RFNGQFKTYA FGGSPGTGVT GGKGREGGRS FCAGEGNERN GKGTAGCEAR
         90        100        110        120        130        140        150        160
DVPGSAAGPA RGRAAPLHPA PGPPLRGAIL QAAVAGTGGG GCSGHCGAEA RRQDGNHASC SQLGLDSTNG DFSYGFELGP
        170        180        190        200        210        220
WCISKCNSAN CNGKHMDRST PHHLGAKRCR LQASSLLENR GLQALEEPAD PGLLA
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2350 | 1 | 835.2854 | -159.01 | 2 | 59.8 | 11.9 | 1 | 38-55 | K.TYAFGGSPGTGVTGGKGR.E | |

# Detailed Protein Report

## Protein 1399: glutamate receptor 3 isoform 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|163659858 | **Score:** | 11.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 101.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MARQKKMGQS | VLRAVFFLVL | GLLGHSHGGF | PNTISIGGLF | MRNTVQEHSA | FRFAVQLYNT | NQNTTEKPFH | LNYHVDHLDS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SNSFSVTNAF | CSQFSRGVYA | IFGFYDQMSM | NTLTSFCGAL | HTSFVTPSFP | TDADVQFVIQ | MRPALKGAIL | SLLGHYKWEK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FVYLYDTERG | FSILQAIMEA | AVQNNWQVTA | RSVGNIKDVQ | EFRRIIEEMD | RRQEKRYLID | CEVERINTIL | EQVVILGKHS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RGYHYMLANL | GFTDILLERV | MHGGANITGF | QIVNNENPMV | QQFIQRWVRL | DEREFPEAKN | APLKYTSALT | HDAILVIAEA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FRYLRRQRVD | VSRRGSAGDC | LANPAVPWSQ | GIDIERALKM | VQVQGMTGNI | QFDTYGRRTN | YTIDVYEMKV | SGSRKAGYWN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EYERFVPFSD | QQISNDSASS | ENRTIVVTTI | LESPYVMYKK | NHEQLEGNER | YEGYCVDLAY | EIAKHVRIKY | KLSIVGDGKY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GARDPETKIW | NGMVGELVYG | RADIAVAPLT | ITLVREEVID | FSKPFMSLGI | SIMIKKPQKS | KPGVFSFLDP | LAYEIWMCIV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FAYIGVSVVL | FLVSRFSPYE | WHLEDNNEEP | RDPQSPPDPP | NEFGIFNSLW | FSLGAFMQQG | CDISPRSLSG | RIVGGVWWFF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TLIIISSYTA | NLAAFLTVER | MVSPIESAED | LAKQTEIAYG | TLDSGSTKEF | FRRSKIAVYE | KMWSYMKSAE | PSVFTKTTAD |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GVARVRKSKG | KFAFLLESTM | NEYIEQRKPC | DTMKVGGNLD | SKGYGVATPK | GSALGNAVNL | AVLKLNEQGL | LDKLKNKWWY |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DKGECGSGGG | DSKDKTSALS | LSNVAGVFYI | LVGGLGLAMM | VALIEFCYKS | RAESKRMKLT | KNTQNFKPAP | ATNTQNYATY |
| 890 | 900 | | | | | | |
| REGYNVYGTE | SVKI | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2723 | 2 | 840.9077 | -17.43 | 2 | 64.4 | 11.9 | 2 | 213-225 | R.QEKRYLIDCEVER.I | |

# Detailed Protein Report

## Protein 1400: diacylglycerol kinase eta isoform 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|325197221 | **Score:** | 11.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 120.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLCAENRKEM | EDWISSLKSV | QTREPYEVAQ | FNVEHFSGMH | NWYACSHARP | TFCNVCRESL | SGVTSHGLSC | EVCKFKAHKR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CAVRATNNCK | WTTLASIGKD | IIEDEDGVAM | PHQWLEGNLP | VSAKCAVCDK | TCGSVLRLQD | WKCLWCKTMV | HTACKDLYHP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ICPLGQCKVS | IIPPIALNST | DSDGFCRATF | SFCVSPLLVF | VNSKSGDNQG | VKFLRRFKQL | LNPAQVFDLM | NGGPHLGLRL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FQKFDNFRIL | VCGGDGSVGW | VLSEIDKLNL | NKQCQLGVLP | LGTGNDLARV | LGWGGSYDDD | TQLPQILEKL | ERASTKMLDR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WSIMTYELKL | PPKASLLPGP | PEASEEFYMT | IYEDSVATHL | TKILNSDEHA | VVISSAKTLC | ETVKDFVAKV | EKTYDKTLEN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AVVADAVASK | CSVLNEKLEQ | LLQALHTDSQ | AAPVLPGLSP | LIVEEDAVES | SSEESLGESK | EQLGDDVTKP | SSQKAVKPRE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IMLRANSLKK | AVRQVIEEAG | KVMDDPTVHP | CEPANQSSDY | DSTETDESKE | EAKDDGAKES | ITVKTAPRSP | DARASYGHSQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TDSVPGPAVA | ASKENLPVLN | TRIICPGLRA | GLAASIAGSS | IINKMLLANI | DPFGATPFID | PDLDSVDGYS | EKCVMNNYFG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IGLDAKISLE | FNNKREEHPE | KCRSRTKNLM | WYGVLGTREL | LQRSYKNLEQ | RVQLECDGQY | IPLPSLQGIA | VLNIPSYAGG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TNFWGGTKED | DIFAAPSFDD | KILEVVAIFD | SMQMAVSRVI | KLQHHRIAQC | RTVKITIFGD | EGVPVQVDGE | AWVQPPGIIK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IVHKNRAQML | TRDRAFESTL | KSWEDKQKCD | SGKPVLRTHL | YIHHAIDLAT | EEVSQMQLCS | QAAEELITRI | CDAATIHCLL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| EQELAHAVNA | CSHALNKANP | RCPESLTRDT | ATEIAINVKA | LYNETESLLV | GRVPLQLESP | HEERVSNALH | SVEVELQKLT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| EIPWLYYILH | PNEDEEPPMD | CTKRNNRSTV | FRIVPKFKKE | KVQKQKTSSQ | PVQKWGTEEV | AAWLDLLNLG | EYKDIFIRHD |
| 1050 | 1060 | 1070 | 1080 | 1090 | | | |
| IRGAELLHLE | RRDLKDLGIP | KVGHVKRILQ | GIKELGRSTP | QSEV | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1474 | 1 | 689.9970 | -3.59 | 3 | 46.8 | 11.9 | 1 | 58-76 | R.ESLSGVTSHGLSCEVCKFK.A | Carbamidomethyl: 13 |

# Detailed Protein Report

## Protein 1401: PREDICTED: palmitoyltransferase ZDHHC17 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530399993 | **Score:** | 11.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 42.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 5.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MINHLQEARQ | AKGYDNPSFL | RKLKADKEFR | QKVMLGTPFL | VIWLVGFIAD | LNIDSWLIKG | LMYGGVWATV | QFLSKSFFDH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SMHSALPLGI | YLATKFWMYV | TWFFWFWNDL | NFLFIHLPFL | ANSVALFYNF | GKSWKSDPGI | IKATEEQKKK | TIVELAETGS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LDLSIFCSTC | LIRKPVRSKH | CGVCNRCIAK | FDHHCPWVGN | CVGAGNHRYF | MGYLFFLLFM | ICWMIYGCIS | YWGLHCETTY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TKDGFWTYIT | QIATCSPWMF | WMFLNSVFHF | MWVAVLLMCQ | MYQISCLGIT | TNERMNARRY | KHFKVTTTSI | ESPFNHGCVR |
| 330 | 340 | 350 | 360 | 370 | | | |
| NIIDFFEFRC | CGLFRPVIVD | WTRQYTIEYD | QISGSGYQLV | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1444 | 1 | 830.0896 | 1.17 | 3 | 48.2 | 11.9 | 2 | 1-21 | -.MINHLQEARQAKGYDNPSFLR.K | |

# Detailed Protein Report

## Protein 1402: PREDICTED: sushi domain-containing protein 3 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578817174 | **Score:** | 11.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.2 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPQCLREGTC | AKLRLPPQAT | FQVLRGNGAS | VGTVLMFRCP | SNHQMVGSGL | LTCTWKGSIA | EWSSGSPVCK | LVPPHETFGF |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| KVAVIASIVS | CAIILLMSMA | FLTCCLLKCV | KKSKRRRSNR | SAQLWSQLKD | EDLETVQAAY | LGLKHFNKPV | SGPSQAHDNH |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| SFTTDHGEST | SKLASVTRSV | DKDPGIPRAL | SLSGSSSSPQ | AQVMVHMANP | RQPLPASGLA | TGMPQQPAAY | ALG |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 589 | 1 | 697.2029 | -172.10 | 2 | 36.9 | 11.9 | 1 | 1-12 | -.MPQCLREGTCAK.L | Carbamidomethyl: 10 |

# Detailed Protein Report

## Protein 1403: PREDICTED: chromobox protein homolog 7 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530419688 | **Score:** | 11.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 17.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| | | **Sequence Coverage [%]:** | 11.4 |
| | | **No. of unique Peptides:** | 1 |

```
         10         20         30         40         50         60         70         80
MELSAIGEQV FAVESIRKKR VRKGKVEYLV KWKGWPPKYS TWEPEEHILD PRLVMAYEEK EERDRASGYR KRGPKPKRLL
         90        100        110        120        130        140        150        160
LQEPPAPDVL QAAGEWEPAA QPPEEEADAD LAEGPPPWTP ALPSSEVTVT DITANSITVT FREAQAAEGF FRDRSGKF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2341 | 1 | 1002.7057 | 145.46 | 2 | 59.1 | 11.9 | 2 | 2-19 | M.ELSAIGEQVFAVESIRKK.R | |

# Detailed Protein Report

**Protein 1404:** **PREDICTED: LOW QUALITY PROTEIN: armadillo repeat-containing protein 4-like [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578818723 | **Score:** | 11.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 3.8 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MCKAKIILED LSLESLDVFL PNRNVLGYFK GISFNEDQQK EKDQLGKAPK KEKAAALHKD ISGSGKRSLE KNQINFWRNQ
        90        100        110        120        130        140        150        160
MTKRWEPSLN WKTTVNYKGK GSAKEIQEDK HTGKLEKPRP SVSHGRAQLL RKSAEKIEET VSDSSSESEE DEEPPDHRQE
       170        180        190        200        210        220
ASADLPSEYW QIQKLVKYLK QKETSQNGRS KRWARKQNTR VIRSTIFDVG KTS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2526 | 1 | 410.2347 | 36.76 | 2 | 61.5 | 11.9 | 1 | 60-67 | K.DISGSGKR.S | |

# Detailed Protein Report

## Protein 1405: PREDICTED: HAUS augmin-like complex subunit 5 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578834213 | **Score:** | 11.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 62.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MELAQEAREL | GCWAVEEMGV | PVAARAPEST | LRRLCLGQGA | DIWAYILQHV | HSQRTVKKIR | GNLLWYGHQD | SPQVRRKLEL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EAAVTRLRAE | IQELDQSLEL | MERDTEAQDT | AMEQARQHTQ | DTQRRALLLR | AQAGAMRRQQ | HTLRDPMQRL | QNQLRRLQDM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ERKAKVDVTF | GSLTSAALGL | EPVVLRDVRT | ACTLRAQFLQ | NLLLPQAKRG | SLPTPHDDHF | GTSYQQWLSS | VETLLTNHPP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GHVLAALEHL | AAEREAEIRS | LCSGDGLGDT | EISRPQAPDQ | SDSSQTLPSM | VHLIQEGWRT | VGVLVSQRST | LLKERQVLTQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RLQGLVEEVE | RRVLGSSERQ | VLILGLRRCC | LWTELKALHD | QSQELQDAAG | HRQLLLRELQ | AKQQRILHWR | QLVEETQEQV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RLLIKGNSAS | KTRLCRSPGE | VLALVQRKVV | PTFEAVAPQS | RELLRCLEEE | VRHLPHILLG | TLLRHRPGEL | KPLPTVLPSI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HQLHPASPRG | SSFIALSHKL | GLPPGKASEL | LLPAAASLRQ | DLLLLQDQRS | LWCWDLLHMK | TSLPPGLPTQ | VPIVC |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1924 | 1 | 902.3552 | -97.62 | 2 | 53.9 | 11.9 | 0 | 89-103 | R.AEIQELDQSLELMER.D | |

# Detailed Protein Report

## Protein 1406: zinc finger protein 575 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|28372567 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 26.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.6 |
| | | **Sequence Coverage [%]:** | 4.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.63 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.19 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578834314 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 575 isoform X3 [Homo sapiens] |
| gi\|530416267 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 575 isoform X2 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLERGAESAA | GATDPSPTGK | EPVTKEAPHQ | GPPQKPSQSA | PGPTASAGSP | PRPRRRPPPQ | RPHRCPDCDK | AFSYPSKLAT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HRLAHGGARP | HPCPDCPKAF | SYPSKLAAHR | LTHSGARPHP | CPHCPKSFGH | RSKLAAHLWT | HAPTRPYPCP | DCPKSFCYPS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KLAAHRHTHH | ATDARPYPCP | HCPKAFSFPS | KLAAHRLCHD | PPTAPGSQAT | AWHRCSSCGQ | AFGQRRLLLL | HQRSHHQVEH |
| 250 | | | | | | | |
| KGERD | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2271 | 1 | 666.3126 | -77.96 | 2 | 56.7 | 11.8 | 1 | 185-196 | K.AFSFPSKLAAHR.L | | WUP:QUP 0.19<br>QU:MU 0.63 |

# Detailed Protein Report

## Protein 1407: coiled-coil domain-containing protein 93 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|82775371 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 73.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.9 |
|  |  | **Sequence Coverage [%]:** | 1.6 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGLPRGPEGQ | GLPEVETRED | EEQNVKLTEI | LELLVAAGYF | RARIKGLSPF | DKVVGGMTWC | ITTCNFDVDV | DLLFQENSTI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GQKIALSEKI | VSVLPRMKCP | HQLEPHQIQG | MDFIHIFPVV | QWLVKRAIET | KEEMGDYIRS | YSVSQFQKTY | SLPEDDDFIK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RKEKAIKTVV | DLSEVYKPRR | KYKRHQGAEE | LLDEESRIHA | TLLEYGRRYG | FSRQSKMEKA | EDKKTALPAG | LSATEKADAH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EEDELRAAEE | QRIQSLMTKM | TAMANEESRL | TASSVGQIVG | LCSAEIKQIV | SEYAEKQSEL | SAEESPEKLG | TSQLHRRKVI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SLNKQIAQKT | KHLEELRASH | TSLQARYNEA | KKTLTELKTY | SEKLDKEQAA | LEKIESKADP | SILQNLRALV | AMNENLKSQE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QEFKAHCREE | MTRLQQEIEN | LKAERAPRGD | EKTLSSGEPP | GTLTSAMTHD | EDLDRRYNME | KEKLYKIRLL | QARRNREIAI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LHRKIDEVPS | RAELIQYQKR | FIELYRQISA | VHKETKQFFT | LYNTLDDKKV | YLEKEISLLN | SIHENFSQAM | ASPAARDQFL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RQMEQIVEGI | KQSRMKMEKK | KQENKMRRDQ | LNDQYLELLE | KQRLYFKTVK | EFKEEGRKNE | MLLSKVKAKA | S |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 308 | 1 | 651.8272 | -75.61 | 2 | 33.8 | 11.8 | 2 | 604-613 | R.LYFKTVKEFK.E |  |

BRUKER

# Detailed Protein Report

## Protein 1408: integrator complex subunit 12 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21361851 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 48.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| | | **Sequence Coverage [%]:** | 4.3 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530378006 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: integrator complex subunit 12 isoform X3 [Homo sapiens] |
| gi\|530378004 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: integrator complex subunit 12 isoform X2 [Homo sapiens] |
| gi\|215599585 | refseq_human (refseq_human_20140103.fasta) | integrator complex subunit 12 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAATVNLELD | PIFLKALGFL | HSKSKDSAEK | LKALLDESLA | RGIDSSYRPS | QKDVEPPKIS | STKNISIKQE | PKISSSLPSG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NNNGKVLTTE | KVKKEAEKRP | ADKMKSDITE | GVDIPKKPRL | EKPETQSSPI | TVQSSKDLPM | ADLSSFEETS | ADDFAMEMGL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ACVVCRQMMV | ASGNQLVECQ | ECHNLYHRDC | HKPQVTDKEA | NDPRLVWYCA | RCTRQMKRMA | QKTQKPPQKP | APAVVSVTPA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VKDPLVKKPE | TKLKQETTFL | AFKRTEVKTS | TVISGNSSSA | SVSSSVTSGL | TGWAAFAAKT | SSAGPSTAKL | SSTTQNNTGK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PATSSANQKP | VGLTGLATSS | KGGIGSKIGS | NNSTTPTVPL | KPPPPLTLGK | TGLSRSVSCD | NVSKVGLPSP | SSLVPGSSSQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | |
| LSGNGNSGTS | GPSGSTTSKT | TSESSSSPSA | SLKGPTSQES | QLNAMKRLQM | VKKKAAQKKL | KK | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 21 | 1 | 736.0052 | -65.71 | 3 | 29.9 | 11.8 | 1 | 33-52 | K.ALLDESLARGIDSSYRPSQK.D | |

# Detailed Protein Report

## Protein 1409: dickkopf-related protein 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|7110719 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 28.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 3.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMALGAAGAT | RVFVAMVAAA | LGGHPLLGVS | ATLNSVLNSN | AIKNLPPPLG | GAAGHPGSAV | SAAPGILYPG | GNKYQTIDNY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QPYPCAEDEE | CGTDEYCASP | TRGGDAGVQI | CLACRKRRKR | CMRHAMCCPG | NYCKNGICVS | SDQNHFRGEI | EETITESFGN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DHSTLDGYSR | RTTLSSKMYH | TKGQEGSVCL | RSSDCASGLC | CARHFWSKIC | KPVLKEGQVC | TKHRRKGSHG | LEIFQRCYCG |
| 250 | 260 | 270 | | | | | |
| EGLSCRIQKD | HHQASNSSRL | HTCQRH | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1338 | 1 | 569.8185 | 115.24 | 2 | 45.1 | 11.8 | 0 | 250-259 | K.DHHQASNSSR.L | |

# Detailed Protein Report

## Protein 1410: monocarboxylate transporter 5 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|319996630 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| | | **Sequence Coverage [%]:** | 4.6 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLKREGKVQP | YTKTLDGGWG | WMIVIHFFLV | NVFVMGMTKT | FAIFFVVFQE | EFEGTSEQIG | WIGSIMSSLR | FCAGLGSAFL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YQVAAVVTTK | YFKKRLALST | AIARSGMGLT | FLLAPFTKFL | IDLYDWTGAL | ILFGAIALNL | VPSSMLLRPI | HIKSENNSGI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KDKGSSLSAH | GPEAHATETH | CHETEESTIK | DSTTQKAGLP | SKNLTVSQNQ | SEEFYNGPNR | NRLLLKSDEE | SDKVISWSCK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QLFDISLFRN | PFFYIFTWSF | LLSQLAYFIP | TFHLVARAKT | LGIDIMDASY | LVSVAGILET | VSQIISGWVA | DQNWIKKYHY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HKSYLILCGI | TNLLAPLATT | FPLLMTYTIC | FAIFAGGYLA | LILPVLVDLC | RNSTVNRFLG | LASFFAGMAV | LSGPPIAGWL |
| 410 | 420 | 430 | 440 | | | | |
| YDYTQTYNGS | FYFSGICYLL | SSVSFFFVPL | AERWKNSLT | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1205 | 1 | 1023.6515 | 108.87 | 2 | 45.2 | 11.8 | 0 | 71-90 | R.FCAGLGSAFLYQVAAVVTTK.Y | |

# Detailed Protein Report

## Protein 1411: zinc finger protein 48 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|333805600 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSDLVKHQRT | HTGEKPYKCG | VCGKGFGDSS | ARIKHQRTHS | GEKPYRARPP | AQGPPKIPRS | RIPAGERPTI | CGECGKSFRQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SSDLVKHQRT | HTGEKPYKCG | ICGKGFGDSS | ARIKHQRTHR | GEQPPRPVVP | RRQPSRAATA | ATQGPKAQDK | PYICTDCGKR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FVLSCSLLSH | QRSHLGPKPF | GCDVCGKEFA | RGSDLVKHLR | VHTGEKPYLC | PECGKGFADS | SARVKHLRTH | SGERPHACPE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CDRTFSLSST | LLRHRLTHME | PQDFSFPGYP | LPALIPSPPP | PPLGTSPPLT | PRSPSHSGEP | FGLPGLEPEP | GGPQAGEPPP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PLAGDKPHKC | PECGKGFRRS | SDLVKHHRVH | TGEKPYLCPE | CGKGFADSSA | RVKHLRTHRG | ERARPPPPST | LLRPHNPPGP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VPMAPRPRVR | AQPSGPSQPH | VCGFCGKEFP | RSSDLVKHRR | THTGEKPYKC | AECGKGFGDS | SARIKHQRGH | LVLTPFGIGD |
| 490 | 500 | | | | | | |
| GRARPLKQEA | ATGLE | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 139 | 1 | 707.7910 | -32.11 | 2 | 31.5 | 11.8 | 1 | 99-112 | K.CGICGKGFGDSSAR.I | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 1412: PREDICTED: receptor-type tyrosine-protein phosphatase T isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578835723 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 155.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLDQAVPTGS | FMMVNSSGRA | SGQKAHLLLP | TLKENDTHCI | DFHYYFSSRD | RSSPGALNVY | VKVNGGPQGN | PVWNVSGVVT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EGWVKAELAI | STFWPHFYQV | IFESVSLKGH | PGYIAVDEVR | VLAHPCRKAP | HFLRLQNVEV | NVGQNATFQC | IAGGKWSQHD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KLWLQQWNGR | DTALMVTRVV | NHRRFSATVS | VADTAQRSVS | KYRCVIRSDG | GSGVSNYAEL | IVKEPPTPIA | PPELLAVGAT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YLWIKPNANS | IIGDGPIILK | EVEYRTTTGT | WAETHIVDSP | NYKLWHLDPD | VEYEIRVLLT | RPGEGGTGPP | GPPLTTRTKC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ADPVHGPQNV | EIVDIRARQL | TLQWEPFGYA | VTRCHSYNLT | VQYQYVFNQQ | QYEAEEVIQT | SSHYTLRGLR | PFMTIRLRLL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LSNPEGRMES | EELVVQTEED | VPGAVPLESI | QGGPFEEKIY | IQWKPPNETN | GVITLYEINY | KAVGSLDPSA | DLSSQRGKVF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KLRNETHHLF | VGLYPGTTYS | FTIKASTAKG | FGPPVTTRIA | TKISAPSMPE | YDTDTPLNET | DTTITVMLKP | AQSRGAPVSV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YQLVVKEERL | QKSRRAADII | ECFSVPVSYR | NASSLDSLHY | FAAELKPANL | PVTQPFTVGD | NKTYNGYWNP | PLSPLKSYSI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| YFQALSKANG | ETKINCVRLA | TKAPMGSAQV | TPGTPLCLLT | TGASTQNSNT | VEPEKQVDNT | VKMAGVIAGL | LMFIIILLGV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| MLTIKRRKLA | KKQKETQSGA | QREMGPVASA | DKPTTKLSAS | RNDEGFSSSS | QDVNGFTDGS | RGELSQPTLT | IQTHPYRTCD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PVEMSYPRDQ | FQPAIRVADL | LQHITQMKRG | QGYGFKEEYE | ALPEGQTASW | DTAKEDENRN | KNRYGNIISY | DHSRVRLLVL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DGDPHSDYIN | ANYIDGYHRP | RHYIATQGPM | QETVKDFWRM | IWQENSASIV | MVTNLVEVGR | VKCVRYWPDD | TEVYGDIKVT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LIETEPLAEY | VIRTFTVQKK | GYHEIRELRL | FHFTSWPDHG | VPCYATGLLG | FVRQVKFLNP | PEAGPIVVHC | SAGAGRTGCF |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| IAIDTMLDMA | ENEGVVDIFN | CVRELRAQRV | NLVQTEEQYV | FVHDAILEAC | LCGNTAIPVC | EFRSLYYNIS | RLDPQTNSSQ |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| IKDEFQTLNI | VTPRVRPEDC | SIGLLPRNHD | KNRSMDVLPL | DRCLPFLISV | DGESSNYINA | ALMDSHKQPA | AFVVTQHPLP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| NTVADFWRLV | FDYNCSSVVM | LNEMDTAQFC | MQYWPEKTSG | CYGPIQVEFV | SADIDEDIIH | RIFRICNMAR | PQDGYRIVQH |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| LQYIGWPAYR | DTPPSKRSLL | KVVRRLEKWQ | EQYDGREGRT | VVHCLNGGGR | SGTFCAICSV | CEMIQQQNII | DVFHIVKTLR |
| 1370 | 1380 | 1390 | | | | | |
| NNKSNMVETL | EQYKFVYEVA | LEYLSSF | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2030 | 1 | 715.9422 | -125.78 | 3 | 53.8 | 11.8 | 1 | 320-338 | K.CADPVHGPQNVEIVDIRAR.Q | Carbamidomethyl: 1 |

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# Detailed Protein Report

## Protein 1413: PREDICTED: beclin-1 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530413037 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 43.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| | | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEGSKTSNNS | TMQVSFVCQR | CSQPLKLDTS | FKILDRVTIQ | ELTAPLLTTA | QAKPGETQEE | ETNSGEEPFI | ETPRQDGVSR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RFIPPARMMS | TESANSFTLI | GEASDGGTME | NLSRRLKVTG | DLFDIMSGQT | DVDHPLCEEC | TDTLLDQLDT | QLNVTENECQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NYKRCLEILE | QMNEDDSEQL | QMELKELALE | EERLIQELED | VEKNRKIVAE | NLEKVQAEAE | RLDQEEAQYQ | REYSEFKRQQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LELDDELKSV | ENQMRYAQTQ | LDKLKKTNVF | NATFHIWHSG | QFGTINNFRL | GRLPSVPVEW | NEINAAWGQT | VLLLHALANK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| MGLKFQRMDV | EKGKIEDTGG | SGGSYSIKTQ | FNSEEQWTKA | LKFMLTNLKW | GLAWVSSQFY | NK | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1558 | 1 | 685.6866 | -202.29 | 2 | 49.2 | 11.8 | 0 | 335-348 | K.IEDTGGSGGSYSIK.T | |

# Detailed Protein Report

## Protein 1414: protein SCO2 homolog, mitochondrial precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|153791313 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 29.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|281182727 | refseq_human (refseq_human_20140103.fasta) | protein SCO2 homolog, mitochondrial precursor [Homo sapiens] |
| gi\|281182722 | refseq_human (refseq_human_20140103.fasta) | protein SCO2 homolog, mitochondrial precursor [Homo sapiens] |
| gi\|281182716 | refseq_human (refseq_human_20140103.fasta) | protein SCO2 homolog, mitochondrial precursor [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLLLTRSPTA | WHRLSQLKPR | VLPGTLGGQA | LHLRSWLLSR | QGPAETGGQG | QPQGPGLRTR | LLITGLFGAG | LGGAWLALRA |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| EKERLQQQKR | TEALRQAAVG | QGDFHLLDHR | GRARCKADFR | GQWVLMYFGF | THCPDICPDE | LEKLVQVVRQ | LEAEPGLPPV |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| QPVFITVDPE | RDDVEAMARY | VQDFHPRLLG | LTGSTKQVAQ | ASHSYRVYYN | AGPKDEDQDY | IVDHSIAIYL | LNPDGLFTDY |
| **250** | **260** | **270** | | | | | |
| YGRSRSAEQI | SDSVRRHMAA | FRSVLS | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 896 | 1 | 512.1549 | -207.64 | 2 | 39.6 | 11.8 | 2 | 113-120 | R.ARCKADFR.G | Carbamidomethyl: 3 |

# Detailed Protein Report

## Protein 1415: ankyrin-1 isoform 2 [Homo sapiens]

**Accession:** gi|70780355
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 11.8
**MW [kDa]:** 188.9
**pI:** 6.2
**Sequence Coverage [%]:** 0.4
**No. of unique Peptides:** 1

## Quantitation

***WUP:QUP*** **Median:** 2.24 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPYSVGFREA | DAATSFLRAA | RSGNLDKALD | HLRNGVDINT | CNQNGLNGLH | LASKEGHVKM | VVELLHKEII | LETTTKKGNT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ALHIAALAGQ | DEVVRELVNY | GANVNAQSQK | GFTPLYMAAQ | ENHLEVVKFL | LENGANQNVA | TEDGFTPLAV | ALQQGHENVV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AHLINYGTKG | KVRLPALHIA | ARNDDTRTAA | VLLQNDPNPD | VLSKTGFTPL | HIAAHYENLN | VAQLLLNRGA | SVNFTPQNGI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TPLHIASRRG | NVIMVRLLLD | RGAQIETKTK | DELTPLHCAA | RNGHVRISEI | LLDHGAPIQA | KTKNGLSPIH | MAAQGDHLDC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VRLLLQYDAE | IDDITLDHLT | PLHVAAHCGH | HRVAKVLLDK | GAKPNSRALN | GFTPLHIACK | KNHVRVMELL | LKTGASIDAV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TESGLTPLHV | ASFMGHLPIV | KNLLQRGASP | NVSNVKVETP | LHMAARAGHT | EVAKYLLQNK | AKVNAKAKDD | QTPLHCAARI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GHTNMVKLLL | ENNANPNLAT | TAGHTPLHIA | AREGHVETVL | ALLEKEASQA | CMTKKGFTPL | HVAAKYGKVR | VAELLLERDA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HPNAAGKNGL | TPLHVAVHHN | NLDIVKLLLP | RGGSPHSPAW | NGYTPLHIAA | KQNQVEVARS | LLQYGGSANA | ESVQGVTPLH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LAAQEGHAEM | VALLLSKQAN | GNLGNKSGLT | PLHLVAQEGH | VPVADVLIKH | GVMVDATTRM | GYTPLHVASH | YGNIKLVKFL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LQHQADVNAK | TKLGYSPLHQ | AAQQGHTDIV | TLLLKNGASP | NEVSSDGTTP | LAIAKRLGYI | SVTDVLKVVT | DETSFVLVSD |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KHRMSFPETV | DEILDVSEDE | GEELISFKAE | RRDSRDVDEE | KELLDFVPKL | DQVVESPAIP | RIPCAMPETV | VIRSEEQEQA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SKEYDEDSLI | PSSPATETSD | NISPVASPVH | TGFLVSFMVD | ARGGSMRGSR | HNGLRVVIPP | RTCAAPTRIT | CRLVKPQKLS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TPPPLAEEEG | LASRIIALGP | TGAQFLSPVI | VEIPHFASHG | RGDRELVVLR | SENGSVWKEH | RSRYGESYLD | QILNGMDEEL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GSLEELEKKR | VCRIITTDFP | LYFVIMSRLC | QDYDTIGPEG | GSLKSKLVPL | VQATFPENAV | TKRVKLALQA | QPVPDELVTK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LLGNQATFSP | IVTVEPRRRK | FHRPIGLRIP | LPPSWTDNPR | DSGEGDTTSL | RLLCSVIGGT | DQAQWEDITG | TTKLVYANEC |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ANFTTNVSAR | FWLSDCPRTA | EAVNFATLLY | KELTAVPYMA | KFVIFAKMND | PREGRLRCYC | MTDDKVDKTL | EQHENFVEVA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| RSRDIEVLEG | MSLFAELSGN | LVPVKKAAQQ | RSFHFQSFRE | NRLAMPVKVR | DSSREPGGSL | SFLRKAMKYE | DTQHILCHLN |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ITMPPCAKGS | GAEDRRRTPT | PLALRYSILS | ESTPGSLSGT | EQAEMKMAVI | SEHLGLSWAE | LARELQFSVE | DINRIRVENP |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| NSLLEQSVAL | LNLWVIREGQ | NANMENLYTA | LQSIDRGEIV | NMLEGSGRQS | RNLKPDRRHT | DRDYSLSPSQ | MNGHQRGQAR |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| ITHSPTVSQV | TERSQDRLQD | WDADGSIVSY | LQDAAQGSWQ | EEVTQGPHSF | QGTSTMTEGL | EPGGSQEYEK | VLVSVSEHTW |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| TEQPEAESSQ | ADRDRRQQGQ | EEQVQEAKNT | FTQVVQGNEF | QNIPGEQVTE | EQFTDEQGNI | VTKKIIRKVV | RQIDLSSADA |
| 1690 | 1700 | 1710 | 1720 | | | | |
| AQEHEEVTVE | GPLEDPSELE | VDIDYFMKHS | KDHTSTPNP | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2604 | 1 | 449.6284 | -302.49 | 2 | 60.8 | 11.8 | 1 | 1492-1498 | R.NLKPDRR.H |  | WUP:QUP 2.24 |

# Detailed Protein Report

## Protein 1416: MAD2L1-binding protein isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|7661918 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 5.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAAPEAEVLS | SAAVPDLEWY | EKSEETHASQ | IELLETSSTQ | EPLNASEAFC | PRDCMVPVVF | PGPVSQEGCC | QFTCELLKHI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MYQRQQLPLP | YEQLKHFYRK | PSPQAEEMLK | KKPRATTEVS | SRKCQQALAE | LESVLSHLED | FFARTLVPRV | LILLGGNALS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PKEFYELDLS | LLAPYSVDQS | LSTAACLRRL | FRAIFMADAF | SELQAPPLMG | TVVMAQGHRN | CGEDWFRPKL | NYRVPSRGHK |
| 250 | 260 | 270 | 280 | | | | |
| LTVTLSCGRP | SIRTTAWEDY | IWFQAPVTFK | GFRE | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1913 | 1 | 599.9134 | -68.59 | 3 | 53.8 | 11.8 | 1 | 220-233 | R.NCGEDWFRPKLNYR.V | |

# Detailed Protein Report

## Protein 1417: bone morphogenetic protein receptor type-1B isoform b precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4502431 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.9 |
| | | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578809323 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: bone morphogenetic protein receptor type-1B isoform X1 [Homo sapiens] |
| gi\|377823731 | refseq_human (refseq_human_20140103.fasta) | bone morphogenetic protein receptor type-1B isoform b precursor [Homo sapiens] |
| gi\|377823723 | refseq_human (refseq_human_20140103.fasta) | bone morphogenetic protein receptor type-1B isoform b precursor [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLLRSAGKLN | VGTKKEDGES | TAPTPRPKVL | RCKCHHHCPE | DSVNNICSTD | GYCFTMIEED | DSGLPVVTSG | CLGLEGSDFQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CRDTPIPHQR | RSIECCTERN | ECNKDLHPTL | PPLKNRDFVD | GPIHHRALLI | SVTVCSLLLV | LIILFCYFRY | KRQETRPRYS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IGLEQDETYI | PPGESLRDLI | EQSQSSGSGS | GLPLLVQRTI | AKQIQMVKQI | GKGRYGEVWM | GKWRGEKVAV | KVFFTTEEAS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| WFRETEIYQT | VLMRHENILG | FIAADIKGTG | SWTQLYLITD | YHENGSLYDY | LKSTTLDAKS | MLKLAYSSVS | GLCHLHTEIF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| STQGKPAIAH | RDLKSKNILV | KKNGTCCIAD | LGLAVKFISD | TNEVDIPPNT | RVGTKRYMPP | EVLDESLNRN | HFQSYIMADM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YSFGLILWEV | ARRCVSGGIV | EEYQLPYHDL | VPSDPSYEDM | REIVCIKKLR | PSFPNRWSSD | ECLRQMGKLM | TECWAHNPAS |
| 490 | 500 | 510 | | | | | |
| RLTALRVKKT | LAKMSESQDI | KL | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2215 | 1 | 1130.1764 | 76.41 | 2 | 58.1 | 11.8 | 2 | 357-376 | K.FISDTNEVDIPPNTRVGTKR.Y | |

# Detailed Protein Report

## Protein 1418: inositol-trisphosphate 3-kinase B [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|194272161 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 102.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 5.55 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.55 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAVYCYALNS | LVIMNSANEM | KSGGGPGPSG | SETPPPPRRA | VLSPGSVFSP | GRGASFLFPP | AESLSPEEPR | SPGGWRSGRR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RLNSSSGSGS | GSSGSSVSSP | SWAGRLRGDR | QQVVAAGTLS | PPGPEEAKRK | LRILQRELQN | VQVNQKVGMF | EAHIQAQSSA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IQAPRSPRLG | RARSPSPCPF | RSSSQPPGRV | LVQGARSEER | RTKSWGEQCP | ETSGTDSGRK | GGPSLCSSQV | KKGMPPLPGR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AAPTGSEAQG | PSAFVRMEKG | IPASPRCGSP | TAMEIDKRGS | PTPGTRSCLA | PSLGLFGASL | TMATEVAARV | TSTGPHRPQD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LALTEPSGRA | RELEDLQPPE | ALVERQGQFL | GSETSPAPER | GGPRDGEPPG | KMGKGYLPCG | MPGSGEPEVG | KRPEETTVSV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QSAESSDSLS | WSRLPRALAS | VGPEEARSGA | PVGGGRWQLS | DRVEGGSPTL | GLLGGSPSAQ | PGTGNVEAGI | PSGRMLEPLP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CWDAAKDLKE | PQCPPGDRVG | VQPGNSRVWQ | GTMEKAGLAW | TRGTGVQSEG | TWESQRQDSD | ALPSPELLPQ | DPDKPFLRKA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| CSPSNIPAVI | ITDMGTQEDG | ALEETQGSPR | GNLPLRKLSS | SSASSTGFSS | SYEDSEEDIS | SDPERTLDPN | SAFLHTLDQQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KPRVSKSWRK | IKNMVHWSPF | VMSFKKKYPW | IQLAGHAGSF | KAAANGRILK | KHCESEQRCL | DRLMVDVLRP | FVPAYHGDVV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KDGERYNQMD | DLLADFDSPC | VMDCKMGIRT | YLEEELTKAR | KKPSLRKDMY | QKMIEVDPEA | PTEEEKAQRA | VTKPRYMQWR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ETISSTATLG | FRIEGIKKED | GTVNRDFKKT | KTREQVTEAF | REFTKGNHNI | LIAYRDRLKA | IRTTLEVSPF | FKCHEVIGSS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | |
| LLFIHDKKEQ | AKVWMIDFGK | TTPLPEGQTL | QHDVPWQEGN | REDGYLSGLN | NLVDILTEMS | QDAPLA | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 672 | 1 | 705.3789 | -4.51 | 2 | 38.4 | 11.8 | 2 | 762-772 | K.KPSLRKDMYQK.M | Oxidation: 8 | WUP:QUP 1.55<br>QU:MU 5.55 |

# Detailed Protein Report

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## Protein 1419: bifunctional glutamate/proline--tRNA ligase [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|62241042 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 170.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.77 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.67 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MATLSLTVNS | GDPPLGALLA | VEHVKDDVSI | SVEEGKENIL | HVSENVIFTD | VNSILRYLAR | VATTAGLYGS | NLMEHTEIDH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| WLEFSATKLS | SCDSFTSTIN | ELNHCLSLRT | YLVGNSLSLA | DLCVWATLKG | NAAWQEQLKQ | KKAPVHVKRW | FGFLEAQQAF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QSVGTKWDVS | TTKARVAPEK | KQDVGKFVEL | PGAEMGKVTV | RFPPEASGYL | HIGHAKAALL | NQHYQVNFKG | KLIMRFDDTN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PEKEKEDFEK | VILEDVAMLH | IKPDQFTYTS | DHFETIMKYA | EKLIQEGKAY | VDDTPAEQMK | AEREQRIDSK | HRKNPIEKNL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QMWEEMKKGS | QFGQSCCLRA | KIDMSSNNGC | MRDPTLYRCK | IQPHPRTGNK | YNVYPTYDFA | CPIVDSIEGV | THALRTTEYH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DRDEQFYWII | EALGIRKPYI | WEYSRLNLNN | TVLSKRKLTW | FVNEGLVDGW | DDPRFPTVRG | VLRRGMTVEG | LKQFIAAQGS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SRSVVNMEWD | KIWAFNKKVI | DPVAPRYVAL | LKKEVIPVNV | PEAQEEMKEV | AKHPKNPEVG | LKPVWYSPKV | FIEGADAETF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SEGEMVTFIN | WGNLNITKIH | KNADGKIISL | DAKLNLENKD | YKKTTKVTWL | AETTHALPIP | VICVTYEHLI | TKPVLGKDED |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FKQYVNKNSK | HEELMLGDPC | LKDLKKGDII | QLQRRGFFIC | DQPYEPVSPY | SCKEAPCVLI | YIPDGHTKEM | PTSGSKEKTK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VEATKNETSA | PFKERPTPSL | NNNCTTSEDS | LVLYNRVAVQ | GDVVRELKAK | KAPKEDVDAA | VKQLLSLKAE | YKEKTGQEYK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PGNPPAEIGQ | NISSNSSASI | LESKSLYDEV | AAQGEVVRKL | KAEKSPKAKI | NEAVECLLSL | KAQYKEKTGK | EYIPGQPPLS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QSSDSSPTRN | SEPAGLETPE | AKVLFDKVAS | QGEVVRKLKT | EKAPKDQVDI | AVQELLQLKA | QYKSLIGVEY | KPVSATGAED |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KDKKKKEKEN | KSEKQNKPQK | QNDGQRKDPS | KNQGGGLSSS | GAGEGQGPKK | QTRLGLEAKK | EENLADWYSQ | VITKSEMIEY |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| HDISGCYILR | PWAYAIWEAI | KDFFDAEIKK | LGVENCYFPM | FVSQSALEKE | KTHVADFAPE | VAWVTRSGKT | ELAEPIAIRP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TSETVMYPAY | AKWVQSHRDL | PIKLNQWCNV | VRWEFKHPQP | FLRTREFLWQ | EGHSAFATME | EAAEEVLQIL | DLYAQVYEEL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LAIPVVKGRK | TEKEKFAGGD | YTTTIEAFIS | ASGRAIQGGT | SHHLGQNFSK | MFEIVFEDPK | IPGEKQFAYQ | NSWGLTTRTI |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| GVMTMVHGDN | MGLVLPPRVA | CVQVVIIPCG | ITNALSEEDK | EALIAKCNDY | RRRLLSVNIR | VRADLRDNYS | PGWKFNHWEL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KGVPIRLEVG | PRDMKSCQFV | AVRRDTGEKL | TVAENEAETK | LQAILEDIQV | TLFTRASEDL | KTHMVVANTM | EDFQKILDSG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KIVQIPFCGE | IDCEDWIKKT | TARDQDLEPG | APSMGAKSLC | IPFKPLCELQ | PGAKCVCGKN | PAKYYTLFGR | SY |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 37 | 1 | 712.6427 | -104.44 | 3 | 30.3 | 11.8 | 2 | 850-867 | K.INEAVECLLSLKAQYKEK.T | Carbamidomethyl: 7 | QU:MU 1.77<br>WUP:QUP 0.67 |

# Detailed Protein Report

## Protein 1420: transmembrane protein 126A isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|14150017 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 14.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MENHKSNNKE | NITIVDISRK | INQLPEAERN | LLENGSVYVG | LNAALCGLIA | NSLFRRILNV | TKARIAAGLP | MAGIPFLTTD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LTYRCFVSFP | LNTGDLDCET | CTITRSGLTG | LVIGGLYPVF | LAIPVNGGLA | ARYQSALLPH | KGNILSYWIR | TSKPVFRKML |
| 170 | 180 | 190 | 200 | | | | |
| FPILLQTMFS | AYLGSEQYKL | LIKALQLSEP | GKEIH | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1779 | 1 | 1011.6290 | 57.94 | 3 | 52.1 | 11.8 | 2 | 57-84 | R.ILNVTKARIAAGLPMAGIPFLTTDLTYR.C | Oxidation: 15 |

# Detailed Protein Report

## Protein 1421: PREDICTED: diphosphomevalonate decarboxylase isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578828983 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 8.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGEQADGKDS | IARQVAPESH | WPELRVLILV | VSAEKKLTGS | TVGMRASVET | SPLLRFRAES | VVPARMAEMA | RCIRERDFPS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FAQLTMKDSN | QFHATCLDTF | PPISYLNAIS | WRIIHLVHRF | NAHHGDTKVA | YTFDAGPNAV | IFTLDDTVAE | FVAAVWHGFP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | |
| PGSNGDTFLK | GLQVRPAPLS | AELQAALAME | PTPGGVKYII | VTQVGPGPQI | LDDPCAHLLG | PDGLPKPAA | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1514 | 1 | 1052.1817 | 93.63 | 2 | 48.6 | 11.8 | 2 | 36-55 | K.KLTGSTVGMRASVETSPLLR.F | |

# Detailed Protein Report

## Protein 1422: PREDICTED: LIM/homeobox protein Lhx9 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530365098 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 37.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MEIVGCRAED NSCPFRPPAM LFHGISGGHI QGIMEEMERR SKTEARLAKG AQLNGRDAGM PPLSPEKPAL CAGCGGKISD

        90        100        110        120        130        140        150        160
RYYLLAVDKQ WHLRCLKCCE CKLALESELT CFAKDGSIYC KEDYYRRFSV QRCARCHLGI SASEMVMRAR DSVYHLSCFT

       170        180        190        200        210        220        230        240
CSTCNKTLTT GDHFGMKDSL VYCRAHFETL LQGEYPPQLS YTELAAKSGG LALPYFNGTG TVQKGRPRKR KSPALGVDIV

       250        260        270        280        290        300        310        320
NYNSGCNENE ADHLDRDQQP YPPSQKTKRM RTSFKHHQLR TMKSYFAINH NPDAKDLKQL AQKTGLTKRV LQGEQILGHY

       330        340
SQTSRRLKIP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1198 | 1 | 612.4376 | 241.33 | 2 | 45.1 | 11.8 | 0 | 167-177 | K.TLTTGDHFGMK.D | Oxidation: 10 |

# Detailed Protein Report

## Protein 1423: PREDICTED: EF-hand calcium-binding domain-containing protein 4A isoform X11 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578820464 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 0.0 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.35 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRPRRRRGNS | RGALQGRGLQ | YWSRLRSCFC | CVTRRLRASS | PSTTCRVSRA | TCPSRQSSWR | LCLKVWTGLT | LASSPPGSSA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| WAWVSLWPAY | PPLPRAGGLI | RRPGTCGALR | AAGASRPPPS | RARALSARTR | AWGLLAAVEC | VELTFLAPSS | SPVLSSGMFV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GVASAQGANP | CRTPEETFES | GGLDVQGTAG | SLDEEEEEEE | RFHTVLEQLG | VAPVLGNSRP | PSRQRAVRTL | WARLQRERPE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LLGSFEDVLI | RASACLEEAA | RERDGLEQAL | RRRESEHERE | VRALYEETEQ | LREQSRRPPS | QVGLGPRPSR | QAQSHLAGLP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GSAFSELIPP | RRPHLRGSRL | PSARGDPTGP | HVSPPSGLLH | PTPLRPGPLP | APGPPCTSFA | WPSGRRRLSG | PPCVPELRPR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GAEKPSGAGA | AEPRAGPGTR | GPAAAGVRAA | AARPGCGAPG | GTGPELPAVA | GARGAANAAG | GGAGADPQAG | ERSTRPPGAN |
| 490 | 500 | 510 | 520 | | | | |
| PTRRGRRLQE | HAERESQPAT | ATGAAQGAEY | TAAG | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1754 | 2 | 577.2577 | -85.92 | 2 | 52.2 | 11.8 | 0 | 473-483 | R.STRPPGANPTR.R | | QU:MU 0.35 |

# Detailed Protein Report

## Protein 1424: fibroleukin precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5730075 | **Score:** | 11.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 50.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.7 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 1.45 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKLANWYWLS | SAVLATYGFL | VVANNETEEI | KDERAKDVCP | VRLESRGKCE | EAGECPYQVS | LPPLTIQLPK | QFSRIEEVFK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EVQNLKEIVN | SLKKSCQDCK | LQADDNGDPG | RNGLLLPSTG | APGEVGDNRV | RELESEVNKL | SSELKNAKEE | INVLHGRLEK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LNLVNMNNIE | NYVDSKVANL | TFVVNSLDGK | CSKCPSQEQI | QSRPVQHLIY | KDCSDYYAIG | KRSSETYRVT | PDPKNSSFEV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YCDMETMGGG | WTVLQARLDG | STNFTRTWQD | YKAGFGNLRR | EFWLGNDKIH | LLTKSKEMIL | RIDLEDFNGV | ELYALYDQFY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VANEFLKYRL | HVGNYNGTAG | DALRFNKHYN | HDLKFFTTPD | KDNDRYPSGN | CGLYYSSGWW | FDACLSANLN | GKYYHQKYRG |
| 410 | 420 | 430 | 440 | | | | |
| VRNGIFWGTW | PGVSEAHPGG | YKSSFKEAKM | MIRPKHFKP | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 675 | 1 | 690.3561 | -24.67 | 2 | 38.4 | 11.8 | 1 | 146-157 | K.NAKEEINVLHGR.L | | QU:MU 1.45 |

# Detailed Protein Report

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**Protein 1425:** **PREDICTED: myb/SANT-like DNA-binding domain-containing protein 2 isoform X4 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530398384 | **Score:** | 11.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 7.9 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578822380 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: myb/SANT-like DNA-binding domain-containing protein 2 isoform X8 [Homo sapiens] |
| gi\|578822376 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: myb/SANT-like DNA-binding domain-containing protein 2 isoform X6 [Homo sapiens] |
| gi\|578822374 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: myb/SANT-like DNA-binding domain-containing protein 2 isoform X5 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEDYSQEDWG | NHSQDLHGYP | TDQELDEIPV | TKRTLKIKQE | SSEEAQKRDI | MQNIVQILES | VQLKWELFQS | WTDFSRLHLS |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| NKLAIFGIGY | NTRWKEDIRY | HYAEISSQVP | LGKRLREYFN | SEKPEGRIIM | TRVQKMNWKN | VYYKFLEITI | SEARCLELHM |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| EIDWIPIAHS | KPTGGNVVQY | LLPGGIPKSP | GLYAIGYEEC | IERPLSPHME | QSSLDPGKEG | RVDLETLSAQ | ASLQVEIEPT |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| RIIYCYLGIA | EVRTLQQCLF | LHFQANTKTF | SKDWVGINGF | LSQNCIVDPG | VSPKSIYIKF | VEVERDFLSA | GSLVECLEKA |
| **330** | | | | | | | |
| IGYPLKFNN | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 975 | 1 | 955.7195 | -97.68 | 3 | 41.8 | 11.7 | 1 | 269-294 | K.TFSKDWVGINGFLSQNCIVDPGVSPK.S | Carbamidomethyl: 17 |

# Detailed Protein Report

## Protein 1426: SH2 domain-containing protein 4B isoform 2 [Homo sapiens]

**Accession:** gi|224591408
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 11.7
**MW [kDa]:** 36.4
**pI:** 7.9
**Sequence Coverage [%]:** 4.9
**No. of unique Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLPEDSGGSP | DAAASDKHIQ | WLLGADGEVW | VWIMGEGPGD | KPYEEISEEL | IAERARLQAQ | REAEELWRQK | EAEITKKFRD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ALANEKARIL | AEKWKVEMED | RKAAKVLEER | IHEEFKRKEE | EERKRGEEQI | RLQEEQRAKE | LYWTLKQAQL | HCQASEKEER |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EWEEQLRRSK | AADEERSRRA | QRARDEYRHH | SLRAIQKGTV | AGLSSMFREL | GQSHEQEARL | YHHLPDPGLP | QPLALPVSRT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | |
| WERPLRPVSR | DVIVRWFKEE | QLPRRAGFER | NTKFIAPWFH | GGNYHCFRRR | VTSGTLRTEG | QPTRLPSVV | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1450 | 1 | 783.3926 | -44.00 | 2 | 47.8 | 11.7 | 1 | 194-208 | R.AIQKGTVAGLSSMFR.E | |

# Detailed Protein Report

## Protein 1427: leucine-rich repeat-containing protein 14B [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|122937351 | **Score:** | 11.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDTMRSLRFI | SAEALVSHPQ | VARQSLDSVA | HNLYPLLFKA | SYLLEQAEVT | RAVLGRWPLE | EFRLGALLGP | GADHPQDLRD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RTCRACLEAL | VRGLADHVLQ | DRSRRRLRVA | DLTGIRDVQV | QRCPCGRALG | RWGRTQLLAR | TCCELQAEPL | AAGRPVEVLA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DLFVTEGNFE | AVVQALRPAG | PAPLRVHCPS | FRADSLSPSQ | LLHVLRLAGP | GALRKLEVVH | NVRLHAGHVQ | QLLAQVGFPR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LASLTLPTKA | FDAPPTYAST | PDGEDPLLAS | IARELSKMAQ | LTELSVAFST | LTGKIPTLLG | PLQTPLRVLD | LANCALNHTD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MAFLADCAHA | AHLEVLDLSG | HNLVSLYPST | FFRLLSQASR | TLRILTLEEC | GIVDSHVGML | ILGLSPCHRL | RQLKFLGNPL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SARALRRLFT | ALCELPELRC | IEFPVPKDCY | PEGAAYPQDE | LAMSKFNQQK | YDEIAEELRA | VLLRADREDI | QVSTPLFGSF |
| 490 | 500 | 510 | 520 | | | | |
| DPDIQETSNE | LGAFLLQAFK | TALENFSRAL | KQIE | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1441 | 1 | 1022.9976 | 61.26 | 2 | 48.2 | 11.7 | 0 | 428-445 | K.DCYPEGAAYPQDELAMSK.F | Carbamidomethyl: 2 |

# Detailed Protein Report

## Protein 1428: PREDICTED: bone morphogenetic protein 5 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530382406 | **Score:** | 11.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 39.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 4.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MHLTVFLLKG IVGFLWSCWV LVGYAKGGLG DNHVHSSFIY RRLRNHERRE IQREILSILG LPHRPRPFSP GKQASSAPLF
        90        100        110        120        130        140        150        160
MLDLYNAMTN EENPEESEYS VRASLAEETR GARKGYPASP NGYPRRIQLS RTTPLTTQSP PLASLHDTNF LNDADMVMSF
       170        180        190        200        210        220        230        240
VNLVERDKDF SHQRRHYKEF RFDLTQIPHG EAVTAAEFRI YKDRSNNRFE NETIKISIYQ IIKEYTNRDA DLFLLDTRKA
       250        260        270        280        290        300        310        320
QALDVGWLVF DITVTSNHWV INPQNNLGLQ LCAETGDGRS INVKSAGLVG RQGPQSKQPF MVAFFKASEV LLRSVRAANK
       330        340        350
RKNQNRNKSS SHQDSSRMSS VGGSSDVS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2529 | 1 | 941.9279 | -93.60 | 2 | 61.6 | 11.7 | 1 | 298-313 | K.QPFMVAFFKASEVLLR.S | |

# Detailed Protein Report

## Protein 1429: PREDICTED: stabilin-2 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578823928 | **Score:** | 11.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 243.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.4 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MMLQHLVIFC LGLVVQNFCS PAETTGQARR CDRKSLLTIR TECRSCALNL GVKCPDGYTM ITSGSVGVRD CRYTFEVRTY
        90        100        110        120        130        140        150        160
SLSLPGCRHI CRKDYLQPRC CPGRWGPDCI ECPGGAGSPC NGRGSCAEGM EGNGTCSCQE GFGGTACETC ADDNLFGPSC
       170        180        190        200        210        220        230        240
SSVCNCVHGV CNSGLDGDGT CECYSAYTGP KCDKPIPECA ALLCPENSRC SPSTEDENKL ECKCLPNYRG DGKYCDPINP
       250        260        270        280        290        300        310        320
CLRKICHPHA HCTYLGPNRH SCTCQEGYRG DGQVCLPVDP CQINFGNCPT KSTVCKYDGP GQSHCECKEH YQNFVPGVGC
       330        340        350        360        370        380        390        400
SMTDICKSDN PCHRNANCTT VAPGRTECIC QKGYVGDGLT CYGNIMERLR ELNTEPRGKW QGRLTSFISL LDKAYAWPLS
       410        420        430        440        450        460        470        480
KLGPFTVLLP TDKGLKGFNV NELLVDNKAA QYFVKLHIIA GQMNIEYMNN TDMFYTLTGK SGEIFNSDKD NQIKLKLHGG
       490        500        510        520        530        540        550        560
KKKVKIIQGD IIASNGLLHI LDRAMDKLEP TFESNNEQTI MTMLQPRYSK FRSLLEETNL GHALDEDGVG GPYTIFVPNN
       570        580        590        600        610        620        630        640
EALNNMKDGT LDYLLSPEGS RKLLELVRYH IVPFTQLEVA TLISTPHIRS MANQLIQFNT TDNGQILAND VAMEEIEITA
       650        660        670        680        690        700        710        720
KNGRIYTLTG VLIPPSIVPI LPHRCDETKR EMKLGTCVSC SLVYWSRCPA NSEPTALFTH RCVYSGRFGS LKSGCARYCN
       730        740        750        760        770        780        790        800
ATVKIPKCCK GFYGPDCNQC PGGFSNPCSG NGQCADSLGG NGTCICEEGF QGSQCQFCSD PNKYGPRCNK KCLCVHGTCN
       810        820        830        840        850        860        870        880
NRIDSDGACL TGTCRDGSAG RLCDKQTSAC GPYVQFCHIH ATCEYSNGTA SCICKAGYEG DGTLCSEMDP CTGLTPGGCS
       890        900        910        920        930        940        950        960
RNAECIKTGT GTHTCVCQQG WTGNGRDCSE INNCLLPSAG GCHDNASCLY VGPGQNECEC KKGFRGNGID CEPITSCLEQ
       970        980        990       1000       1010       1020       1030       1040
TGKCHPLASC QSTSSGVWSC VCQEGYEGDG FLCYGNAAVE LSFLSEAAIF NRWINNASLQ PTLSATSNLT VLVPSQQATE
      1050       1060       1070       1080       1090       1100       1110       1120
DMDQDEKSFW LSQSNIPALI KYHMLLGTYR VADLQTLSSS DMLATSLQGN FLHLAKVDGN ITIEGASIVD GDNAATNGVI
      1130       1140       1150       1160       1170       1180       1190       1200
HIINKVLVPQ RRLTGSLPNL LMRLEQMPDY SIFRGYIIQY NLANAIEAAD AYTVFAPNNN AIENYIREKK VLSLEEDVLR
      1210       1220       1230       1240       1250       1260       1270       1280
YHVVLEEKLL KNDLHNGMHR ETMLGFSYFL SFFLHNDQLY VNEAPINYTN VATDKGVIHG LGKVLEIQKN RCDNNDTTII
      1290       1300       1310       1320       1330       1340       1350       1360
RGRCRTCSSE LTCPFGTKSL GNEKRRCIYT SYFMGRRTLF IGCQPKCVRT VITRECCAGF FGPQCQPCPG NAQNVCFGNG
      1370       1380       1390       1400       1410       1420       1430       1440
ICLDGVNGTG VCECGEGFSG TACETCTEGK YGIHCDQACS CVHGRCNQGP LGDGSCDCDV GWRGVHCDNA TTEDNCNGTC
      1450       1460       1470       1480       1490       1500       1510       1520
HTSANCLTNS DGTASCKCAA GFQGNGTICT AINACEISNG GCSAKADCKR TTPGRRVCTC KAGYTGDGIV CLEINPCLEN
      1530       1540       1550       1560       1570       1580       1590       1600
HGGCDKNAEC TQTGPNQAAC NCLPAYTGDG KVCTLINVCL TKNGGCSEFA ICNHTGQVER TCTCKPNYIG DGFTCRGSIY
      1610       1620       1630       1640       1650       1660       1670       1680
QELPKNPKTS QYFFQLQEHF VKDLVGPGPF TVFAPLSAAF DEEARVKDWD KYGLMPQVLR YHVVACHQLL LENLKLISNA
      1690       1700       1710       1720       1730       1740       1750       1760
TSLQGEPIVI SVSQSTVYIN NKAKIISSDI ISTNGIVHII DKLLSPKNLL ITPKDNSGRI LQNLTTLATN NGYIKFSNLI
      1770       1780       1790       1800       1810       1820       1830       1840
QDSGLLSVIT DPIHTPVTLF WPTDQALHAL PAEQQDFLFN QDNKDKLKEY LKFHVIRDAK VLAVDLPTST AWKTLQGSEL
      1850       1860       1870       1880       1890       1900       1910       1920
SVKCGAGRDI GDLFLNGQTC RIVQRELLFD LGVAYGIDCL LIDPTLGGRC DTFTTFDASG ECGSCVNTPS CPRWSKPKGV
      1930       1940       1950       1960       1970       1980       1990       2000
KQKCLYNLPF KRNLEGCRER CSLVIQIPRC CKGYFGRDCQ ACPGGPDAPC NNRGVCLDQY SATGECKCNT GFNGTACEMC
      2010       2020       2030       2040       2050       2060       2070       2080
WPGRFGPDCL PCGCSDHGQC DDGITGSGQC LCETGWTGPS CDTQAVLPAV CTPPCSAHAT CKENNTCECN LDYEGDGITC
      2090       2100       2110       2120       2130       2140       2150       2160
TVVDFCKQDN GGCAKVARCS QKGTKVSCSC QKGYKGDGHS CTEIDPCADG LNGGCHEHAT CKMTGPGKHK CECKSHYVGD
      2170       2180       2190       2200       2210       2220       2230       2240
```

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2882 | 2 | 648.3630 | 73.51 | 2 | 64.8 | 11.7 | 1 | 220-229 | K.LECKCLPNYR.G | Carbamidomethyl: 3 |

# Detailed Protein Report

## Protein 1430: SLC2A4 regulator [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|31982931 | **Score:** | 11.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 5.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***WUP:QUP*** | **Median:** | 0.56 | **CV:** | 0.00 % | **No. of Peptides:** | 1 | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MERPPPRAAG | RDPSALRAEA | PWLRAEGPGP | RAAPVTVPTP | PQGSSVGGGF | AGLEFARPQE | SEPRASDLGA | PRTWTGAAAG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PRTPSAHIPV | PAQRATPGKA | RLDEVMAAAA | LTSLSTSPLL | LGAPVAAFSP | EPGLEPWKEA | LVRPPGSYSS | SSNSGDWGWD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LASDQSSPST | PSPPLPPEAA | HFLFGEPTLR | KRKSPAQVMF | QCLWKSCGKV | LSTASAMQRH | IRLVHLGRQA | EPEQSDGEED |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FYYTELDVGV | DTLTDGLSSL | TPVSPTASMP | PAFPRLELPE | LLEPPALPSP | LRPPAPPLPP | PPVLSTVANP | QSCHSDRVYQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| GCLTPARLEP | QPTEVGACPP | ALSSRIGVTL | RKPRGDAKKC | RKVYGMERRD | LWCTACRWKK | ACQRFLD | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2046 | 1 | 1073.4473 | -106.13 | 2 | 53.9 | 11.7 | 2 | 12-31 | R.DPSALRAEAPWLRAEGPGPR.A | | WUP:QUP | 0.56 |

# Detailed Protein Report

## Protein 1431: PREDICTED: uncharacterized protein LOC102724043 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578808329 | **Score:** | 11.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MLSCFTPCPP PLRISEALVG RFREQVVSSE QPRLLTPLGE APCLGPLGLT LSGEFWRASA AVPAPTHEAP QNRRVLRLLS
        90        100        110        120        130        140        150        160
SCRLPEPMWD IVLGWPRFCS SGLEVGRKPL LSRWVVKAVG GPEIWGLWGK GPWREGIRYG GLDSLQGAAA SAPGPATAHS
       170        180        190        200        210        220        230        240
AAPPTGSPGP VAVDSPGPER PRGESPTYVN IPVSPSSRKQ LHYMGLELQE ASEGVRGAGA SLYAQIDIMA TETAHRVGVR
       250        260        270
HARAREEQLS ELEQRKAAPQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2081 | 1 | 731.3837 | 37.61 | 2 | 56.4 | 11.7 | 0 | 1-13 | -.MLSCFTPCPPPLR.I | |

# Detailed Protein Report

## Protein 1432: PREDICTED: probable JmjC domain-containing histone demethylation protein 2C isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530393275 | **Score:** | 11.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 188.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 0.5 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MAVETRAELV GKRFLCVAVG DEARSERWES GRGWRSWRAG VIRAVSHRDS RNPDLAVYVE FDDLEWDKRE WVKVYEDFST

        90        100        110        120        130        140        150        160
FLVEYHLIWA KRNDPSQTQG SKSKQIQWPA LTFKPLVERN IPSSVTAVEF LVDKQLDFLT EDSAFQPYQD DIDSLNPVLR

       170        180        190        200        210        220        230        240
DNPQLHEEVK VWVKEQKVQE IFMQGPYSLN GYRVRVYRQD SATQWFTGII THHDLFTRTM IVMNDQVLEP QNVDPSMVQM

       250        260        270        280        290        300        310        320
TFLDDVVHSL LKGENIGITS RRRSRANQNV NAVHSHYTRA QANSPRPAMN SQAAVPKQNT HQQQQQRSIR PNKRKGSDSS

       330        340        350        360        370        380        390        400
IPDEEKMKEE KYDYISRGEN PKGKNKHLMN KRRKPEEDEK KLNMKRLRTD NVSDFSESSD SENSNKRIID NSSEQKPENE

       410        420        430        440        450        460        470        480
LKNKNTSKIN GEEGKPHNNE KAGEETLKNS QPPWDQIQED KKHEEAEKRK SVDTQLQEDM IIHSSEQSTV SDHNSNDLLP

       490        500        510        520        530        540        550        560
QECNMDKTHT MELLPKEKFV SRPPTPKCVI DITNDTNLEK VAQENSSTFG LQTLQKMDPN VSDSKHSIAN AKFLETAKKD

       570        580        590        600        610        620        630        640
SDQSWVSDVV KVDLTQSSVT NASSGNDHLN MEKEKYVSYI SPLSAVSVME DKLHKRSPPP ETIKSKLNTS VDTHKIKSSP

       650        660        670        680        690        700        710        720
SPEVVKPKIT HSPDSVKSKA TYVNSQATGE RRLANKIEHE LSRCSFHPIP TRSSTLETTK SPLIIDKNEH FTVYRDPALI

       730        740        750        760        770        780        790        800
GSETGANHIS PFLSQHPFPL HSSSHRTCLN PGTHHPALTP APHLLAGSSS QTPLPTINTH PLTSGPHHAV HHPHLLPTVL

       810        820        830        840        850        860        870        880
PGVPTASLLG GHPRLESAHA SSLSHLALAH QQQQQLLQHQ SPHLLGQAHP SASYNQLGLY PIIWQYPNGT HAYSGLGLPS

       890        900        910        920        930        940        950        960
SKWVHPENAV NAEASLRRNS PSPWLHQPTP VTSADGIGLL SHIPVRPSSA EPHRPLKITA HSSPPLTKTL VDHHKEELER

       970        980        990       1000       1010       1020       1030       1040
KAFMEPLRSV ASTSAKNDLD LNRSQTGKDC HLHRHFVDPV LNQLQRPPQE TGERLNKYKE EHRRILQESI DVAPFTTKIK

      1050       1060       1070       1080       1090       1100       1110       1120
GLEGERENYS RVASSSSSPK SHIIKQDMDV ERSVSDLYKM KHSVPQSLPQ SNYFTTLSNS VVNEPPRSYP SKEVSNIYGD

      1130       1140       1150       1160       1170       1180       1190       1200
KQSNALAAAA ANPQTLTSFI TSLSKPPPLI KHQPESEGLV GKIPEHLPHQ IASHSVTTFR NDCRSPTHLT VSSTNTLRSM

      1210       1220       1230       1240       1250       1260       1270       1280
PALHRAPVFH PPIHHSLERK EGSYSSLSPP TLTPVMPVNA GGKVQESQKP PTLIPEPKDS QANFKSSSEQ SLTEMWRPNN

      1290       1300       1310       1320       1330       1340       1350       1360
NLSKEKTEWH VEKSSGKLQA AMASVIVRPS SSTKTDSMPA MQLASKDRVS ERSSAGAHKT DCLKLAEAGE TGRIILPNVN

      1370       1380       1390       1400       1410       1420       1430       1440
SDSVHTKSEK NFQAVSQGSV PSSVMSAVNT MCNTKTDVIT SAADTTSVSS WGGSEVISSL SNTILASTSS ECVSSKSVSQ

      1450       1460       1470       1480       1490       1500       1510       1520
PVAQKQECKV STTAPVTLAS SKTGSVVQPS SGFSGTTDFI HLKKHKAALA AAQYKSSNAS ETEPNAIKNQ TLSASLPLDS

      1530       1540       1550       1560       1570       1580       1590       1600
TVICSTINKA NSVGNGQASQ TSQPNYHTKL KKAWLTRHSE EDKNTNKMEN SGNSVSEIIK PCSVNLIAST SSDIQNSVDS

      1610       1620       1630       1640       1650       1660       1670       1680
KIIVDKYVKD DKVNRRKAKR TYESGSESGD SDESESKSEQ RTKRQPKPTY KKKQNDLQKR KGEIEEDLKP NGVLSRSAKE

      1690       1700       1710
RSKLKLQSNS NSMLHNAEST
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 343 | 1 | 528.7540 | -68.44 | 2 | 33.9 | 11.7 | 2 | 345-352 | K.NKHLMNKR.R | Oxidation: 5 |

# Detailed Protein Report

## Protein 1433: Krueppel-related zinc finger protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|32401441 | **Score:** | 11.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 75.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.6 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRVNHTVSTM | LPTCMVHRQT | MSCSGAGGIT | AFVAFRDVAV | YFTQEEWRLL | SPAQRTLHRE | VMLETYNHLV | SLEIPSSKPK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LIAQLERGEA | PWREERKCPL | DLCPESKPEI | QLSPSCPLIF | SSQQALSQHV | WLSHLSQLFS | SLWAGNPLHL | GKHYPEDQKQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QQDPFCFSGK | AEWIQEGEDS | RLLFGRVSKN | GTSKALSSPP | EEQQPAQSKE | DNTVVDIGSS | PERRADLEET | DKVLHGLEVS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GFGEIKYEEF | GPGFIKESNL | LSLQKTQTGE | TPYMYTEWGD | SFGSMSVLIK | NPRTHSGGKP | YVCRECGRGF | TWKSNLITHQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RTHSGEKPYV | CKDCGRGFTW | KSNLFTHQRT | HSGLKPYVCK | ECGQSFSLKS | NLITHQRAHT | GEKPYVCREC | GRGFRQHSHL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VRHKRTHSGE | KPYICRECEQ | GFSQKSHLIR | HLRTHTGEKP | YVCTECGRHF | SWKSNLKTHQ | RTHSGVKPYV | CLECGQCFSL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KSNLNKHQRS | HTGEKPFVCT | ECGRGFTRKS | TLSTHQRTHS | GEKPFVCAEC | GRGFNDKSTL | ISHQRTHSGE | KPFMCRECGR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RFRQKPNLFR | HKRAHSGAFV | CRECGQGFCA | KLTLIKHQRA | HAGGKPHVCR | ECGQGFSRQS | HLIRHQRTHS | GEKPYICRKC |
| 650 | 660 | | | | | | |
| GRGFSRKSNL | IRHQRTHSG | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 952 | 1 | 584.2074 | -228.39 | 2 | 41.5 | 11.7 | 1 | 564-572 | R.QKPNLFRHK.R | |

# Detailed Protein Report

## Protein 1434: signal transducer and activator of transcription 3 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|47458820 | **Score:** | 11.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 83.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAQWNQLQQL | DTRYLEQLHQ | LYSDSFPMEL | RQFLAPWIES | QDWAYAASKE | SHATLVFHNL | LGEIDQQYSR | FLQESNVLYQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HNLRRIKQFL | QSRYLEKPME | IARIVARCLW | EESRLLQTAA | TAAQQGGQAN | HPTAAVVTEK | QQMLEQHLQD | VRKRVQDLEQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KMKVVENLQD | DFDFNYKTLK | SQGDMQDLNG | NNQSVTRQKM | QQLEQMLTAL | DQMRRSIVSE | LAGLLSAMEY | VQKTLTDEEL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ADWKRRQQIA | CIGGPPNICL | DRLENWITSL | AESQLQTRQQ | IKKLEELQQK | VSYKGDPIVQ | HRPMLEERIV | ELFRNLMKSA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FVVERQPCMP | MHPDRPLVIK | TGVQFTTKVR | LLVKFPELNY | QLKIKVCIDK | DSGDVAALRG | SRKFNILGTN | TKVMNMEESN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NGSLSAEFKH | LTLREQRCGN | GGRANCDASL | IVTEELHLIT | FETEVYHQGL | KIDLETHSLP | VVVISNICQM | PNAWASILWY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NMLTNNPKNV | NFFTKPPIGT | WDQVAEVLSW | QFSSTTKRGL | SIEQLTTLAE | KLLGPGVNYS | GCQITWAKFC | KENMAGKGFS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FWVWLDNIID | LVKKYILALW | NEGYIMGFIS | KERERAILST | KPPGTFLLRF | SESSKEGGVT | FTWVEKDISG | KTQIQSVEPY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TKQQLNNMSF | AEIIMGYKIM | DATNILVSPL | VYLYPDIPKE | EAFGKYCRPE | SQEHPEADPG | SAAPYLKTKF | ICVTPFIDAV |
| 730 | | | | | | | |
| WK | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1378 | 1 | 977.5477 | 34.77 | 2 | 47.4 | 11.7 | 0 | 216-233 | R.SIVSELAGLLSAMEYVQK.T | Oxidation: 13 |

# Detailed Protein Report

## Protein 1435: proliferating cell nuclear antigen [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4505641 | **Score:** | 11.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 28.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|33239451 | refseq_human (refseq_human_20140103.fasta) | proliferating cell nuclear antigen [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MFEARLVQGS | ILKKVLEALK | DLINEACWDI | SSSGVNLQSM | DSSHVSLVQL | TLRSEGFDTY | RCDRNLAMGV | NLTSMSKILK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CAGNEDIITL | RAEDNADTLA | LVFEAPNQEK | VSDYEMKLMD | LDVEQLGIPE | QEYSCVVKMP | SGEFARICRD | LSHIGDAVVI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SCAKDGVKFS | ASGELGNGNI | KLSQTSNVDK | EEEAVTIEMN | EPVQLTFALR | YLNFFTKATP | LSSTVTLSMS | ADVPLVVEYK |
| 250 | 260 | 270 | | | | | |
| IADMGHLKYY | LAPKIEDEEG | S | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1448 | 1 | 428.2129 | 16.30 | 3 | 47.7 | 11.7 | 1 | 139-149 | K.MPSGEFARICR.D | Oxidation: 1 |

# Detailed Protein Report

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## Protein 1436: glutathione peroxidase 3 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|6006001 | **Score:** | 11.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 25.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 7.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MARLLQASCL | LSLLLAGFVS | QSRGQEKSKM | DCHGGISGTI | YEYGALTIDG | EEYIPFKQYA | GKYVLFVNVA | SYUGLTGQYI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ELNALQEELA | PFGLVILGFP | CNQFGKQEPG | ENSEILPTLK | YVRPGGGFVP | NFQLFEKGDV | NGEKEQKFYT | FLKNSCPPTS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | |
| ELLGTSDRLF | WEPMKVHDIR | WNFEKFLVGP | DGIPIMRWHH | RTTVSNVKMD | ILSYMRRQAA | LGVKRK | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2604 | 1 | 973.9996 | -12.90 | 2 | 62.6 | 11.7 | 1 | 186-201 | K.FLVGPDGIPIMRWHHR.T | Oxidation: 11 |

# Detailed Protein Report

## Protein 1437: E3 ubiquitin-protein ligase parkin isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|169790971 | **Score:** | 11.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 48.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.9 |
| | | **Sequence Coverage [%]:** | 5.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MIVFVRFNSS | HGFPVEVDSD | TSIFQLKEVV | AKRQGVPADQ | LRVIFAGKEL | RNDWTVQNCD | LDQQSIVHIV | QRPWRKGQEM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NATGGDDPRN | AAGGCEREPQ | SLTRVDLSSS | VLPGDSVGLA | VILHTDSRKD | SPPAGSPAGR | SIYNSFYVYC | KGPCQRVQPG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KLRVQCSTCR | QATLTLTQEF | FFKCGAHPTS | DKETSVALHL | IATNSRNITC | ITCTDVRSPV | LVFQCNSRHV | ICLDCFHLYC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VTRLNDRQFV | HDPQLGYSLP | CVAGCPNSLI | KELHHFRILG | EEQYNRYQQY | GAEECVLQMG | GVLCPRPGCG | AGLLPEPDQR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KVTCEGGNGL | GCGFAFCREC | KEAYHEGECS | AVFEASGTTT | QAYRVDERAA | EQARWEAASK | ETIKKTTKPC | PRCHVPVEKN |
| 410 | 420 | 430 | 440 | | | | |
| GGCMHMKCPQ | PQCRLEWCWN | CGCEWNRVCM | GDHWFDV | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2156 | 1 | 836.3125 | -111.36 | 3 | 55.3 | 11.7 | 2 | 129-151 | R.KDSPPAGSPAGRSIYNSFYVYCK.G | |

# Detailed Protein Report

## Protein 1438: centrosomal protein kizuna isoform 3 [Homo sapiens]

**Accession:** gi|247301334
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 11.7
**MW [kDa]:** 59.2
**pI:** 4.9
**Sequence Coverage [%]:** 2.8
**No. of unique Peptides:** 1

## Quantitation

***QU:MU*** **Median:** 0.97 **CV:** 0.00 % **No. of Peptides:** 1
***WUP:QUP*** **Median:** 1.05 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQVAVHEGIN | SGTAMSRGLY | QPATIFMGRQ | MSAILSMRDF | STEHKSPQPT | KNFSIPDPHS | HRQTAQSSNV | TDSCVVQTSN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DTQCLNKSDN | IDGKASLQIG | EKMPVTASVL | SEEEQTHCLE | IGSNTRHGKS | NLSEGKKSAE | LNSPLRERLS | PENRTTDLKC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DSSSGSEGEI | LTREHIEVEE | KRASPPVSPI | PVSEYCESEN | KWSQEKHSPW | EGVSDHLAHR | EPKSQKPFRK | MQEEEEESWS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TSSDLTISIS | EDDLILESPE | PQPNPGGKME | GEDGIEALKL | IHAEQERVAL | STEKNCILQT | LSSPDSEKES | STNAPTREPG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QTPDSDVPRA | QVGQHVATLK | EHDNSVKEEA | TALLRKALTE | ECGRRSAIHS | SESSCSLPSI | LNDNSGIKEA | KPAVWLNSVP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TREQEVSSGC | GDKSKKENVA | ADIPITETEA | YQLLKKATLQ | DNTNQTENRF | QKTDASVSHL | SGLNIGSGAF | ETKTANKIAS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | |
| EASFSSSEGS | PLSRHENKKK | PVINLKSNAL | WDESDDSNSE | IEAALRPRNH | NTDDSDDFYD | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 30 | 1 | 856.3760 | -67.86 | 2 | 30.1 | 11.7 | 1 | 341-355 | K.EHDNSVKEEATALLR.K | | WUP:QUP 1.05<br>QU:MU 0.97 |

# Detailed Protein Report

## Protein 1439: PREDICTED: uncharacterized protein LOC102725509 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578796799 | **Score:** | 11.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.1 |
| | | **Sequence Coverage [%]:** | 7.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRTAVCTCSV | RTVAGTRRSF | REGAGAKSTF | RVFRAPAEVV | AGRGGCWESC | SGAHVPIPNY | KFRSRAPTLG | GCGALASRSP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FAAGSYEVLI | SIIQFLCHTV | RGTPVPMTES | TCGLSGGGVG | GGEKKFWRHL | EDPSIPESSV | KKVVLANRIN | MVGLGLVGGA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GAGLVRGAKW | SPYFRIRPHL | ANASFGVPWL | RGCGVYPVLG | RGGERPPRPP | RRPQNGGPAL | WAFVAWALSC | RKTKVTIPVA |
| 250 | 260 | 270 | 280 | 290 | 300 | | |
| NWKEMEFFLH | SPHDRDGPFL | KCVLFNSLFK | TPRIWTTCTQ | DPLRVWRASL | SVAVF | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1023 | 2 | 955.6838 | 135.95 | 2 | 42.4 | 11.7 | 1 | 149-169 | R.INMVGLGLVGGAGAGLVRGAK.W | |

# Detailed Protein Report

## Protein 1440: fibrillin-3 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|56237021 | **Score:** | 11.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 300.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTLEGLYLAR | GPLARLLLAW | SALLCMAGGQ | GRWDGALEAA | GPGRVRRRGS | PGILQGPNVC | GSRFHAYCCP | GWRTFPGRSQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CVVPICRRAC | GEGFCSQPNL | CTCADGTLAP | SCGVSRGSGC | SVSCMNGGTC | RGASCLCQKG | YTGTVCGQPI | CDRGCHNGGR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CIGPNRCACV | YGFMGPQCER | DYRTGPCFGQ | VGPEGCQHQL | TGLVCTKALC | CATVGRAWGL | PCELCPAQPH | PCRRGFIPNI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HTGACQDVDE | CQAVPGLCQG | GSCVNMVGSF | HCRCPVGHRL | SDSSAACEDY | RAGACFSVLF | GGRCAGDLAG | HYTRRQCCCD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RGRCWAAGPV | PELCPPRGSN | EFQQLCAQRL | PLLPGHPGLF | PGLLGFGSNG | MGPPLGPARL | NPHGSDARGI | PSLGPGNSNI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GTATLNQTID | ICRHFTNLCL | NGRCLPTPSS | YRCECNVGYT | QDVRGECIDV | DECTSSPCHH | GDCVNIPGTY | HCRCYPGFQA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TPTRQACVDV | DECIVSGGLC | HLGRCVNTEG | SFQCVCNAGF | ELSPDGKNCV | DHNECATSTM | CVNGVCLNED | GSFSCLCKPG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FLLAPGGHYC | MDIDECQTPG | ICVNGHCTNT | EGSFRCQCLG | GLAVGTDGRV | CVDTHVRSTC | YGAIEKGSCA | RPFPGTVTKS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ECCCANPDHG | FGEPCQLCPA | KDSAEFQALC | SSGLGITTDG | RDINECALDP | EVCANGVCEN | LRGSYRCVCN | LGYEAGASGK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DCTDVDECAL | NSLLCDNGWC | QNSPGSYSCS | CPPGFHFWQD | TEICKDVDEC | LSSPCVSGVC | RNLAGSYTCK | CGPGSRLDPS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GTFCLDSTKG | TCWLKIQESR | CEVNLQGASL | RSECCATLGA | AWGSPCERCE | IDPACARGFA | RMTGVTCDDV | NECESFPGVC |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PNGRCVNTAG | SFRCECPEGL | MLDASGRLCV | DVRLEPCFLR | WDEDECGVTL | PGKYRMDVCC | CSIGAVWGVE | CEACPDPESL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| EFASLCPRGL | GFASRDFLSG | RPFYKDVNEC | KVFPGLCTHG | TCRNTVGSFH | CACAGGFALD | AQERNCTDID | ECRISPDLCG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QGTCVNTPGS | FECECFPGYE | SGFMLMKNCM | DVDECARDPL | LCRGGTCTNT | DGSYKCQCPP | GHELTAKGTA | CEDIDECSLS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DGLCPHGQCV | NVIGAFQCSC | HAGFQSTPDR | QGCVDINECR | VQNGGCDVHC | INTEGSYRCS | CGQGYSLMPD | GRACADVDEC |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| EENPRVCDQG | HCTNMPGGHR | CLCYDGFMAT | PDMRTCVDVD | ECDLNPHICL | HGDCENTKGS | FVCHCQLGYM | VRKGATGCSD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VDECEVGGHN | CDSHASCLNI | PGSFSCRCLP | GWVGDGFECH | DLDECVSQEH | RCSPRGDCLN | VPGSYRCTCR | QGFAGDGFFC |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| EDRDECAENV | DLCDNGQCLN | APGGYRCECE | MGFDPTEDHR | ACQDVDECAQ | GNLCAFGSCE | NLPGMFRCIC | NGGYELDRGG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| GNCTDINECA | DPVNCINGVC | INTPGSYLCS | CPQDFELNPS | GVGCVDTRAG | NCFLETHDRG | DSGISCSAEI | GVGVTRASCC |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| CSLGRAWGNP | CELCPMANTT | EYRTLCPGGE | GFQPNRITVI | LEDIDECQEL | PGLCQGGDCV | NTFGSFQCEC | PPGYHLSEHT |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| RICEDIDECS | THSGICGPGT | CYNTLGNYTC | VCPAEYLQVN | GGNNCMDMRK | SVCFRHYNGT | CQNELAFNVT | RKMCCCSYNI |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| GQAWNRPCEA | CPTPISPDYQ | ILCGNQAPGF | LTDIHTGKPL | DIDECGEIPA | ICANGICINQ | IGSFRCECPA | GFNYNSILLA |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| CEDVDECGSR | ESPCQQNADC | INIPGSYRCK | CTRGYKLSPG | GACVGRNECR | EIPNVCSHGD | CMDTEGSYMC | LCHRGFQASA |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| DQTLCMDIDE | CDRQPCGNGT | CKNIIGSYNC | LCFPGFVVTH | NGDCVDFDEC | TTLVGQVCRF | GHCLNTAGSF | HCLCQDGFEL |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| TADGKNCVDT | NECLSLAGTC | LPGTCQNLEG | SFRCICPPGF | QVQSDHCIDI | DECSEEPNLC | LFGTCTNSPG | SFQCLCPPGF |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| VLSDNGHRCF | DTRQSFCFTR | FEAGKCSVPK | AFNTTKTRCC | CSKRPGEGWG | DPCELCPQEG | SAAFQELCPF | GHGAVPGPDD |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| SREDVNECAE | NPGVCTNGVC | VNTDGSFRCE | CPFGYSLDFT | GINCVDTDEC | SVGHPCGQGT | CTNVIGGFEC | ACADGFEPGL |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2042 | 1 | 733.5869 | -72.63 | 3 | 53.9 | 11.7 | 2 | 304-321 | R.CAGDLAGHYTRRQCCCDR.G | Carbamidomethyl: 14, 15, 16 |

BRUKER

# Detailed Protein Report

## Protein 1441: zinc finger protein 721 [Homo sapiens]

**Accession:** gi|119120877

**Database:** refseq_human(refseq_human_20140103.fasta)

**Database Date:** 2015-11-30

**Modification(s):** Carbamidomethyl

**Score:** 11.7

**MW [kDa]:** 106.4

**pI:** 10.4

**Sequence Coverage [%]:** 1.7

**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MLENYRNLVS LAMCSHFTQD FLPVQGIEDS FHKLILRRYE KCGHDNLQLR KGCKSMNVCK VQKGVYNGIN KCLSNTQSKI
        90        100        110        120        130        140        150        160
FQCNARVKVF SKFANSNKDK TRHTGEKHFK CNECGKSFQK FSDLTQHKGI HAGEKPYTCE ERGKDFGWYT DLNQHKKIHT
       170        180        190        200        210        220        230        240
GEKPYKCEEC GKAFNRSTNL TAHKRIHNRE KAYTGEDRDR AFGWSTNLNE YKKIHTGDKP YKCKECGKAF MHSSHLNKHE
       250        260        270        280        290        300        310        320
KIHTGEKPYK CKECGKVISS SSSFAKHKRI HTGEKPFKCL ECGKAFNIST TLTKHRRIHT GEKPYTCEVC GKAFRQSANL
       330        340        350        360        370        380        390        400
YVHRRIHTGE KPYTCGECGK TFRQSANLYV HRRIHTGEKP YKCEDCGKAF GRYTALNQHK KIHTGEKPYK CEECGKAFNS
       410        420        430        440        450        460        470        480
STNLTAHKRI HTREKPYTCE DRGRAFGLST NLNEYKKIHT GDKPYKCKEC GKAFIHSLHL NKHEKIHTGK KPYKCKQCGK
       490        500        510        520        530        540        550        560
VITSSSSFAK HKRIHTGEKP FECLECGKAF TSSTTLTKHR RIHTGEKPYT CEVCGKAFRQ SAILYVHRRI HTGEKPYTCE
       570        580        590        600        610        620        630        640
ECGKTFRQSA NLYVHRRIHT GEKPYKCEEC GKAFGRYTDL NQHKKIHTGE KLYKCEECGK DFVWYTDLNQ QKKIYTGEKP
       650        660        670        680        690        700        710        720
YKCEECGKAF APSTDLNQHT KILTGEQSYK CEECGKAFGW SIALNQHKKI HTGEKPYKCE ECGKAFSRSR NLTTHRRVHT
       730        740        750        760        770        780        790        800
REKPYKCEDR GRSFGWSTNL NEYKKIHTGD KLYKCKECGK VFKQSSHLNR HEKIHTGKKP YKCKECGKVI TSSSSFAKHK
       810        820        830        840        850        860        870        880
RIHTGEKPFK CLECGKAFTS STTLTKHRRI HTGEKPYTCE ECGKAFRQSA ILYVHRRIHT GEKPYTCGEC GKTFRQSANL
       890        900        910        920        930
YAHKKIHTGE KPYTCGDCGK TFRQSANLYA HKKIHTGDKT IQV
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1666 | 1 | 938.9110 | -24.87 | 2 | 50.6 | 11.7 | 2 | 223-238 | K.CKECGKAFMHSSHLNK.H | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 1442: PREDICTED: neuronal PAS domain-containing protein 2 isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530368679 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 87.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| | | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MYAYGFVGRC | APFPAEEGRT | FDLSEELGRS | VTREGTGTTR | LNSEPVPLLC | LPLLNCSRKN | CIENLMDEDE | KDRAKRASRN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KSEKKRRDQF | NVLIKELSSM | LPGNTRKMDK | TTVLEKVIGF | LQKHNEVSAQ | TEICDIQQDW | KPSFLSNEEF | TQLMLEALDG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FIIAVTTDGS | IIYVSDSITP | LLGHLPSDVM | DQNLLNFLPE | QEHSEVYKIL | SSHMLVTDSP | SPEYLKSDSD | LEFYCHLLRG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SLNPKEFPTY | EYIKFVGNFR | SYNNVMQFGK | GKSCCYRFLT | KGQQWIWLQT | HYYITYHQWN | SKPEFIVCTH | SVVSYADVRV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ERRQELALED | PPSEALHSSA | LKDKGSSLEP | RQHFNTLDVG | ASGLNTSHSP | SASSRSSHKS | SHTAMSEPTS | TPTKLMAEAS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TPALPRSATL | PQELPVPGLS | QAATMPAPLP | SPSSCDLTQQ | LLPQTVLQST | PAPMAQFSAQ | FSMFQTIKDQ | LEQRTRILQA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NIRWQQEELH | KIQEQLCLVQ | DSNVQMFLQQ | PAVSLSFSST | QRPEAQQQLQ | QRSAAVTQPQ | LGAGPQLPGQ | ISSAQVTSQH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LLRESSVIST | QGPKPMRSSQ | LMQSSGRSGS | SLVSPFSSAT | AALPPSLNLT | TPASTSQDAS | QCQPSPDFSH | DRQLRLLLSQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PIQPMMPGSC | DARQPSEVSR | TGRQVKYAQS | QTVFQNPDAH | PANSSSAPMP | VLLMGQAVLH | PSFPASQPSP | LQPAQARQQP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | |
| PQHYLQVQAP | TSLHSEQQDS | LLLSTYSQQP | GTLGYPQPPP | AQPQPLRPPR | RVSSLSESSG | LQQPPR | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 169 | 1 | 492.6415 | 18.04 | 3 | 31.8 | 11.6 | 1 | 111-123 | K.TTVLEKVIGFLQK.H | |

# Detailed Protein Report

## Protein 1443: PREDICTED: zinc finger MIZ domain-containing protein 2 isoform X10 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530385040 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 81.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNSMNPMKPA | LPPAPHGDGS | FAYESVPWQQ | SATQPAGSLS | VVTTVWGVGN | ATQSQVLGNP | MGPAGSPSGS | SMMPGVAGGS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SALTSPQCLG | QQAFAEGGAN | KGYVQQGVYS | RGGYPGAPGF | TTGYAGGPGG | LGLPSHAARP | STDFTQAAAA | AAVAAAAATA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TATATATVAA | LQEKQSQELS | QYGAMGAGQS | FNSQFLQHGG | PRGPSVPAGM | NPTGIGGVMG | PSGLSPLAMN | PTRAAGMTPL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YAGQRLPQHG | YPGPPQAQPL | PRQGVKRTYS | EVYPGQQYLQ | GGQYAPSTAQ | FAPSPGQPPA | PSPSYPGHRL | PLQQGMTQSL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SVPGPTGLHY | KPTEQFNGQG | ASFNGGSVSY | SQPGLSGPTR | SIPGYPSSPL | PGNPTPPMTP | SSSVPYMSPN | QEVKSPFLPD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LKPNLNSLHS | SPSAHSQWPL | LPGSGPCDEL | RLTFPVRDGV | VLEPFRLQHN | LAVSNHVFQL | RDSVYKTLIM | RPDLELQFKC |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YHHEDRQMNT | NWPASVQVSV | NATPLTIERG | DNKTSHKPLY | LKHVCQPGRN | TIQITVTACC | CSHLFVLQLV | HRPSVRSVLQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GLLKKRLLPA | EHCITKIKRN | FSSGTIPGTP | GPNGEDGVEQ | TAIKVSLKCP | ITFRRIQLPA | RGHDCRHIQC | FDLESYLQLN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CERGTWRCPV | CNKTALLEGL | EVDQYMLGIL | IYIQNSDYEE | ITIDPTCSWK | PVPVKPDMHI | KEEPDGPALK | RCRTVSPAHV |
| 730 | 740 | 750 | 760 | 770 | | | |
| LMPSVMEMIA | ALGPGAAPFA | PLQPPSVPAP | SDYPGQGMSQ | GQFPWQQ | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 76 | 1 | 750.8206 | -121.89 | 2 | 30.9 | 11.6 | 1 | 510-522 | R.GDNKTSHKPLYLK.H | |

# Detailed Protein Report

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**Protein 1444:** **carcinoembryonic antigen-related cell adhesion molecule 20 isoform 4S precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|156564388 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 5.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.31 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.73 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGPADSWGHH | WMGILLSASL | CTVWSPPAAA | QLTLNANPLD | ATQSEDVVLP | VFGTPRTPQI | HGRSRELAKP | SIAVSPGTAI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EQKDMVTFYC | TTKDVNITIH | WVSNNLSVVF | HERMQLSKDG | KILTILIVQR | EDSGTYQCEA | RDALLSQRSD | PIFLDVKYGP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DPVEIKLESG | VASGEVVEVM | EGSSMTFLAE | TKSHPPCAYT | WFLLDSILSH | TTRTFTIHAV | SREHEGLYRC | LVSNSATHLS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SLGTLKVRVL | ETLTMPQVVP | SSLNLVENAR | SVDLTCQTVN | QSVNVQWFLS | GQPLLPSEHL | QLSADNRTLI | IHGLQRNDTG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PYACEVWNWG | SRARSEPLEL | TINCPQSSSL | SSGAIAGIVI | GILAVIAVAS | ELGYFLYIRN | ARRPSRKTTE | DPSHETSQPI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PKEEHPTEPS | SESLSPEYCN | ISQLQGRIRV | ELTKLPSASR | RGNSFSPWKP | PPKPLMPPLR | LVSTVPKNME | SIYEELVNPE |
| 490 | 500 | | | | | | |
| PNTYIQINPS | V | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 95 | 1 | 896.4310 | -0.22 | 3 | 30.1 | 11.6 | 0 | 167-192 | K. LESGVASGEVVEVMEGSSMTFLA S | | QU:MU 2.31<br>WUP:QUP 0.73 |

# Detailed Protein Report

## Protein 1445: fibulin-5 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|19743803 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 50.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MPGIKRILTV TILALCLPSP GNAQAQCTNG FDLDRQSGQC LDIDECRTIP EACRGDMMCV NQNGGYLCIP RTNPVYRGPY

        90        100        110        120        130        140        150        160
SNPYSTPYSG PYPAAAPPLS APNYPTISRP LICRFGYQMD ESNQCVDVDE CATDSHQCNP TQICINTEGG YTCSCTDGYW

       170        180        190        200        210        220        230        240
LLEGQCLDID ECRYGYCQQL CANVPGSYSC TCNPGFTLNE DGRSCQDVNE CATENPCVQT CVNTYGSFIC RCDPGYELEE

       250        260        270        280        290        300        310        320
DGVHCSDMDE CSFSEFLCQH ECVNQPGTYF CSCPPGYILL DDNRSCQDIN ECEHRNHTCN LQQTCYNLQG GFKCIDPIRC

       330        340        350        360        370        380        390        400
EEPYLRISDN RCMCPAENPG CRDQPFTILY RDMDVVSGRS VPADIFQMQA TTRYPGAYYI FQIKSGNEGR EFYMRQTGPI

       410        420        430        440        450
SATLVMTRPI KGPREIQLDL EMITVNTVIN FRGSSVIRLR IYVSQYPF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2359 | 1 | 911.7720 | -114.30 | 2 | 57.8 | 11.6 | 1 | 327-342 | R.ISDNRCMCPAENPGCR.D | Carbamidomethyl: 6 |

# Detailed Protein Report

## Protein 1446: zinc finger protein 514 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|14249456 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 4.8 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578805042 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 514 isoform X3 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTFEDVAVEF | SQWEWGQLNP | AQKDLYREVM | LENFRNLAIL | GLLVSKPYVI | CQLEEGGEPF | MVEREISTGA | HSDWKRRSKS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KESMPSWGIS | KEELFQVVSV | EKHIQDVLQF | SKLKAACGCD | GQLEMQQIKQ | ERHLKQMSTI | HKSATTLSRD | YKWNGFGRSL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GLRSVLVNQH | SILMGEGSYK | CDTEFRQTLG | GNNSQRTHPE | KKSCKCNECG | KSFHFQSELR | RHQRCHTGEK | PYECSDCGRA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FGHISSLIKH | QRTHTGEKPY | ECSECGRAFS | QSSSLVLHYR | FHTGEKPYKC | NECGRAFGHT | SSLIKHQRTH | TGEKPYECRE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CGRTFSQSSS | LIVHYRFHTG | EKPYKCNKCG | RAFSQSSSLT | QHYRFHTGEK | PYKCNECGRA | FAHTASLIKH | QRSHAGKKTL |
| 410 | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2043 | 1 | 714.6158 | -98.66 | 3 | 55.9 | 11.6 | 2 | 374-392 | K.CNECGRAFAHTASLIKHQR.S | |

# Detailed Protein Report

**Protein 1447: PREDICTED: myotubularin-related protein 5 isoform X5 [Homo sapiens]**

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|530420851 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 208.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
|  |  | **Sequence Coverage [%]:** | 0.5 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MARLADYFVL | VAFGPHPRGS | GEGQGQILQR | FPEKDWEDNP | FPQGIELFCQ | PSGWQLCPER | NPPTFFVAVL | TDINSERHYC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ACLTFWEPAE | PSQETTRVED | ATEREEEGDE | GGQTHLSPTA | PAPSAQLFAP | KTLVLVSRLD | HTEVFRNSLG | LIYAIHVEGL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NVCLENVIGN | LLTCTVPLAG | GSQRTISLGA | GDRQVIQTPL | ADSLPVSRCS | VALLFRQLGI | TNVLSLFCAA | LTEHKVLFLS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RSYQRLADAC | RGLLALLFPL | RYSFTYVPIL | PAQLLEVLST | PTPFIIGVNA | AFQAETQELL | DVIVADLDGG | TVTIPECVHI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PPLPEPLQSQ | THSVLSMVLD | PELELADLAF | PPPTTSTSSL | KMQDKELRAV | FLRLFAQLLQ | GYRWCLHVVR | IHPEPVIRFH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KAAFLGQRGL | VEDDFLMKVL | EGMAFAGFVS | ERGVPYRPTD | LFDELVAHEV | ARMRADENHP | QRVLRHVQEL | AEQLYKNENP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YPAVAMHKVQ | RPGESSHLRR | VPRPFPRLDE | GTVQWIVDQA | AAKMQGAPPA | VKAERRTTVP | SGPPMTAILE | RCSGLHVNSA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RRLEVVRNCI | SYVFEGKMLE | AKKLLPAVLR | ALKGRAARRC | LAQELHLHVQ | QNRAVLDHQQ | FDFVVRMMNC | CLQDCTSLDE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HGIAAALLPL | VTAFCRKLSP | GVTQFAYSCV | QEHVVWSTPQ | FWEAMFYGDV | QTHIRALYLE | PTEDLAPAQE | VGEAPSQEDE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RSALDVASEQ | RRLWPTLSRE | KQQELVQKEE | STVFSQAIHY | ANRMSYLLLP | LDSSKSRLLR | ERAGLGDLES | ASNSLVTNSM |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| AGSVAESYDT | ESGFEDAETC | DVAGAVVRFI | NRFVDKVCTE | SGVTSDHLKG | LHVMVPDIVQ | MHIETLEAVQ | RESRRLPPIQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KPKLLRPRLL | PGEECVLDGL | RVYLLPDGRE | EGAGGSAGGP | ALLPAEGAVF | LTTYRVIFTG | MPTDPLVGEQ | VVVRSFPVAA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LTKEKRISVQ | TPVDQLLQDG | LQLRSCTFQL | LKMAFDEEVG | SDSAELFRKQ | LHKLRYPPDI | RATFAFTLGS | AHTPGRPPRV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TKDKGPSLRT | LSRNLVKNAK | KTIGRQHVTR | KKYNPPSWEH | RGQPPPEDQE | DEISVSEELE | PSTLTPSSAL | KPSDRMTMSS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LVERACCRDY | QRLGLGTLSS | SLSRAKSEPF | RISPVNRMYA | ICRSYPGLLI | VPQSVQDNAL | QRVSRCYRQN | RFPVVCWRSG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| RSKAVLLRSG | GLHGKGVVGL | FKAQNAPSPG | QSQADSSSLE | QEKYLQAVVS | SMPRYADASG | RNTLSGFSSA | HMGSHGKWGS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VRTSGRSSGL | GTDVGSRLAG | RDALAPPQAN | GGPPDPGFLR | PQRAALYILG | DKAQLKGVRS | DPLQQWELVP | IEVFEARQVK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ASFKKLLKAC | VPGCPAAEPS | PASFLRSLED | SEWLIQIHKL | LQVSVLVVEL | LDSGSSVLVG | LEDGWDITTQ | VVSLVQLLSD |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| PFYRTLEGFR | LLVEKEWLSF | GHRFSHRGAH | TLAGQSSGFT | PVFLQFLDCV | HQVHLQFPME | FEFSQFYLKF | LGYHHVSRRF |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| RTFLLDSDYE | RIELGLLYEE | KGERRGQVPC | RSVWEYVDRL | SKRTPVFHNY | MYAPEDAEVL | RPYSNVSNLK | VWDFYTEETL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| AEGPPYDWEL | AQGPPEPPEE | ERSDGGAPQS | RRRVVWPCYD | SCPRAQPDAI | SRLLEELQRL | ETELGQPAER | WKDTWDRVKA |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| AQRLEGRPDG | RGTPSSLLVS | TAPHHRRSLG | VYLQEGPVGS | TLSLSLDSDQ | SSGSTTSGSR | QAARRSTSTL | YSQFQTAESE |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| NRSYEGTLYK | KGAFMKPWKA | RWFVLDKTKH | QLRYYDHRVD | TECKGVIDLA | EVEAVAPGTP | TMGAPKTVDE | KAFFDVKTTR |
| 1850 | 1860 | 1870 |  |  |  |  |  |
| RVYNFCAQDV | PSAQQWVDRI | QSCLSDA |  |  |  |  |  |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 292 | 1 | 591.6596 | -216.66 | 2 | 33.3 | 11.6 | 1 | 242-251 | R.SYQRLADACR.G | |

# Detailed Protein Report

## Protein 1448: receptor-type tyrosine-protein phosphatase C isoform 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|392307009 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 131.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTMYLWLKLL | AFGFAFLDTE | VFVTGQSPTP | SPTDAYLNAS | ETTTLSPSGS | AVISTTTIAT | TPSKPTCDEK | YANITVDYLY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NKETKLFTAK | LNVNENVECG | NNTCTNNEVH | NLTECKNASV | SISHNSCTAP | DKTLILDVPP | GVEKFQLHDC | TQVEKADTTI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CLKWKNIETF | TCDTQNITYR | FQCGNMIFDN | KEIKLENLEP | EHEYKCDSEI | LYNNHKFTNA | SKIIKTDFGS | PGEPQIIFCR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SEAAHQGVIT | WNPPQRSFHN | FTLCYIKETE | KDCLNLDKNL | IKYDLQNLKP | YTKYVLSLHA | YIIAKVQRNG | SAAMCHFTTK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SAPPSQVWNM | TVSMTSDNSM | HVKCRPPRDR | NGPHERYHLE | VEAGNTLVRN | ESHKNCDFRV | KDLQYSTDYT | FKAYFHNGDY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PGEPFILHHS | TSYNSKALIA | FLAFLIIVTS | IALLVVLYKI | YDLHKKRSCN | LDEQQELVER | DDEKQLMNVE | PIHADILLET |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YKRKIADEGR | LFLAEFQSIP | RVFSKFPIKE | ARKPFNQNKN | RYVDILPYDY | NRVELSEING | DAGSNYINAS | YIDGFKEPRK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YIAAQGPRDE | TVDDFWRMIW | EQKATVIVMV | TRCEEGNRNK | CAEYWPSMEE | GTRAFGDVVV | KINQHKRCPD | YIIQKLNIVN |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KKEKATGREV | THIQFTSWPD | HGVPEDPHLL | LKLRRRVNAF | SNFFSGPIVV | HCSAGVGRTG | TYIGIDAMLE | GLEAENKVDV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YGYVVKLRRQ | RCLMVQVEAQ | YILIHQALVE | YNQFGETEVN | LSELHPYLHN | MKKRDPPSEP | SPLEAEFQRL | PSYRSWRTQH |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IGNQEENKSK | NRNSNVIPYD | YNRVPLKHEL | EMSKESEHDS | DESSDDDSDS | EEPSKYINAS | FIMSYWKPEV | MIAAQGPLKE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TIGDFWQMIF | QRKVKVIVML | TELKHGDQEI | CAQYWGEGKQ | TYGDIEVDLK | DTDKSSTYTL | RVFELRHSKR | KDSRTVYQYQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| YTNWSVEQLP | AEPKELISMI | QVVKQKLPQK | NSSEGNKHHK | STPLLIHCRD | GSQQTGIFCA | LLNLLESAET | EEVVDIFQVV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KALRKARPGM | VSTFEQYQFL | YDVIASTYPA | QNGQVKKNNH | QEDKIEFDNE | VDKVKQDANC | VNPLGAPEKL | PEAKEQAEGS |
| 1130 | 1140 | 1150 | | | | | |
| EPTSGTEGPE | HSVNGPASPA | LNQGS | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2545 | 2 | 625.3171 | 71.20 | 2 | 62.4 | 11.6 | 1 | 370-379 | R.NESHKNCDFR.V | |

# Detailed Protein Report

## Protein 1449: PREDICTED: zinc finger protein 334 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578836054 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 78.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578836058 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 334 isoform X6 [Homo sapiens] |
| gi\|578836056 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 334 isoform X5 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAATGPCSEA | PVQGCDAGEL | QQLGLCGVSD | VQRSWSKFCN | FPLTGYHVSK | PDVIFKLEQG | EEPWIVEEFS | NQNYPDIDDA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LEKNKEIQDK | HLTQTVFFSN | KTLITERENV | FGKTLNLGMN | SVPSRKMPYK | CNPGGNSLKT | NSEVIVAKKS | KENRKIPDGY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SGFGKHEKSH | LGMKKYRYNP | MRKASNQNEN | LILHQNIQIL | KQPFDYNKCG | KTFFKRAILI | TQKGRQTERK | PNECNECRKT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FSKRSTLIVH | QRIHTGEKPY | VCSDCRKTFR | VKTSLTRHRR | IHTGERPYEC | SECRKTFIDK | SALIVHQKIH | GGEKSYECNE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CGKTFFRKSA | LAEHFRSHTG | EKPYECKECG | NAFSKKSYLV | VHQRTHRGEK | PNECKECGKT | FFCQSALTAH | QRIHTGEKPY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ECSECEKTFF | CQSALNVHRR | SHTGEKPYEC | SQCGKFLCTK | SALIAHQITH | RGKKSYECNE | CGKFFCHKST | LTIHQRTHTG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EKHGVFNKCG | RISIVKSNCS | QCKRMNTKEN | LYECSEHGHA | VSKNSHLIVH | QRTIWERPYE | CNECGRTYCR | KSALTHHQRT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HTGQRPYECN | ECGKTFCQKF | SFVEHQRTHT | GEKPYECNEC | GKSFCHKSAF | RVHRRIHTGE | KPYECNQCGK | TYRRLWTLTE |
| 650 | 660 | 670 | 680 | | | | |
| HQKIHTGEKP | YECNKCEKTF | RHKSNFLLHQ | KSHKE | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1665 | 1 | 967.4326 | -7.08 | 2 | 49.1 | 11.6 | 2 | 224-238 | K.GRQTERKPNECNECR.K | Carbamidomethyl: 11, 14 |

# Detailed Protein Report

## Protein 1450: tankyrase-2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|13376842 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 126.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| | | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSGRRCAGGG | AACASAAAEA | VEPAARELFE | ACRNGDVERV | KRLVTPEKVN | SRDTAGRKST | PLHFAAGFGR | KDVVEYLLQN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GANVQARDDG | GLIPLHNACS | FGHAEVVNLL | LRHGADPNAR | DNWNYTPLHE | AAIKGKIDVC | IVLLQHGAEP | TIRNTDGRTA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LDLADPSAKA | VLTGEYKKDE | LLESARSGNE | EKMMALLTPL | NVNCHASDGR | KSTPLHLAAG | YNRVKIVQLL | LQHGADVHAK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DKGDLVPLHN | ACSYGHYEVT | ELLVKHGACV | NAMDLWQFTP | LHEAASKNRV | EVCSLLLSYG | ADPTLLNCHN | KSAIDLAPTP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QLKERLAYEF | KGHSLLQAAR | EADVTRIKKH | LSLEMVNFKH | PQTHETALHC | AAASPYPKRK | QICELLLRKG | ANINEKTKEF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LTPLHVASEK | AHNDVVEVVV | KHEAKVNALD | NLGQTSLHRA | AYCGHLQTCR | LLLSYGCDPN | IISLQGFTAL | QMGNENVQQL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LQEGISLGNS | EADRQLLEAA | KAGDVETVKK | LCTVQSVNCR | DIEGRQSTPL | HFAAGYNRVS | VVEYLLQHGA | DVHAKDKGGL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VPLHNACSYG | HYEVAELLVK | HGAVVNVADL | WKFTPLHEAA | AKGKYEICKL | LLQHGADPTK | KNRDGNTPLD | LVKDGDTDIQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DLLRGDAALL | DAAKKGCLAR | VKKLSSPDNV | NCRDTQGRHS | TPLHLAAGYN | NLEVAEYLLQ | HGADVNAQDK | GGLIPLHNAA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SYGHVDVAAL | LIKYNACVNA | TDKWAFTPLH | EAAQKGRTQL | CALLLAHGAD | PTLKNQEGQT | PLDLVSADDV | SALLTAAMPP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SALPSCYKPQ | VLNGVRSPGA | TADALSSGPS | SPSSLSAASS | LDNLSGSFSE | LSSVVSSSGT | EGASSLEKKE | VPGVDFSITQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| FVRNLGLEHL | MDIFEREQIT | LDVLVEMGHK | ELKEIGINAY | GHRHKLIKGV | ERLISGQQGL | NPYLTLNTSG | SGTILIDLSP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DDKEFQSVEE | EMQSTVREHR | DGGHAGGIFN | RYNILKIQKV | CNKKLWERYT | HRRKEVSEEN | HNHANERMLF | HGSPFVNAII |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| HKGFDERHAY | IGGMFGAGIY | FAENSSKSNQ | YVYGIGGGTG | CPVHKDRSCY | ICHRQLLFCR | VTLGKSFLQF | SAMKMAHSPP |
| 1130 | 1140 | 1150 | 1160 | 1170 | | | |
| GHHSVTGRPS | VNGLALAEYV | IYRGEQAYPE | YLITYQIMRP | EGMVDG | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2748 | 1 | 694.8549 | -29.42 | 2 | 64.7 | 11.6 | 1 | 59-71 | K.STPLHFAAGFGRK.D | |

# Detailed Protein Report

## Protein 1451: condensin complex subunit 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|178056552 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 157.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAPQMYEFHL | PLSPEELLKS | GGVNQYVVQE | VLSIKHLPPQ | LRAFQAAFRA | QGPLAMLQHF | DTIYSILHHF | RSIDPGLKED |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TLQFLIKVVS | RHSQELPAIL | DDTTLSGSDR | NAHLNALKMN | CYALIRLLES | FETMASQTNL | VDLDLGGKGK | KARTKAAHGF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DWEEERQPIL | QLLTQLLQLD | IRHLWNHSII | EEEFVSLVTG | CCYRLLENPT | INHQKNRPTR | EAITHLLGVA | LTRYNHMLSA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TVKIIQMLQH | FEHLAPVLVA | AVSLWATDYG | MKSIVGEIVR | EIGQKCPQEL | SRDPSGTKGF | AAFLTELAER | VPAILMSSMC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ILLDHLDGEN | YMMRNAVLAA | MAEMVLQVLS | GDQLEAAARD | TRDQFLDTLQ | AHGHDVNSFV | RSRVLQLFTR | IVQQKALPLT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RFQAVVALAV | GRLADKSVLV | CKNAIQLLAS | FLANNPFSCK | LSDADLAGPL | QKETQKLQEM | RAQRRTAAAS | AVLDPEEEWE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AMLPELKSTL | QQLLQLPQGE | EEIPEQIANT | ETTEDVKGRI | YQLLAKASYK | KAIILTREAT | GHFQESEPFS | HIDPEESEET |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RLLNILGLIF | KGPAASTQEK | NPRESTGNMV | TGQTVCKNKP | NMSDPEESRG | NDELVKQEML | VQYLQDAYSF | SRKITEAIGI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ISKMMYENTT | TVVQEVIEFF | VMVFQFGVPQ | ALFGVRRMLP | LIWSKEPGVR | EAVLNAYRQL | YLNPKGDSAR | AKAQALIQNL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SLLLVDASVG | TIQCLEEILC | EFVQKDELKP | AVTQLLWERA | TEKVACCPLE | RCSSVMLLGM | MARGKPEIVG | SNLDTLVSIG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LDEKFPQDYR | LAQQVCHAIA | NISDRRKPSL | GKRHPPFRLP | QEHRLFERLR | ETVTKGFVHP | DPLWIPFKEV | AVTLIYQLAE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GPEVICAQIL | QGCAKQALEK | LEEKRTSQED | PKESPAMLPT | FLLMNLLSLA | GDVALQQLVH | LEQAVSGELC | RRRVLREEQE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| HKTKDPKEKN | TSSETTMEEE | LGLVGATADD | TEAELIRGIC | EMELLDGKQT | LAAFVPLLLK | VCNNPGLYSN | PDLSAAASLA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LGKFCMISAT | FCDSQLRLLF | TMLEKSPLPI | VRSNLMVATG | DLAIRFPNLV | DPWTPHLYAR | LRDPAQQVRK | TAGLVMTHLI |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| LKDMVKVKGQ | VSEMAVLLID | PEPQIAALAK | NFFNELSHKG | NAIYNLLPDI | ISRLSDPELG | VEEEPFHTIM | KQLLSYITKD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KQTESLVEKL | CQRFRTSRTE | RQQRDLAYCV | SQLPLTERGL | RKMLDNFDCF | GDKLSDESIF | SAFLSVVGKL | RRGAKPEGKA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| IIDEFEQKLR | ACHTRGLDGI | KELEIGQAGS | QRAPSAKKPS | TGSRYQPLAS | TASDNDFVTP | EPRRTTRRHP | NTQQRASKKK |
| 1370 | 1380 | 1390 | 1400 | 1410 | | | |
| PKVVFSSDES | SEEDLSAEMT | EDETPKKTTP | ILRASARRHR | S | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2825 | 1 | 913.4475 | -27.71 | 2 | 63.9 | 11.6 | 0 | 1086-1100 | R.FPNLVDPWTPHLYAR.L | |

## Protein 1452: olfactory receptor 5M9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|52317128 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 35.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 5.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPNFTDVTEF | TLLGLTCRQE | LQVLFFVVFL | AVYMITLLGN | IGMIILISIS | PQLQSPMYFF | LSHLSFADVC | FSSNVTPKML |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ENLLSETKTI | SYVGCLVQCY | FFIAVVHVEV | YILAVMAFDR | YMAGCNPLLY | GSKMSRTVCV | RLISVPYVYG | FSVSLICTLW |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TYGLYFCGNF | EINHFYCADP | PLIQIACGRV | HIKEITMIVI | AGINFTYSLS | VVLISYTLIV | VAVLRMRSAD | GRRKAFSTCG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SHLTAVSMFY | GTPIFMYLRR | PTEESVEQGK | MVAVFYTTVI | PMLNPMIYSL | RNKDVKEAVN | KAITKTYVRQ | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1533 | 1 | 911.7754 | -156.20 | 2 | 49.4 | 11.6 | 1 | 121-136 | R.YMAGCNPLLYGSKMSR.T | Oxidation: 2, 14 |

# Detailed Protein Report

## Protein 1453: jerky protein homolog isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|525342477 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 61.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.66 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.64 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578816229 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: jerky protein homolog isoform X3 [Homo sapiens] |
| gi\|525342488 | refseq_human (refseq_human_20140103.fasta) | jerky protein homolog isoform b [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASKPAAGKS | RGEKRKRVVL | TLKEKIDICT | RLEKGESRKA | LMQEYNVGMS | TLYDIRAHKA | QLLRFFASSD | SNKALEQRRT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LHTPKLEHLD | RVLYEWFLGK | RSEGVPVSGP | MLIEKAKDFY | EQMQLTEPCV | FSGGWLWRFK | ARHGIKKLDA | SSEKQSADHQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AAEQFCAFFR | SLAAEHGLSA | EQVYNADETG | LFWRCLPNPT | PEGGAVPGPK | QGKDRLTVLM | CANATGSHRL | KPLAIGKCSG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PRAFKGIQHL | PVAYKAQGNA | WVDKEIFSDW | FHHIFVPSVR | EHFRTIGLPE | DSKAVLLLDS | SRAHPQEAEL | VSSNVFTIFL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PASVASLVQP | MEQGIRRDFM | RNFINPPVPL | QGPHARYNMN | DAIFSVACAW | NAVPSHVFRR | AWRKLWPSVA | FAEGSSSEEE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LEAECFPVKP | HNKSFAHILE | LVKEGSSCPG | QLRQRQAASW | GVAGREAEGG | RPPAATSPAE | VVWSSEKTPK | ADQDGRGDPG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EGEEVAWEQA | AVAFDAVLRF | AERQPCFSAQ | EVGQLRALRA | VFRSQQQETV | GLEDVVVTSP | EELAIPKCCL | EASTET |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 69 | 1 | 773.7368 | -181.03 | 2 | 29.8 | 11.6 | 0 | 216-229 | R.LTVLMCANATGSHR.L | Carbamidomethyl: 6;<br>Oxidation: 5 | WUP:QUP<br>QU:MU | 0.64<br>0.66 |

# Detailed Protein Report

## Protein 1454: protein phosphatase 1M isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|171460934 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 10.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGGCTALVAV | SLQGKLYMAN | AGDSRAILVR | RDEIRPLSFE | FTPETERQRI | QQLAFVYPEL | LAGEFTRLEF | PRRLKGDDLG |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| QKVLFRDHHM | SGWSYKRVEK | SDLKYPLIHG | QGRQARLLGT | LAVSRGLGDH | QLRVLDTNIQ | LKPFLLSVPQ | VTVLDVDQLE |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| LQEDDVVVMA | TDGLWDVLSN | EQVAWLVRSF | LPGNQEDPHR | FSKLAQMLIH | STQGKEDSLT | EEGQVSYDDV | SVFVIPLHSQ |
| **250** | | | | | | | |
| GQESSDH | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 444 | 1 | 862.7948 | 47.40 | 3 | 35.5 | 11.6 | 1 | 1-25 | -.MGGCTALVAVSLQGKLYMANAGDSR.A | Carbamidomethyl: 4;<br>Oxidation: 18 |

# Detailed Protein Report

## Protein 1455: rhomboid-related protein 1 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|523704585 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 4.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MDRSSLLQLI QEQQLDPENT GFIGADTFTG LVHSHELPLD PAKLDMLVAL AQSNEQGQVC YQELVDLISS KRSSSFKRAI
        90        100        110        120        130        140        150        160
ANGQRALPRD GPLDEPGLGV YKRFVRYVAY EILPCEVDRR WYFYRHRSCP PPVFMASVTL AQIIVFLCYG ARLNKWVLQT
       170        180        190        200        210        220        230        240
YHPEYMKSPL VYHPGHRARA WRFLTYMFMH VGLEQLGFNA LLQLMIGVPL EMVHGLLRIS LLYLAGVLAG SLTVSITDMR
       250        260        270        280        290        300        310        320
APVVGGSGGV YALCSAHLAN VVMNWAGMRC PYKLLRMVLA LVCMSSEVGR AVWLRFSPPL PASGPQPSFM AHLAGAVVGV
       330        340        350        360        370        380
SMGLTILRSY EERLRDQCGW WVVLLAYGTF LLFAVFWNVF AYDLLGAHIP PPP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1780 | 1 | 898.8434 | -152.71 | 2 | 52.1 | 11.6 | 1 | 86-102 | R.ALPRDGPLDEPGLGVYK.R | |

# Detailed Protein Report

## Protein 1456: endophilin-A2 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|317108193 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| | | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 4.28 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.35 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSVAGLKKQF YKASQLVSEK VGGAEGTKLD DDFKEMEKKV DVTSKAVTEV LARTIEYLQP NPASRAKLTM LNTVSKIRGQ
        90        100        110        120        130        140        150        160
NLCEKDLKEI QHHLKKLEGR RLDFDYKKKR QGKIPDEELR QALEKFEESK EVAETSMHNL LETDIEQVSQ LSALVDAQLD
       170        180        190        200        210        220        230        240
YHRQAVQILD ELAEKLKRRM REASSRPKRE YKPKPREPFD LGEPEQSNGG FPCTTAPKIA ASSSFRSSDK PIRTPSRSMP
       250        260        270        280        290        300        310
PLDQPSCKAL YDFEPENDGE LGFHEGDVIT LTNQIDENWY EGMLDGQSGF FPLSYVEVLV PLPQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 818 | 1 | 635.1543 | -208.98 | 2 | 38.6 | 11.6 | 1 | 29-38 | K.LDDDFKEMEK.K | | WUP:QUP 0.35<br>QU:MU 4.28 |

# Detailed Protein Report

## Protein 1457: NEDD4 family-interacting protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|13386480 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 7.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.76 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.31 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MALALAALAA | VEPACGSRYQ | QLQNEEESGE | PEQAAGDAPP | PYSSISAESA | AYFDYKDESG | FPKPPSYNVA | TTLPSYDEAE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RTKAEATIPL | VPGRDEDFVG | RDDFDDADQL | RIGNDGIFML | TFFMAFLFNW | IGFFLSFCLT | TSAAGRYGAI | SGFGLSLIKW |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | |
| ILIVRFSTYF | PGYFDGQYWL | WWVFLVLGFL | LFLRGFINYA | KVRKMPETFS | NLPRTRVLFI | Y | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1839 | 1 | 547.6443 | 24.04 | 3 | 51.3 | 11.6 | 0 | 2-18 | M.ALALAALAAVEPACGSR.Y | Carbamidomethyl: 14 | QU:MU 0.76<br>WUP:QUP 1.31 |

# Detailed Protein Report

## Protein 1458: DNA damage-inducible transcript 4-like protein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21687001 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 5.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530377132 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: DNA damage-inducible transcript 4-like protein isoform X1 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MVATGSLSSK NPASISELLD CGYHPESLLS DFDYWDYVVP EPNLNEVIFE ESTCQNLVKM LENCLSKSKQ TKLGCSKVLV
        90        100        110        120        130        140        150        160
PEKLTQRIAQ DVLRLSSTEP CGLRGCVMHV NLEIENVCKK LDRIVCDSSV VPTFELTLVF KQENCSWTSF RDFFFSRGRF
       170        180        190        200
SSGFRRTLIL SSGFRLVKKK LYSLIGTTVI EGS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2065 | 1 | 575.2075 | -231.33 | 2 | 55.7 | 11.6 | 1 | 166-175 | R.RTLILSSGFR.L | |

# Detailed Protein Report

## Protein 1459: ferrochelatase, mitochondrial isoform b precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|60499021 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 47.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRSLGANMAA | ALRAAGVLLR | DPLASSSWRV | CQPWRWKSGA | AAAAVTTETA | QHAQGAKPQV | QPQKRKPKTG | ILMLNMGGPE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TLGDVHDFLL | RLFLDRDLMT | LPIQNKLAPF | IAKRRTPKIQ | EQYRRIGGGS | PIKIWTSKQG | EGMVKLLDEL | SPNTAPHKYY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IGFRYVHPLT | EEAIEEMERD | GLERAIAFTQ | YPQYSCSTTG | SSLNAIYRYY | NQVGRKPTMK | WSTIDRWPTH | HLLIQCFADH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ILKELDHFPL | EKRSEVVILF | SAHSLPMSVV | NRGDPYPQEV | SATVQKVMER | LEYCNPYRLV | WQSKVGPMPW | LGPQTDESIK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GLCERGRKNI | LLVPIAFTSD | HIETLYELDI | EYSQVLAKEC | GVENIRRAES | LNGNPLFSKA | LADLVHSHIQ | SNELCSKQLT |
| 410 | 420 | 430 | | | | | |
| LSCPLCVNPV | CRETKSFFTS | QQL | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2339 | 1 | 1029.7232 | 144.15 | 2 | 57.5 | 11.6 | 2 | 1-20 | -.MRSLGANMAAALRAAGVLLR.D | Oxidation: 8 |

# Detailed Protein Report

## Protein 1460: xylosyltransferase 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|28269693 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 107.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVAAPCARRL | ARRSHSALLA | ALTVLLLQTL | VVWNFSSLDS | GAGERRGGAA | VGGGEQPPPA | PAPRRERRDL | PAEPAAARGG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GGGGGGGGGG | RGPQARARGG | GPGEPRGQQP | ASRGALPARA | LDPHPSPLIT | LETQDGYFSH | RPKEKVRTDS | NNENSVPKDF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ENVDNSNFAP | RTQKQKHQPE | LAKKPPSRQK | ELLKRKLEQQ | EKGKGHTFPG | KGPGEVLPPG | DRAAANSSHG | KDVSRPPHAR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KTGGSSPETK | YDQPPKCDIS | GKEAISALSR | AKSKHCRQEI | GETYCRHKLG | LLMPEKVTRF | CPLEGKANKN | VQWDEDSVEY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MPANPVRIAF | VLVVHGRASR | QLQRMFKAIY | HKDHFYYIHV | DKRSNYLHRQ | VLQVSRQYSN | VRVTPWRMAT | IWGGASLLST |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YLQSMRDLLE | MTDWPWDFFI | NLSAADYPIR | TNDQLVAFLS | RYRDMNFLKS | HGRDNARFIR | KQGLDRLFLE | CDAHMWRLGD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RRIPEGIAVD | GGSDWFLLNR | RFVEYVTFST | DDLVTKMKQF | YSYTLLPAES | FFHTVLENSP | HCDTMVDNNL | RITNWNRKLG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| CKCQYKHIVD | WCGCSPNDFK | PQDFHRFQQT | ARPTFFARKF | EAVVNQEIIG | QLDYYLYGNY | PAGTPGLRSY | WENVYDEPDG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IHSLSDVTLT | LYHSFARLGL | RRAETSLHTD | GENSCRYYPM | GHPASVHLYF | LADRFQGFLI | KHHATNLAVS | KLETLETWVM |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PKKVFKIASP | PSDFGRLQFS | EVGTDWDAKE | RLFRNFGGLL | GPMDEPVGMQ | KWGKGPNVTV | TVIWVDPVNV | IAATYDILIE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| STAEFTHYKP | PLNLPLRPGV | WTVKILHHWV | PVAETKFLVA | PLTFSNRQPI | KPEEALKLHN | GPLRNAYMEQ | SFQSLNPVLS |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LPINPAQVEQ | ARRNAASTGT | ALEGWLDSLV | GGMWTAMDIC | ATGPTACPVM | QTCSQTAWSS | FSPDPKSELG | AVKPDGRLR |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2175 | 1 | 701.2622 | -127.85 | 3 | 57.6 | 11.6 | 0 | 388-406 | R.MATIWGGASLLSTYLQSMR.D | Oxidation: 18 |

# Detailed Protein Report

## Protein 1461: tricarboxylate transport protein, mitochondrial isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|568786339 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 23.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MFEFLSNHMR | DAQGRLDSTR | GLLCGLGAGV | AEAVVVVCPM | ETIKVKFIHD | QTSPNPKYRG | FFHGVREIVR | EQGLKGTYQG |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| LTATVLKQGS | NQAIRFFVMT | SLRNWYRGDN | PNKPMNPLIT | GVFGAIAGAA | SVFGNTPLDV | IKTRMQGLEA | HKYRNTWDCG |
| **170** | **180** | **190** | **200** | **210** | | | |
| LQILKKEGLK | AFYKGTVPRL | GRVCLDVAIV | FVIYDEVVKL | LNKVWKTD | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 610 | 1 | 593.6757 | -215.17 | 2 | 36.0 | 11.6 | 1 | 143-152 | K.TRMQGLEAHK.Y | Oxidation: 3 |

# Detailed Protein Report

## Protein 1462: homeobox protein BarH-like 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|153218470 | **Score:** | 11.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| | | **Sequence Coverage [%]:** | 7.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MQRPGEPGAA | RFGPPEGCAD | HRPHRYRSFM | IEEILTEPPG | PKGAAPAAAA | AAAGELLKFG | VQALLAARPF | HSHLAVLKAE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QAAVFKFPLA | PLGCSGLSSA | LLAAGPGLPG | AAGAPHLPLE | LQLRGKLEAA | GPGEPGTKAK | KGRRSRTVFT | ELQLMGLEKR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FEKQKYLSTP | DRIDLAESLG | LSQLQVKTWY | QNRRMKWKKI | VLQGGGLESP | TKPKGRPKKN | SIPTSEQLTE | QERAKDAEKP |
| 250 | 260 | | | | | | |
| AEVPGEPSDR | SRED | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1733 | 1 | 697.3497 | -100.24 | 3 | 50.0 | 11.6 | 2 | 200-219 | K.IVLQGGGLESPTKPKGRPKK.N | |

# Detailed Protein Report

## Protein 1463: PREDICTED: transcriptional repressor p66-beta isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530365126 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 65.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKISNMMDRM | TEDALRLNLL | KRSLDPADER | DDVLAKRLKM | EGHEAMERLK | MLALLKRKDL | ANLEVPHELP | TKQDGSGVKG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YEEKLNGNLR | PHGDNRTAGR | PGKENINDEP | VDMSARRSEP | ERGRLTPSPD | IIVLSDNEAS | SPRSSSRMEE | RLKAANLEMF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KGKGIEERQQ | LIKQLRDELR | LEEARLVLLK | KLRQSQLQKE | NVVQKTPVVQ | NAASIVQPSP | AHVGQQGLSK | LPSRPGAQGV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EPQNLRTLQG | HSVIRSATNT | TLPHMLMSQR | VIAPNPAQLQ | GQRGPPKPGL | VRTTTPNMNP | AINYQPQSSS | SVPCQRTTSS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AIYMNLASHI | QPGTVNRVSS | PLPSPSAMTD | AANSQAAAKL | ALRKQLEKTL | LEIPPPKPPA | PLLHFLPSAA | NSEFIYMVGL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EEVVQSVIDS | QGKSCASLLR | VEPFVCAQCR | TDFTPHWKQE | KNGKILCEQC | MTSNQKKALK | AEHTNRLKNA | FVKALQQEQE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IEQRLQQQAA | LSPTTAPAVS | SVSKQETIMR | HHTLRQAPQP | QSSLQRGIPT | SARSMLSNFA | QAPQLSVPGG | LLGMPGVNIA |
| 570 | 580 | 590 | 600 | | | | |
| YLNTGIGGHK | GPSLADRQRE | YLLDMIPPRS | ISQSISGQK | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1072 | 1 | 571.1338 | -223.95 | 2 | 43.5 | 11.5 | 1 | 1-9 | -.MKISNMMDR.M | Oxidation: 7 |

# Detailed Protein Report

## Protein 1464: PREDICTED: rho GTPase-activating protein 29 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578800119 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 134.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.98 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.03 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MERRDCFKEV | IHIRLEELLR | VLKSIMNKHQ | NLNSVDLQNA | AEMLTAKVKA | VNFTEVNEEN | KNDLFQEVFS | SIETLAFTFG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NILTNFLMGD | VGNDSLLRLP | VSRETKSFEN | VSVESVDSSS | EKGNFSPLEL | DNVLLKNTDS | IELALSYAKT | WSKYTKNIVS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WVEKKLNLEL | ESTRNMVKLA | EATRTNIGIQ | EFMPLQSLFT | NALLNDIESS | HLLQQTIAAL | QANKFVQPLL | GRKNEMEKQR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KEIKELWKQE | QNKMLEAENA | LKKAKLLCMQ | RQDEYEKAKS | SMFRAEEEHL | SSSGGLAKNL | NKQLEKKRRL | EEEALQKVEE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ANELYKVCVT | NVEERRNDLE | NTKREILAQL | RTLVFQCDLT | LKAVTVNLFH | MQHLQAASLA | DSLQSLCDSA | KLYDPGQEYS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EFVKATNSTE | EEKVDGNVNK | HLNSSQPSGF | GPANSLEDVV | RLPDSSNKIE | EDRCSNSADI | TGPSFIRSWT | FGMFSDSEST |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GGSSESRSLD | SESISPGDFH | RKLPRTPSSG | TMSSADDLDE | REPPSPSETG | PNSLGTFKKT | LMSKAALTHK | FRKLRSPTKC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RDCEGIVVFQ | GVECEECLLV | CHRKCLENLV | IICGHQKLPG | KIHLFGAEFT | QVAKKEPDGI | PFILKICASE | IENRALCLQG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IYRVCGNKIK | TEKLCQALEN | GMHLVDISEF | SSHDICDVLK | LYLRQLPEPF | ILFRLYKEFI | DLAKEIQHVN | EEQETKKNSL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EDKKWPNMCI | EINRILLKSK | DLLRQLPASN | FNSLHFLIVH | LKRVVDHAEE | NKMNSKNLGV | IFGPSLIRPR | PTTAPITISS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LAEYSNQARL | VEFLITYSQK | IFDGSLQPQD | VMCSIGVVDQ | GCFPKPLLSP | EERDIERSMK | SLFFSSKEDI | HTSESESKIF |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ERATSFEESE | RKQNALGKCD | ACLSDKAQLL | LDQEAESASQ | KIEDGKTPKP | LSLKSDRSTN | NVERHTPRTK | IRPVSLPVDR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LLLASPPNER | NGRNMGNVNL | DKFCKNPAFE | GVNRKDAATT | VCSKFNGFDQ | QTLQKIQDKQ | YEQNSLTAKT | TMIMPSALQE |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KGVTTSLQIS | GDHSINATQP | SKPYAEPVRS | VREASERRSS | DSYPLAPVRA | PRTLQPQHWT | TFYKPHAPII | SIRGNEEKPA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SPSAAVPPGT | DHDPHGLVVK | SMPDPDKASA | CPGQATGQPK | EDSEELGLPD | VNPMCQRPRL | KRMQQFEDLE | GEIPQFV |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 648 | 3 | 512.1373 | -240.75 | 2 | 36.5 | 11.5 | 1 | 995-1004 | R.KDAATTVCSK.F | | WUP:QUP 1.03<br>QU:MU 0.98 |

# Detailed Protein Report

## Protein 1465: Krueppel-like factor 9 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4557375 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 4.94 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.32 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSAAAYMDFV AAQCLVSISN RAAVPEHGVA PDAERLRLPE REVTKEHGDP GDTWKDYCTL VTIAKSLLDL NKYRPIQTPS

        90        100        110        120        130        140        150        160
VCSDSLESPD EDMGSDSDVT TESGSSPSHS PEERQDPGSA PSPLSLLHPG VAAKGKHASE KRHKCPYSGC GKVYGKSSHL

       170        180        190        200        210        220        230        240
KAHYRVHTGE RPFPCTWPDC LKKFSRSDEL TRHYRTHTGE KQFRCPLCEK RFMRSDHLTK HARRHTEFHP SMIKRSKKAL

       250
ANAL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 344 | 1 | 646.6642 | -214.55 | 2 | 34.0 | 11.5 | 2 | 142-152 | K.RHKCPYSGCGK.V | Carbamidomethyl: 4 | QU:MU 4.94<br>WUP:QUP 0.32 |

# Detailed Protein Report

## Protein 1466: V-type proton ATPase subunit E 1 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|87159818 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 22.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 1.12 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MALSDADVQK | QIKHMMAFIE | QEANEKAEEI | DAKAEEEFNI | EKGRLVQTQR | LKIMEYYEKK | EKQIEQQKKI | QMSNLMNQAR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LKVLRARDDL | ITGLYQLLEP | RMIVRCRKQD | FPLVKAAVQK | AIPMYKIATK | NDVDVQIDQE | SYLPEDIAGG | VEIYNGDRKI |
| 170 | 180 | 190 | 200 | | | | |
| KVSNTLESRL | DLIAQQMMPE | VRGALFGANA | NRKFLD | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 428 | 1 | 645.8393 | -21.26 | 2 | 35.0 | 11.5 | 2 | 106-115 | R.CRKQDFPLVK.A | Carbamidomethyl: 1 | QU:MU 1.12 |

# Detailed Protein Report

## Protein 1467: PREDICTED: sorting nexin-32 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578821254 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.0 |
| | | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| METYAEVGKE | GKPSCASVDL | QGDSSLQVEI | SDAVSERDKV | KFTVQTKSCL | PHFAQTEFSV | VRQHEEFIWL | HDAYVENEEY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AGLIIPPAPP | RPDFEASREK | LQKLGEGDSS | VTREEFAKMK | QELEAEYLAI | FKKTVAMHEV | FLQRLAAHPT | LRRDHNFFVF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LEYGQDLSVR | GKNRKELLGG | FLRNIVKSAD | EALITGMSGL | KEVDDFFEHE | RTFLLEYHTR | IRDACLRADR | VMRAHKCLAD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DYIPISAALS | SLGTQEVNQL | RTSFLKLAEL | FERLRKLEGR | VASDEDLKLS | DMLRYYMRDS | QAAKDLLYRR | LRALADYENA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NKALDKARTR | NREVRPAESH | QQLCCQRFER | LSDSAKQELM | DFKSRRVSSF | RKNLIELAEL | ELKHAKLKGP | PGTLSAKAV |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 880 | 1 | 695.3494 | -29.98 | 2 | 41.1 | 11.5 | 1 | 101-113 | K.LQKLGEGDSSVTR.E | |

# Detailed Protein Report

## Protein 1468: PREDICTED: diacylglycerol kinase iota isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578814733 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 116.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDAAGRGCHL | LPLPAARGPA | RAPAAAAAAA | ASPPGPCSGA | ACAPSAAAGA | GAMNPSSSAG | EEKGATGGSS | SSGSGAGSCC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LGAEGGADPR | GAGSAAAAGA | AALDEPAAAG | QKEKDEALEE | KLRNLTFRKQ | VSYRKAISRA | GLQHLAPAHP | LSLPVANGPA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KEPRATLDWS | ENAVNGEHLW | LETNVSGDLC | YLGEENCQVR | FAKSALRRKC | AVCKIVVHTA | CIEQLEKINF | RCKPTFREGG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SRSPRENFVR | HHWVHRRRQE | GKCKQCGKGF | QQKFSFHSKE | IVAISCSWCK | QAFHNKVTCF | MLHHIEEPCS | LGAHAAVIVP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PTWIIKVKKP | QNSLKASNRK | KKRTSFKRKA | SKRGMEQENK | GRPFVIKPIS | SPLMKPLLVF | VNPKSGGNQG | TKVLQMFMWY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LNPRQVFDLS | QEGPKDALEL | YRKVPNLRIL | ACGGDGTVGW | ILSILDELQL | SPQPPVGVLP | LGTGNDLART | LNWGGGYTDE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PVSKILCQVE | DGTVVQLDRW | NLHVERNPDL | PPEELEDGVC | KLPLNVFNNY | FSLGFDAHVT | LEFHESREAN | PEKFNSRFRN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KMFYAGAAFS | DFLQRSSRDL | SKHVKVVCDG | TDLTPKIQEL | KFQCIVFLNI | PRYCAGTMPW | GNPGDHHDFE | PQRHDDGYIE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VIGFTMASLA | ALQVGGHGER | LHQCREVMLL | TYKSIPMQVD | GEPCRLAPAM | IRISLRNQAN | MVQKSKRRTS | MPLLNDPQSV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PDRLRIRVNK | ISLQDYEGFH | YDKEKLREAS | IPLGILVVRG | DCDLETCRMY | IDRLQEDLQS | VSSGSQRVHY | QDHETSFPRA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LSAQRLSPRW | CFLDATSADR | FYRIDRSQEH | LHFVMEISQD | EIFILDPDMV | VSQPAGTPPG | MPDLVVEQAS | GISDWWNPAL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RKRMLSDSGL | GMIAPYYEDS | DLKDLSHSRV | LQSPVSSEDH | AILQAVIAGD | LMKLIESYKN | GGSLLIQGPD | HCSLLHYAAK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TGNGEIVKYI | LDHGPSELLD | MADSETGETA | LHKAACQRNR | AVCQLLVDAG | ASLRKTDSKG | KTPQERAQQA | GDPDLAAYLE |
| 1050 | 1060 | | | | | | |
| SRQNYKVIGH | EDLETAV | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1696 | 1 | 1102.1837 | 102.80 | 2 | 51.0 | 11.5 | 2 | 1-21 | -.MDAAGRGCHLLPLPAARGPAR.A | Carbamidomethyl: 8;<br>Oxidation: 1 |

# Detailed Protein Report

## Protein 1469: PREDICTED: protein EMSY isoform X10 [Homo sapiens]

**Accession:** gi|578821618
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 11.5
**MW [kDa]:** 122.8
**pI:** 10.2
**Sequence Coverage [%]:** 1.3
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPVVWPTLLD | LSRDECKRIL | RKLELEAYAG | VISALRAQGD | LTKEKKDLLG | ELSKVLSIST | ERHRAEVRRA | VNDERLTTIA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HNMSGPNSSS | EWSIEGRRLV | PLMPRLVPQT | AFTVTANAVA | NAAIQHNASL | PVPAETGSKE | GVSCSDEDEK | PRKRRRTNSS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SSSPVVLKEV | PKAVVPVSKT | ITVPVSGSPK | MSNIMQSIAN | SLPPHMSPVK | ITFTKPSTQT | TNTTTQKVII | VTTSPSSTFV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PNILSKSHNY | AAVTKLVPTS | VIASTTQKPP | VVITASQSSL | VSNSSSGSSS | STPSPIPNTV | AVTAVVSSTP | SVVMSTVAQG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VSTSAIKMAS | TRLPSPKSLV | SAPTQILAQF | PKQHQQSPKQ | QLYQVQQQTQ | QQVAQPSPVS | HQQQPQQSPL | PPGIKPTIQI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KQESGVKIIT | QQVQPSKILP | KPVTATLPTS | SNSPIMVVSS | NGAIMTTKLV | TTPTGTQATY | TRPTVSPSIG | RMAATPGAAT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YVKTTSGSII | TVVPKSLATL | GGKIISSNIV | SGTTTKITTI | PMTSKPNVIV | VQKTTGKGTT | IQGLPGKNVV | TTLLNAGGEK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TIQTVPTGAK | PAILTATRPI | TKMIVTQPKG | IGSTVQPAAK | IIPTKIVYGQ | QGKTQVLIKP | KPVTFQATVV | SEQTRQLVTE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TLQQASRVAE | AGNSSIQEGK | EEPQNYTDSS | SSSTESSQSS | QVSHRSQPQQ | PSQPQRTLLQ | HVAQSQTATQ | TSVVVKSIPA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SSPGAITHIM | QQALSSHTAF | TKHSEELGTE | EGEVEEMDTL | DPQTGLFYRS | ALTQSQSAKQ | QKLSQPPLEQ | TQLQVKTLQC |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FQTKQKQTIH | LQADQLQHKL | PQMPQLSIRH | QKLTPLQQEQ | AQPKPDVQHT | QHPMVAKDRQ | LPTLMAQPPQ | TVVQVLAVKT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| TQQLPKLQQA | PNQPKIYVQP | QTPQSQMSLP | ASSEKQTASQ | VEQPIITQGS | SVTKITFEGR | QPPTVTKITG | GSSVPKLTSP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VTSISPIQAS | EKTAVSDILK | MSLMEAQIDT | NVEHMIVDPP | KKALATSMLT | GEAGSLPSTH | MVVAGMANST | PQQQKCRESC |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SSPSTVGSSL | TTRKIDPPAV | PATGQFMRIQ | NVGQKKAEES | PAEIIIQAIP | QYAIPCHSSS | NVVVEPSGLL | ELNNFTSQQL |
| 1130 | 1140 | 1150 | 1160 | | | | |
| DDEETAMEQD | IDSSTEDGTE | PSPSQSSAER | S | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2683 | 2 | 822.4436 | 13.69 | 2 | 64.6 | 11.5 | 1 | 1054-1068 | R.KIDPPAVPATGQFMR.I | Oxidation: 14 |

# Detailed Protein Report

## Protein 1470: protein RRP5 homolog [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|70980549 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 208.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MANLEESFPR | GGTRKIHKPE | KAFQQSVEQD | NLFDISTEEG | STKRKKSQKG | PAKTKKLKIE | KRESSKSARE | KFEILSVESL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CEGMRILGCV | KEVNELELVI | SLPNGLQGFV | QVTEICDAYT | KKLNEQVTQE | QPLKDLLHLP | ELFSPGMLVR | CVVSSLGITD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RGKKSVKLSL | NPKNVNRVLS | AEALKPGMLL | TGTVSSLEDH | GYLVDIGVDG | TRAFLPLLKA | QEYIRQKNKG | AKLKVGQYLN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CIVEKVKGNG | GVVSLSVGHS | EVSTAIATEQ | QSWNLNNLLP | GLVVKAQVQK | VTPFGLTLNF | LTFFTGVVDF | MHLDPKKAGT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YFSNQAVRAC | ILCVHPRTRV | VHLSLRPIFL | QPGRPLTRLS | CQNLGAVLDD | VPVQGFFKKA | GATFRLKDGV | LAYARLSHLS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DSKNVFNPEA | FKPGNTHKCR | IIDYSQMDEL | ALLSLRTSII | EAQYLRYHDI | EPGAVVKGTV | LTIKSYGMLV | KVGEQMRGLV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PPMHLADILM | KNPEKKYHIG | DEVKCRVLLC | DPEAKKLMMT | LKKTLIESKL | PVITCYADAK | PGLQTHGFII | RVKDYGCIVK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FYNNVQGLVP | KHELSTEYIP | DPERVFYTGQ | VVKVVVLNCE | PSKERMLLSF | KLSSDPEPKK | EPAGHSQKKG | KAINIGQLVD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VKVLEKTKDG | LEVAVLPHNI | RAFLPTSHLS | DHVANGPLLH | HWLQAGDILH | RVLCLSQSEG | RVLLCRKPAL | VSTVEGGQDP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KNFSEIHPGM | LLIGFVKSIK | DYGVFIQFPS | GLSGLAPKAI | MSDKFVTSTS | DHFVEGQTVA | AKVTNVDEEK | QRMLLSLRLS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DCGLGDLAIT | SLLLLNQCLE | ELQGVRSLMS | NRDSVLIQTL | AEMTPGMFLD | LVVQEVLEDG | SVVFSGGPVP | DLVLKASRYH |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RAGQEVESGQ | KKKVVILNVD | LLKLEVHVSL | HQDLVNRKAR | KLRKGSEHQA | IVQHLEKSFA | IASLVETGHL | AAFSLTSHLN |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DTFRFDSEKL | QVGQGVSLTL | KTTEPGVTGL | LLAVEGPAAK | RTMRPTQKDS | ETVDEDEEVD | PALTVGTIKK | HTLSIGDMVT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GTVKSIKPTH | VVVTLEDGII | GCIHASHILD | DVPEGTSPTT | KLKVGKTVTA | RVIGGRDMKT | FKYLPISHPR | FVRTIPELSV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RPSELEDGHT | ALNTHSVSPM | EKIKQYQAGQ | TVTCFLKKYN | VVKKWLEVEI | APDIRGRIPL | LLTSLSFKVL | KHPDKKFRVG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| QALRATVVGP | DSSKTLLCLS | LTGPHKLEEG | EVAMGRVVKV | TPNEGLTVSF | PFGKIGTVSI | FHMSDSYSET | PLEDFVPQKV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VRCYILSTAD | NVLTLSLRSS | RTNPETKSKV | EDPEINSIQD | IKEGQLLRGY | VGSIQPHGVF | FRLGPSVVGL | ARYSHVSQHS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| PSKKALYNKH | LPEGKLLTAR | VLRLNHQKNL | VELSFLPGDT | GKPDVLSASL | EGQLTKQEER | KTEAEERDQK | GEKKNQKRNE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KKNQKGQEEV | EMPSKEKQQP | QKPQAQKRGG | RECRESGSEQ | ERVSKKPKKA | GLSEEDDSLV | DVYYREGKEE | AEETNVLPKE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| KQTKPAEAPR | LQLSSGFAWN | VGLDSLTPAL | PPLAESSDSE | EDEKPHQATI | KKSKKERELE | KQKAEKELSR | IEEALMDPGR |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QPESADDFDR | LVLSSPNSSI | LWLQYMAFHL | QATEIEKARA | VAERALKTIS | FREEQEKLNV | WVALLNLENM | YGSQESLTKV |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| FERAVQYNEP | LKVFLHLADI | YAKSEKFQEA | GELYNRMLKR | FRQEKAVWIK | YGAFLLRRSQ | AAASHRVLQR | ALECLPSKEH |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| VDVIAKFAQL | EFQLGDAERA | KAIFENTLST | YPKRTDVWSV | YIDMTIKHGS | QKDVRDIFER | VIHLSLAPKR | MKFFFKRYLD |
| 1850 | 1860 | 1870 | 1880 | | | | |
| YEKQHGTEKD | VQAVKAKALE | YVEAKSSVLE | D | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1880 | 1 | 835.3213 | -94.03 | 2 | 53.4 | 11.5 | 0 | 72-85 | K.FEILSVESLCEGMR.I | Carbamidomethyl: 10 |

# Detailed Protein Report

## Protein 1471: protein sidekick-1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|119220550 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 74.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MQVRELPRGE | WQTYSSSISH | EATACVVDRL | RPFTSYKLRL | KATNDIGDSD | FSSETEAVTT | LQDVPGEPPG | SVSATPHTTS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SVLIQWQPPR | DESLNGLLQG | YRIYYRELEY | EAGSGTEAKT | LKNPIALHAE | LTAQSSFKTV | NSSSTSTMCE | LTHLKKYRRY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EVIMTAYNII | GESPASAPVE | VFVGEAAPAM | APQNVQVTPL | TASQLEVTWD | PPPPESQNGN | IQGYKIYYWE | ADSQNETEKM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KVLFLPEPVV | RLKNLTSHTK | YLVSISAFNA | AGDGPKSDPQ | QGRTHQAAPG | APSFLAFSEI | TSTTLNVSWG | EPAAANGILQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GYRVVYEPLA | PVQGVSKVVT | VEVRGNWQRW | LKVRDLTKGV | TYFFRVQART | ITYGPELQAN | ITAGPAEGSP | GSPRDVLVTK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SASELTLQWT | EGHSGDTPTT | GYVIEARPSD | EGLWDMFVKD | IPRSATSYTL | SLDKLRQGVT | YEFRVVAVNE | AGYGEPSNPS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TAVSAQVEAP | FYEEWWFLLV | MALSSLIVIL | LVVFALVLHG | QNKKYKNCST | GKGISTMEES | VTLDNGGFAA | LELSSRHLNV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KSTFSKKNGT | RSPPRPSPGG | LHYSDEDICN | KYNGAVLTES | VSLKEKSADA | SESEATDSDY | EDALPKHSFV | NHYMSDPTYY |
| 650 | 660 | 670 | 680 | | | | |
| NSWKRRAQGR | APAPHSVAIL | LTSNPSAYLS | VAPRGSASW | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2162 | 1 | 618.9457 | -18.66 | 3 | 55.4 | 11.5 | 0 | 139-155 | K.TVNSSSTSTMCELTHLK.K | Oxidation: 10 |

# Detailed Protein Report

## Protein 1472: presqualene diphosphate phosphatase [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|66773040 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 32.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.2 |
| | | **Sequence Coverage [%]:** | 6.4 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPSPRRSMEG | RPLGVSASSS | SSSPGSPAHG | GGGGGSRFEF | QSLLSSRATA | VDPTCARLRA | SESPVHRRGS | FPLAAAGPSQ |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| SPAPPLPEED | RMDLNPSFLG | IALRSLLAID | LWLSKKLGVC | AGESSSWGSV | RPLMKLLEIS | GHGIPWLLGT | LYCLCRSDSW |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| AGREVLMNLL | FALLLDLLLV | ALIKGLVRRR | RPAHNQMDMF | VTLSVDKYSF | PSGHATRAAL | MSRFILNHLV | LAIPLRVLVV |
| **250** | **260** | **270** | **280** | **290** | **300** | | |
| LWAFVLGLSR | VMLGRHNVTD | VAFGFFLGYM | QYSIVDYCWL | SPHNAPVLFL | LWSQR | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 97 | 1 | 767.6746 | -69.94 | 3 | 30.9 | 11.5 | 2 | 189-207 | R.RRRPAHNQMDMFVTLSVDK.Y | |

# Detailed Protein Report

## Protein 1473: Lebercilin [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|170650670 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 80.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| | | **Sequence Coverage [%]:** | 3.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530383030 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: Lebercilin isoform X2 [Homo sapiens] |
| gi\|170650672 | refseq_human (refseq_human_20140103.fasta) | Lebercilin [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGERAGSPGT | DQERKAGKHH | YSYLSDFETP | QSSGRSSLVS | SSPASVRRKN | PKRQTSDGQV | HHQAPRKPSP | KGLPNRKGVR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VGFRSQSLNR | EPLRKDTDLV | TKRILSARLL | KINELQNEVS | ELQVKLAELL | KENKSLKRLQ | YRQEKALNKF | EDAENEISQL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IFRHNNEITA | LKERLRKSQE | KERATEKRVK | DTESELFRTK | FSLQKLKEIS | EARHLPERDD | LAKKLVSAEL | KLDDTERRIK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ELSKNLELST | NSFQRQLLAE | RKRAYEAHDE | NKVLQKEVQR | LYHKLKEKER | ELDIKNIYSN | RLPKSSPNKE | KELALRKNAA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CQSDFADLCT | KGVQTMEDFK | PEEYPLTPET | IMCYENKWEE | PGHLTLDLQS | QKQDRHGEAG | ILNPIMEREE | KFVTDEELHV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VKQEVEKLED | EWEREELDKK | QKEKASLLER | EEKPEWETGR | YQLGMYPIQN | MDKLQGEEEE | RLKREMLLAK | LNEIDRELQD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SRNLKYPVLP | LLPDFESKLH | SPERSPKTYR | FSESSERLFN | GHHLQDISFS | TPKGEGQNSG | NVRSPASPNE | FAFGSYVPSF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AKTSERSNPF | SQKSSFLDFQ | RNSMEKLSKD | GVDLITRKEK | KANLMEQLFG | ASGSSTISSK | SSDPNSVASS | KGDIDPLNFL |
| 650 | 660 | 670 | 680 | 690 | 700 | | |
| PGNKGSRDQE | HDEDEGFFLS | EGRSFNPNRH | RLKHADDKPA | VKAADSVEDE | IEEVALR | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 96 | 1 | 820.3387 | -82.67 | 3 | 30.9 | 11.5 | 1 | 621-644 | K.SSDPNSVASSKGDIDPLNFLPGNK.G | |

# Detailed Protein Report

## Protein 1474: PREDICTED: 5-azacytidine-induced protein 1 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530411826 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 117.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKGTRAIGSV | PERSPAGVDL | SLTGLPPPVS | RRPGSAATTK | PIVRSVSVVT | GSEQKRKVLE | ATGPGGSQAI | NNLRRSNSTT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QVSQPRSGSP | RPTEPTDFLM | LFEGSPSGKK | RPASLSTAPS | EKGATWNVLD | DQPRGFTLPS | NARSSSALDS | PAGPRRKECT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VALAPNFTAN | NRSNKGAVGN | CVTTMVHNRY | TPSERAPPLK | SSNQTAPSLN | NIIKAATCEG | SESSGFGKLP | KNVSSATHSA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RNNTGGSTGL | PRRKEVTEEE | AERFIHQVNQ | ATVTIQRWYR | HQVQRRGAGA | ARLEHLLQAK | REEQRQRSGE | GTLLDLHQQK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EAARRKAREE | KARQARRAAI | QELQQKRALR | AQKASTAERG | PPENPRETRV | PGMRQPAQEL | SPTPGGTAHQ | ALKANNTGGG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LPAAGPGDRC | LPTSDSSPEP | QQPPEDRTQD | VLAQDAAGDN | LEMMAPSRGS | AKSRGPLEEL | LHTLQLLEKE | PDVLPRPRTH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HRGRYAWASE | EDDASSLTAD | NLEKFGKLSA | FPEPPEDGTL | LSEAKLQSIM | SFLDEMEKSG | QDQLDSQQEG | WVPEAGPGPL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ELGSEVSTSV | MRLKLEVEEK | KQAMLLLQRA | LAQQRDLTAR | RVKETEKALS | RQLQRQREHY | EATIQRHLAF | IDQLIEDKKV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LSEKCEAVVA | ELKQEDQRCT | ERVAQAQAQH | ELEIKKLKEL | MSATEKARRE | KWISEKTKKI | KEVTVRGLEP | EIQKLIARHK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QEVRRLKSLH | EAELLQSDER | ASQRCLRQAE | ELREQLEREK | EALGQQERER | ARQRQRAELE | ELRQQLEESS | SALTRALRAE |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FEKGREEQER | RHQMELNTLK | QQLELERQAW | EAGRTRKEEA | WLLNREQELR | EEIRKGRDKE | IELVIHRLEA | DMALAKEESE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KAAESRIKRL | RDKYEAELSE | LEQSERKLQE | RCSELKGQLG | EAEGENLRLQ | GLVRQKERAL | EDAQAVNEQL | SSERSNLAQV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| IRQEFEDRLA | ASEEETRQAK | AELATLQARQ | QLELEEVHRR | VKTALARKEE | AVSSLRTQHE | VSPCGQPCWT | SGLGAGLTLW |
| 1050 | | | | | | | |
| VCCRLR | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 497 | 1 | 945.4933 | 40.80 | 2 | 36.2 | 11.5 | 1 | 912-928 | R.CSELKGQLGEAEGENLR.L | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 1475: PREDICTED: collagen alpha-1(III) chain-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530436794 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 29.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.7 |
| | | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTPSRAQEGP | PRVERAECGA | SAGALTIVSS | HGGDSDKDLC | ARTQIYGAQP | REDQMGSVEK | LTTSAFLSAK | PGSVPAPRPL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RRAPGLGKSI | DGEAGHSEAA | GEKGECGIPW | TEGQVWRPLE | RRASVASPGE | KGECGVPWRE | GRVWRPLDRR | GSVASPGEKG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QCGVPWREGG | VWRPLERRGS | VASPGEKGEC | GVPWREGPVW | RPLERRGEKG | ECGVPWREGG | VWRPLDRRGS | VASPGEKGEC |
| 250 | 260 | 270 | 280 | | | | |
| GVRWREGRVW | YSLDRRGSVP | AALASQRHAL | LALPQPQG | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 355 | 1 | 528.6942 | -187.78 | 2 | 34.1 | 11.5 | 0 | 257-267 | R.GSVPAALASQR.H | |

# Detailed Protein Report

## Protein 1476: epithelial splicing regulatory protein 1 isoform 5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|170763533 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 67.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTASPDYLVV | LFGITAGATG | AKLGSDEKEL | ILLFWKVVDL | ANKKVGQLHE | VLVRPDQLEL | TEDCKEETKI | DVESLSSASQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LDQALRQFNQ | SVSNELNIGV | GTSFCLCTDG | QLHVRQILHP | EASKKNVLLP | ECFYSFFDLR | KEFKKCCPGS | PDIDKLDVAT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MTEYLNFEKS | SSVSRYGASQ | VEDMGNIILA | MISEPYNHRF | SDPERVNYKF | ESGTCSKMEL | IDDNTVVRAR | GLPWQSSDQD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IARFFKGLNI | AKGGAALCLN | AQGRRNGEAL | VRFVSEEHRD | LALQRHKHHM | GTRYIEVYKA | TGEDFLKIAG | GTSNEVAQFL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SKENQVIVRM | RGLPFTATAE | EVVAFFGQHC | PITGGKEGIL | FVTYPDGRPT | GDAFVLFACE | EYAQNALRKH | KDLLGKRYIE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LFRSTAAEVQ | QVLNRFSSAP | LIPLPTPPII | PVLPQQFVPP | TNVRDCIRLR | GLPYAATIED | ILDFLGEFAT | DIRTHGVHMV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LNHQGRPSGD | AFIQMKSADR | AFMAAQKCHK | KNMKDRYVEV | FQCSAEEMNF | VLMGGTLNRN | GLSPPPCLSP | PSYTFPAPAA |
| 570 | 580 | 590 | 600 | 610 | | | |
| VIPTEAAIYQ | PSVILNPRAL | QPSTAYYPAG | TQLFMNYTAY | YPSV | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2627 | 1 | 863.9392 | -38.81 | 2 | 62.9 | 11.5 | 1 | 247-264 | K.GLNIAKGGAALCLNAQGR.R | |

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# Detailed Protein Report

## Protein 1477: fatty acid-binding protein 12 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|157427691 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 15.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 12.9 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578815695 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: fatty acid-binding protein 12 isoform X2 [Homo sapiens] |
| gi\|530388530 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: fatty acid-binding protein 12 isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MIDQLQGTWK | SISCENSEDY | MKELGIGRAS | RKLGRLAKPT | VTISTDGDVI | TIKTKSIFKN | NEISFKLGEE | FEEITPGGHK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | |
| TKSKVTLDKE | SLIQVQDWDG | KETTITRKLV | DGKMVVESTV | NSVICTRTYE | KVSSNSVSNS | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1717 | 1 | 1023.8660 | -90.78 | 2 | 51.8 | 11.5 | 1 | 11-28 | K.SISCENSEDYMKELGIGR.A | Oxidation: 11 |

# Detailed Protein Report

## Protein 1478: PREDICTED: signal-induced proliferation-associated 1-like protein 2 isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578802290 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 188.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSDPRQSQEE | KHKLGRASSK | FKDPPRIMQS | DDYFARKFKA | INGNMGPTTS | LNASNSNETG | GGGPANGTPA | VPKMGVRARV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SEWPPKKDCS | KELTCKALWE | SRSQTSYESI | TSVLQNGQSD | QSEGQQDEQL | DLDFVEAKYT | IGDIFVHSPQ | RGLHPIRQRS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NSDVTISDID | AEDVLDQNAV | NPNTGAALHR | EYGSTSSIDR | QGLSGENFFA | MLRGYRVENY | DHKAMVPFGF | PEFFRCDPAI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SPSLHAAAQI | SRGEFVRISG | LDYVDSALLM | GRDRDKPFKR | RLKSESVETS | LFRKLRTVKS | EHETFKFTSE | LEESRLERGI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RPWNCQRCFA | HYDVQSILFN | INEAMATRAN | VGKRKNITTG | ASAASQTQMP | TGQTGNCESP | LGSKEDLNSK | ENLDADEGDG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KSNDLVLSCP | YFRNETGGEG | DRRIALSRAN | SSSFSSGESC | SFESSLSSHC | TNAGVSVLEV | PRENQPIHRE | KVKRYIIEHI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DLGAYYYRKF | FYGKEHQNYF | GIDENLGPVA | VSIRREKVED | AKEKEGSQFN | YRVAFRTSEL | TTLRGAILED | AIPSTARHGT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ARGLPLKEVL | EYVIPELSIQ | CLRQASNSPK | VSEQLLKLDE | QGLSFQHKIG | ILYCKAGQST | EEEMYNNETA | GPAFEEFLDL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LGQRVRLKGF | SKYRAQLDNK | TDSTGTHSLY | TTYKDYELMF | HVSTLLPYMP | NNRQQLLRKR | HIGNDIVTIV | FQEPGALPFT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PKSIRSHFQH | VFVIVKVHNP | CTENVCYSVG | VSRSKDVPPF | GPPIPKGVTF | PKSAVFRDFL | LAKVINAENA | AHKSEKFRAM |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ATRTRQEYLK | DLAENFVTTA | TVDTSVKFSF | ITLGAKKKEK | VKPRKDAHLF | SIGAIMWHVI | ARDFGQSADI | ECLLGISNEF |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| IMLIEKDSKN | VVFNCSCRDV | IGWTSGLVSI | KVFYERGECV | LLSSVDNCAE | DIREIVQRLV | IVTRGCETVE | MTLRRNGLGQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LGFHVNFEGI | VADVEPFGFA | WKAGLRQGSR | LVEICKVAVA | TLTHEQMIDL | LRTSVTVKVV | IIQPHDDGSP | RRGCSELCRI |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PMVEYKLDSE | GTPCEYKTPF | RRNTTWHRVP | TPALQPLSRA | SPIPGTPDRL | PCQQLLQQAQ | AAIPRSTSFD | RKLPDGTRSS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PSNQSSSSDP | GPGGSGPWRP | QVGYDGCQSP | LLLEHQGSGP | LECDGARERE | DTMEASRHPE | TKWHGPPSKV | LGSYKERALQ |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KDGSCKDSPN | KLSHIGDKSC | SSHSSSNTLS | SNTSSNSDDK | HFGSGDLMDP | ELLGLTYIKG | ASTDSGIDTA | PCMPATILGP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VHLAGSRSLI | HSRAEQWADA | ADVSGPDDEP | AKLYSVHGYA | STISAGSAAE | GSMGDLSEIS | SHSSGSHHSG | SPSAHCSKSS |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| GSLDSSKVYI | VSHSSGQQVP | GSMSKPYHRQ | GAVNKYVIGW | KKSEGSPPPE | EPEVTECPGM | YSEMDVMSTA | TQHQTVVGDA |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| VAETQHVLSK | EDFLKLMLPD | SPLVEEGRRK | FSFYGNLSPR | RSLYRTLSDE | SICSNRRGSS | FGSSRSSVLD | QALPNDILFS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| TTPPYHSTLP | PRAHPAPSMG | SLRNEFWFSD | GSLSDKSKCA | DPGLMPLPDT | ATGLDWTHLV | DAARAFEDQR | VASFCTLTDM |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| QHGQDLEGAQ | ELPLCVDPGS | GKEFMDTTGE | RSPSPLTGKV | NQLELILRQL | QTDLRKEKQD | KAVLQAEVQH | LRQDNMRLQE |
| 1690 | 1700 | 1710 | | | | | |
| ESQTATAQLR | KFTEWFFTTI | DKKS | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1759 | 1 | 1057.1731 | 7.31 | 3 | 51.8 | 11.5 | 0 | 40-73 | K.AINGNMGPTTSLNASNSNETGGGGPANGTPAVPK.M | Oxidation: 6 |

# Detailed Protein Report

## Protein 1479: PREDICTED: zinc finger protein 62 homolog isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578811209 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 79.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| | | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.78 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.66 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578811217 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 62 homolog isoform X8 [Homo sapiens] |
| gi\|578811215 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 62 homolog isoform X7 [Homo sapiens] |
| gi\|578811213 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 62 homolog isoform X6 [Homo sapiens] |
| gi\|578811211 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 62 homolog isoform X5 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRNQLKNMKM | LEMQHLSGQK | WRILCLNLSS | VLDQHKRIHT | GEKPYECGEC | GKAFRNSSGL | RVHKRIHTGE | KPYECDICGK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TFSNSSGLRV | HKRIHTGEKP | YECDECGKAF | ITCRTLLNHK | SIHFGDKPYK | CDECEKSFNY | SSLLIQHKVI | HTGEKPYECD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ECGKAFRNSS | GLIVHKRIHT | GEKPYKCDVC | GKAFSYSSGL | AVHKSIHPGK | KAHECKECGK | SFSYNSLLLQ | HRTIHTGERP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YVCDVCGKTF | RNNAGLKVHR | RLHTGEKPYK | CDVCGKAYIS | RSSLKNHKGI | HLGEKPYKCS | YCEKSFNYSS | ALEQHKRIHT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| REKPFGCDEC | GKAFRNNSGL | KVHKRIHTGE | RPYKCEECGK | AYISLSSLIN | HKSVHPGEKP | FKCDECEKAF | ITYRTLTNHK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KVHLGEKPYK | CDVCEKSFNY | TSLLSQHRRV | HTREKPYECD | RCEKVFRNNS | SLKVHKRIHT | GERPYECDVC | GKAYISHSSL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| INHKSTHPGR | TPHTCDECGK | AFFSSRTLIS | HKRVHLGEKP | FKCVECGKSF | SYSSLLSQHK | RIHTGEKPYV | CDRCGKAFRN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SSGLTVHKRI | HTGEKPYECD | ECGKAYISHS | SLINHKSVHQ | GKQPYNCECG | KSFNYRSVLD | QHKRIHTGKK | PYRCNECGKA |
| 650 | 660 | 670 | 680 | 690 | 700 | | |
| FNIRSNLTKH | KRTHTGEESL | NVIYVGSYSG | TSQKRTYEGG | NALDGGRMRM | PL | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 903 | 1 | 700.3064 | 5.36 | 2 | 41.3 | 11.5 | 1 | 434-444 | R.EKPYECDRCEK.V | | WUP:QUP 0.66<br>QU:MU 1.78 |

# Detailed Protein Report

## Protein 1480: PREDICTED: zinc finger protein 839 isoform X1 [Homo sapiens]

**Accession:** gi|530404173
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 11.5
**MW [kDa]:** 72.5
**pI:** 8.7
**Sequence Coverage [%]:** 2.4
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MADAEPEAGG | GSEDGGGGGG | PAPPGQSGSV | ARVAPLGPEQ | LRQVLEQVTK | AQPPPPPPPF | VLRDAARRLR | DAAQQAALQR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GRGTEPPRLP | RLLPPQQLEA | ICVKVTSGET | KGQERPMLLP | TTIQPQTARK | SQLPRGNSCL | VGLHIASPQL | LRVQPLVRTE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PQSCFLSDLC | QPPAQGFVQR | PLPALQVVPA | KRVPAPKAPD | EQGSMLTPLS | ASDPLAVTSL | SSSSAHPFIS | NLHTRHTEKL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KKSLKVKTRS | GRVSRPPKYK | AKDYKFIKTE | DLADGHLSDS | DDYSELCVEE | DEDQRERHAL | FDLSSCSLRP | KSFKCQTCEK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SYIGKGGLAR | HFKLNPGHGQ | LDPEMVLSEK | ASGSTLRGCT | EERTLSLTSL | GLSMPADPCE | GGARSCLVTE | SARGGLQNGQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SVDVEETLPS | EPENGALLRS | ERYQGPRRRA | CSETLAESRT | AVLQQRRAAQ | LPGGPAAAGE | QRASPSKARL | KEFLQQCDRE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DLVELALPQL | AQVVTVYEFL | LMKVEKDHLA | KPFFPAIYKE | FEELHKMVKK | MCQDYLSSSG | LCSQETLEIN | NDKVAESLGI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TEFLRKKEIH | PDNLGPKHLS | RDMDGEQLEG | ASSEKREREA | AEEGLASVKR | PRREALSNDT | TESLAANSRG | REKPRPLHAL |
| 650 | 660 | 670 | | | | | |
| AAGTIVSQEE | DIVTVTDAEG | RACGWAR | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2340 | 1 | 899.3808 | -112.44 | 2 | 59.7 | 11.5 | 2 | 597-612 | R.EREAAEEGLASVKRPR.R | |

# Detailed Protein Report

## Protein 1481: sorting nexin-5 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|540344544 | **Score:** | 11.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| | | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQKLGEGEGS | MTKEEFAKMK | QELEAEYLAV | FKKTVSSHEV | FLQRLSSHPV | LSKDRNFHVF | LEYDQDLSVR | RKNTKEMFGG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FFKSVVKSAD | EVLFTGVKEV | DDFFEQEKNF | LINYYNRIKD | SCVKADKMTR | SHKNVADDYI | HTAACLHSLA | LEEPTVIKKY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLKVAELFEK | LRKVEGRVSS | DEDLKLTELL | RYYMLNIEAA | KDLLYRRTKA | LIDYENSNKA | LDKARLKSKD | VKLAEAHQQE |
| 250 | 260 | 270 | 280 | 290 | 300 | | |
| CCQKFEQLSE | SAKEELINFK | RKRVAAFRKN | LIEMSELEIK | HARNNVSLLQ | SCIDLFKNN | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2099 | 1 | 938.3578 | -137.94 | 2 | 56.1 | 11.5 | 1 | 192-206 | R.YYMLNIEAAKDLLYR.R | |

# Detailed Protein Report

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**Protein 1482:** **PREDICTED: echinoderm microtubule-associated protein-like 4 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530367490 | **Score:** | 11.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 84.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDGFAGSLDD | SISAASTSDV | QDRLSALESR | VQQQEDEITV | LKAALADVLR | RLAISEDHVA | SVKKSVSSKG | QPSPRAVIPM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SCITNGSGAN | RKPSHTSAVS | IAGKETLSSA | AKSGTEKKKE | KPQGQREKKE | ESHSNDQSPQ | IRASPSPQPS | SQPLQIHRQT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PESKNATPTK | SIKRPSPAEK | SHNSWENSDD | SRNKLSKIPS | TPKLIPKVTK | TADKHKDVII | NQAKMSTREK | NSQEGEYIKM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FMRGRPITMF | IPSDVDNYDD | IRTELPPEKL | KLEWAYGYRG | KDCRANVYLL | PTGKIVYFIA | SVVVLFNYEE | RTQRHYLGHT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DCVKCLAIHP | DKIRIATGQI | AGVDKDGRPL | QPHVRVWDSV | TLSTLQIIGL | GTFERGVGCL | DFSKADSGVH | LCIIDDSNEH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MLTVWDWQKK | AKGAEIKTTN | EVVLAVEFHP | TDANTIITCG | KSHIFFWTWS | GNSLTRKQGI | FGKYEKPKFV | QCLAFLGNGD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VLTGDSGGVM | LIWSKTTVEP | TPGKGPKGVY | QISKQIKAHD | GSVFTLCQMR | NGMLLTGGGK | DRKIILWDHD | LNPEREIEVP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DQYGTIRAVA | EGKADQFLVG | TSRNFILRGT | FNDGFQIEVQ | GHTDELWGLA | THPFKDLLLT | CAQDRQVCLW | NSMEHRLEWT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RLVDEPGHCA | DFHPSGTVVA | IGTHSGRWFV | LDAETRDLVS | IHTDGNEQLS | VMRYSIDGTF | LAVGSHDNFI | YLYVVSENGR |
| 730 | 740 | 750 | 760 | 770 | | | |
| KYSRYGRCTG | HSSYITHLDW | SPDNKYIMSN | SGDYEILYLY | GL | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1879 | 1 | 1059.3311 | -131.92 | 2 | 53.9 | 11.4 | 0 | 728-745 | R.CTGHSSYITHLDWSPDNK.Y | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 1483: glutamate-rich protein 1 [Homo sapiens]

**Accession:** gi|46409304
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 11.4
**MW [kDa]:** 49.0
**pI:** 4.5
**Sequence Coverage [%]:** 3.8
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAHRKHVFV | EKVLQRLFPP | VPSGQGKREP | QTLAVQNPPK | KVTSEKVSQK | HAEPLTDTGS | ETPTARRLYT | ASGPPEGYVP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CWPEPSSCGS | PENASSGDDT | EDQDPHDQPK | RRRIRKHKSK | KKFKNPNNVL | IEQAELEKQQ | SLLQEKSQRQ | HTDGTTISKN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KKRKLKKKQQ | IKRKKAAGLA | AKAAGVSFMY | QPEDSSNEGE | GVGEACEEDG | VDTSEEDPTL | AGEEDVKDTR | EEDGADASEE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DLTRARQEEG | ADASEEDPTP | AGEEDVKDAR | EEDGVDTIEE | DLTRAGEEDG | KDTREEDGAD | ASEEDPTWAG | EEEGADSGEE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DGADASEEDD | TITNEKAHSI | LNFLKSTQEM | YFYDGVSRDA | ASAALADAAE | ELLDRLASHS | MLPSDVSILY | HMKTLLLLQD |
| 410 | 420 | 430 | 440 | 450 | | | |
| TERLKHALEM | FPEHCTMPPD | HARVISAFFS | YWITHILPEK | SSD | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1666 | 1 | 981.9452 | -2.85 | 2 | 51.1 | 11.4 | 1 | 268-284 | K.DAREEDGVDTIEEDLTR.A | |

# Detailed Protein Report

## Protein 1484: PREDICTED: formin-binding protein 1 isoform X20 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530390795 | **Score:** | 11.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 64.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.35 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.21 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSWGTELWDQ FDNLEKHTQW GIDILEKYIK FVKERTEIEL SYAKQLRNLS KKYQPKKNSK EEEEYKYTSC KAFISNLNEM

        90        100        110        120        130        140        150        160
NDYAGQHEVI SENMASQIIV DLARYVQELK QERKSNFHDG RKAQQHIETC WKQLESSKRR FERDCKEADR AQQYFEKMDA

       170        180        190        200        210        220        230        240
DINVTKADVE KARQQAQIRH QMAEDSKADY SSILQKFNHE QHEYYHTHIP NIFQKIQEME ERRIVRMGES MKTYAEVDRQ

       250        260        270        280        290        300        310        320
VIPIIGKCLD GIVKAAESID QKNDSQLVIE AYKSGFEPPG DIEFEDYTQP MKRTVSDNSL SNSRGEGKPD LKFGGKSKGK

       330        340        350        360        370        380        390        400
LWPFIKKNKG ATPEDFSNLP PEQRRKKLQQ KVDELNKEIQ KEMDQRDAIT KMKDVYLKNP QMGDPASLDH KLAEVSQNIE

       410        420        430        440        450        460        470        480
KLRVETQKFE AWLAEVEGRL PARSEQARRQ SGLYDSQNPP TVNNCAQDRE SPDGSYTEEQ SQESEMKVLA TDFDDEFDDE

       490        500        510        520        530        540        550        560
EPLPAIGTCK ALYTFEGQNE GTISVVEGET LYVIEEDKGD GWTRIRRNED EEGYVPTSYV EVCLDKNAKD S
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 812 | 1 | 603.7427 | -137.75 | 2 | 39.7 | 11.4 | 2 | 223-232 | R.RIVRMGESMK.T | | WUP:QUP 0.21<br>QU:MU 1.35 |

# Detailed Protein Report

## Protein 1485: zinc finger and BTB domain-containing protein 10 isoform c [Homo sapiens]

**Accession:** gi|460417313
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 11.4
**MW [kDa]:** 64.9
**pI:** 5.2
**Sequence Coverage [%]:** 2.6
**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MTRLERSSHR TVICKVPGEL VAREGKCASR ARESEIPSEE GYCDFNSRPN ENSYCYQLLR QLNEQRKKGI LCDVSIVVSG
        90        100        110        120        130        140        150        160
KIFKAHKNIL VAGSRFFKTL YCFSNKESPN QNNTTHLDIA AVQGFSVILD FLYSGNLVLT SQNAIEVMTV ASYLQMSEVV
       170        180        190        200        210        220        230        240
QTCRNFIKDA LNISIKSEAP ESVVVDYNNR KPVNRDGLSS SRDQKIASFW ATRNLTNLAS NVKIENDGCN VDEGQIENYQ
       250        260        270        280        290        300        310        320
MNDSSWVQDG SPEMAENESE GQTKVFIWNN MGSQGIQETG KTRRKNQTTK RFIYNIPPNN ETNLEDCSVM QPPVAYPEEN
       330        340        350        360        370        380        390        400
TLLIKEEPDL DGALLSGPDG DRNVNANLLA EAGTSQDGGD AGTSHDFKYG LMPGPSNDFK YGLIPGTSND FKYGLIPGAS
       410        420        430        440        450        460        470        480
NDFKYGLLPE SWPKQETWEN GESSLIMNKL KCPHCSYVAK YRRTLKRHLL IHTGVRSFSC DICGKLFTRR EHVKRHSLVH
       490        500        510        520        530        540        550        560
KKDKKYKCMV CKKIFMLAAS VGIRHGSRRY GVCVDCADKS QPGGQEGVDQ GQDTEFPRDE EYEENEVGEA DEELVDDGED
       570        580
QNDPSRWDES GEVCMSLDD
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1822 | 1 | 861.7800 | -131.73 | 2 | 52.6 | 11.4 | 2 | 505-519 | R.HGSRRYGVCVDCADK.S | Carbamidomethyl: 12 |

# Detailed Protein Report

## Protein 1486: PREDICTED: clusterin-associated protein 1 isoform X1 [Homo sapiens]

**Accession:** gi|578828036
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 11.4
**MW [kDa]:** 39.5
**pI:** 4.5
**Sequence Coverage [%]:** 3.8
**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MATKAHIKLN TKKLYQADGY AVKELLKITS VLYNAMKTKG MEGSEIVEED VNKFKFDLGS KIADLKAARQ LASEITSKGA
        90        100        110        120        130        140        150        160
SLYDLLGMEV ELREMRTEAI ARPLEINETE KVMRIAIKEI LTQVQKTKDL LNNVASDEAN LEAKIEKRKL ELERNRKRLE
       170        180        190        200        210        220        230        240
TLQSVRPCFM DEYEKTEEEL QKQYDTYLEK FQNLTYLEQQ LEDHHRMEQE RFEEAKNTLC LIQNKLKEEE KRLLKSGSND
       250        260        270        280        290        300        310        320
DSDIDIQEDD ESDSELEERR LPKPQTAMEM LMQGRPGKRI VGTMQGGDSD DNEDSEESEI DMEDDDDEDD DLEDESISLS
       330        340        350
PTKPNRRVRK SEPLDESDND F
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2301 | 1 | 741.3566 | -87.91 | 2 | 57.1 | 11.4 | 2 | 54-66 | K.FKFDLGSKIADLK.A | |

# Detailed Protein Report

**Protein 1487:** **PREDICTED: activating transcription factor 7-interacting protein 2 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578828278 | **Score:** | 11.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| | | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MASPDRSKRK ILKAKKTMPL SCRKQVEMLN KSRNVEALKT AIGSNVPSGN QSFSPSVITR TTEITKCSPS ENGASSLDSN
        90        100        110        120        130        140        150        160
KNSISEKSKV FSQNCIKPVE EIVHSETKLE QVVCSYQKPS RTTESPSRVF TEEAKDSLNT SENDSEHQTN VTRSLFEHEG
       170        180        190        200        210        220        230        240
ACSLKSSCCP PSVLSGVVQM PESTVTSTVG DKKTDQMVFH LETNSNSESH DKRQSDNILC SEDSGFVPVE KTPNLVNSVT
       250        260        270        280        290        300        310        320
SNNCADDILK TDECSRTSIS NCESADSTWQ SSLDTNNNSH YQKKRMFSEN EENVKRMKTS EQINENICVS LERQTAFLEQ
       330        340        350        360        370
VRHLIQQEIY SINYELFDKK LKELNQRIGK TECRNKHEGI ADKLLR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 53 | 1 | 750.8261 | -51.63 | 2 | 30.6 | 11.4 | 2 | 351-363 | K.TECRNKHEGIADK.L | |

# Detailed Protein Report

## Protein 1488: putative GTP cyclohydrolase 1 type 2 NIF3L1 isoform 3 [Homo sapiens]

**Accession:** gi|215272362
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 11.4
**MW [kDa]:** 32.1
**pI:** 9.9
**Sequence Coverage [%]:** 4.6
**No. of unique Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578804706 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: putative GTP cyclohydrolase 1 type 2 NIF3L1 isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLSSCVRPVP | TTVRFVDSLI | CNSSRSFMDL | KALLSSLNDF | ASLSFAESWD | NVGLLVEPSP | PHTVNTLFLT | NDLTEEVMEE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VLQKKADLIL | SYHPPIFRPM | KRITWNTWKE | RLVIRALENR | VGIYSPHTAY | DAAPQGVNNW | LAKGLGACTS | RPIHPSKAPN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YPTEGNHRVE | FNVNYTQDLD | KVMSAVKGID | GVSVTSFSAR | TGNEEQTRIN | LNCTQKALMQ | VVDFLSRNKQ | LYQKTEILSL |
| 250 | 260 | 270 | 280 | 290 | | | |
| EKSLKSKSWP | CVLVLGAAFC | RVLRLTFTSQ | VRCPIMILWM | LLPKE | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 531 | 1 | 472.2515 | -30.65 | 3 | 35.1 | 11.4 | 0 | 2-14 | M.LSSCVRPVPTTVR.F | |

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# Detailed Protein Report

**Protein 1489:** **PREDICTED: persulfide dioxygenase ETHE1, mitochondrial isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530416070 | **Score:** | 11.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 14.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 11.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.00 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.98 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
         10         20         30         40         50         60         70         80
MLALETRASP GHTPGCVTFV LNDHSMAFTG DALLIRGCGR TDFQQGCAKT LYHSVHEKIF TLPGDCLIYP AHDYHGFTVS
         90        100        110        120        130        140
TVEEERTLNP RLTLSCEEFV KIMGNLNLPK PQQIDFAVPA NMRCGVQTPT A
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 197 | 1 | 903.9342 | -44.66 | 2 | 32.2 | 11.4 | 1 | 87-101 | R.TLNPRLTLSCEEFVK.I | Carbamidomethyl: 10 | WUP:QUP 0.98<br>QU:MU 1.00 |

# Detailed Protein Report

## Protein 1490: proteasome activator complex subunit 3 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|30410794 | **Score:** | 11.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 29.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 6.3 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MASLLKVDQE VKLKVDSFRE RITSEAEDLV ANFFPKKLLE LDSFLKEPIL NIHDLTQIHS DMNLPVPDPI LLTNSHDGLD
        90        100        110        120        130        140        150        160
GPTYKKRRLD ECEEAFQGTK VFVMPNGMLK SNQQLVDIIE KVKPEIRLLI EKCNTVKMWV QLLIPRIEDG NNFGVSIQEE
       170        180        190        200        210        220        230        240
TVAELRTVES EAASYLDQIS RYYITRAKLV SKIAKYPHVE DYRRTVTEID EKEYISLRLI ISELRNQYVT LHDMILKNIE
       250        260
KIKRPRSSNA ETLY
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2745 | 1 | 941.9477 | -120.25 | 2 | 62.8 | 11.4 | 2 | 122-137 | K.VKPEIRLLIEKCNTVK.M | |

# Detailed Protein Report

## Protein 1491: PREDICTED: E3 ubiquitin-protein ligase RNF220 isoform X7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578799381 | **Score:** | 11.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 35.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| | | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.97 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MDLHRAAFKM ENSSYLPNPL ASPALMVLAS TAEASRDASI PCQQPRPFGV PVSVDKDVHI PFTNGSYTFA SMYHRQGGVP
        90        100        110        120        130        140        150        160
GTFANRDFPP SLLHLHPQFA PPNLDCTPIS MLNHSGVGAF RPFASTEDRE SYQSAFTPAK RLKNCHDTES PHLRFSDADG
       170        180        190        200        210        220        230        240
KEYDFGTQLP SSSPGSLKVD DTGKKIFAVS GLISDREASS SPEDRNDRCK KKAAALFDSQ APICPICQVL LRPSELQEHM
       250        260        270        280        290        300        310        320
EQELEQLAQL PSSKNSLLKD AMAPGTPKSL LLSASIKREG ESPTASPHSS ATDDLHHSDR YQTFLRVRAN RQTRLNEGRL
       330
LHG
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2277 | 1 | 775.3245 | -72.44 | 2 | 56.8 | 11.4 | 1 | 142-154 | R.LKNCHDTESPHLR.F | | QU:MU 0.97 |

# Detailed Protein Report

## Protein 1492: interleukin-17F precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|16418375 | **Score:** | 11.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 18.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 14.7 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MTVKTLHGPA MVKYLLLSIL GLAFLSEAAA RKIPKVGHTF FQKPESCPPV PGGSMKLDIG IINENQRVSM SRNIESRSTS
        90        100        110        120        130        140        150        160
PWNYTVTWDP NRYPSEVVQA QCRNLGCINA QGKEDISMNS VPIQQETLVV RRKHQGCSVS FQLEKVLVTV GCTCVTPVIH
       170
HVQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 429 | 1 | 881.1700 | 63.88 | 3 | 35.3 | 11.4 | 1 | 33-56 | K.IPKVGHTFFQKPESCPPVPGGSMK.L | Carbamidomethyl: 15;<br>Oxidation: 23 |

# Detailed Protein Report

## Protein 1493: PREDICTED: autism susceptibility gene 2 protein isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530385715 | **Score:** | 11.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 90.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFAPPTALPP | PPPLTSGSLQ | VAGHPAGSTY | SEQDILRQEL | NTRFLASQSA | DRGASLGPPP | YLRTEFHQHQ | HQHQHTHQHT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HQHTFTPFPH | AIPPTAIMPT | PAPPMVRTPG | RNFDKYPTKV | DPFYRHSLFH | SYPPAVSGIP | PMIPPTGPFG | SLQGAFQPKT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SNPIDVAARP | GTVPHTLLQK | DPRLTDPFRP | MLRKPGKWCA | MHVHIAWQIY | HHQQKVKKQM | QSDPHKLDFG | LKPEFLSRPP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GPSLFGAIHH | PHDLARPSTL | FSAAGAAHPT | GTPFGPPPHH | SNFLNPAAHL | EPFNRPSTFT | GLAAVGGNAF | GGLGNPSVTP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NSMFGHKDGP | SVQNFSNPHE | PWNRLHRTPP | SFPTPPPWLK | PGELERSASA | AAHDRDRDVD | KRDSSVSKDD | KERESVEKRH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SSHPSPAPVL | PVNALGHTRS | STEQIRAHLN | TEAREKDKPK | ERERDHSESR | KDLAADEHKA | KEGHLPEKDG | HGHEGRAAGE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EAKQLARVPS | PYVRTPVVES | ARPNSTSSRE | AEPRKGEPAY | ENPKKSSEVK | VKEERKEDHD | LPPEAPQTHR | ASEPPPPNSS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SSVHPGPLAS | MPMTVGVTGI | HPMNSISSLD | RTRMMTPFMG | ISPLPGGERF | PYPSFHWDPI | RDPLRDPYRE | LDIHRRDPLG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RDFLLRNDPL | HRLSTPRLYE | ADRSFRDREP | HDYSHHHHHH | HHPLSVDPRR | EHERGGHLDE | RERLHMLRED | YEHTRLHSVH |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PASLDGHLPH | PSLITPGLPS | MHYPRISPTA | GNQNGLLNKT | PPTAALSAPP | PLISTLGGRP | VSPRRTTPLS | AEIRERPPSH |
| 810 | | | | | | | |
| TLKDIEAR | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1863 | 1 | 860.9061 | -9.89 | 2 | 51.6 | 11.4 | 0 | 594-609 | R.MMTPFMGISPLPGGER.F | |

# Detailed Protein Report

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## Protein 1494: PREDICTED: cell death activator CIDE-A isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578832070 | **Score:** | 11.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 13.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| | | **Sequence Coverage [%]:** | 10.0 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MILEKGQKWM PGSQHVPTCS PPKRSGIARV TFDLYRLNPK DFIGCLNVKA TMYEMYSVSY DIRCTGLKGL LRSLLRFLSY
        90        100        110        120        130
SAQVTGQFLI YLGTYMLRVL DDKEERPSLR SQAKGRFTCG
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1540 | 1 | 699.3756 | -6.91 | 2 | 48.9 | 11.4 | 1 | 25-36 | R.SGIARVTFDLYR.L | |

# Detailed Protein Report

## Protein 1495: zinc finger and SCAN domain-containing protein 29 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|109715825 | **Score:** | 11.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 96.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 1.65 **CV:** 0.00 % **No. of Peptides:** 1

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578826641 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger and SCAN domain-containing protein 29 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMAKSALREN | GTNSETFRQR | FRRFHYQEVA | GPREAFSQLW | ELCCRWLRPE | VRTKEQIVEL | LVLEQFLTVL | PGEIQNWVQE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QCPENGEEAV | TLVEDLEREP | GRPRSSVTVS | VKGQEVRLEK | MTPPKSSQEL | LSVRQESVEP | QPRGVPKKER | ARSPDLGPQE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QMNPKEKLKP | FQRSGLPFPK | SGVVSRLEQG | EPWIPDLLGS | KEKELPSGSH | IGDRRVHADL | LPSKKDRRSW | VEQDHWSFED |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EKVAGVHWGY | EETRTLLAIL | SQTEFYEALR | NCHRNSQVYG | AVAERLREYG | FLRTLEQCRT | KFKGLQKSYR | KVKSGHPPET |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CPFFEEMEAL | MSAQVIALPS | NGLEAAASHS | GLVGSDAETE | EPGQRGWQHE | EGAEEAVAQE | SDSDDMDLEA | TPQDPNSAAP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VVFRSPGGVH | WGYEETKTYL | AILSETQFYE | ALRNCHRNSQ | LYGAVAERLW | EYGFLRTPEQ | CRTKFKSLQT | SYRKVKNGQA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PETCPFFEEM | DALVSVRVAA | PPNDGQEETA | SCPVQGTSEA | EAQKQAEEAD | EATEEDSDDD | EEDTEIPPGA | VITRAPVLFQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SPRGFEAGFE | NEDNSKRDIS | EEVQLHRTLL | ARSERKIPRY | LHQGKGNESD | CRSGRQWAKT | SGEKRGKLTL | PEKSLSEVLS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QQRPCLGERP | YKYLKYSKSF | GPNSLLMHQV | SHQVENPYKC | ADCGKSFSRS | ARLIRHRRIH | TGEKPYKCLD | CGKSFRDSSN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| FITHRRIHTG | EKPYQCGECG | KCFNQSSSLI | IHQRTHTGEK | PYQCEECGKS | FNNSSHFSAH | RRIHTGERPH | VCPDCGKSFS |
| 810 | 820 | 830 | 840 | 850 | 860 | | |
| KSSDLRAHHR | THTGEKPYGC | HDCGKCFSKS | SALNKHGEIH | AREKLLTQSA | PK | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 200 | 1 | 849.4012 | -12.44 | 2 | 32.5 | 11.4 | 1 | 153-167 | R.SPDLGPQEQMNPKEK.L | | QU:MU 1.65 |

# Detailed Protein Report

## Protein 1496: cryptochrome-2 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|188536103 | **Score:** | 11.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 60.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| | | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPAPPGRTHT | WFLLQSLEDL | DTSLRKLNSR | LFVVRGQPAD | VFPRLFKEWG | VTRLTFEYDS | EPFGKERDAA | IMKMAKEAGV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EVVTENSHTL | YDLDRIIELN | GQKPPLTYKR | FQAIISRMEL | PKKPVGLVTS | QQMESCRAEI | QENHDETYGV | PSLEELGFPT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EGLGPAVWQG | GETEALARLD | KHLERKAWVA | NYERPRMNAN | SLLASPTGLS | PYLRFGCLSC | RLFYYRLWDL | YKKVKRNSTP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PLSLFGQLLW | REFFYTAATN | NPRFDRMEGN | PICIQIPWDR | NPEALAKWAE | GKTGFPWIDA | IMTQLRQEGW | IHHLARHAVA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CFLTRGDLWV | SWESGVRVFD | ELLLDADFSV | NAGSWMWLSC | SAFFQQFFHC | YCPVGFGRRT | DPSGDYIRRY | LPKLKAFPSR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YIYEPWNAPE | SIQKAAKCII | GVDYPRPIVN | HAETSRLNIE | RMKQIYQQLS | RYRGLCLLAS | VPSCVEDLSH | PVAEPSSSQA |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| GSMSSAGPRP | LPSGPASPKR | KLEAAEEPPG | EELSKRARVA | ELPTPELPSK | DA | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 874 | 1 | 960.4724 | -57.70 | 2 | 41.0 | 11.4 | 2 | 437-451 | R.LNIERMKQIYQQLSR.Y | |

# Detailed Protein Report

**Protein 1497:** **bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2 isoform a [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|34447231 | **Score:** | 11.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSGIKKQKTE | NQQKSTNVVY | QAHHVSRNKR | GQVVGTRGGF | RGCTVWLTGL | SGAGKTTISF | ALEEYLVSHA | IPCYSLDGDN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VRHGLNRNLG | FSPGDREENI | RRIAEVAKLF | ADAGLVCITS | FISPFAKDRE | NARKIHESAG | LPFFEIFVDA | PLNICESRDV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KGLYKRARAG | EIKGFTGIDS | DYEKPETPER | VLKTNLSTVS | DCVHQVVELL | QEQNIVPYTI | IKDIHELFVP | ENKLDHVRAE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AETLPSLSIT | KLDLQWVQVL | SEGWATPLKG | FMREKEYLQV | MHFDTLLDDG | VINMSIPIVL | PVSAEDKTRL | EGCSKFVLAH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GGRRVAILRD | AEFYEHRKEE | RCSRVWGTTC | TKHPHIKMVM | ESGDWLVGGD | LQVLEKIRWN | DGLDQYRLTP | LELKQKCKEM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NADAVFAFQL | RNPVHNGHAL | LMQDTRRRLL | ERGYKHPVLL | LHPLGGWTKD | DDVPLDWRMK | QHAAVLEEGV | LDPKSTIVAI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FPSPMLYAGP | TEVQWHCRSR | MIAGANFYIV | GRDPAGMPHP | ETKKDLYEPT | HGGKVLSMAP | GLTSVEIIPF | RVAAYNKAKK |
| 570 | 580 | 590 | 600 | 610 | 620 | | |
| AMDFYDPARH | NEFDFISGTR | MRKLAREGEN | PPDGFMAPKA | WKVLTDYYRS | LEKN | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1674 | 1 | 882.9064 | -71.21 | 2 | 51.2 | 11.4 | 1 | 459-474 | R.MKQHAAVLEEGVLDPK.S | |

# Detailed Protein Report

## Protein 1498: probable ATP-dependent RNA helicase DDX20 [Homo sapiens]

**Accession:** gi|256223453
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 11.4
**MW [kDa]:** 92.2
**pI:** 6.5
**Sequence Coverage [%]:** 1.7
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAAFEASGA | LAAVATAMPA | EHVAVQVPAP | EPTPGPVRIL | RTAQDLSSPR | TRTGDVLLAE | PADFESLLLS | RPVLEGLRAA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GFERPSPVQL | KAIPLGRCGL | DLIVQAKSGT | GKTCVFSTIA | LDSLVLENLS | TQILILAPTR | EIAVQIHSVI | TAIGIKMEGL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ECHVFIGGTP | LSQDKTRLKK | CHIAVGSPGR | IKQLIELDYL | NPGSIRLFIL | DEADKLLEEG | SFQEQINWIY | SSLPASKQML |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AVSATYPEFL | ANALTKYMRD | PTFVRLNSSD | PSLIGLKQYY | KVVNSYPLAH | KVFEEKTQHL | QELFSRIPFN | QALVFSNLHS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RAQHLADILS | SKGFPAECIS | GNMNQNQRLD | AMAKLKHFHC | RVLISTDLTS | RGIDAEKVNL | VVNLDVPLDW | ETYMHRIGRA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GRFGTLGLTV | TYCCRGEEEN | MMMRIAQKCN | INLLPLPDPI | PSGLMEECVD | WDVEVKAAVH | TYGIASVPNQ | PLKKQIQKIE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RTLQIQKAHG | DHMASSRNNS | VSGLSVKSKN | NTKQKLPVKS | HSECGIIEKA | TSPKELGCDR | QSEEQMKNSV | QTPVENSTNS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QHQVKEALPV | SLPQIPCLSS | FKIHQPYTLT | FAELVEDYEH | YIKEGLEKPV | EIIRHYTGPG | DQTVNPQNGF | VRNKVIEQRV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PVLASSSQSG | DSESDSDSYS | SRTSSQSKGN | KSYLEGSSDN | QLKDSESTPV | DDRISLEQPP | NGSDTPNPEK | YQESPGIQMK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| TRLKEGASQR | AKQSRRNLPR | RSSFRLQTEA | QEDDWYDCHR | EIRLSFSDTY | QDYEEYWRAY | YRAWQEYYAA | ASHSYYWNAQ |
| 810 | 820 | 830 | | | | | |
| RHPSWMAAYH | MNTIYLQEMM | HSNQ | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1828 | 1 | 807.3949 | -77.75 | 2 | 51.2 | 11.4 | 2 | 39-52 | R.ILRTAQDLSSPRTR.T | |

# Detailed Protein Report

## Protein 1499: dynein heavy chain 7, axonemal [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|151301127 | **Score:** | 11.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 460.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 0.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSSEQDKSAS | KEKSKKPVRF | LPQLSMEKLA | SKEKFKAPAR | ALPQLSMVST | KPHWQQAAPS | FHLSVKQDDE | SPEPFSVKNE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QSHAEYMERF | GKKGKLPHQV | DDSYVGPSTS | KSKGKSPHKE | RENFRSTLVN | VIMQQDADLD | SAVPDGSTIP | KPTASAIEKD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ILRYYYYIHH | GIDTDHVAPM | EDSWLEHVLD | LVPQHLKVFT | DSIVTLSDEM | REDYLLSVRK | SIVDFVLKDP | REKGDDKKTD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ELPAHRAEME | ILPKPWRKSF | LAASSYIRDH | LNAMNPTMLA | VLDLWHTNFK | KLRLVDIKEF | HNCQDALELS | SFQNIIMRHM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DSAKETLLKM | WFPEVQNIYY | QGNKKKQLPT | GDSSAKLESF | FNCAAALMTL | QLQDLTLVSM | QDFTDLIAQP | PDSVRAFEHP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GFIMRLILDN | DTIKFEPELS | DYIDIFLNVY | DVMIKAVSFV | PRVETKLYSK | WESKSKPTTL | KPIILNEIVD | AHKEKIKEVI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| MKESVAPTEH | LRLYDKYDFL | ITRKAERDVD | NFLAENHSYE | KIIDEICKYQ | KLIEEIQYTS | IKTIRLGMFE | MHCEELIRAL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VKRADIICGK | LLAKMFRDHQ | EVNTRLCDEF | ERIAEKALST | PPNTAELMEM | KAYIQKVEVT | DMIELEQRLV | DSKNCLAFLI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EYVNFSPADM | RLNNSVFQWY | GRMGEIFEEH | RKIIKEKIEQ | YQEGLKLRCE | RFVEELESYA | KQSEEFYSFG | DLQDVQRYLK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KAQILNGKLD | LAADKIEQFN | AEEEAFGWLP | SVYPQRKKIQ | DGLNPYLRLY | ETAVEFSSNY | RAWTEGPYHK | VNPDQVEADI |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GNYWRGLYKL | EKTFHDSPYA | LAMTKKVRSK | VEDFKQHIPL | IQVICNPGLR | PRHWEAMSAI | VGYPLQPSDD | STVSSFLDMN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LEPYIDRFEG | ISEAASKEYS | LEKAMEKMIT | EWDAVEFVIH | SYRETGTFIL | ASVDEIQMLL | DDHIIKTQTM | RGSPFIKPYE |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KQMREWEGKL | LLLQEILDEW | LKVQATWLYL | EPIFSSPDIM | SQMPEEGRRF | TAVDKTWRDI | MRSVMQDKHV | LTVVTIDRML |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ERLKKSNELL | ELILKGLNEY | LEKKRLFFPR | FFFLSNDELL | EILSETKDPT | RVQPHLKKCF | EGIAKVEFTE | TLDITHMKSS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EGEVVELIEI | ISTAKARGQV | EKWLVELERV | MINSIHKVTG | DATFAYTKYE | RINWVRDWPG | QTVLCVSQIF | WTKEVQTAIP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| MGIKALEQYL | KTCNRQIDDI | VTLVRGKLSM | QNRVTLGALV | VLDVHARDVL | SSLVKKNISD | DSDFEWLSQL | RYYWQENHLE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TKMINAGLRY | GYEYLGNSPR | LVITPLTDRC | YRTLFGALHL | HLGGAPEGPA | GTGKTETTKD | LAKAVAKQCV | VFNCSDGLDY |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LALGKFFKGL | LSCGAWACFD | EFNRIDLEVL | SVVAQQILTI | QRGINAGADI | LMFEGTELKL | DPTCAVFITM | NPGYAGRSEL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| PDNLKALFRT | VAMMVPDYAM | IAEIVLYSCG | FVTARPLSVK | IVATYRLCSE | QLSSQHHYDY | GMRAVKSVLT | AAGNLKLKYP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| NENEEILLLR | SIIDVNLPKF | LSHDLPLFEG | ITSDLFPGVK | LPKPDYNDLL | AAIKDNCASM | NLQMTAFFSE | KILQVYEMMI |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| VRHGFMIVGE | PFGGKTSAYR | VLAGALNDIC | EKGLMEENKV | QITVLNPKSV | TMGQLYGQFD | SVSHEWSDGV | LAVSFRAFAS |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| SVTPDRKWLI | FDGPVDAVWI | ENMNTVLDDN | KKLCLMSGEI | IQMSPQMNLI | FEPMDLEVAS | PATVSRCGMI | YMEPHMLGWR |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| PLMLSWVNLL | PASVSVIQKE | FIMGLFDRMV | PVSVEFIRKH | TKELSPTSDT | NLVRSLMNLI | DCFMDDFADE | VKLKERNDRE |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| TYSLLEGIFL | FSLIWSVGAS | CTDDDRLKFN | KILRELMESP | ISDRTRNTFK | LQSGTEQTSS | KALTVPFPEK | GTIYDYQFVT |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| EGIGKWEPWI | KKLKEAPPIP | KDVMFNEIIV | PTLDTIRYSA | LMELLTTHQK | PSIFVGPTGT | GKSVYITNFL | LNQLNKEIYK |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| PLLINFSAQT | TAAQTQNIVM | SKLDKRRKGV | FGPPLGKRMV | VFVDDVNMPA | REVYGAQPPI | ELLRQWLDHW | NWYDLKDCSM |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| IKLVDIQIMC | AMGPPGGGRN | PVTPRYMRHF | NIITINEFSD | KSMYTIFSRI | LTWHLEICYK | FPDEFLDLTT | QIVNGTMTLY |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2726 | 1 | 862.4253 | -75.80 | 2 | 65.2 | 11.4 | 2 | 436-450 | K.AVSFVPRVETKLYSK.W | |

# Detailed Protein Report

## Protein 1500: PREDICTED: coiled-coil domain-containing protein 9 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578834259 | **Score:** | 11.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.24 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.51 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAATLDLKSK | EEKDAELDKR | IEALRRKNEA | LIRRYQEIEE | DRKKAELEGV | AVTAPRKGRS | VEKENVAVES | EKNLGPSRRS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PGTPRPPGAS | KGGRTPPQQG | GRAGMGRASR | SWEGSPGEQP | RGGGAGGRGR | RGRGRGSPHL | SGAGDTSISD | RKSKEWEERR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RQNIEKMNEE | MEKIAEYERN | QREGVLEPNP | VRNFLDDPRR | RSGPLEESER | DRREESRRHG | RNWGGPDFER | VRCGLEHERQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GRRAGLGSAG | DMTLSMTGRE | RSEYLRWKQE | REKIDQERLQ | RHRKPTGQWR | REWDAEKTDG | MFKDGPVPAH | EPSHRYDDQA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WARPPKPPTF | GEFLSQHKAE | ASSRRRRKSS | RPQAKAAPRA | YSDHDDRWET | KEGAASPAPE | TPQPTSPETS | PKETPMQPPE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IPAPAHRPPE | DEGEENEGEE | DEEWEDISED | EEEEEIEVEE | GGGQSAPAFP | ESGPSLRGTQ | EAEEEGSEAT | PEAGPEGQET |
| 490 | 500 | 510 | | | | | |
| AEITDFQRVR | FCKVVAAPPL | PGAAR | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 795 | 1 | 848.9510 | 49.56 | 2 | 39.5 | 11.4 | 1 | 243-259 | R.RAGLGSAGDMTLSMTGR.E | Oxidation: 14 | QU:MU 1.24<br>WUP:QUP 0.51 |

# Detailed Protein Report

## Protein 1501: homeobox protein TGIF1 isoform d [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|28178851 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 6.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.33 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.28 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530424923 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: homeobox protein TGIF1 isoform X2 [Homo sapiens] |
| gi\|522838246 | refseq_human (refseq_human_20140103.fasta) | homeobox protein TGIF1 isoform d [Homo sapiens] |
| gi\|28178857 | refseq_human (refseq_human_20140103.fasta) | homeobox protein TGIF1 isoform d [Homo sapiens] |
| gi\|28178855 | refseq_human (refseq_human_20140103.fasta) | homeobox protein TGIF1 isoform d [Homo sapiens] |
| gi\|28178853 | refseq_human (refseq_human_20140103.fasta) | homeobox protein TGIF1 isoform d [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MDIPLDLSSS AGSGKRRRRG NLPKESVQIL RDWLYEHRYN AYPSEQEKAL LSQQTHLSTL QVCNWFINAR RRLLPDMLRK
        90        100        110        120        130        140        150        160
DGKDPNQFTI SRRGAKISET SSVESVMGIK NFMPALEETP FHSCTAGPNP TLGRPLSPKP SSPGSVLARP SVICHTTVTA
       170        180        190        200        210        220        230        240
LKDVPFSLCQ SVGVGQNTDI QQIAAKNFTD TSLMYPEDTC KSGPSTNTQS GLFNTPPPTP PDLNQDFSGF QLLVDVALKR
       250        260
AAEMELQAKL TA
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1061 | 2 | 751.8882 | -7.89 | 2 | 41.5 | 11.3 | 1 | 2-16 | M.DIPLDLSSSAGSGKR.R | | WUP:QUP 1.28<br>QU:MU 1.33 |

# Detailed Protein Report

## Protein 1502: deoxyribonuclease-1-like 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5803007 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 33.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530430464 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: deoxyribonuclease-1-like 1 isoform X1 [Homo sapiens] |
| gi\|58430946 | refseq_human (refseq_human_20140103.fasta) | deoxyribonuclease-1-like 1 precursor [Homo sapiens] |
| gi\|58430944 | refseq_human (refseq_human_20140103.fasta) | deoxyribonuclease-1-like 1 precursor [Homo sapiens] |
| gi\|58430942 | refseq_human (refseq_human_20140103.fasta) | deoxyribonuclease-1-like 1 precursor [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MHYPTALLFL ILANGAQAFR ICAFNAQRLT LAKVAREQVM DTLVRILARC DIMVLQEVVD SSGSAIPLLL RELNRFDGSG
        90        100        110        120        130        140        150        160
PYSTLSSPQL GRSTYMETYV YFYRSHKTQV LSSYVYNDED DVFAREPFVA QFSLPSNVLP SLVLVPLHTT PKAVEKELNA
       170        180        190        200        210        220        230        240
LYDVFLEVSQ HWQSKDVILL GDFNADCASL TKKRLDKLEL RTEPGFHWVI ADGEDTTVRA STHCTYDRVV LHGERCRSLL
       250        260        270        280        290        300        310
HTAAAFDFPT SFQLTEEEAL NISDHYPVEV ELKLSQAHSV QPLSLTVLLL LSLLSPQLCP AA
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 35 | 1 | 1080.5173 | 4.02 | 2 | 30.1 | 11.3 | 2 | 220-237 | R.ASTHCTYDRVVLHGERCR.S | Carbamidomethyl: 5 |

# Detailed Protein Report

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**Protein 1503:** **PREDICTED: EF-hand calcium-binding domain-containing protein 4B isoform X6 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578822705 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 77.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.97 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.51 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAPDGRVVS | RPQRLGQGSG | QGPKGSGACL | HPLDSLEQKE | TQEQTSGQLV | MLRKAQEFFQ | TCDAEGKGFI | ARKDMQRLHK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ELPLSLEELE | DVFDALDADG | NGYLTPQEFT | TGFSHFFFSQ | NNPSQEDAGE | QVAQRHEEKV | YLSRGDEDLG | DMGEDEEAQF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RMLMDRLGAQ | KVLEDESDVK | QLWLQLKKEE | PHLLSNFEDF | LTRIISQLQE | AHEEKNELEC | ALKRKIAAYD | EEIQHLYEEM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EQQIKSEKEQ | FLLKDTERFQ | ARSQELEQKL | LCKEQELEQL | TQKQKRLEGQ | CTALHHDKHE | TKAENTKLKL | TNQELARELE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RTSWELQDAQ | QQLESLQQEA | CKLHQEKEME | VYRVTESLQR | EKAGLLKQLD | FLSSQSEEEE | EVFGIPRRSS | LGLSGYPLTE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EEPGTGEPGP | GGPYPRPLRR | IISVEEDPLP | QLLDGGFEQP | LSKCSEEEEV | SDQGVQGQIP | EAPPLKLTPT | SPRGQPVGKE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ALCKEESSPS | APDRLFKIVF | VGNSAVGKTS | FLRRFCEDRF | SPGMAATVGI | DYRVKTLNVD | NSQVALQLWD | TAGQERYRCI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TQQFFRKADG | VIVMYDLTDK | QSFLSVRRWL | SSVEEAVGDR | VPVLLLGNKL | DNEKEREVPR | GLGEQLATVK | SKHFHLSGQS |
| 650 | 660 | 670 | 680 | 690 | | | |
| VTPREVGQVP | KSLGGDFLWK | CHGKEATGKH | GCLGILGMAQ | LLCM | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1025 | 3 | 508.1580 | -265.04 | 2 | 41.1 | 11.3 | 0 | 621-630 | R.GLGEQLATVK.S | | QU:MU 0.97<br>WUP:QUP 0.51 |

# Detailed Protein Report

## Protein 1504: protein AKNAD1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|91754185 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 92.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDEADFSEHT | TYKQEDLPYD | GDLSQIKIGN | DYSFTSKKDG | LEVLNQIIFI | ADDPQEKAMH | SETCGNTAVT | IPLGKITENA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ANKKDEKEKQ | CTAALHIPAN | EGDASKSSIS | DILLHHLSKE | PFLRGQGIDC | ETLPEISNAD | SFEEEAIIKS | IISCYNKNSW |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PKEQTPELTD | QLNPKRDGEN | SNKPGSATTT | EENTSDLEGP | VAAGDSSHQE | NVNVLTKTKG | PGDKQKSYQG | QSPQKQQTEK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ANSGNTFKYG | QGQVHYQLPD | FSKIAPKVKI | PKNKIINKPL | AIAKQASFSS | KSRDKPTLVQ | DSLETTPESN | CVEKQHQEQK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GKITEPSQQI | QMEPIVHIHQ | ELLTGIESEA | SLSKLSPTSQ | KGTSSSSSYI | FQKISQGKQM | CQKLKEQTDQ | LKTKVQEFSK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RIKQDSPYHL | QDKKLVLEKL | QGHLELLEQN | FLATKDKHLT | LQQQVHKHES | TIVGDFDPER | KVEGEIFKLE | MLLEDVKEKM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DESKYTSAPS | LPVSSPVTLD | DLASTFSSLS | NEIPKEHPGH | PSGPRGSGGS | EVTGTPQGGP | QEAPNEELCE | LAPQTYLNGH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YGDAAAQNKP | DQVAMRLSSN | SGEDPNGTPR | RQDCAEMTAP | SPSCAFCRRL | LEWKQNVEKK | GHGRINCGRF | SIVLHEKAPH |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SDSTPNSDTG | HSFCSDSGTE | MQSNKCQDCG | TKIPTSRRAC | RKEPTKEFHY | RYNTPGQNYS | NHSKRGAFVQ | PHSLDESKNS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SPSFLKPKRI | CSQRVNSKSF | KGEHEPTPGK | KKLQAFMTYS | SDPATPSPHF | YSCRISGSKS | LCDFDSTEEI | KSEILNSALD |
| 810 | 820 | 830 | 840 | | | | |
| HALRTATILK | ETTDQMIKTI | AEDLAKAQRW | RNRLKY | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 182 | 1 | 795.4018 | 96.81 | 2 | 31.1 | 11.3 | 0 | 1-13 | -.MDEADFSEHTTYK.Q | Oxidation: 1 |

# Detailed Protein Report

## Protein 1505: leukocyte immunoglobulin-like receptor subfamily B member 1 isoform 6 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|508772614 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTPILTVLIC | LGLSLGPRTH | VQAGHLPKPT | LWAEPGSVIT | QGSPVTLRCQ | GGQETQEYRL | YREKKTALWI | TRIPQELVKK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GQFPIPSITW | EHAGRYRCYY | GSDTAGRSES | SDPLELVVTG | AYIKPTLSAQ | PSPVVNSGGN | VILQCDSQVA | FDGFSLCKEG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EDEHPQCLNS | QPHARGSSRA | IFSVGPVSPS | RRWWYRCYAY | DSNSPYEWSL | PSDLLELLVL | GVSKKPSLSV | QPGPIVAPEE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TLTLQCGSDA | GYNRFVLYKD | GERDFLQLAG | AQPQAGLSQA | NFTLGPVSRS | YGGQYRCYGA | HNLSSEWSAP | SDPLDILIAG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QFYDRVSLSV | QPGPTVASGE | NVTLLCQSQG | WMQTFLLTKE | GAADDPWRLR | STYQSQKYQA | EFPMGPVTSA | HAGTYRCYGS |
| 410 | 420 | 430 | 440 | 450 | 460 | | |
| QSSKPYLLTH | PSDPLELVVS | GPSGGPSSPT | TGPTSTSAGP | EDQPLTPTGS | DPQSGE | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1584 | 1 | 949.1716 | 123.54 | 2 | 48.1 | 11.3 | 0 | 1-18 | -.MTPILTVLICLGLSLGPR.T | |

# Detailed Protein Report

## Protein 1506: DAN domain family member 5 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|22749329 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 20.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.3 |
| | | **Sequence Coverage [%]:** | 9.5 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MLLGQLSTLL CLLSGALPTG SGRPEPQSPR PQSWAAANQT WALGPGALPP LVPASALGSW KAFLGLQKAR QLGMGRLQRG
        90        100        110        120        130        140        150        160
QDEVAAVTLP LNPQEVIQGM CKAVPFVQVF SRPGCSAIRL RNHLCFGHCS SLYIPGSDPT PLVLCNSCMP ARKRWAPVVL
       170        180        190
WCLTGSSASR RRVKISTMLI EGCHCSPKA
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2762 | 1 | 1023.0288 | -17.53 | 2 | 65.7 | 11.3 | 2 | 155-172 | R.WAPVVLWCLTGSSASRRR.V | |

# Detailed Protein Report

## Protein 1507: PREDICTED: phosphatidylinositide phosphatase SAC2 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578819140 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 74.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.5 |
| | | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.98 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.01 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MELFQAKDHY ILQQGERALW CSRRDGGLQL RPATDLLLAW NPICLGLVEG VIGKIQLHSD LPWWLILIRQ KALVGKLPGD
        90        100        110        120        130        140        150        160
HEVCKVTKIA VLSLSEMEPQ DLELELCKKH HFGINKPEKI IPSPDDSKFL LKTFTHIKSN VSAPNKKKVK ESKEKEKLER
       170        180        190        200        210        220        230        240
RLLEELLKMF MDSESFYYSL TYDLTNSVQR QSTGERDGRP LWQKVDDRFF WNKYMIQDLT EIGTPDVDFW IIPMIQGFVQ
       250        260        270        280        290        300        310        320
IEELVVNYTE SSDDEKSSPE TPPQESTCVD DIHPRFLVAL ISRRSRHRAG MRYKRRGVDK NGNVANYVET EQLIHVHNHT
       330        340        350        360        370        380        390        400
LSFVQTRGSV PVFWSQVGYR YNPRPRLDRS EKETVAYFCA HFEEQLNIYK KQVIINLVDQ AGREKIIGDA YLKQVLLFNN
       410        420        430        440        450        460        470        480
SHLTYVSFDF HEHCRGMKFE NVQTLTDAIY DIILDMKWCW VDEAGVICKQ EGIFRVNCMD CLDRTNVVQA AIARVVMEQQ
       490        500        510        520        530        540        550        560
LKKLGVMPPE QPLPVKCNRI YQIMWANNGD SISRQYAGTA ALKGDFTRTG ERKLAGVMKD GVNSANRYYL NRFKDAYRQA
       570        580        590        600        610        620        630        640
VIDLMQGIPV TEDLYSIFTK EKEHEALHKE NQRSHQELIS QLLQSYMKLL LPDDEKFHGG WALIDCDPRK PPTLSTAGKR
       650
L
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1347 | 1 | 727.4089 | -26.13 | 2 | 46.5 | 11.3 | 1 | 371-383 | K.KQVIINLVDQAGR.E | | QU:MU 1.98<br>WUP:QUP 1.01 |

# Detailed Protein Report

## Protein 1508: nuclear RNA export factor 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|11545757 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 60.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSLPSGHTTG | HTDQVVQRRA | RCWDIYQRRF | SSRSEPVNPG | MHSSSHQQQD | GDAAMHGAHM | DSPVRYTPYT | ISPYNRKGSF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RKQDQTHVNM | EREQKPPERR | MEGNMPDGTL | GSWFKITVPF | GIKYNEKWLL | NLIQNECSVP | FVPVEFHYEN | MHASFFVENA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SIAYALKNVS | GKIWDEDNEK | ISIFVNPAGI | PHFVHRELKS | EKVEQIKLAM | NQQCDVSQEA | LDIQRLPFYP | DMVNRDTKMA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SNPRKCMAAS | LDVHEENIPT | VMSAGEMDKW | KGIEPGEKCA | DRSPVCTTFS | DTSSNINSIL | ELFPKLLCLD | GQQSPRATLC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GTEAHKRLPT | CKGSFFGSEM | LKNLVLQFLQ | QYYLIYDSGD | RQGLLSAYHD | EACFSLSIPF | NPEDSAPSSF | CKFFKDSRNI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KILKDPYLRG | ELLKHTKLDI | VDSLSALPKT | QHDLSSFLVD | MWYQTEWMLC | FSVNGVFKEV | EGQSQGSVLA | FTRTFIATPG |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| SSSSLCIVND | KLFVRDTSHQ | GTQSALFTLV | PTAFSSSVPA | FSQEQQKMLP | S | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2683 | 1 | 835.4519 | 96.70 | 2 | 61.9 | 11.3 | 0 | 101-115 | R.MEGNMPDGTLGSWFK.I | |

# Detailed Protein Report

## Protein 1509: PREDICTED: amyotrophic lateral sclerosis 2 chromosomal region candidate gene 12 protein isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578803684 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 6.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MYPNPLIYCT | CWDPWNLGPR | KLIKTPQLPR | KNSTGSSKLT | PLVPAPKNHN | YLQPTKPVVS | PKMKIHSARQ | EETNKSFYEV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| INVSPGYQLV | RNREQISVTL | GDEMFDRKKR | WESEIPDKGR | FSRTNIISDL | EEQISELTAI | IEQMNRDHQS | AQKLLSSEMD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LRCAEMKQNF | ENKNRELKEA | HEAELSELEN | NYKAALKAEK | LAAQEKLEEM | GKEYKYLKNM | FRTYQDSIYD | EMEEKWSKQK |
| 250 | 260 | 270 | | | | | |
| AKWKKDEKFE | RENILLQQKK | KR | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2079 | 1 | 715.9597 | -76.99 | 3 | 54.4 | 11.3 | 1 | 176-193 | R.ELKEAHEAELSELENNYK.A | |

# Detailed Protein Report

**Protein 1510:** **PREDICTED: brain-specific angiogenesis inhibitor 1-associated protein 2 isoform X11 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578830259 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 58.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MIGVKQEYQQ | EMGSVQPRNH | SESSILPACL | GRRQGWACVT | YAAKGYFDAL | VKMGELASES | QGSKELGDVL | FQMAEVHRQI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QNQLEEMLKS | FHNELLTQLE | QKVELDSRYL | SAALKKYQTE | QRSKGDALDK | CQAELKKLRK | KSQGSKNPQK | YSDKELQYID |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AISNKQGELE | NYVSDGYKTA | LTEERRRFCF | LVEKQCAVAK | NSAAYHSKGK | ELLAQKLPLW | QQACADPSKI | PERAVQLMQQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VASNGATLPS | ALSASKSNLV | ISDPIPGAKP | LPVPPELAPF | VGRMSAQEST | PIMNGVTGPD | GEDYSPWADR | KAAQPKSLSP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PQSQSKLSDS | YSNTLPVRKS | VTPKNSYATT | AENKTLPRSS | SMAAGLERNG | RMRVKAIFSH | AAGDNSTLLS | FKEGDLITLL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VPEARDGWHY | GESEKTKMRG | WFPFSYTRVL | DSDGSDRLHM | SLQQGKSSST | GNLLDKDDLA | IPPPDYGAAS | RAFPAQTASG |
| 490 | 500 | 510 | 520 | 530 | | | |
| FKQRPYSVAV | PAFSQGLDDY | GARSMSRNPF | AHVQLKPTVT | NDRSAPLLS | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 807 | 1 | 677.1961 | -212.84 | 2 | 40.1 | 11.3 | 1 | 33-44 | R.RQGWACVTYAAK.G | |

# Detailed Protein Report

## Protein 1511: alpha-synuclein isoform NACP112 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|6806898 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 11.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 11.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.04 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MDVFMKGLSK AKEGVVAAAE KTKQGVAEAA GKTKEGVLYV GSKTKEGVVH GVATVAEKTK EQVTNVGGAV VTGVTAVAQK
         90        100        110        120
TVEGAGSIAA ATGFVKKDQL GKEGYQDYEP EA
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2558 | 1 | 648.3654 | 21.74 | 2 | 62.0 | 11.3 | 0 | 46-58 | K.EGVVHGVATVAEK.T | | WUP:QUP 0.04 |

# Detailed Protein Report

## Protein 1512: prostate-specific antigen isoform 4 preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|71834855 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 23.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.9 |
| | | **Sequence Coverage [%]:** | 11.9 |
| | | **No. of unique Peptides:** | 1 |

```
         10         20         30         40         50         60         70         80
MWVPVVFLTL SVTWIGAAPL ILSRIVGGWE CEKHSQPWQV LVASRGRAVC GGVLVHPQWV LTAAHCIRKP GDDSSHDLML
         90        100        110        120        130        140        150        160
LRLSEPAELT DAVKVMDLPT QEPALGTTCY ASGWGSIEPE EFLTPKKLQC VDLHVISNDV CAQVHPQKVT KFMLCAGRWT
        170        180        190        200        210        220
GGKSTCSGDS GGPLVCNGVL QGITSWGSEP CALPERPSLY TKVVHYRKWI KDTIVANP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 801 | 1 | 1419.2740 | 37.23 | 2 | 39.6 | 11.3 | 1 | 69-94 | R.KPGDDSSHDLMLLRLSEPAELTDAVK.V | |

# Detailed Protein Report

## Protein 1513: glycine receptor subunit alpha-2 isoform C [Homo sapiens]

**Accession:** gi|284925161
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 11.3
**MW [kDa]:** 42.0
**pI:** 9.6
**Sequence Coverage [%]:** 5.8
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDYRVNIFLR | QQWNDSRLAY | SEYPDDSLDL | DPSMLDSIWK | PDLFFANEKG | ANFHDVTTDN | KLLRISKNGK | VLYSIRLTLT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LSCPMDLKNF | PMDVQTCTMQ | LESFGYTMND | LIFEWLSDGP | VQVAEGLTLP | QFILKEEKEL | GYCTKHYNTG | KFTCIEVKFH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LERQMGYYLI | QMYIPSLLIV | ILSWVSFWIN | MDAAPARVAL | GITTVLTMTT | QSSGSRASLP | KVSYVKAIDI | WMAVCLLFVF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AALLEYAAVN | FVSRQHKEFL | RLRRRQKRQN | KEEDVTRESR | FNFSGYGMGH | CLQVKDGTAV | KATPANPLPQ | PPKDGDAIKK |
| 330 | 340 | 350 | 360 | 370 | | | |
| KFVDRAKRID | TISRAAFPLA | FLIFNIFYWI | TYKIIRHEDV | HKK | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2213 | 1 | 753.7852 | 120.48 | 3 | 58.1 | 11.3 | 1 | 281-301 | R.FNFSGYGMGHCLQVKDGTAVK.A | |

# Detailed Protein Report

## Protein 1514: zinc finger protein 41 homolog [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|27883846 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 22.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| | | **Sequence Coverage [%]:** | 5.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|403048741 | refseq_human (refseq_human_20140103.fasta) | zinc finger protein 41 homolog [Homo sapiens] |

```
         10         20         30         40         50         60         70         80
MEKPAGRKKK TPTPREEADV QKSALREEKV SGDRKPPERP TVPRKPRTEP CLSPEDEEHV FDAFDASFKD DFEGVPVFIP
         90        100        110        120        130        140        150        160
FQRKKPYECS ECGRIFKHKT DHIRHQRVHT GEKPFKCAQC GKAFRHSSDV TKHQRTHTGE KPFKCGECGK AFNCGSNLLK
        170        180        190        200
HQKTHTGEKP YECTHCGKAF AYSSCLIRHQ KRHPRKKKP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1184 | 1 | 586.1188 | -218.96 | 2 | 43.0 | 11.3 | 0 | 85-94 | K.KPYECSECGR.I | |

# Detailed Protein Report

## Protein 1515: PREDICTED: enhancer of polycomb homolog 2 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578804049 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 77.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDSEDETLLN | RLNRKMEIKP | LQFEIMIDRL | EKASSNQLVT | LQEAKLLLNE | DDYLIKAVYD | YWVRKRKNCR | GPSLIPQIKQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EKRDGSTNND | PYVAFRRRTE | KMQTRKNRKN | DEASYEKMLK | LRREFSRAIT | ILEMIKRREK | TKRELLHLTL | EVVEKRYHLG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DYGGEILNEV | KISRSEKELY | ATPATLHNGN | HHKVQECKTK | HPHHLSLKEE | ASDVVRQKKK | YPKKPKAEAL | ITSQQPTPET |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LPVINKSDIK | QYDFHSSDED | EFPQVLSPVS | EPEEENDPDG | PCAFRRRAGC | QYYAPRLDQA | NHSCENSELA | DLDKLRYRHC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LTTLTVPRRC | IGFARRRIGR | GGRVIMDRIS | TEHDPVLKQI | DPEMLNSFSS | SSQTIDFSSN | FSRTNASSKH | CENRLSLSEI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LSNIRSCRLQ | CFQPRLLNLQ | DSDSEECTSR | KPGQTVNNKR | VSAASVALLN | TSKNGISGGI | TEEQFQTHQQ | QLVQMQRQQL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AQLQQKQQSQ | HSSQQTHPKA | QGSSTSDCMS | KTLDSASAHF | AASAVVSAPV | PSRSEVAKEQ | NTGHNNINGV | VQPSGTSKTL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| YSTNMALSSS | PGISAVQLVR | TVGHTTTNHL | IPALCTSSPQ | TLPMNNSCLT | NAVHLNNVSV | VSPVNVHINT | RTSAPSPTAL |
| 650 | 660 | 670 | 680 | 690 | | | |
| KLATVAASMD | RVPKVTPSSA | ISSIARENHE | PERLGLNGIA | ETTVAMEVT | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 956 | 1 | 757.0581 | 154.93 | 2 | 40.3 | 11.3 | 1 | 652-666 | R.VPKVTPSSAISSIAR.E | |

# Detailed Protein Report

## Protein 1516: ferritin, heavy polypeptide-like 18 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|410991933 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 25.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 5.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.45 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.23 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVVLRGPHRC | RHCPRRCRYP | LRAPGKPTAF | PLLPAPALPA | LGPLSQVQRY | HHPSCEAAIN | THISLELHAS | YVYLSMAFYF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DQDDAALEHF | DCYFLCQLQE | KREHAQELMR | LHNLRGGRIC | LHDVGKPEGQ | GWESGLKAME | CAFHLEKNIN | QSLLELHQLA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | |
| KENGDPQLCD | FLENHFLNQQ | AKTIKELGGY | LSNLRKMGSP | EAGLAEYLFN | KLTLGRSQKH | T | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1531 | 1 | 698.8072 | -95.99 | 2 | 49.3 | 11.3 | 2 | 1-11 | -.MVVLRGPHRCR.H | Carbamidomethyl: 10;<br>Oxidation: 1 | WUP:QUP 1.23<br>QU:MU 1.45 |

# Detailed Protein Report

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**Protein 1517:** **PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 isoform X9 [Homo sapiens]**

**Accession:** gi|530380539
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 11.3
**MW [kDa]:** 56.5
**pI:** 9.0
**Sequence Coverage [%]:** 2.8
**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MPALACLRRL CRHVSPQAVL FLLFIFCLFS VFISAYYLYG WKRGLEPSAD APEPDCGDPP PVAPSRLLPL KPVQAATPSR
        90        100        110        120        130        140        150        160
TDPLVLVFVE SLYSQLGQEV VAILESSRFK YRTEIAPGKG DMPTLTDKGR GRFALIIYEN ILKYVNLDAW NRELLDKYCV
       170        180        190        200        210        220        230        240
AYGVGIIGFF KANENSLLSA QLKGFPLFLH SNLGLKDCSI NPKSPLLYVT RPSEVEKGVL PGEDWTVFQS NHSTYEPVLL
       250        260        270        280        290        300        310        320
AKTRSSESIP HLGADAGLHA ALHATVVQDL GLHDGIQRVL FGNNLNFWLH KLVFVDAVAF LTGKRLSLPL DRYILVDIDD
       330        340        350        360        370        380        390        400
IFVGKEGTRM KVEDVKALFD TQNELRAHIP NFTFNLGYSG KFFHTGTNAE DAGDDLLLSY VKEFWWFPHM WSHMQPHLFH
       410        420        430        440        450        460        470        480
NQSVLAEQMA LNKKFAVVRA WHSHRHGVCS GAPPLGRVPR ARAAVRGLEA GVEHPRDQHG GVPPPEASPL PPWLHPQWHH
       490        500        510
GSPTADLRPL HTHHLLQRVP WRLQ
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 35 | 1 | 731.3198 | -109.15 | 2 | 30.3 | 11.3 | 1 | 443-456 | R.AAVRGLEAGVEHPR.D | |

## Protein 1518: 39S ribosomal protein L18, mitochondrial [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21265080 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 20.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.6 |
| | | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MALRSRFWGL | FSVCRNPGCR | FAALSTSSEP | AAKPEVDPVE | NEAVAPEFTN | RNPRNLELLS | VARKERGWRT | VFPSREFWHR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LRVIRTQHHV | EALVEHQNGK | VVVSASTREW | AIKKHLYSTR | NVVACESIGR | VLAQRCLEAG | INFMVYQPTP | WEAASDSMKR |
| 170 | 180 | 190 | | | | | |
| LQSAMTEGGV | VLREPQRIYE | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 373 | 1 | 524.1226 | -273.97 | 2 | 33.3 | 11.3 | 0 | 121-130 | R.NVVACESIGR.V | |

## Protein 1519: CD109 antigen isoform 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|227430301 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 159.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQGPPLLTAA | HLLCVCTAAL | AVAPGPRFLV | TAPGIIRPGG | NVTIGVELLE | HCPSQVTVKA | ELLKTASNLT | VSVLEAEGVF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EKGSFKTLTL | PSLPLNSADE | IYELRVTGRT | QDEILFSNST | RLSFETKRIS | VFIQTDKALY | KPKQEVKFRI | VTLFSDFKPY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KTSLNILIKD | PKSNLIQQWL | SQQSDLGVIS | KTFQLSSHPI | LGDWSIQVQV | NDQTYYQSFQ | VSEYVLPKFE | VTLQTPLYCS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MNSKHLNGTI | TAKYTYGKPV | KGDVTLTFLP | LSFWGKKKNI | TKTFKINGSA | NFSFNDEEMK | NVMDSSNGLS | EYLDLSSPGP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VEILTTVTES | VTGISRNVST | NVFFKQHDYI | IEFFDYTTVL | KPSLNFTATV | KVTRADGNQL | TLEERRNNVV | ITVTQRNYTE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YWSGSNSGNQ | KMEAVQKINY | TVPQSGTFKI | EFPILEDSSE | LQLKAYFLGS | KSSMAVHSLF | KSPSKTYIQL | KTRDENIKVG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SPFELVVSGN | KRLKELSYMV | VSRGQLVAVG | KQNSTMFSLT | PENSWTPKAC | VIVYYIEDDG | EIISDVLKIP | VQLVFKNKIK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LYWSKVKAEP | SEKVSLRISV | TQPDSIVGIV | AVDKSVNLMN | ASNDITMENV | VHELELYNTG | YYLGMFMNSF | AVFQECGLWV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LTDANLTKDY | IDGVYDNAEY | AERFMEENEG | HIVDIHDFSL | GSSPHVRKHF | PETWIWLDTN | MGYRIYQEFE | VTVPDSITSW |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VATGFVISED | LGLGLTTTPV | ELQAFQPFFI | FLNLPYSVIR | GEEFALEITI | FNYLKDATEV | KVIIEKSDKF | DILMTSNEIN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ATGHQQTLLV | PSEDGATVLF | PIRPTHLGEI | PITVTALSPT | ASDAVTQMIL | VKAEGIEKSY | SQSILLDLTD | NRLQSTLKTL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SFSFPPNTVT | GSERVQITAI | GDVLGPSING | LASLIRMPYG | CGEQNMINFA | PNIYILDYLT | KKKQLTDNLK | EKALSFMRQG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| YQRELLYQRE | DGSFSAFGNY | DPSGSTWLSA | FVLRCFLEAD | PYIDIDQNVL | HRTYTWLKGH | QKSNGEFWDP | GRVIHSELQG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GNKSPVTLTA | YIVTSLLGYR | KYQPNIDVQE | SIHFLESEFS | RGISDNYTLA | LITYALSSVG | SPKAKEALNM | LTWRAEQEGG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| MQFWVSSESK | LSDSWQPRSL | DIEVAAYALL | SHFLQFQTSE | GIPIMRWLSR | QRNSLGGFAS | TQDTTVALKA | LSEFAALMNT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| ERTNIQVTVT | GPSSPSPLAV | VQPTAVNISA | NGFGFAICQL | NVVYNVKASG | SSRRRRSIQN | QEAFDLDVAV | KENKDDLNHV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DLNVCTSFSG | PGRSGMALME | VNLLSGFMVP | SEAISLSETV | KKVEYDHGKL | NLYLDSVNET | QFCVNIPAVR | NFKVSNTQDA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | |
| SVSIVDYYEP | RRQAVRSYNS | EVKLSSCDLC | SDVQGCRPCE | DGASGSHHHS | SVIFIFCFKL | LYFMELWL | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1508 | 2 | 705.9840 | -55.85 | 3 | 47.2 | 11.3 | 1 | 110-127 | R.TQDEILFSNSTRLSFETK.R | |

# Detailed Protein Report

## Protein 1520: PREDICTED: transmembrane channel-like protein 6 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530411463 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 64.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPWRYALKRI | GGQFGSSVLS | YFLFLKTLLA | FNALLLLLLV | AFIMGPQVAF | PPALPGPAPV | CTGLELLTGA | GCFTHTVMYY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GHYSNATLNQ | PCGSPLDGSQ | CTPRVGGLPY | NMPLAYLSTV | GVSFFITCIT | LVYSMAHSFG | ESYRVGSTSG | IHAITVFCSW |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DYKVTQKRAS | RLQQDNIRTR | LKELLAEWQL | RHSPRSVCGR | LRQAAVLGLV | WLLCLGTALG | CAVAVHVFSE | FMIQSPEAAG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QEAVLLVLPL | VVGLLNLGAP | YLCRVLAALE | PHDSPVLEVY | VAICRNLILK | LAILGTLCYH | WLGRRVGVLQ | GQCWEDFVGQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ELYRFLVMDF | VLMLLDTLFG | ELVWRIISEK | KLKRRRKPEF | DIARNVLELI | YGQTLTWLGV | LFSPLLPAVQ | IIKLLLVFYV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KKTSLLANCQ | APRRPWLASH | MSTVFLTLLC | FPAFLGAAVF | LCYAVWQVKP | SSTCGPFRTL | DTMYEAGRVW | VRHLEAAGPR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VSWLPWVHRY | LMENTFFVFL | VSALLLAVIY | LNIQVVRGQR | KVICLLKEQI | SNEGEDKIFL | INKLHSIYER | KEREERSRVG |
| 570 | 580 | | | | | | |
| TTEEAAAPPA | LLTDEQDA | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 300 | 1 | 646.8066 | -31.67 | 4 | 33.4 | 11.3 | 1 | 145-167 | R.VGSTSGIHAITVFCSWDYKVTQK.R | Carbamidomethyl: 14 |

# Detailed Protein Report

## Protein 1521: PREDICTED: mitochondrial sodium/hydrogen exchanger 9B2 isoform X6 [Homo sapiens]

**Accession:** gi|578808778

**Database:** refseq_human(refseq_human_20140103.fasta)

**Database Date:** 2015-11-30

**Modification(s):** Carbamidomethyl

**Score:** 11.3

**MW [kDa]:** 45.1

**pI:** 8.9

**Sequence Coverage [%]:** 3.1

**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGDEDKRITY | EDSEPSTGMN | YTPSMHQEAQ | EETVMKLKGI | DANEPTEGSI | LLKSSEKKLQ | ETPTEANHVQ | RLRQMLACPP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HGLLDRVITN | GMLLAGFLIR | NIPVINDNVQ | IKHKWSSSLR | SIALSIILVR | AGLGLDSKAL | KKLKGVCVRL | SMGPCIVEAC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TSALLAHYLL | GLPWQWGFIL | GFVLGAVSPA | VVVPSMLLLQ | GGGYGVEKGV | PTLLMAAGSF | DDILAITGFN | TCLGIAFSTG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| STVFNVLRGV | LEVVIGVATG | SVLGFFIQYF | PSRDQDKLVC | KRTFLVLGLS | VLAVFSSVHF | GFPGSGGLCT | LVMAFLAGMG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WTSEKAEVEK | IIAVAWDIFQ | PLLFGLIGAE | VSIASLRPET | VGCNRICGFG | HSKVTWRETI | RRLWNGCVDS | GIFVHPHHSP |
| 410 | 420 | | | | | | |
| NWKSAYWFTG | PQASAES | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2407 | 1 | 754.4199 | 54.17 | 2 | 58.4 | 11.3 | 0 | 74-86 | R.QMLACPPHGLLDR.V | Carbamidomethyl: 5 |

# Detailed Protein Report

## Protein 1522: PREDICTED: uncharacterized protein C9orf84 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578817110 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 127.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.8 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFSALKYHAI | DYLYENVVRK | KFYRDALLLR | IPSCLYQDES | YHVAVTDNKF | RRPWTRVSAV | SVPGMTDTSV | LDQWKASFFV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EDFLEKKTIT | RMVTQINCEF | EEVVPSSNPD | SQIEVEEVSL | YTHMDYNEVF | TPVSCLEKCS | ALQNQNQDLF | IDDKGILFVS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SRKHLPTLPT | LLSRLKLFLV | KDPLLDFKGQ | IFTEANFSRE | CFSLQETLEA | FVKEDFCMDK | VNFCQEKLED | TICLNEPSSF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LIEYEFLIPP | SLKPEIDIPS | LSELKELLNP | VPEIINYVDE | KEKLFERDLT | NKHGIEDIGD | IKFSSTEILT | IQSQSEPEEC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SKPGELEMPL | TPLFLTCQHS | SVNSLRTELQ | TFPLSPVCKI | NLLTAEESAN | EYYMMWQLER | CRSPLNPFLL | TVPRIQEPHS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QYSVTDLKKI | FSVKEESLVI | NLEKAEWWKQ | AGLNLKMMET | LEHLNTYLCH | DNLSSNDTKI | EIFLPTKVLQ | LESCLEHKSH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SSPIALIDEK | STNAHLSLPQ | KSPSLAKEVP | DLCFSDDYFS | DKGAAKEEKP | KNDQEPVNRI | IQKKENNDHF | ELDCTGPSIK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SPSSSIIKKA | SFEHGKKQEN | DLDLLSDFIM | LRNKYKTCTS | KTEVTNSDEK | HDKEACSLTL | QEESPIVHIN | KTLEEINQER |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GTDSVIEIQA | SDSQCQAFCL | LEAAASPILK | NLVSLCTLPT | ANWKFATVIF | DQTRFLLKEQ | EKVVSDAVRQ | GTIDEREMTF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KHAALLHLLV | TIRDVLLTCS | LDTALGYLSK | AKDIYNSILG | PYLGDIWRQL | EIVQFIRGKK | PETNYKIQEL | QCQILSWMQS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QQQIKVLIII | RMDSDGEKHF | LIKILNKIEG | LTLTVLHSNE | RKDFLESEGV | LRGTSSCVVV | HNQYIGADFP | WSNFSFVVEY |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| NYVEDSCWTK | HCKELNIPYM | AFKVILPDTV | LERSTLLDRF | GGFLLEIQIP | YVFFASEGLL | NTPDILQLLE | SNYNISLVER |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GCSESLKLFG | SSECYVVVTI | DEHTAIILQD | LEELNYEKAS | DNIIMRLMAL | SLQYRYCWII | LYTKETLNSE | YLLTEKTLHH |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LALIYAALVS | FGLNSEELDV | KLIIAPGVEA | TALIIRQIAD | HSLMTSKRDP | HEWLDKSWLK | VSPSEEEMYL | LVE |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1652 | 1 | 911.3660 | -99.01 | 2 | 50.9 | 11.3 | 0 | 578-592 | K.QENDLDLLSDFIMLR.N | |

# Detailed Protein Report

## Protein 1523: short-chain dehydrogenase/reductase family 42E member 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|116268111 | **Score:** | 11.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 44.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.2 |
| | | **Sequence Coverage [%]:** | 4.8 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530424544 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: short-chain dehydrogenase/reductase family 42E member 1 isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDPKRSQKES | VLITGGSGYF | GFRLGCALNQ | NGVHVILFDI | SSPAQTIPEG | IKFIQGDIRH | LSDVEKAFQD | ADVTCVFHIA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SYGMSGREQL | NRNLIKEVNV | RGTDNILQVC | QRRRVPRLVY | TSTFNVIFGG | QVIRNGDESL | PYLPLHLHPD | HYSRTKSIAE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QKVLEANATP | LDRGDGVLRT | CALRPAGIYG | PGEQRHLPRI | VSYIEKGLFK | FVYGDPRSLV | EFVHVDNLVQ | AHILASEALR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ADKGHIASGQ | PYFISDGRPV | NNFEFFRPLV | EGLGYTFPST | RLPLTLVYCF | AFLTEMVHFI | LGRLYNFQPF | LTRTEVYKTG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VTHYFSLEKA | KKELGYKAQP | FDLQEAVEWF | KAHGHGRSSG | SRDSECFVWD | GLLVFLLIIA | VLMWLPSSVI | LSL |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2676 | 1 | 1045.0263 | -17.77 | 2 | 63.6 | 11.3 | 2 | 5-23 | K.RSQKESVLITGGSGYFGFR.L | |

# Detailed Protein Report

## Protein 1524: arginase-2, mitochondrial precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4502215 | **Score:** | 11.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 4.5 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSLRGSLSRL LQTRVHSILK KSVHSVAVIG APFSQGQKRK GVEHGPAAIR EAGLMKRLSS LGCHLKDFGD LSFTPVPKDD
        90        100        110        120        130        140        150        160
LYNNLIVNPR SVGLANQELA EVVSRAVSDG YSCVTLGGDH SLAIGTISGH ARHCPDLCVV WVDAHADINT PLTTSSGNLH
       170        180        190        200        210        220        230        240
GQPVSFLLRE LQDKVPQLPG FSWIKPCISS ASIVYIGLRD VDPPEHFILK NYDIQYFSMR DIDRLGIQKV MERTFDLLIG
       250        260        270        280        290        300        310        320
KRQRPIHLSF DIDAFDPTLA PATGTPVVGG LTYREGMYIA EEIHNTGLLS ALDLVEVNPQ LATSEEEAKT TANLAVDVIA
       330        340        350        360
SSFGQTREGG HIVYDQLPTP SSPDESENQA RVRI
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 812 | 1 | 908.4359 | -50.77 | 2 | 40.2 | 11.2 | 2 | 51-66 | R.EAGLMKRLSSLGCHLK.D | Carbamidomethyl: 13;<br>Oxidation: 5 |

# Detailed Protein Report

## Protein 1525: PREDICTED: serine/threonine-protein kinase TAO3 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578823854 | **Score:** | 11.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 101.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.3 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRKGVLKDPE | IADLFYKDDP | EELFIGLHEI | GHGSFGAVYF | ATNAHTSEVV | AIKKMSYSGK | QTHEKWQDIL | KEVKFLRQLK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HPNTIEYKGC | YLKEHTAWLV | MEYCLGSASD | LLEVHKKPLQ | EVEIAAITHG | ALHGLAYLHS | HALIHRDIKA | GNILLTEPGQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VKLADFGSAS | MASPANSFVG | TPYWMAPEVI | LAMDEGQYDG | KVDIWSLGIT | CIELAERKPP | LFNMNAMSAL | YHIAQNDSPT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LQSNEWTDSF | RRFVDYCLQK | IPQERPTSAE | LLRHDFVRRD | RPLRVLIDLI | QRTKDAVREL | DNLQYRKMKK | ILFQETRNGP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LNESQEDEED | SEHGTSLNRE | MDSLGSNHSI | PSMSVSTGSQ | SSSVNSMQEV | MDESSSELVM | MHDDESTINS | SSSVVHKKVG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FLVPSTEDHV | FIRDEAGHGD | PRPEPRPTQS | VQSQALHYRN | RERFATIKSA | SLVTRQIHEH | EQENELREQM | SGYKRMRRQH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QKQLIALENK | LKAEMDEHRL | KLQKEVETHA | NNSSIELEKL | AKKQVAIIEK | EAKVAAADEK | KFQQQILAQQ | KKDLTTFLES |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QKKQYKICKE | KIKEEMNEDH | STPKKEKQER | ISKHKENLQH | TQAEEEAHLL | TQQRLYYDKN | CRFFKRKIMI | KRHEVEQQNI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| REELNKKRTQ | KEMEHAMLIR | HDESTRELEY | RQLHTLQKLR | MDLIRLQHQT | ELENQLEYNK | RRERELHRKH | VMELRQQPKN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LKAMEMQIKK | QFQDTCKVQT | KQYKALKNHQ | LEVTPKNEHK | TILKTLKDEQ | TRKLAILAEQ | YEQSINEMMA | SQALRLDEAQ |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| EAECQALRLQ | LQQEMELLNA | YQSKIKMQTE | AQHERELQKL | EQRVSLRRAH | LEQKETLNVP | SQRNDVGCWG | G |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1644 | 1 | 803.6077 | 180.34 | 2 | 50.3 | 11.2 | 2 | 478-490 | R.RQHQKQLIALENK.L | |

# Detailed Protein Report

## Protein 1526: PREDICTED: zinc finger protein 513 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530367236 | **Score:** | 11.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQTHSGEKPF | RCGRCPYASA | QLVNLTRHTR | THTGEKPYRC | PHCPFACSSL | GNLRRHQRTH | AGPPTPPCPT | CGFRCCTPRP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ARPPSPTEQE | GAVPRRPEDA | LLLPDLSLHV | PPGGASFLPD | CGQLRGEGEG | LCGTGSEPLP | ELLFPWTCRG | CGQELEEGEG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SRLGAAMCGR | CMRGEAGGGA | SGGPQGPSDK | GFACSLCPFA | THYPNHLARH | MKTHSGEKPF | RCARCPYASA | HLDNLKRHQR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VHTGEKPYKC | PLCPYACGNL | ANLKRHGRIH | SGDKPFRCSL | CNYSCNQSMN | LKRHMLRHTG | EKPFRCATCA | YTTGHWDNYK |
| 330 | 340 | 350 | 360 | 370 | 380 | | |
| RHQKVHGHGG | AGGPGLSASE | GWAPPHSPPS | VLSSRGPPAL | GTAGSRAVHT | DSS | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1243 | 1 | 715.1105 | 125.80 | 3 | 43.8 | 11.2 | 2 | 250-268 | K.CPLCPYACGNLANLKRHGR.I | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 1527: caldesmon isoform 5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|15149465 | **Score:** | 11.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 61.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLGGSGSHGR | RSLAALSQIA | YQRNDDDEEE | AARERRRRAR | QERLRQKQEE | ESLGQVTDQV | EVNAQNSVPD | EEAKTTTTNT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QVEGDDEAAF | LERLARREER | RQKRLQEALE | RQKEFDPTIT | DASLSLPSRR | MQNDTAENET | TEKEEKSESR | QERYEIEETE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TVTKSYQKND | WRDAEENKKE | DKEKEEEEEE | KPKRGSIGEN | QIKDEKIKKD | KEPKEEVKSF | MDRKKGFTEV | KSQNGEFMTH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KLKHTENTFS | RPGGRASVDT | KEAEGAPQVE | AGKRLEELRR | RRGETESEEF | EKLKQKQQEA | ALELEELKKK | REERRKVLEE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EEQRRKQEEA | DRKLREEEEK | RRLKEEIERR | RAEAAEKRQK | MPEDGLSDDK | KPFKCFTPKG | SSLKIEERAE | FLNKSVQKSS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GVKSTHQAAI | VSKIDSRLEQ | YTSAIEGTKS | AKPTKPAASD | LPVPAEGVRN | IKSMWEKGNV | FSSPTAAGTP | NKETAGLKVG |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| VSSRINEWLT | KTPDGNKSPA | PKPSDLRPGD | VSSKRNLWEK | QSVDKVTSPT | KV | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1301 | 1 | 829.0598 | 117.96 | 2 | 46.4 | 11.2 | 2 | 297-310 | K.QQEAALELEELKKK.R | |

# Detailed Protein Report

## Protein 1528: matrin-3 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|533112484 | **Score:** | 11.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.15 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGDPFMLQQS | TNPAPGILGP | PPPSFHLGGP | AVGPRGNLGA | GNGNLQGPRH | MQKGRVETSR | VVHIMDFQRG | KNLRYQLLQL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VEPFGVISNH | LILNKINEAF | IEMATTEDAQ | AAVDYYTTTP | ALVFGKPVRV | HLSQKYKRIK | KPEGKPDQKF | DQKQELGRVI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HLSNLPHSGY | SDSAVLKLAE | PYGKIKNYIL | MRMKSQAFIE | METREDAMAM | VDHCLKKALW | FQGRCVKVDL | SEKYKKLVLR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IPNRGIDLLK | KDKSRKRSYS | PDGKESPSDK | KSKTDGSQKT | ESSTEGKEQE | EKSGEDGEKD | TKDDQTEQEP | NMLLESEDEL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LVDEEEAAAL | LESGSSVGDE | TDLANLGDVA | SDGKKEPSDK | AVKKDGSASA | AAKKKLKKVD | KIEELDQENE | AALENGIKNE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ENTEPGAESS | ENADDPNKDT | SENADGQSDE | NKDDYTIPDE | YRIGPYQPNV | PVGIDYVIPK | TGFYCKLCSL | FYTNEEVAKN |
| 490 | 500 | 510 | | | | | |
| THCSSLPHYQ | KLKKFLNKLA | EERRQKKET | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2783 | 1 | 973.5180 | 13.43 | 2 | 65.2 | 11.2 | 2 | 54-69 | K.GRVETSRVVHIMDFQR.G | Oxidation: 12 | WUP:QUP 0.15 |

# Detailed Protein Report

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## Protein 1529: fatty aldehyde dehydrogenase isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|73466520 | **Score:** | 11.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MELEVRRVRQ | AFLSGRSRPL | RFRLQQLEAL | RRMVQEREKD | ILTAIAADLC | KSEFNVYSQE | VITVLGEIDF | MLENLPEWVT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AKPVKKNVLT | MLDEAYIQPQ | PLGVVLIIGA | WNYPFVLTIQ | PLIGAIAAGN | AVIIKPSELS | ENTAKILAKL | LPQYLDQDLY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IVINGGVEET | TELLKQRFDH | IFYTGNTAVG | KIVMEAAAKH | LTPVTLELGG | KSPCYIDKDC | DLDIVCRRIT | WGKYMNCGQT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CIAPDYILCE | ASLQNQIVWK | IKETVKEFYG | ENIKESPDYE | RIINLRHFKR | ILSLLEGQKI | AFGGETDEAT | RYIAPTVLTD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VDPKTKVMQE | EIFGPILPIV | PVKNVDEAIN | FINEREKPLA | LYVFSHNHKL | IKRMIDETSS | GGVTGNDVIM | HFTLNSFPFG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GVGSSGMGAY | HGKHSFDTFS | HQRPCLLKSL | KREGANKLRY | PPNSQSKVDW | GKFFLLKRFN | KEKLGLLLLT | FLGIVAAVLV |
| 490 | 500 | 510 | | | | | |
| KKYQAVLRRK | ALLIFLVVHR | LRWSSKQR | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1203 | 1 | 661.1025 | -12.99 | 3 | 44.6 | 11.2 | 1 | 464-482 | K.LGLLLLTFLGIVAAVLVKK.Y | |

# Detailed Protein Report

**Protein 1530:** **PREDICTED: NACHT, LRR and PYD domains-containing protein 9 isoform X1 [Homo sapiens]**

**Accession:** gi|530416403
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 11.2
**MW [kDa]:** 102.4
**pI:** 6.4
**Sequence Coverage [%]:** 1.3
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRNKLNPYRK | HMKETFQLIW | EKETCLHVPE | HFYKETMKNE | YKELNDAYTA | AARRHTVVLE | GPDGIGKTTL | LRKVMLDWAE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GNLWKDRFTF | VFFLNVCEMN | GIAETSLLEL | LSRDWPESSE | KIEDIFSQPE | RILFIMDGFE | QLKFNLQLKA | DLSDDWRQRQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PMPIILSSLL | QKKMLPESSL | LIALGKLAMQ | KHYFMLRHPK | LIKLLGFSES | EKKSYFSYFF | GEKSKALKVF | NFVRDNGPLF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ILCHNPFTCW | LVCTCVKQRL | ERGEDLEINS | QNTTYLYASF | LTTVFKAGSQ | SFPPKVNRAR | LKSLCALAAE | GIWTYTFVFS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HGDLRRNGLS | ESEGVMWVGM | RLLQRRGDCF | AFMHLCIQEF | CAAMFYLLKR | PKDDPNPAIG | SITQLVRASV | VQPQTLLTQV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GIFMFGISTE | EIVSMLETSF | GFPLSKDLKQ | EITQCLESLS | QCEADREAIA | FQELFIGLFE | TQEKEFVTKV | MNFFEEVFIY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IGNIEHLVIA | SFCLKHCQHL | TTLRMCVENI | FPDDSGCISD | YNEKLVYWRE | LCSMFITNKN | FQILDMENTS | LDDPSLAILC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KALAQPVCKL | RKLIFTSVYF | GHDSELFKAV | LHNPHLKLLS | LYGTSLSQSD | IRHLCETLKH | PMCKIEELIL | GKCDISSEVC |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EDIASVLACN | SKLKHLSLVE | NPLRDEGMTL | LCEALKHSHC | ALERLMLMYC | CLTSVSCDSI | SEVLLCSKSL | SLLDLGSNAL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EDNGVASLCA | ALKHPGCSIR | ELWLMGCFLT | SDSCKDIAAV | LICNGKLKTL | KLGHNEIGDT | GVRQLCAALQ | HPHCKLECLG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LQTCPITRAC | CDDIAAALIA | CKTLRSLNLD | WIALDADAVV | VLCEALSHPD | CALQMLGNCQ | KSLGDTVAPG | ENHCSIKHLL |
| 890 | 900 | 910 | | | | | |
| LTLPINMQRQ | LRLQKGFWNG | LRS | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1989 | 1 | 703.2718 | -104.11 | 2 | 53.2 | 11.2 | 0 | 784-795 | R.QLCAALQHPHCK.L | Carbamidomethyl: 11 |

# Detailed Protein Report

## Protein 1531: mitogen-activated protein kinase 4 [Homo sapiens]

**Accession:** gi|89276769
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 11.2
**MW [kDa]:** 65.9
**pI:** 5.1
**Sequence Coverage [%]:** 3.1
**No. of unique Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530413856 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: mitogen-activated protein kinase 4 isoform X2 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAEKGDCIAS | VYGYDLGGRF | VDFQPLGFGV | NGLVLSAVDS | RACRKVAVKK | IALSDARSMK | HALREIKIIR | RLDHDNIVKV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YEVLGPKGTD | LQGELFKFSV | AYIVQEYMET | DLARLLEQGT | LAEEHAKLFM | YQLLRGLKYI | HSANVLHRDL | KPANIFISTE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DLVLKIGDFG | LARIVDQHYS | HKGYLSEGLV | TKWYRSPRLL | LSPNNYTKAI | DMWAAGCILA | EMLTGRMLFA | GAHELEQMQL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ILETIPVIRE | EDKDELLRVM | PSFVSSTWEV | KRPLRKLLPE | VNSEAIDFLE | KILTFNPMDR | LTAEMGLQHP | YMSPYSCPED |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EPTSQHPFRI | EDEIDDIVLM | AANQSQLSNW | DTCSSRYPVS | LSSDLEWRPD | RCQDASEVQR | DPRAGSAPLA | EDVQVDPRKD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SHSSSERFLE | QSHSSMERAF | EADYGRSCDY | KVGSPSYLDK | LLWRDNKPHH | YSEPKLILDL | SHWKQAAGAP | PTATGLADTG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AREDEPASLF | LEIAQWVKST | QGGPEHASPP | ADDPERRLSA | SPPGRPAPVD | GGASPQFDLD | VFISRALKLC | TKPEDLPDNK |
| 570 | 580 | 590 | | | | | |
| LGDLNGACIP | EHPGDLVQTE | AFSKERW | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1554 | 1 | 977.3310 | -137.30 | 2 | 49.1 | 11.2 | 0 | 209-226 | K.AIDMWAAGCILAEMLTGR.M | Oxidation: 4, 14 |

# Detailed Protein Report

## Protein 1532: COP9 signalosome complex subunit 4 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|384367993 | **Score:** | 11.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 4.8 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAAAVRQDLA | QLMNSSGSHK | DLAGKYRQIL | EKAIQLSGAE | QLEALKAFVE | AMVNENVSLV | ISRQLLTDFC | THLPNLPDST |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| AKEIYHFTLE | KIQPRVISFE | EQVASIRQHL | ASIYEKEEDW | RNAAQVLVGI | PLETGQKQYN | VDYKLETYLK | IARLYLEDDD |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| PVQAEAYINR | ASLLQNESTN | EQLQIHYKVC | YARVLDYRRK | FIEAAQRYNE | LSYKTIVHES | ERLEALKHAL | HCTILASAGQ |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| QRSRMLATLF | KDERCQQLAA | YGILEKMYLD | RIIRGNQLQE | FAAMLMPHQK | ATTADGSSIL | DRAVIEHNLL | SASKLYNNIT |
| **330** | **340** | **350** | **360** | | | | |
| FEELGALLEI | PAAKHEKPCQ | RGISRSNHFV | SK | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2784 | 1 | 696.7062 | 37.74 | 3 | 65.2 | 11.2 | 1 | 255-271 | R.CQQLAAYGILEKMYLDR.I | Carbamidomethyl: 1;<br>Oxidation: 13 |

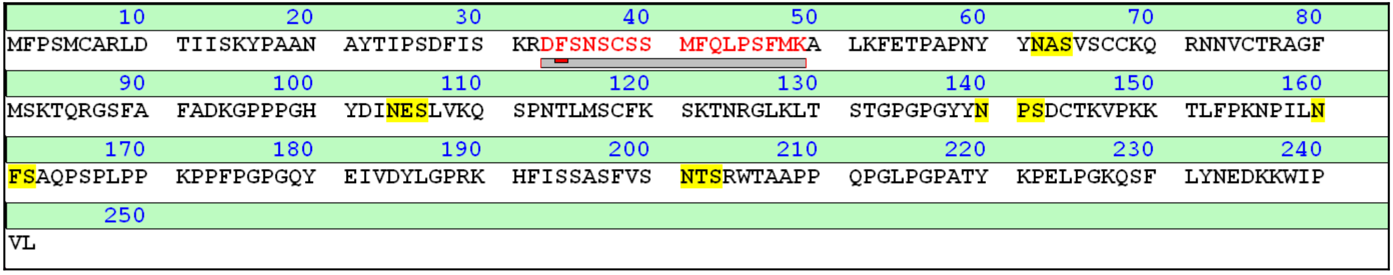
# Detailed Protein Report

## Protein 1533: O(6)-methylguanine-induced apoptosis 2 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|312222707 | **Score:** | 11.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 26.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 7.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530361428 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: O(6)-methylguanine-induced apoptosis 2 isoform X2 [Homo sapiens] |



```
        10         20         30         40         50         60         70         80
MFPSMCARLD TIISKYPAAN AYTIPSDFIS KRDFSNSCSS MFQLPSFMKA LKFETPAPNY YNASVSCCKQ RNNVCTRAGF
        90        100        110        120        130        140        150        160
MSKTQRGSFA FADKGPPPGH YDINESLVKQ SPNTLMSCFK SKTNRGLKLT STGPGPGYYN PSDCTKVPKK TLFPKNPILN
       170        180        190        200        210        220        230        240
FSAQPSPLPP KPPFPGPGQY EIVDYLGPRK HFISSASFVS NTSRWTAAPP QPGLPGPATY KPELPGKQSF LYNEDKKWIP
       250
VL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1822 | 2 | 682.2710 | -22.76 | 3 | 53.1 | 11.2 | 0 | 33-49 | R.DFSNSCSSMFQLPSFMK.A | Carbamidomethyl: 6;<br>Oxidation: 9, 16 |

# Detailed Protein Report

## Protein 1534: zinc finger MYM-type protein 3 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|283837894 | **Score:** | 11.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 151.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530421842 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger MYM-type protein 3 isoform X2 [Homo sapiens] |

```
        10          20          30          40          50          60          70          80
MDPSDFPSPF  DPLTLPEKPL  AGDLPVDMEF  GEDLLESQTA  PTRGWAPPGP  SPSSGALDLL  DTPAGLEKDP  GVLDGATELL

        90         100         110         120         130         140         150         160
GLGGLLYKAP  SPPEVDHGPE  GTLAWDAGDQ  TLEPGPGGQT  PEVVPPDPGA  GANSCSPEGL  LEPLAPDSPI  TLQSPHIEEE

       170         180         190         200         210         220         230         240
ETTSIATARR  GSPGQEEELP  QGQPQSPNAP  PSPSVGETLG  DGINSSQTKP  GGSSPPAHPS  LPGDGLTAKA  SEKPPERKRS

       250         260         270         280         290         300         310         320
ERVRRAEPPK  PEVVDSTESI  PVSDEDSDAM  VDDPNDEDFV  PFRPRRSPRM  SLRSSVSQRA  GRSAVGTKMT  CAHCRTPLQK

       330         340         350         360         370         380         390         400
GQTAYQRKGL  PQLFCSSSCL  TTFSKKPSGK  KTCTFCKKEI  WNTKDSVVAQ  TGSGGSFHEF  CTSVCLSLYE  AQQQRPIPQS

       410         420         430         440         450         460         470         480
GDPADATRCS  ICQKTGEVLH  EVSNGSVVHR  LCSDSCFSKF  RANKGLKTNC  CDQCGAYIYT  KTGSPGPELL  FHEGQQKRFC

       490         500         510         520         530         540         550         560
NTTCLGAYKK  KNTRVYPCVW  CKTLCKNFEM  LSHVDRNGKT  SLFCSLCCTT  SYKVKQAGLT  GPPRPCSFCR  RSLSDPCYYN

       570         580         590         600         610         620         630         640
KVDRTVYQFC  SPSCWTKFQR  TSPEGGIHLS  CHYCHSLFSG  KPEVLDWQDQ  VFQFCCRDCC  EDFKRLRGVV  SQCEHCRQEK

       650         660         670         680         690         700         710         720
LLHEKLRFSG  VEKSFCSEGC  VLLYKQDFTK  KLGLCCITCT  YCSQTCQRGV  TEQLDGSTWD  FCSEDCKSKY  LLWYCKAARC

       730         740         750         760         770         780         790         800
HACKRQGKLL  ETIHWRGQIR  HFCNQQCLLR  FYSQQNQPNL  DTQSGPESLL  NSQSPESKPQ  TPSQTKVENS  NTIPVKTRSA

       810         820         830         840         850         860         870         880
PTAPTPPPPP  PPATPRKNKA  AMCKPLMQNR  GVSCKVEMKS  KGSQTEEWKP  QVIVLPIPVP  IFVPVPMHLY  CQKVPVPFSM

       890         900         910         920         930         940         950         960
PIPVPVPMFL  PTTLESTDKI  VETIEELKVK  IPSNPLEADI  LAMAEMIAEA  EELDKASSDL  CDLVSNQSAE  GLLEDCDLFG

       970         980         990        1000        1010        1020        1030        1040
PARDDVLAMA  VKMANVLDEP  GQDLEADFPK  NPLDINPSVD  FLFDCGLVGP  EDVSTEQDLP  RTMRKGQKRL  VLSESCSRDS

      1050        1060        1070        1080        1090        1100        1110        1120
MSSQPSCTGL  NYSYGVNAWK  CWVQSKYANG  ETSKGDELRF  GPKPMRIKED  ILACSAAELN  YGLAQFVREI  TRPNGERYEP

      1130        1140        1150        1160        1170        1180        1190        1200
DSIYYLCLGI  QQYLLENNRM  VNIFTDLYYL  TFVQELNKSL  STWQPTLLPN  NTVFSRVEEE  HLWECKQLGV  YSPFVLLNTL

      1210        1220        1230        1240        1250        1260        1270        1280
MFFNTKFFGL  QTAEEHMQLS  FTNVVRQSRK  CTTPRGTTKV  VSIRYYAPVR  QRKGRDTGPG  KRKREDEAPI  LEQRENRMNP

      1290        1300        1310        1320        1330        1340        1350        1360
LRCPVKFYEF  YLSKCPESLR  TRNDVFYLQP  ERSCIAESPL  WYSVIPMDRS  MLESMLNRIL  AVREIYEELG  RPGEEDLD
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1640 | 1 | 720.2941 | -66.09 | 2 | 50.8 | 11.2 | 1 | 1067-1079 | K.YANGETSKGDELR.F | |

# Detailed Protein Report

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## Protein 1535: liprin-beta-1 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|312032471 | **Score:** | 11.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 96.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLQQELLSRT | SLETQKLDLM | AEISNLKLKL | TAVEKDRLDY | EDKFRDTEGL | IQEINDLRLK | VSEMDSERLQ | YEKKLKSTKS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LMAKLSSMKI | KVGQMQYEKQ | RMEQKWESLK | DELASLKEQL | EEKESEVKRL | QEKLVCKMKG | EGVEIVDRDI | EVQKMKKAVE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SLMAANEEKD | RKIEDLRQCL | NRYKKMQDTV | VLAQGKDGEY | EELLNSSSIS | SLLDAQGFSD | LEKSPSPTPV | MGSPSCDPFN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TSVPEEFHTT | ILQVSIPSLL | PATVSMETSE | KSKLTPKPET | SFEENDGNII | LGATVDTQLC | DKLLTSSLQK | SSSLGNLKKE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TSDGEKETIQ | KTSEDRAPAE | SRPFGTLPPR | PPGQDTSMDD | NPFGTRKVRS | SFGRGFFKIK | SNKRTASAPN | LAETEKETAE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HLDLAGASSR | PKDSQRNSPF | QIPPPSPDSK | KKSRGIMKLF | GKLRRSQSTT | FNPDDMSEPE | FKRGGTRATA | GPRLGWSRDL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GQSNSDLDMP | FAKWTKEQVC | NWLMEQGLGS | YLNSGKHWIA | SGQTLLQASQ | QDLEKELGIK | HSLHRKKLQL | ALQALGSEEE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TNHGKLDFNW | VTRWLDDIGL | PQYKTQFDEG | RVDGRMLHYM | TVDDLLSLKV | VSVLHHLSIK | RAIQVLRINN | FEPNCLRRRP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SDENTIAPSE | VQKWTNHRVM | EWLRSVDLAE | YAPNLRGSGV | HGGLMVLEPR | FNVETMAQLL | NIPPNKTLLR | RHLATHFNLL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| IGAEAQHQKR | DAMELPDYVL | LTATAKVKPK | KLAFSNFGNL | RKKKQEDGEE | YVCPMELGQA | SGSASKKGFK | PGLDMRLYEE |
| 810 | 820 | 830 | 840 | 850 | 860 | | |
| DDLDRLEQME | DSEGTVRQIG | AFSEGINNLT | HMLKEDDMFK | DFAARSPSAS | ITDEDSNV | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 901 | 1 | 559.2818 | -42.07 | 2 | 39.7 | 11.2 | 0 | 1-9 | -.MLQQELLSR.T | |

# Detailed Protein Report

## Protein 1536: zinc finger protein 341 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|544711270 | **Score:** | 11.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 83.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAKEQSLIRQ | ARVSMRPLLS | SHWISTYITV | PPSPLIQTLV | QGNILVSDDV | LMSAMSAFTS | LDQPMPQGPP | PVQSSLNMHS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VPSYLTQPPP | PPPPPPPLPP | PPPPQPPPPP | PQSLGPPGRP | NPGGNGVVEV | YSAAAPLAGS | GTVEIQALGM | QPYPPLEVPN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QCVEPPVYPT | PTVYSPGKQG | FKPKGPNPAA | PMTSATGGTV | ATFDSPATLK | TRRAKGARGL | PEAAGKPKAQ | KLKCSYCDKS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FTKNFDLQQH | IRSHTGEKPF | QCIACGRAFA | QKSNVKKHMQ | THKVWPPGHS | GGTVSRNSVT | VQVMALNPSR | QEDEESTGLG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QPLPGAPQPQ | ALSTAGEEEG | DKPESKQVVL | IDSSYLCQFC | PSKFSTYFQL | KSHMTQHKNE | QVYKCVVKSC | AQTFPKLDTF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LEHIKSHQEE | LSYRCHLCGK | DFPSLYDLGV | HQYSHSLLPQ | HSPKKDNAVY | KCVKCVNKYS | TPEALEHHLQ | TATHNFPCPH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CQKVFPCERY | LRRHLPTHGS | GGRFKCQVCK | KFFRREHYLK | LHAHIHSGEK | PYKCSVCESA | FNRKDKLKRH | MLIHEPFKKY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KCPFSTHTGC | SKEFNRPDKL | KAHILSHSGM | KLHKCALCSK | SFSRRAHLAE | HQRAHTGNYK | FRCAGCAKGF | SRHKYLKDHR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CRLGPQKDKD | LQTRRPPQRR | AAPRSCGSGG | RKVLTPLPDP | LGLEELKDTG | AGLVPEAVPG | KPPFAEPDAV | LSIVVGGAVG |
| 730 | 740 | 750 | 760 | 770 | | | |
| AETELVVPGH | AEGLGSNLAL | AELQAGAEGP | CAMLAVPVYI | QASE | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2222 | 1 | 1022.6455 | 144.68 | 2 | 58.2 | 11.2 | 0 | 347-363 | K.QVVLIDSSYLCQFCPSK.F | Carbamidomethyl: 11, 14 |

# Detailed Protein Report

**Protein 1537:** **pentatricopeptide repeat domain-containing protein 3, mitochondrial precursor [Homo sapiens]**

**Accession:** gi|38683855
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 11.2
**MW [kDa]:** 78.5
**pI:** 6.0
**Sequence Coverage [%]:** 2.0
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAVVSAVRWL | GLRSRLGQPL | TGRRAGLCEQ | ARSCRFYSGS | ATLSKVEGTD | VTGIEEVVIP | KKKTWDKVAV | LQALASTVNR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DTTAVPYVFQ | DDPYLMPASS | LESRSFLLAK | KSGENVAKFI | INSYPKYFQK | DIAEPHIPCL | MPEYFEPQIK | DISEAALKER |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IELRKVKASV | DMFDQLLQAG | TTVSLETTNS | LLDLLCYYGD | QEPSTDYHFQ | QTGQSEALEE | ENDETSRRKA | GHQFGVTWRA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KNNAERIFSL | MPEKNEHSYC | TMIRGMVKHR | AYEQALNLYT | ELLNNRLHAD | VYTFNALIEA | TVCAINEKFE | EKWSKILELL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RHMVAQKVKP | NLQTFNTILK | CLRRFHVFAR | SPALQVLREM | KAIGIEPSLA | TYHHIIRLFD | QPGDPLKRSS | FIIYDIMNEL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MGKRFSPKDP | DDDKFFQSAM | SICSSLRDLE | LAYQVHGLLK | TGDNWKFIGP | DQHRNFYYSK | FFDLICLMEQ | IDVTLKWYED |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LIPSAYFPHS | QTMIHLLQAL | DVANRLEVIP | KIWKDSKEYG | HTFRSDLREE | ILMLMARDKH | PPELQVAFAD | CAADIKSAYE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SQPIRQTAQD | WPATSLNCIA | ILFLRAGRTQ | EAWKMLGLFR | KHNKIPRSEL | LNELMDSAKV | SNSPSQAIEV | VELASAFSLP |
| 650 | 660 | 670 | 680 | 690 | | | |
| ICEGLTQRVM | SDFAINQEQK | EALSNLTALT | SDSDTDSSSD | SDSDTSEGK | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1587 | 1 | 820.8460 | -154.50 | 2 | 49.6 | 11.2 | 1 | 345-358 | R.FHVFARSPALQVLR.E | |

# Detailed Protein Report

## Protein 1538: PREDICTED: cAMP-dependent protein kinase catalytic subunit PRKX isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530421195 | **Score:** | 11.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 36.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| | | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEAPGLAQAA | AAESDSRKVA | EETPDGAPAL | CPSPEALSPE | PPVYSLQDFD | TLATVGTGTF | GRVHLVKEKT | AKHFFALKVM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SIPDVIRLKQ | EQHVHNEKSV | LKEVSHPFLI | RLFWTWHDER | FLYMLMEYVP | GGELFSYLRN | RGRFSSTTGL | FYSAEIICAI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EYLHSKEIVY | RDLKPENILL | DRDGHIKLTD | FGFAKKLVDR | FPPFFDDNPF | GIYQKILAGK | IDFPRHLDFH | VKDLIKKLLV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VDRTRRLGNM | KNGANDVKHH | RWFRSVDWEA | VPQRKLKPPI | VPKIAGDGDT | SNFETYPEND | WDTAAPVPQK | DLEIFKNF |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1124 | 1 | 593.6547 | -238.34 | 2 | 44.2 | 11.2 | 0 | 265-274 | R.SVDWEAVPQR.K | |

# Detailed Protein Report

## Protein 1539: PREDICTED: ras association domain-containing protein 3 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578823589 | **Score:** | 11.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 26.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.8 |
| | | **Sequence Coverage [%]:** | 4.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSHCAWPAIW | IFKSTLASSA | YSLPTLQDVE | KEKETHSYLS | KEEIKEKVHK | YNLAVTDKLK | MTLNSNGIYT | GFIKVQMELC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KPPQTSPNSG | KLSPSSNGCM | NTLHISSTNT | VGEVIEALLK | KFLVTESPAK | FALYKRCHRE | DQVYACKLSD | REHPLYLRLV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | |
| AGPRTDTLSF | VLREHEIGEW | EAFSLPELQN | FLRILDKEED | EQLQNLKRRY | TAYRQKLEEA | LREVWKPD | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 727 | 2 | 676.1762 | -179.70 | 2 | 38.6 | 11.2 | 1 | 137-147 | R.CHREDQVYACK.L | |

# Detailed Protein Report

## Protein 1540: RNA-binding protein 40 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|40538732 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 58.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.5 |
| | | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.46 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAPEQPLAI | SRGCTSSSSL | SPPRGDRTLL | VRHLPAELTA | EEKEDLLKYF | GAQSVRVLSD | KGRLKHTAFA | TFPNEKAAIK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ALTRLHQLKL | LGHTLVVEFA | KEQDRVHSPC | PTSGSEKKKR | SDDPVEDDKE | KKELGYLTVE | NGIAPNHGLT | FPLNSCLKYM |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YPPPSSTILA | NIVNALASVP | KFYVQVLHLM | NKMNLPTPFG | PITARPPMYE | DYMPLHAPLP | PTSPQPPEEP | PLPDEDEELS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SEESEYESTD | DEDRQRMNKL | MELANLQPKR | PKTIKQRHVR | KKRKIKDMLN | TPLCPSHSSL | HPVLLPSDVF | DQPQPVGNKR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IEFHISTDMP | AAFKKDLEKE | QNCEEKNHDL | PATEVDASNI | GFGKIFPKPN | LDITEEIKED | SDEMPSECIS | RRELEKGRIS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| REEMETLSVF | RSYEPGEPNC | RIYVKNLAKH | VQEKDLKYIF | GRYVDFSSET | QRIMFDIRLM | KEGRMKGQAF | IGLPNEKAAA |
| 490 | 500 | 510 | 520 | | | | |
| KALKEANGYV | LFGKPMVVQF | ARSARPKQDP | KEGKRKC | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1430 | 1 | 955.9503 | -90.67 | 2 | 47.5 | 11.1 | 2 | 257-272 | R.MNKLMELANLQPKRPK.T | | QU:MU 0.46 |

# Detailed Protein Report

## Protein 1541: PREDICTED: zinc finger protein 844 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578833194 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 58.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQEKAHTGEK | LYDCKECGKT | FISHSSIQRH | MIMHNGDGTY | KCKFCGKACP | CLSIYLIHER | VHTGEKPYKC | KQCGKAFSYS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TSLQIHERTH | TGEKPYECKE | CGKAFGSPNS | LYEHRRTHTG | EKPYECKQCG | KAFRWFHSFQ | IHERTHSEEK | AYECTKCGKA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FKCPSYLCRH | EVTHSGKKPC | ECKQCGKALS | YLNFQRHMKM | HTRMRPYKCK | TVEKPLILPV | RFEDMKELTL | ERNLMNASTV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VKPSIVPVPF | TIMKGLTLER | NPMNVSSVVK | PSFLPLPFDI | MKGLTLERNR | MSVSNVGKPS | DLPHTFKCME | GLTLKRNPMN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VSSVVKPSFF | PLPFDIMKGL | TLERNPMSVS | NVGKPSHLPH | TFKCMKGLTL | ESNCMNLNNV | KKPLDLSETF | KFMKRHTLER |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NPIRNMEKHS | TISLPFKYMQ | QCTEDRMPMN | VKSVTKHSYL | PRSFEYMQEH | TLERNPMNVR | NAEKRSIIFL | LCVYTKGCTL |
| 490 | 500 | 510 | | | | | |
| ERNHINVRIV | GKHSVCLVPF | VDIKGLTLE | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 85 | 1 | 695.6045 | -76.90 | 3 | 30.0 | 11.1 | 1 | 364-381 | K.CMKGLTLESNCMNLNNVK.K | Carbamidomethyl: 11;<br>Oxidation: 12 |

# Detailed Protein Report

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**Protein 1542:** **PREDICTED: dedicator of cytokinesis protein 5 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530388077 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 119.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.9 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDLIRPRVSL | VCQIVRVGHM | ELKEGKKHTC | GLRRPFGVAV | MDITDIIHGK | VDDEEKQHFI | PFQQIAMETY | IRQRQLIMSP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LITSHVIGEN | EPLTSVLNKV | IAAKEVNHKG | QGLWVSLKLL | PGDLTQVQKN | FSHLVDRSTA | IARKMGFPEI | ILPGDVRNDI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YVTLIHGEFD | KGKKKTPKNV | EVTMSVHDEE | GKLLEKAIHP | GAGYEGISEY | KSVVYYQVKQ | PCWYETVKVS | IAIEEVTRCH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IRFTFRHRSS | QETRDKSERA | FGVAFVKLMN | PDGTTLQDGR | HDLVVYKGDN | KKMEDAKFYL | TLPGTKMEME | EKELQASKNL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VTFTPSKDST | KDSFQIATLI | CSTKLTQNVD | LLGLLNWRSN | SQNIKHNLKK | LMEVDGGEIV | KFLQDTLDAL | FNIMMEMSDS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ETYDFLVFDA | LVFIISLIGD | IKFQHFNPVL | ETYIYKHFSA | TLAYVKLSKV | LNFYVANADD | SSKTELLFAA | LKALKYLFRF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IIQSRVLYLR | FYGQSKDGDE | FNNSIRQLFL | AFNMLMDRPL | EEAVKIKGAA | LKYLPSIIND | VKLVFDPVEL | SVLFCKFIQS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IPDNQLVRQK | LNCMTKIVES | TLFRQSECRE | VLLPLLTDQL | SGQLDDNSNK | PDHEASSQLL | SNILEVLDRK | DVGATAVHIQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LIMERLLRRI | NRTVIGMNRQ | SPHIGSFVAC | MIALLQQMDD | SHYSHYISTF | KTRQDIIDFL | METFIMFKDL | IGKNVYAKDW |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| MVMNMTQNRV | FLRAINQFAE | VLTRFFMDQA | SFELQLWNNY | FHLAVAFLTH | ESLQLETFSQ | AKRNKIVKKY | GDMRKEIGFR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IRDMWYNLGP | HKIKFIPSMV | GPILEVTLTP | EVELRKATIP | IFFDMMQCEF | NFSGNGNFHM | FENELITKLD | QEVEGGRGDE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QYKVLLEKLL | LEHCRKHKYL | SSSGEVFALL | VSSLLENLLD | YRTIIMQDES | KENRMSCTVN | VLNFYKEKKR | EDIYIRYLYK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LRDLHRDCEN | YTEAAYTLLL | HAELLQVNGS | ESLFQQGGVQ | CPFRLNSIHF | MILMGKNFIP | GISFYTSFFS | SF |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1070 | 1 | 630.9825 | -2.66 | 3 | 41.6 | 11.1 | 0 | 694-708 | R.QDIIDFLMETFIMFK.D | |

# Detailed Protein Report

## Protein 1543: PREDICTED: uncharacterized protein LOC102723865 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578795329 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.7 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578843767 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: uncharacterized protein LOC102723865 [Homo sapiens] |
| gi\|578810067 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: uncharacterized protein LOC102723865 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEIRSSHLPG | CLPPTIPRFL | KRAHQDSWLT | QRDALPAAGL | ARGNPRPPCY | SCRGIPAPRP | CHSGKGVPAP | RINQGEGIPA |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| HPGGSADPLR | SEARSGPQRR | CVPAPGSGTR | RGGGCRQPRS | RRPNPRHRDC | ASRGCRRTAA | LQLGAGAAAA | PVVAAVAAAA |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| RGPAGRRLGL | DARGSRGSLG | QAASRLRRLR | GSRICLDERC | SLAAVSLSVS | VQQEKGEKPA | KHYGADQCTC | CM |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2508 | 1 | 701.6144 | -172.95 | 2 | 61.3 | 11.1 | 0 | 222-232 | K.HYGADQCTCCM.- | Carbamidomethyl: 7, 9, 10 |

# Detailed Protein Report

## Protein 1544: PREDICTED: centrosomal protein of 120 kDa isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530379724 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 107.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVSKSDQLLI | VVSILEGRHF | PKRPKHMLVV | EAKFDGEQLA | TDPVDHTDQP | EFATELAWEI | DRKALHQHRL | QRTPIKLQCF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ALDPVTSAKE | TIGYIVLDLR | TAQETKQAPK | WYQLLSNKYT | KFKSEIQISI | ALETDTKPPV | DSFKAKGAPP | RDGKVPAILA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GLDPRDIVAV | LNEEGGYHQI | GPAEYCTDSF | IMSVTIAFAT | QLEQLIPCTM | KLPERQPEFF | FYYSLLGNDV | TNEPFNDLIN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PNFEPERASV | RIRSSVEILR | VYLALQSKLQ | IHLCCGDQSL | GSTEIPLTGL | LKKGSTEINQ | HPVTVEGAFT | LDPPNRAKQK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LAPIPVELAP | TVGVSVALQR | EGIDSQSPPT | KDDATESEVE | SLQYDKDTKP | NPKASSSVPA | SLAQLVTTSN | ASEVASGQKI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AVPATSHHFC | FSIDLRSIHA | LEIGFPINCI | LRYSYPFFGS | AAPIMTNPPV | EVRKNMEVFL | PQSYCAFDFA | TMPHQLQDTF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LRIPLLVELW | HKDKMSKDLL | LGIARIQLSN | ILSSEKTRFL | GSNGEQCWRQ | TYSESVPVIA | AQGSNNRIAD | LSYTVTLEDY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GLVKMREIFI | SDSSQGVSAV | QQKPSSLPPA | PCPSEIQTEP | RETLEYKAAL | ELEMWKEMQE | DIFENQLKQK | ELAHMQALAE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EWKKRDRERE | SLVKKKVAEY | TILEGKLQKT | LIDLEKREQQ | LASVESELQR | EKKELQSERQ | RNLQELQDSI | RRAKEDCIHQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VELERLKIKQ | LEEDKHRLQQ | QLNDAENKYK | ILEKEFQQFK | DQQNNKPEIR | LQSEINLLTL | EKVELERKLE | SATKSKLHYK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QQWGRALKEL | ARLKQREQES | QMARLKKQQE | ELEQMRLRYL | AAEEKDTVKT | ERQELLDIRN | ELNRLRQQEQ | KQYQDSTEIA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | |
| SGKKDGPHGS | VLEEGLDDYL | TRLIEERDTL | MRTGVYNHED | RIISELDRQI | REILAKSNAS | N | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 605 | 1 | 1106.2245 | 18.50 | 3 | 36.0 | 11.1 | 2 | 617-643 | K.EMQEDIFENQLKQKELAHMQALAEEWK.K | |

# Detailed Protein Report

## Protein 1545: dickkopf-related protein 3 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|40548389 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.4 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 7.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578820415 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: dickkopf-related protein 3 isoform X2 [Homo sapiens] |
| gi\|66346689 | refseq_human (refseq_human_20140103.fasta) | dickkopf-related protein 3 precursor [Homo sapiens] |
| gi\|40548393 | refseq_human (refseq_human_20140103.fasta) | dickkopf-related protein 3 precursor [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQRLGATLLC | LLLAAAVPTA | PAPAPTATSA | PVKPGPALSY | PQEEATLNEM | FREVEELMED | TQHKLRSAVE | EMEAEEAAAK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ASSEVNLANL | PPSYHNETNT | DTKVGNNTIH | VHREIHKITN | NQTGQMVFSE | TVITSVGDEE | GRRSHECIID | EDCGPSMYCQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FASFQYTCQP | CRGQRMLCTR | DSECCGDQLC | VWGHCTKMAT | RGSNGTICDN | QRDCQPGLCC | AFQRGLLFPV | CTPLPVEGEL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CHDPASRLLD | LITWELEPDG | ALDRCPCASG | LLCQPHSHSL | VYVCKPTFVG | SRDQDGEILL | PREVPDEYEV | GSFMEEVRQE |
| 330 | 340 | 350 | 360 | | | | |
| LEDLERSLTE | EMALREPAAA | AAALLGGEEI | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2160 | 1 | 1045.4020 | -30.23 | 3 | 56.9 | 11.1 | 2 | 176-201 | R.MLCTRDSECCGDQLCVWGHCTKMATR.G | Carbamidomethyl: 3, 15, 20; Oxidation: 23 |

# Detailed Protein Report

## Protein 1546: vacuole membrane protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|20070349 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| | | **Sequence Coverage [%]:** | 4.4 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAENGKNCDQ | RRVAMNKEHH | NGNFTDPSSV | NEKKRREREE | RQNIVLWRQP | LITLQYFSLE | ILVILKEWTS | KLWHRQSIVV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SFLLLLAVLI | ATYYVEGVHQ | QYVQRIEKQF | LLYAYWIGLG | ILSSVGLGTG | LHTFLLYLGP | HIASVTLAAY | ECNSVNFPEP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PYPDQIICPD | EEGTEGTISL | WSIISKVRIE | ACMWGIGTAI | GELPPYFMAR | AARLSGAEPD | DEEYQEFEEM | LEHAESAQDF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ASRAKLAVQK | LVQKVGFFGI | LACASIPNPL | FDLAGITCGH | FLVPFWTFFG | ATLIGKAIIK | MHIQKIFVII | TFSKHIVEQM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VAFIGAVPGI | GPSLQKPFQE | YLEAQRQKLH | HKSEMGTPQG | ENWLSWMFEK | LVVVMVCYFI | LSIINSMAQS | YAKRIQQRLN |
| 410 | | | | | | | |
| SEEKTK | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 357 | 1 | 699.2645 | -100.79 | 3 | 33.1 | 11.1 | 2 | 18-35 | K.EHHNGNFTDPSSVNEKKR.R | |

# Detailed Protein Report

## Protein 1547: PREDICTED: microspherule protein 1 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530399608 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 42.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVKDYIEVSK | APSTPVPPSP | APAPGLTKRV | KKSKQPLQVT | KDLGRWKPAD | DLLLINAVLQ | TNDLTSVHLG | VKFSCRFTLR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EVQERWYALL | YDPVISKLAC | QAMRQLHPEA | IAAIQSKALF | SKAEEQLLSK | VGSTSQPTLE | TFQDLLHRHP | DAFYLARTAK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ALQAHWQLMK | QYYLLEDQTV | QPLPKGDQVL | NFSDAEDLID | DSKLKDMRDE | VLEHELMVAD | RRQKREIRQL | EQELHKWQVL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VDSITGMSSP | DFDNQTLAVL | RGRMVRYLMR | SREITLGRAT | KDNQIDVDLS | LEGPAWKISR | KQGVIKLKNN | GDFFIANEGR |
| 330 | 340 | 350 | 360 | 370 | 380 | | |
| RPIYIDGRPV | LCGSKWRLSN | NSVVEIASLR | FVFLINQDLI | ALIRAEAAKI | TPQ | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1814 | 1 | 689.9700 | -142.87 | 3 | 51.0 | 11.1 | 2 | 11-31 | K.APSTPVPPSPAPAPGLTKRVK.K | |

# Detailed Protein Report

## Protein 1548: zinc finger protein 497 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|333033771 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.0 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|333033775 | refseq_huma (refseq_human_20140103.fasta) | zinc finger protein 497 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MESPRGWTLQ | VAPEEGQVLC | NVKTATRGLS | EGAVSGGWGA | WENSTEVPRE | AGDGQRQQAT | LGAADEQGGP | GRELGPADGG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RDGAGPRSEP | ADRALRPSPL | PEEPGCRCGE | CGKAFSQGSY | LLQHRRVHTG | EKPYTCPECG | KAFAWSSNLS | QHQRIHSGEK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PYACRECGKA | FRAHSQLIHH | QETHSGLKPF | RCPDCGKSFG | RSTTLVQHRR | THTGEKPYEC | PECGKAFSWN | SNFLEHRRVH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TGARPHACRD | CGKAFSQSSN | LAEHLKIHAG | ARPHACPDCG | KAFVRVAGLR | QHRRTHSSEK | PFPCAECGKA | FRESSQLLQH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QRTHTGERPF | ECAECGQAFV | MGSYLAEHRR | VHTGEKPHAC | AQCGKAFSQR | SNLLSHRRTH | SGAKPFACAD | CGKAFRGSSG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LAHHRLSHTG | ERPFACAECG | KAFRGSSELR | QHQRLHSGER | PFVCAHCSKA | FVRKSELLSH | RRTHTGERPY | ACGECGKPFS |
| 490 | 500 | | | | | | |
| HRCNLNEHQK | RHGGRAAP | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 244 | 1 | 766.7454 | -154.75 | 2 | 33.1 | 11.1 | 0 | 267-281 | K.IHAGARPHACPDCGK.A | |

# Detailed Protein Report

## Protein 1549: protein shisa-7 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|223633890 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.1 |
| | | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPALLLLVLL | ASSAGQARAR | PSNATSAEPA | GPLPALLAHL | RRLTGALTGG | GGAASPGANG | TRTGPAGGAG | AAARAPPPAE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LCHGYYDVMG | QYDATFNCST | GSYRFCCGTC | HYRFCCEHRH | MRLAQASCSN | YDTPRWATTP | PPLAGGAGGA | GGAGGGPGPG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QAGWLEGGRT | GGAGGRGGEG | PGGSTAYVVC | GVISFALAVG | VGAKVAFSKA | SRAPRAHRDI | NVPRALVDIL | RHQAGPGTRP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DRARSSSLTP | GIGGPDSMPP | RTPKNLYNTV | KTPNLDWRAL | PPPSPSLHYS | TLSCSRSFHN | LSHLPPSYEA | AVKSELNRYS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SLKRLAEKDL | DEAYLKRRPL | ELPRGTLPLH | ALRRPGTGGG | YRMEAWGGPE | ELGLAPAPNP | RRVMSQEHLL | GDGGRSRYEF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TLPRARLVSQ | EHLLLSSPEA | LRQSREHLLS | PPRSPALPPD | PTARASLAAS | HSNLLLGPGG | PPTPLRGLPP | PSSLHAHHHH |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| ALHGSPQPAW | MSDAGGGGGT | LARRPPFQRQ | GTLEQLQFIP | GHHLPQHLRT | ASKNEVTV | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2765 | 1 | 941.9760 | 0.36 | 2 | 63.1 | 11.1 | 1 | 243-261 | R.ARSSSLTPGIGGPDSMPPR.T | |

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# Detailed Protein Report

## Protein 1550: PREDICTED: phospholipid scramblase family member 5 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530374589 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 28.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| | | **Sequence Coverage [%]:** | 8.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MASKDAQNQR | RGLPGFLPGA | PDPDQSLPAS | SNPGNQAWQL | SLPLPSSFLP | TLDLIIIHQQ | VELLGMILGT | ETSNKYEIKN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SLGQRIYFAV | EESICFNRTF | CSTLRSCTLR | ITDNSGREVI | TVNRPLRCNS | CWCPCYLQEL | EIQAPPGTIV | GYVTQKWDPF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LPKFTIQNAN | KEDILKIVGP | CVTCGCFGDV | DFEVKTINEK | LTIGKISKYW | SGFVNDVFTN | ADNFGIHVPA | DLDVTVKAAM |
| 250 | 260 | | | | | | |
| IGACFLFDFM | FFEHSLAGL | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1375 | 1 | 927.1378 | 4.22 | 3 | 47.3 | 11.1 | 2 | 76-98 | K.YEIKNSLGQRIYFAVEESICFNR.T | |

# Detailed Protein Report

## Protein 1551: receptor-type tyrosine-protein kinase FLT3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|121114304 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 112.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPALARDGGQ | LPLLVVFSAM | IFGTITNQDL | PVIKCVLINH | KNNDSSVGKS | SSYPMVSESP | EDLGCALRPQ | SSGTVYEAAA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VEVDVSASIT | LQVLVDAPGN | ISCLWVFKHS | SLNCQPHFDL | QNRGVVSMVI | LKMTETQAGE | YLLFIQSEAT | NYTILFTVSI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RNTLLYTLRR | PYFRKMENQD | ALVCISESVP | EPIVEWVLCD | SQGESCKEES | PAVVKKEEKV | LHELFGTDIR | CCARNELGRE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CTRLFTIDLN | QTPQTTLPQL | FLKVGEPLWI | RCKAVHVNHG | FGLTWELENK | ALEEGNYFEM | STYSTNRTMI | RILFAFVSSV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ARNDTGYYTC | SSSKHPSQSA | LVTIVEKGFI | NATNSSEDYE | IDQYEEFCFS | VRFKAYPQIR | CTWTFSRKSF | PCEQKGLDNG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YSISKFCNHK | HQPGEYIFHA | ENDDAQFTKM | FTLNIRRKPQ | VLAEASASQA | SCFSDGYPLP | SWTWKKCSDK | SPNCTEEITE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GVWNRKANRK | VFGQWVSSST | LNMSEAIKGF | LVKCCAYNSL | GTSCETILLN | SPGPFPFIQD | NISFYATIGV | CLLFIVVLTL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LICHKYKKQF | RYESQLQMVQ | VTGSSDNEYF | YVDFREYEYD | LKWEFPRENL | EFGKVLGSGA | FGKVMNATAY | GISKTGVSIQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VAVKMLKEKA | DSSEREALMS | ELKMMTQLGS | HENIVNLLGA | CTLSGPIYLI | FEYCCYGDLL | NYLRSKREKF | HRTWTEIFKE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| HNFSFYPTFQ | SHPNSSMPGS | REVQIHPDSD | QISGLHGNSF | HSEDEIEYEN | QKRLEEEEDL | NVLTFEDLLC | FAYQVAKGME |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FLEFKSCVHR | DLAARNVLVT | HGKVVKICDF | GLARDIMSDS | NYVVRGNARL | PVKWMAPESL | FEGIYTIKSD | VWSYGILLWE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| IFSLGVNPYP | GIPVDANFYK | LIQNGFKMDQ | PFYATEEIYI | IMQSCWAFDS | RKRPSFPNLT | SFLGCQLADA | EEAMYQNVDG |
| 970 | 980 | 990 | 1000 | | | | |
| RVSECPHTYQ | NRRPFSREMD | LGLLSPQAQV | EDS | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1473 | 1 | 655.3406 | 24.71 | 2 | 46.8 | 11.1 | 2 | 645-655 | K.MLKEKADSSER.E | Oxidation: 1 |

# Detailed Protein Report

## Protein 1552: PREDICTED: HMG domain-containing protein 3 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578810822 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 109.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLPLPAYSVV | ENPTSIKLTT | TYTRRGHGTC | TSPGCSFTYV | TRHKPPKCPT | CGNFLGGKWI | PKEKPAKVKV | ELASGVSSKG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SVVKRNQQPV | TTEQNSSKEN | ASKLTLENSE | AVSQLLNVAP | PREVGEESEW | EEVIISDAHV | LVKEAPGNCG | TAVTKTPVVK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SGVQPEVTLG | TTDNDSPGAD | VPTPSEGTST | SSPLPAPKKP | TGADLLTPGS | RAPELKGRAR | GKPSLLAAAR | PMRAILPAPV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NVGRGSSMGL | PRARQAFSLS | DKTPSVRTCG | LKPSTLKQLG | QPIQQPSGPG | EVKLPSGPSN | RTSQVKVVEV | KPDMFPPYKY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SCTVTLDLGL | ATSRGRGKCK | NPSCSYVYTN | RHKPRICPSC | GVNLAKDRTE | KTTKAIEVSS | PLPDVLNATE | PLSTAQREIQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RQSTLQLLRK | VLQIPENESE | LAEVFALIHE | LNSSRLILSN | VSEETVTIEQ | TSWSNYYESP | STQCLLCSSP | LFKGGQNSLA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GPQECWLLTA | SRLQTVTAQV | KMCLNPHCLA | LHSFIDIYTG | LFNVGNKLLV | SLDLLFAIRN | QIKLGEDPRV | SINVVLKSVQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EQTEKTLTSE | ELSQLQELLC | NGYWAFECLT | VRDYNDMICG | ICGVAPKVEM | AQRSEENVLA | LKSVEFTWPE | FLGSNEVNVE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DFWATMETEV | IEQVAFPASI | PITKFDASVI | APFFPPLMRG | AVVVNTEKDK | NLDVQPVPGS | GSALVRLLQE | GTCKLDEIGS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YSEEKLQHLL | RQCGIPFGAE | DSKDQLCFSL | LALYESVQNG | ARAIRPPRHF | TGGKIYKVCP | HQVVCGSKYL | VRGESARDHV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DLLASSRHWP | PVYVVDMATS | VALCADLCYP | ELTNQMWGRN | QGCFSSPTEP | PVSVSCPELL | DQHYTVDMTE | TEHSIQHPVT |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KTATRRIVHA | GLQPNPGDPS | AGHHSLALCP | ELAPYATILA | SIVDSKPNGV | RQRPIAFDNA | THYYLYNRLM | DFLTSREIVN |
| 970 | 980 | 990 | 1000 | 1010 | | | |
| RQIHDIVQSC | QPGEVVIRDT | LYRLGVAQIK | TETEEEGEEE | EVAAVAE | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1930 | 2 | 682.2633 | -103.38 | 3 | 54.5 | 11.1 | 0 | 474-492 | K.GGQNSLAGPQECWLLTASR.L | Carbamidomethyl: 12 |

# Detailed Protein Report

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## Protein 1553: tyrosine-protein kinase CSK [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4758078 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 50.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| | | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530405396 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: tyrosine-protein kinase CSK isoform X1 [Homo sapiens] |
| gi\|187475373 | refseq_human (refseq_human_20140103.fasta) | tyrosine-protein kinase CSK [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MSAIQAAWPS GTECIAKYNF HGTAEQDLPF CKGDVLTIVA VTKDPNWYKA KNKVGREGII PANYVQKREG VKAGTKLSLM
        90        100        110        120        130        140        150        160
PWFHGKITRE QAERLLYPPE TGLFLVREST NYPGDYTLCV SCDGKVEHYR IMYHASKLSI DEEVYFENLM QLVEHYTSDA
       170        180        190        200        210        220        230        240
DGLCTRLIKP KVMEGTVAAQ DEFYRSGWAL NMKELKLLQT IGKGEFGDVM LGDYRGNKVA VKCIKNDATA QAFLAEASVM
       250        260        270        280        290        300        310        320
TQLRHSNLVQ LLGVIVEEKG GLYIVTEYMA KGSLVDYLRS RGRSVLGGDC LLKFSLDVCE AMEYLEGNNF VHRDLAARNV
       330        340        350        360        370        380        390        400
LVSEDNVAKV SDFGLTKEAS STQDTGKLPV KWTAPEALRE KKFSTKSDVW SFGILLWEIY SFGRVPYPRI PLKDVVPRVE
       410        420        430        440        450        460
KGYKMDAPDG CPPAVYEVMK NCWHLDAAMR PSFLQLREQL EHIKTHELHL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1966 | 2 | 616.2745 | -102.45 | 2 | 54.5 | 11.1 | 0 | 57-67 | R.EGIIPANYVQK.R | |

# Detailed Protein Report

## Protein 1554: PREDICTED: uncharacterized protein LOC102725205, partial [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578845222 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 95.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.90 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.36 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
TLSHTLHPPT HTPNLTHSTH THTTPPTHTP HPTHHSTPLT HSTPHTSHTH STPLTHSTPH SWAAKSLERL LWVVASSPPR

        90        100        110        120        130        140        150        160
RTAVVGRIPG AGMPAGAGGP ACRCPCLSRV GWRDLDAEPS SQEFRQLSLD SHQVAAFQTE MECWARGSGM DATEPLCCDC

       170        180        190        200        210        220        230        240
QTSDLVCWSQ QGHQGPERGA LGSLEEPGLL SAREAWPVSC SSIFLEVSGR RLESRMPPGG AAINISPGDK RTNQSPAGYR

       250        260        270        280        290        300        310        320
GEDKSGKRLM SELWLQVAAA RDGLQDFPGL LVAGRGSSSG DWSERAYGWE LEELMEKRGR VGWSSREALW SGEGEEEPNK

       330        340        350        360        370        380        390        400
EKQQSTWNIS IPPSKAVLEE QPQSPIVPKS GKSVKTFIRN RYEPAKRCEE LICAELIRMN KVTTDSAMGI ADKDLSEELQ

       410        420        430        440        450        460        470        480
HRLQHALASL QVAQGEDLTA DIMYSPSASE PLPFMQCDGE QETGTASPIW LWNLWAGESH PHGVHALATL GWEGPMVNAG

       490        500        510        520        530        540        550        560
EKVQEEEGAP ATGPSCGQHR EGCCGGEDVG VEGCGGGHLL ALGCPSKTLT ARGILPVGGA ASTTSLQEAM FVFRTTLIRA

       570        580        590        600        610        620        630        640
VGCKEQRPLK GEGGAVKDVE SRRCAGLWFR EPCGRQVKME LHKSAGETPG KLKVEYADGG MPEARLWEGT HIFETKVKLS

       650        660        670        680        690        700        710        720
TVIHEAAVQW PSGDIEKTHL SSGLFSELIR GLCSFDMFLP DTVVCWPLPW SAFHPVLLQT MSAPGLSPAL DPLCPQLLAD

       730        740        750        760        770        780        790        800
LGSEKQSCPS REFGWGLAEV PSVSNLCKGG LALQAADGGS GGGVRTPSYY LNECMGITAA LYEHLKTTLS NPSFSKEKES

       810        820        830        840        850        860        870        880
VNFPFSMHEV TGVCHSGGPV FKKNREETVR LSAGGAARQK ELMLYPVVSF PKGLHQLPSF LALIMTISVV TSLLSKESIF

       890
SSCQE
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1138 | 1 | 983.4246 | -85.91 | 2 | 44.4 | 11.1 | 1 | 82-103 | R.<br>TAVVGRIPGAGMPAGAGGPACR.<br>C | | QU:MU 1.90<br>WUP:QUP 1.36 |

# Detailed Protein Report

## Protein 1555: uncharacterized protein CXorf22 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|90963001 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 110.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNTQKGSLTI | NVHRGSLAMS | IQRGSLVPRD | MDSSGRDMQL | RVIPAEVKFL | DTMAGRVYRL | PITVHNICRW | NQKIRFKEPV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KPQFKLMLTS | LDKELASGLQ | MTAMVEYHPD | KDEDTFDRLL | ISIENKTTEI | PLIGLIPSCQ | LEIESVVNFG | TLVANSKVYS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KEITITNHGK | APGIFKAEYH | GQLPILIFPT | SGIVDAKSSM | VIKVDFCADQ | PRIVDEEAIV | ILQGQPEMLL | SIKAHVVEQI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IELLSMSSDR | RLECIHFGPV | FFGSSKIKHA | RVYNNSPEPI | NWVAIIQDDA | VGEELGTDIQ | QRTDIALNNL | TYIRKIKNID |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TTIIISCLPN | EGTLQPYQKT | VITFCFTPKL | MAVGKKDIGP | SYRQDYALFL | RFESVGSKDG | FLRDDDYKTI | KSERFQKVEL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ALTGTGLPVL | LQFDPGPVLN | FKPCFMGERS | EIQCIIKNQC | ELLPVTYHFK | KTANFEIDPE | KGKITGGGMV | DVMCSFVPHQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LGVFKVKQMI | EIIGLVAEED | LQSLSVKSFH | HVYLAFNSIC | KASTKKVVMK | FDPGILPSIR | NPTGKFVVKD | LAKRKNYAPV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AMLQSAMTRT | HNHRSCEEPV | KDMLLAFPND | RAATIRSKDH | HKHFRPIFTK | VPRFNYVNHD | FAYTTFEKQQ | KKLHENYYAM |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| YLKYLRSVRL | QKKQAERERM | YSYDDTDIGL | EPGSGLKSPS | LSEAEIEEEL | SSAANSIRAN | RLLTTRGIAS | QEEESVRRKV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LKGLKSEPST | PQEKHDCSLM | LTPKQIHQVI | VGPSVLNFGN | ICVNSPNTHL | LHVINMLPMH | VLLQLDTDLE | ELQKTNQFSY |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VILPTSSTYI | SMVFDSPTIG | KFWKSFTFTV | NNVPSGHILV | VAVVQPVTLE | LSSNELVLRP | RGFFMKTCFR | GTVRLYNRQN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| CCAQFQWQPV | NTGRGIAFSI | CPAKGTVEAY | SSLECEVTWQ | QGFSSPEEGE | FILHVFQGNA | LKLKCVAHVI | IFLEHGFCFE |
| 970 | 980 | | | | | | |
| GYEFVGYTLV | YIVTYI | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1409 | 1 | 786.4063 | -58.78 | 2 | 47.8 | 11.1 | 1 | 527-540 | K.VVMKFDPGILPSIR.N | |

# Detailed Protein Report

## Protein 1556: alpha-2,8-sialyltransferase 8F precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|54234057 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 44.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 7.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRPGGALLAL | LASLLLLLLL | RLLWCPADAP | GRARILVEES | REATHGTPAA | LRTLRSPATA | VPRATNSTYL | NEKSLQLTEK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CKNLQYGIES | FSNKTKGYSE | NDYLQIITDI | QSCPWKRQAE | EYANFRAKLA | SCCDAVQNFV | VSQNNTPVGT | NMSYEVESKK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EIPIKKNIFH | MFPVSQPFVD | YPYNQCAVVG | NGGILNKSLC | GTEIDKSDFV | FRCNLPPTTG | DVSKDVGSKT | NLVTINPSII |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TLKYGNLKEK | KALFLEDIAT | YGDAFFLLPA | FSFRANTGTS | FKVYYTLEES | KARQKVLFFH | PKYLKDLALF | WRTKGVTAYR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LSTGLMITSV | AVELCKNVKL | YGFWPFSKTV | EDIPVSHHYY | DNKLPKHGFH | QMPKEYSQIL | QLHMKGILKL | QFSKCEVA |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1694 | 1 | 1131.2170 | 33.19 | 3 | 49.5 | 11.1 | 0 | 129-159 | K.LASCCDAVQNFVVSQNNTPVGTNMSYEVESK.K | Carbamidomethyl: 4 |

## Protein 1557: E3 ubiquitin-protein ligase HECW1 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|559098413 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 175.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| | | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLLHLCSVKN | LYQNRFLGLA | AMASPSRNSQ | SRRRCKEPLR | YSYNPDQFHN | MDLRGGPHDG | VTIPRSTSDT | DLVTSDSRST |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LMVSSSYYSI | GHSQDLVIHW | DIKEEVDAGD | WIGMYLIDEV | LSENFLDYKN | RGVNGSHRGQ | IIWKIDASSY | FVEPETKICF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KYYHGVSGAL | RATTPSVTVK | NSAAPIFKSI | GADETVQGQG | SRRLISFSLS | DFQAMGLKKG | MFFNPDPYLK | ISIQPGKHSI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FPALPHHGQE | RRSKIIGNTV | NPIWQAEQFS | FVSLPTDVLE | IEVKDKFAKS | RPIIKRFLGK | LSMPVQRLLE | RHAIGDRVVS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YTLGRRLPTD | HVSGQLQFRF | EITSSIHPDD | EEISLSTEPE | SAQIQDSPMN | NLMESGSGEP | RSEAPESSES | WKPEQLGEGS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VPDGPGNQSI | ELSRPAEEAA | VITEAGDQGM | VSVGPEGAGE | LLAQVQKDIQ | PAPSAEELAE | QLDLGEEASA | LLLEDGEAPA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| STKEEPLEEE | ATTQSRAGRE | EEEKEQEEEG | DVSTLEQGEG | RLQLRASVKR | KSRPCSLPVS | ELETVIASAC | GDPETPRTHY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IRIHTLLHSM | PSAQGGSAAE | EEDGAEEEST | LKDSSEKDGL | SEVDTVAADP | SALEEDREEP | EGATPGTAHP | GHSGGHFPSL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ANGAAQDGDT | HPSTGSESDS | SPRQGGDHSC | EGCDASCCSP | SCYSSSCYST | SCYSSSCYSA | SCYSPSCYNG | NRFASHTRFS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SVDSAKISES | TVFSSQDDEE | EENSAFESVP | DSMQSPELDP | ESTNGAGPWQ | DELAAPSGHV | ERSPEGLESP | VAGPSNRRED |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| WEARIDSHGR | VFYVDHVNRT | TTWQRPTAAA | TPDGMRRSGS | IQQMEQLNRR | YQNIQRTIAT | ERSEEDSGSQ | SCEQAPAGGG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GGGGSDSEAE | SSQSSLDLRR | EGSLSPVNSQ | KITLLLQSPA | VKFITNPEFF | TVLHANYSAY | RVFTSSTCLK | HMILKVRRDA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RNFERYQHNR | DLVNFINMFA | DTRLELPRGW | EIKTDQQGKS | FFVDHNSRAT | TFIDPRIPLQ | NGRLPNHLTH | RQHLQRLRSY |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SAGEASEVSR | NRGASLLARP | GHSLVAAIRS | QHQHESLPLA | YNDKIVAFLR | QPNIFEMLQE | RQPSLARNHT | LREKIHYIRT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EGNHGLEKLS | CDADLVILLS | LFEEEIMSYV | PLQAAFHPGY | SFSPRCSPCS | SPQNSPGLQR | ASARAPSPYR | RDFEAKLRNF |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| YRKLEAKGFG | QGPGKIKLII | RRDHLLEGTF | NQVMAYSRKE | LQRNKLYVTF | VGEEGLDYSG | PSREFFFLLS | QELFNPYYGL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| FEYSANDTYT | VQISPMSAFV | ENHLEWFRFS | GRILGLALIH | QYLLDAFFTR | PFYKALLRLP | CDLSDLEYLD | EEFHQSLQWM |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KDNNITDILD | LTFTVNEEVF | GQVTERELKS | GGANTQVTEK | NKKEYIERMV | KWRVERGVVQ | QTEALVRGFY | EVVDSRLVSV |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| FDARELELVI | AGTAEIDLND | WRNNTEYRGG | YHDGHLVIRW | FWAAVERFNN | EQRLRLLQFV | TGTSSVPYEG | FAALRGSNGL |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | | |
| RRFCIEKWGK | ITSLPRAHTC | FNRLDLPPYP | SYSMLYEKLL | TAVEETSTFG | LE | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1838 | 2 | 731.2905 | -123.49 | 2 | 52.8 | 11.1 | 1 | 1387-1400 | R.ELKSGGANTQVTEK.N | |

# Detailed Protein Report

## Protein 1558: slit homolog 3 protein isoform 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|11321571 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 167.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.50 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.90 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAPGWAGVGA | AVRARLALAL | ALASVLSGPP | AVACPTKCTC | SAASVDCHGL | GLRAVPRGIP | RNAERLDLDR | NNITRITKMD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FAGLKNLRVL | HLEDNQVSVI | ERGAFQDLKQ | LERLRLNKNK | LQVLPELLFQ | STPKLTRLDL | SENQIQGIPR | KAFRGITDVK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NLQLDNNHIS | CIEDGAFRAL | RDLEILTLNN | NNISRILVTS | FNHMPKIRTL | RLHSNHLYCD | CHLAWLSDWL | RQRRTVGQFT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LCMAPVHLRG | FNVADVQKKE | YVCPAPHSEP | PSCNANSISC | PSPCTCSNNI | VDCRGKGLME | IPANLPEGIV | EIRLEQNSIK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AIPAGAFTQY | KKLKRIDISK | NQISDIAPDA | FQGLKSLTSL | VLYGNKITEI | AKGLFDGLVS | LQLLLLNANK | INCLRVNTFQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DLQNLNLLSL | YDNKLQTISK | GLFAPLQSIQ | TLHLAQNPFV | CDCHLKWLAD | YLQDNPIETS | GARCSSPRRL | ANKRISQIKS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KKFRCSGSED | YRSRFSSECF | MDLVCPEKCR | CEGTIVDCSN | QKLVRIPSHL | PEYVTDLRLN | DNEVSVLEAT | GIFKKLPNLR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KINLSNNKIK | EVREGAFDGA | ASVQELMLTG | NQLETVHGRV | FRGLSGLKTL | MLRSNLIGCV | SNDTFAGLSS | VRLLSLYDNR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ITTITPGAFT | TLVSLSTINL | LSNPFNCNCH | LAWLGKWLRK | RRIVSGNPRC | QKPFFLKEIP | IQDVAIQDFT | CDGNEESSCQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LSPRCPEQCT | CMETVVRCSN | KGLRALPRGM | PKDVTELYLE | GNHLTAVPRE | LSALRHLTLI | DLSNNSISML | TNYTFSNMSH |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LSTLILSYNR | LRCIPVHAFN | GLRSLRVLTL | HGNDISSVPE | GSFNDLTSLS | HLALGTNPLH | CDCSLRWLSE | WVKAGYKEPG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| IARCSSPEPM | ADRLLLTTPT | HRFQCKGPVD | INIVAKCNAC | LSSPCKNNGT | CTQDPVELYR | CACPYSYKGK | DCTVPINTCI |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| QNPCQHGGTC | HLSDSHKDGF | SCSCPLGFEG | QRCEINPDDC | EDNDCENNAT | CVDGINNYVC | ICPPNYTGEL | CDEVIDHCVP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ELNLCQHEAK | CIPLDKGFSC | ECVPGYSGKL | CETDNDDCVA | HKCRHGAQCV | DTINGYTCTC | PQGFSGPFCE | HPPPMVLLQT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SPCDQYECQN | GAQCIVVQQE | PTCRCPPGFA | GPRCEKLITV | NFVGKDSYVE | LASAKVRPQA | NISLQVATDK | DNGILLYKGD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| NDPLALELYQ | GHVRLVYDSL | SSPPTTVYSV | ETVNDGQFHS | VELVTLNQTL | NLVVDKGTPK | SLGKLQKQPA | VGINSPLYLG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| GIPTSTGLSA | LRQGTDRPLG | GFHGCIHEVR | INNELQDFKA | LPPQSLGVSP | GCKSCTVCKH | GLCRSVEKDS | VVCECRPGWT |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| GPLCDQEARD | PCLGHRCHHG | KCVATGTSYM | CKCAEGYGGD | LCDNKNDSAN | ACSAFKCHHG | QCHISDQGEP | YCLCQPGFSG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| EHCQQENPCL | GQVVREVIRR | QKGYASCATA | SKVPIMECRG | GCGPQCCQPT | RSKRRKYVFQ | CTDGSSFVEE | VERHLECGCL |
| 1530 | | | | | | | |
| ACS | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 907 | 1 | 547.2124 | -176.66 | 3 | 41.4 | 11.1 | 0 | 1176-1190 | K.VRPQANISLQVATDK.D | | QU:MU 1.50<br>WUP:QUP 0.90 |

# Detailed Protein Report

## Protein 1559: spermatogenesis-associated protein 31D1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|48717285 | **Score:** | 11.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 175.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MENILCFLNS | YTETGLSPDS | HWLDIDPNFI | CLSGLGLFIL | YLFYVVLTLY | SSPTEKNNDI | QKHQGRAKRR | RKGGTFKGFP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DWKSFQREEE | EERKLLSLLK | SFGPPVSCSP | RGQHHDTNHF | RRLLCPDPVC | RVCKRATADI | QQLLSWESLK | DAAPSVSPLA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SSASATESSF | TLASTPSATP | PEDLILSPRP | KASPPPPLIL | SPDLITTLAD | LFSPSPLRDP | LPPQPVSPLD | SKFPIDHSPP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QQLPFPLLPP | HHIERVESSL | QPEASLSLNT | IFSFGSTLCQ | DISQAMNPID | SCARHHGPPI | PSALPPEDCT | VTQSKSSLTI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LKTFPEMLSL | GGSGGSSTSA | PTIKGIDHSH | LASSEFTWWQ | PHAKDSFSSN | FVPSDFMEEL | LTLHSSEAFL | GGHSVANLIE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PVNISFLSHD | ILALLERQVK | KRGDFLMWKE | NGKKPGSFPK | QLRPNYQLNS | SRNMLTSIAV | KHDLAESFPF | WASKGKLEWQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HIHQQPPHSK | CFEDHLEQKY | VQLFWGLPSL | HSESLHPTVL | VQRGHSSMFV | FFNGITNTSI | SHESPVLPPP | QPLSLPSTQP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LPLPQTLPQG | QSPHLTQVKS | LAQPQSPFRA | LLPSPLFLIR | ICGVCFHRPQ | NEARSLLPSE | INHLEWNVLQ | KVQESLWGLP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SVVQKSQEDF | CPPAPNPELV | RKSFKVHVPI | SIIPGDFPLS | SEVRKKLEQH | IRRRLIQRRW | GLPRRIHESL | SLLRPQSKIS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ELSVSERIHG | PLNISLVEGQ | RCNVLKKSAS | SFPRSFHERS | SNMLSMENVG | NYQGYSQETV | PKDHLLHGPE | TSSDKDLRSN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| SERDLETHMM | HLSGNDSGVR | LGQKQLENAL | TVRLSKKFEE | INEGRMPGTV | HSSWHSVKQT | MSLPEKSHSQ | IKHRNLVTLV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SEDHCVDTSQ | EISFLSSNKQ | KMLEAHIKTF | RMRMLWGLPL | KVLESIEIFK | SKADLSTSFS | HFDLPSSATF | ISQGDSKDGV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SKSRSRSTFQ | GEKLGTTSSV | PILDRPHPVS | SPVVQEGQGT | LRRQFSDTDH | DLIETDSKDG | ASTSLRRGTT | DFQSEKLDST |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SSFPILGHSY | LVTSPVNQEK | QGTLRREFSD | TDNDLTESVR | TTEDGRQTFL | PPPHSIVDEV | SQKQTVLASR | CSAELPIMQA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GAGCESWDKR | KSSFHNVDRL | QGSRKTFPVT | NALQSQTRNN | LTTSKSGSCS | LTNVKASTSN | ETEIFPPRIS | VPQDPKSSYL |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| KNQMLSQLKL | VQRKHSQPQS | HFTDMSFALD | NLSSKDLLTN | SQGISSGDMG | TSQVVHVHLE | DSGIRVAQKQ | EPRVPTCVLQ |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| KCQVTNFPPA | VNRVSPVRPK | GGELDGGDAG | LGTSQRRRKS | LPVHNKTSGE | VLGSKSSPTL | KTQPPPENLF | RKWMKTSLQW |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| FNKPSISYEE | QESSWEKGSS | LSSCVQNIGR | VIRAAFTGTT | EAQKIRKDTR | EFLEEKLGHR | HGIDITCPQE | PLSFPVGLGK |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| AQHNPEVHVR | AEPVQGCPCN | YRAPSCKVTR | TKSCSQQAIF | VGQNYPTRIR | QIIDKDRQPQ | KVEAFKGKIL | CQSHPQSMPH |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | | |
| RKPVPHPNPT | CRRQVSLVCP | AVPTSAKSPV | FSDVPFLTGQ | KMLPKHLQGG | KFPPTK | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1691 | 1 | 900.9255 | -88.98 | 2 | 50.9 | 11.1 | 1 | 95-111 | K.LLSLLKSFGPPVSCSPR.G | |

# Detailed Protein Report

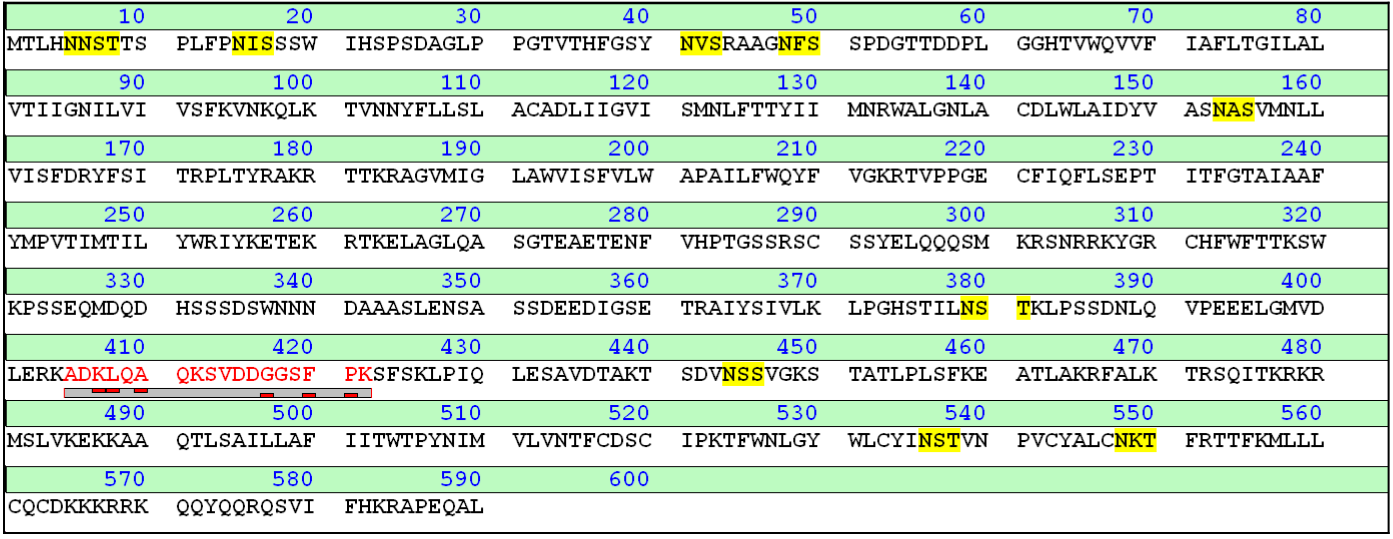
## Protein 1560: muscarinic acetylcholine receptor M3 [Homo sapiens]

**Accession:** gi|4502819
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 11.0
**MW [kDa]:** 66.1
**pI:** 10.0
**Sequence Coverage [%]:** 3.1
**No. of unique Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578802131 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: muscarinic acetylcholine receptor M3 isoform X5 [Homo sapiens] |
| gi\|530366001 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: muscarinic acetylcholine receptor M3 isoform X4 [Homo sapiens] |
| gi\|530365999 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: muscarinic acetylcholine receptor M3 isoform X3 [Homo sapiens] |
| gi\|530365997 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: muscarinic acetylcholine receptor M3 isoform X2 [Homo sapiens] |



```
        10         20         30         40         50         60         70         80
MTLHNNSTTS PLFPNISSSW IHSPSDAGLP PGTVTHFGSY NVSRAAGNFS SPDGTTDDPL GGHTVWQVVF IAFLTGILAL
        90        100        110        120        130        140        150        160
VTIIGNILVI VSFKVNKQLK TVNNYFLLSL ACADLIIGVI SMNLFTTYII MNRWALGNLA CDLWLAIDYV ASNASVMNLL
       170        180        190        200        210        220        230        240
VISFDRYFSI TRPLTYRAKR TTKRAGVMIG LAWVISFVLW APAILFWQYF VGKRTVPPGE CFIQFLSEPT ITFGTAIAAF
       250        260        270        280        290        300        310        320
YMPVTIMTIL YWRIYKETEK RTKELAGLQA SGTEAETENF VHPTGSSRSC SSYELQQQSM KRSNRRKYGR CHFWFTTKSW
       330        340        350        360        370        380        390        400
KPSSEQMDQD HSSSDSWNNN DAAASLENSA SSDEEDIGSE TRAIYSIVLK LPGHSTILNS TKLPSSDNLQ VPEEELGMVD
       410        420        430        440        450        460        470        480
LERKADKLQA QKSVDDGGSF PKSFSKLPIQ LESAVDTAKT SDVNSSVGKS TATLPLSFKE ATLAKRFALK TRSQITKRKR
       490        500        510        520        530        540        550        560
MSLVKEKKAA QTLSAILLAF IITWTPYNIM VLVNTFCDSC IPKTFWNLGY WLCYINSTVN PVCYALCNKT FRTTFKMLLL
       570        580        590        600
CQCDKKKRRK QQYQQRQSVI FHKRAPEQAL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 943 | 1 | 630.8946 | -151.26 | 3 | 41.3 | 11.0 | 2 | 405-422 | K.ADKLQAQKSVDDGGSFPK.S | |

# Detailed Protein Report

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## Protein 1561: probable E3 ubiquitin-protein ligase DTX3 isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|30425428 | **Score:** | 11.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.6 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|555943685 | refseq_human (refseq_human_20140103.fasta) | probable E3 ubiquitin-protein ligase DTX3 isoform a [Homo sapiens] |
| gi\|530399882 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: probable E3 ubiquitin-protein ligase DTX3 isoform X7 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MSFVLSRMAA CGGTCKNKVT VSKPVWDFLS KETPARLARL REEHRVSILI DGETSDIYVL QLSPQGPPPA PPNGLYLARK
        90        100        110        120        130        140        150        160
ALKGLLKEAE KELKKAQRQG ELMGCLALGG GGEHPEMHRA GPPPLRAAPL LPPGARGLPP PPPPLPPPLP PRLREEAEEQ
       170        180        190        200        210        220        230        240
ESTCPICLGE IQNAKTLEKC RHSFCEGCIT RALQVKKACP MCGRFYGQLV GNQPQNGRML VSKDATLLLP SYEKYGTIVI
       250        260        270        280        290        300        310        320
QYVFPPGVQG AEHPNPGVRY PGTTRVAYLP DCPEGNKVLT LFRKAFDQRL TFTIGTSMTT GRPNVITWND IHHKTSCTGG
       330        340        350
PQLFGYPDPT YLTRVQEELR AKGITDD
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 728 | 1 | 839.4181 | 42.29 | 2 | 39.1 | 11.0 | 1 | 1-16 | -.MSFVLSRMAACGGTCK.N | Oxidation: 1 |

# Detailed Protein Report

## Protein 1562: calcium-activated chloride channel regulator 2 precursor [Homo sapiens]

**Accession:** gi|5729769
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 11.0
**MW [kDa]:** 103.9
**pI:** 6.6
**Sequence Coverage [%]:** 1.6
**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MTQRSIAGPI CNLKFVTLLV ALSSELPFLG AGVQLQDNGY NGLLIAINPQ VPENQNLISN IKEMITEASF YLFNATKRRV
        90        100        110        120        130        140        150        160
FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGAH GDDPYTLQYR GCGKEGKYIH FTPNFLLNDN LTAGYGSRGR
       170        180        190        200        210        220        230        240
VFVHEWAHLR WGVFDEYNND KPFYINGQNQ IKVTRCSSDI TGIFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI
       250        260        270        280        290        300        310        320
MFMQSLSSVV EFCNASTHNQ EAPNLQNQMC SLRSAWDVIT DSADFHHSFP MNGTELPPPP TFSLVQAGDK VVCLVLDVSS
       330        340        350        360        370        380        390        400
KMAEADRLLQ LQQAAEFYLM QIVEIHTFVG IASFDSKGEI RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSGLKKGF
       410        420        430        440        450        460        470        480
EVVEKLNGKA YGSVMILVTS GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLEELSRLT GGLKFFVPDI SNSNSMIDAF
       490        500        510        520        530        540        550        560
SRISSGTGDI FQQHIQLEST GENVKPHHQL KNTVTVDNTV GNDTMFLVTW QASGPPEIIL FDPDGRKYYT NNFITNLTFR
       570        580        590        600        610        620        630        640
TASLWIPGTA KPGHWTYTLN NTHHSLQALK VTVTSRASNS AVPPATVEAF VERDSLHFPH PVMIYANVKQ GFYPILNATV
       650        660        670        680        690        700        710        720
TATVEPETGD PVTLRLLDDG AGADVIKNDG IYSRYFFSFA ANGRYSLKVH VNHSPSISTP AHSIPGSHAM YVPGYTANGN
       730        740        750        760        770        780        790        800
IQMNAPRKSV GRNEEERKWG FSRVSSGGSF SVLGVPAGPH PDVFPPCKII DLEAVKVEEE LTLSWTAPGE DFDQGQATSY
       810        820        830        840        850        860        870        880
EIRMSKSLQN IQDDFNNAIL VNTSKRNPQQ AGIREIFTFS PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN
       890        900        910        920        930        940        950
IAQAPLFIPP NSDPVPARDY LILKGVLTAM GLIGIICLII VVTHHTLSRK KRADKKENGT KLL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1242 | 1 | 786.5105 | 159.93 | 2 | 45.1 | 11.0 | 0 | 410-424 | K.AYGSVMILVTSGDDK.L | Oxidation: 6 |

# Detailed Protein Report

## Protein 1563: RING finger protein 207 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|124487387 | **Score:** | 11.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 70.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | |
|---|---|---|---|
| ***WUP:QUP*** | **Median:** 2.64 | **CV:** 0.00 % | **No. of Peptides:** 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSGAIFGPLE | GPSSLDAPSI | HPLVCPLCHV | QYERPCLLDC | FHDFCAGCLR | GRATDGRLTC | PLCQHQTVLK | GPSGLPPVDR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LLQFLVDSSG | DGVEAVRCAN | CDLECSEQDV | ETTYFCNTCG | QPLCARCRDE | THRARMFARH | DIVALGQRSR | DVPQKCTLHA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EPYLLFSTDK | KLLLCIRCFR | DMQKESRAHC | VDLESAYVQG | CERLEQAVLA | VKALQTATRE | AIALLQAMVE | EVRHSAAEEE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DAIHALFGSM | QDRLAERKAL | LLQAVQSQYE | EKDKAFKEQL | SHLATLLPTL | QVHLVICSSF | LSLANKAEFL | DLGYELMERL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QGIVTRPHHL | RPIQSSKIAS | DHRAEFARCL | EPLLLLGPRR | VAAAASGANT | LAGGLGPKAL | TGPHCPSPVG | KMSGSPVQKP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TLHRSISTKV | LLAEGENTPF | AEHCRHYEDS | YRHLQAEMQS | LKDQVQELHR | DLTKHHSLIK | AEIMGDVLHK | SLQLDVQIAS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EHASLEGMRV | VFQEIWEEAY | QRVANEQEIY | EAQLHDLLQL | RQENAYLTTI | TKQITPYVRS | IAKVKERLEP | RFQAPVDEQS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ESLQNTHDDS | RNNAASARNN | PGSVPEKREK | TSEPKGNSWA | PNGLSEEPLL | KNMDHHRSKQ | KNGGDVPTWR | EHPT |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2156 | 1 | 841.3920 | -93.73 | 2 | 57.3 | 11.0 | 1 | 360-378 | R.RVAAAASGANTLAGGLGPK.A | | WUP:QUP 2.64 |

# Detailed Protein Report

**Protein 1564:** **membrane-associated phosphatidylinositol transfer protein 1 isoform b [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|195927017 | **Score:** | 11.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 134.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLIKEYHILL | PMSLDEYQVA | QLYMIQKKSR | EESSGEGSGV | EILANRPYTD | GPGGSGQYTH | KVYHVGSHIP | GWFRALLPKA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ALQVEEESWN | AYPYTRTRYT | CPFVEKFSIE | IETYYLPDGG | QQPNVFNLSG | AERRQRILDT | IDIVRDAVAP | GEYKAEEDPR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LYHSVKTGRG | PLSDDWARTA | AQTGPLMCAY | KLCKVEFRYW | GMQAKIEQFI | HDVGLRRVML | RAHRQAWCWQ | DEWTELSMAD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IRALEEETAR | MLAQRMAKCN | TGSEGSEAQP | PGKPSTEARS | AASNTGTPDG | PEAPPGPDAS | PDASFGKQWS | SSSRSSYSSQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HGGAVSPQSL | SEWRMQNIAR | DSENSSEEEF | FDAHEGFSDS | EEVFPKEMTK | WNSNDFIDAF | ASPVEAEGTP | EPGAEAAKGI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EDGAQAPRDS | EGLDGAGELG | AEACAVHALF | LILHSGNILD | SGPGDANSKQ | ADVQTLSSAF | EAVTRIHFPE | ALGHVALRLV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PCPPICAAAY | ALVSNLSPYS | HDGDSLSRSQ | DHIPLAALPL | LATSSSRYQG | AVATVIARTN | QAYSAFLRSP | EGAGFCGQVA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LIGDGVGGIL | GFDALCHSAN | AGTGSRGSSR | RGSMNNELLS | PEFGPVRDPL | ADGVEGLGRG | SPEPSALPPQ | RIPSDMASPE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PEGSQNSLQA | APATTSSWEP | RRASTAFCPP | AASSEAPDGP | SSTARLDFKV | SGFFLFGSPL | GLVLALRKTV | MPALEAQMRP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ACEQIYNLFH | AADPCASRLE | PLLAPKFQAI | APLTVPRYQK | FPLGDGSSLL | LADTLQTHSS | LFLEELEMLV | PSTPTSTSGA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FWKGSELATD | PPAQPAAPST | TSEVVKILER | WWGTKRIDYS | LYCPEALTAF | PTVTLPHLFH | ASYWESADVV | AFILRQVIEK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ERPQLAECEE | PSIYSPAFPR | EKWQRKRTQV | KIRNVTSNHR | ASDTVVCEGR | PQVLSGRFMY | GPLDVVTLTG | EKVDVYIMTQ |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PLSGKWIHFG | TEVTNSSGRL | TFPVPPERAL | GIGVYPVRMV | VRGDHTYAEC | CLTVVARGTE | AVVFSIDGSF | TASVSIMGSD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PKVRAGAVDV | VRHWQDSGYL | IVYVTGRPDM | QKHRVVAWLS | QHNFPHGVVS | FCDGLTHDPL | RQKAMFLQSL | VQEVELNIVA |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GYGSPKDVAV | YAALGLSPSQ | TYIVGRAVRK | LQAQCQFLSD | GYVAHLGQLE | AGSHSHASSG | PPRAALGKSS | YGVAAPVDFL |
| 1210 | 1220 | 1230 | 1240 | 1250 | | | |
| RKQSQLLRSR | GPSQAEREGP | GTPPTTLARG | KARSISLKLD | SEE | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1309 | 1 | 598.8020 | -25.24 | 2 | 46.5 | 11.0 | 0 | 1218-1229 | R.EGPGTPPTTLAR.G | |

# Detailed Protein Report

---

## Protein 1565: PREDICTED: myoferlin isoform X3 [Homo sapiens]

**Accession:** gi|578819249
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 11.0
**MW [kDa]:** 221.1
**pI:** 5.9
**Sequence Coverage [%]:** 1.5
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGGDGEEDEG | DEDRLDNAVR | GPGPKGPVGT | VSEAQLARRL | TKVKNSRRML | SNKPQDFQIR | VRVIEGRQLS | GNNIRPVVKV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HVCGQTHRTR | IKRGNNPFFD | ELFFYNVNMT | PSELMDEIIS | IRVYNSHSLR | ADCLMGEFKI | DVGFVYDEPG | HAVMRKWLLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NDPEDTSSGS | KGYMKVSMFV | LGTGDEPPPE | RRDRDNDSDD | VESNLLLPAG | IALRWVTFLL | KIYRAEDIPQ | MDDAFSQTVK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EIFGGNADKK | NLVDPFVEVS | FAGKKVCTNI | IEKNANPEWN | QVVNLQIKFP | SVCEKIKLTI | YDWDRLTKND | VVGTTYLHLS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KIAASGGEVE | DFSSSGTGAA | SYTVNTGETE | VGFVPTFGPC | YLNLYGSPRE | YTGFPDPYDE | LNTGKGEGVA | YRGRILVELA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TFLEKTPPDK | KLEPISNDDL | LVVEKYQRRR | KYSLSAVFHS | ATMLQDVGEA | IQFEVSIGNY | GNKFDTTCKP | LASTTQYSRA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VFDGNYYYYL | PWAHTKPVVT | LTSYWEDISH | RLDAVNTLLA | MAERLQTNIE | ALKSGIQGKI | PANQLAELWL | KLIDEVIEDT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RYTLPLTEGK | ANVTVLDTQI | RKLRSRSLSQ | IHEAAVRMRS | EATDVKSTLA | EIEDWLDKLM | QLTEEPQNSM | PDIIIWMIRG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EKRLAYARIP | AHQVLYSTSG | ENASGKYCGK | TQTIFLKYPQ | EKNNGPKVPV | ELRVNIWLGL | SAVEKKFNSF | AEGTFTVFAE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| MYENQALMFG | KWGTSGLVGR | HKFSDVTGKI | KLKREFFLPP | KGWEWEGEWI | VDPERSLLTE | ADAGHTEFTD | EVYQNESRYP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GGDWKPAEDT | YTDANGDKAA | SPSELTCPPG | WEWEDDAWSY | DINRAVDEKG | WEYGITIPPD | HKPKSWVAAE | KMYHTHRRRR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LVRKRKKDLT | QTASSTARAM | EELQDQEGWE | YASLIGWKFH | WKQRSSDTFR | RRRWRRKMAP | SETHGAAAIF | KLEGALGADT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TEDGDEKSLE | KQKHSATTVF | GANTPIVSCN | FDRVYIYHLR | CYVYQARNLL | ALDKDSFSDP | YAHICFLHRS | KTTEIIHSTL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| NPTWDQTIIF | DEVEIYGEPQ | TVLQNPPKVI | MELFDNDQVG | KDEFLGRSIF | SPVVKLNSEM | DITPKLLWHP | VMNGDKACGD |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| VLVTAELILR | GKDGSNLPIL | PPQRAPNLYM | VPQGIRPVVQ | LTAIEILAWG | LRNMKNFQMA | SITSPSLVVE | CGGERVESVV |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| IKNLKKTPNF | PSSVLFMKVF | LPKEELYMPP | LVIKVIDHRQ | FGRKPVVGQC | TIERLDRFRC | DPYAGKEDIV | PQLKASLLSA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PPCRDIVIEM | EDTKPLLASK | CLSSMSTALS | KMASPATVHL | TEKEEEIVDW | WSKFYASSGE | HEKCGQYIQK | GYSKLKIYNC |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ELENVAEFEG | LTDFSDTFKL | YRGKSDENED | PSVVGEFKGS | FRIYPLPDDP | SVPAPPRQFR | ELPDSVPQEC | TVRIYIVRGL |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ELQPQDNNGL | CDPYIKITLG | KKVIEDRDHY | IPNTLNPVFG | RMYELSCYLP | QEKDLKISVY | DYDTFTRDEK | VGETIIDLEN |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| RFLSRFGSHC | GIPEEYCVSG | VNTWRDQLRP | TQLLQNVARF | KGFPQPILSE | DGSRIRYGGR | DYSLDEFEAN | KILHQHLGAP |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| EERLALHILR | TQGLVPEHVE | TRTLHSTFQP | NISQGKLQMW | VDVFPKSLGP | PGPPFNITPR | KAKKYYLRVI | IWNTKDVILD |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| EKSITGEEMS | DIYVKGWIPG | NEENKQKTDV | HYRSLDGEGN | FNWRFVFPFD | YLPAEQLCIV | AKKEHFWSID | QTEFRIPPRL |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| IIQIWDNDKF | SLDDYLGFLE | LDLRHTIIPA | KSPEKCRLDM | IPDLKAMNPL | KAKTASLFEQ | KSMKGWWPCY | AEKDGARVMA |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| GKVEMTLEIL | NEKEADERPA | GKGRDEPNMN | PKLDLPNRPE | TSFLWFTNPC | KTMKFIVWRR | FKWVIIGLLF | LLILLLFVAV |
| 1930 | 1940 | | | | | | |
| LLYSLPNYLS | MKIVKPNV | | | | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1791 | 1 | 1011.5611 | 83.52 | 3 | 52.2 | 11.0 | 1 | 938-967 | K.MAPSETHGAAAIFKLEGALGADTTEDGDEK.S | |

# Detailed Protein Report

## Protein 1566: cyclin-dependent kinase 15 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21040235 | **Score:** | 11.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 43.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.2 |
| | | **Sequence Coverage [%]:** | 4.9 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530370812 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: cyclin-dependent kinase 15 isoform X2 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTSFHPRGLQ | AARAQKFKSK | RPRSNSDCFQ | EEDLRQGFQW | RKSLPFGAAS | SYLNLEKLGE | GSYATVYKGI | SRINGQLVAL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KVISMNAEEG | VPFTAIREAS | LLKGLKHANI | VLLHDIIHTK | ETLTFVFEYM | HTDLAQYMSQ | HPGGLHPHNV | RLFMFQLLRG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LAYIHHQHVL | HRDLKPQNLL | ISHLGELKLA | DFGLARAKSI | PSQTYSSEVV | TLWYRPPDAL | LGATEYSSEL | DIWGAGCIFI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EMFQGQPLFP | GVSNILEQLE | KIWEVLGVPT | EDTWPGVSKL | PNYNPEWFPL | PTPRSLHVVW | NRLGRVPEAE | DLASQMLKGF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| PRDRVSAQEA | LVHDYFSALP | SQLYQLPDEE | SLFTVSGVRL | KPEMCDLLAS | YQKGHHPAQF | SKCW | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2792 | 1 | 1079.9998 | -45.87 | 2 | 65.3 | 11.0 | 2 | 306-324 | R.VPEAEDLASQMLKGFPRDR.V | |

# Detailed Protein Report

## Protein 1567: 28S ribosomal protein S9, mitochondrial [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|33188463 | **Score:** | 11.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MAAPCVSYGG AVSYRLLLWG RGSLARKQGL WKTAAPELQT NVRSQILRLR HTAFVIPKKN VPTSKRETYT EDFIKKQIEE
        90        100        110        120        130        140        150        160
FNIGKRHLAN MMGEDPETFT QEDIDRAIAY LFPSGLFEKR ARPVMKHPEQ IFPRQRAIQW GEDGRPFHYL FYTGKQSYYS
       170        180        190        200        210        220        230        240
LMHDVYGMLL NLEKHQSHLQ AKSLLPEKTV TRDVIGSRWL IKEELEEMLV EKLSDLDYMQ FIRLLEKLLT SQCGAAEEEF
       250        260        270        280        290        300        310        320
VQRFRRSVTL ESKKQLIEPV QYDEQGMAFS KSEGKRKTAK AEAIVYKHGS GRIKVNGIDY QLYFPITQDR EQLMFPFHFV
       330        340        350        360        370        380        390        400
DRLGKHDVTC TVSGGGRSAQ AGAIRLAMAK ALCSFVTEDE VEWMRQAGLL TTDPRVRERK KPGQEGARRK FTWKKR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 598 | 1 | 700.7029 | -188.45 | 2 | 37.0 | 11.0 | 0 | 2-15 | M.AAPCVSYGGAVSYR.L | |

# Detailed Protein Report

## Protein 1568: protein Jade-1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|19923609 | **Score:** | 11.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 58.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|566006111 | refseq_human (refseq_human_20140103.fasta) | protein Jade-1 isoform 2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKRGRLPSSS | EDSDDNGSLS | TTWSQNSRSQ | HRRSSCSRHE | DRKPSEVFRT | DLITAMKLHD | SYQLNPDEYY | VLADPWRQEW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EKGVQVPVSP | GTIPQPVARV | VSEEKSLMFI | RPKKYIVSSG | SEPPELGYVD | IRTLADSVCR | YDLNDMDAAW | LELTNEEFKE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MGMPELDEYT | MERVLEEFEQ | RCYDNMNHAI | ETEEGLGIEY | DEDVVCDVCQ | SPDGEDGNEM | VFCDKCNICV | HQACYGILKV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PEGSWLCRTC | ALGVQPKCLL | CPKKGGAMKP | TRSGTKWVHV | SCALWIPEVS | IGSPEKMEPI | TKVSHIPSSR | WALVCSLCNE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KFGASIQCSV | KNCRTAFHVT | CAFDRGLEMK | TILAENDEVK | FKSYCPKHSS | HRKPEESLGK | GAAQENGAPE | CSPRNPLEPF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ASLEQNREEA | HRVSVRKQKL | QQLEDEFYTF | VNLLDVARAL | RLPEEVVDFL | YQYWKLKRKV | NFNKPLITPK | KDEEDNLAKR |
| 490 | 500 | 510 | | | | | |
| EQDVLFRRLQ | LFTHLRQDLE | RVMIDTDTL | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 565 | 1 | 661.8568 | 62.79 | 2 | 35.5 | 11.0 | 0 | 311-321 | R.WALVCSLCNEK.F | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 1569: neuroblastoma breakpoint family member 3 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|374088176 | **Score:** | 11.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 65.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.2 |
| | | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPLTPTVQGF | QWTLRGPDVE | TSPFGAPRAA | SHGVGRHQEL | RDPTDYEDCK | DLIKSMLRDE | RLLTEEKLAE | ELGQAEELRQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YKVLVHSQER | ELTQLREKLQ | EGRDASRSLN | QHLQALLTPD | EPDNSQGRDL | REQLAEGCRL | AQHLVQKLSP | ENDDDEDEDV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KVEEAEKVQE | LYAPREVQKA | EEKEVPEDSL | EECAITCSNS | HHPCESNQPY | GNTRITFEED | QVDSTLIDSS | SHDEWLDAVC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IIPENESDHE | QEEEKGPVSP | RNLQESEEEE | APQESWDEGD | WTLSIPPDMS | ASYQSDRSTF | HSVEEQQVGL | ALDIGRHWCD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QVKKEDQEAT | SPRLSRELLD | EKEPEVLQDS | LDRFYSTPFE | YLELPDLCQP | YRSDFYSLQE | QHLGLALDLD | RMKKDQEEEE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DQGPPCPRLS | RELPEVVEPE | DLQDSLDRWY | STPFSYPELP | DSCQPYGSCF | YSLEEEHVGF | SLDVDEIEKY | QEGEEDQKPP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CPRLNEVLME | AEEPEVLQDS | LDRCYSTTST | YFQLHASFQQ | YRSAFYSFEE | QDVSLALDVD | NRFFTLTVIR | HHLAFQMGVI |
| 570 | | | | | | | |
| FPH | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2286 | 1 | 665.3174 | -11.91 | 2 | 59.0 | 11.0 | 0 | 16-28 | R.GPDVETSPFGAPR.A | |

# Detailed Protein Report

## Protein 1570: leucine-rich repeat and IQ domain-containing protein 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|122937315 | **Score:** | 11.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 63.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| | | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.90 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.16 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578807342 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: leucine-rich repeat and IQ domain-containing protein 4 isoform X2 [Homo sapiens] |
| gi\|530374547 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: leucine-rich repeat and IQ domain-containing protein 4 isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSKDIKSVEH | SPKIHQRNDP | QHVNDRTFFI | DASNQSLTAI | PLEIFTFTEL | EEVHLENNQI | EEIPQEIQRL | KNIRVLYLDK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NNLRSLCPAL | GLLSSLESLD | LSYNPIFSSS | LVVVSFLHAL | RELRLYQTDL | KEIPVVIFKN | LHHLELLGLT | GNHLKCLPKE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IVNQTKLREI | YLKRNQFEVF | PQELCVLYTL | EIIDLDENKI | GAIPEEIGHL | TGLQKFYMAS | NNLPVLPASL | CQCSQLSVLD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LSHNLLHSIP | KSFAELRKMT | EIGLSGNRLE | KVPRLICRWT | SLHLLYLGNT | GLHRLRGSFR | CLVNLRFLDL | SQNHLHHCPL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QICALKNLEV | LGLDDNKIGQ | LPSELGSLSK | LKILGLTGNE | FLSFPEEVLS | LASLEKLYIG | QDQGFKLTYV | PEHIRKLQSL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KELYIENNHL | EYLPVSLGSM | PNLEVLDCRH | NLLKQLPDAI | CQAQALKELR | LEDNLLTHLP | ENLDSLVNLK | VLTLMDNPME |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EPPKEVCAEG | NEAIWKYLKE | NRNRNIMATK | IQAWWRGTMV | QRGFGKFGEL | LKPQKKGKTS | PKDKKGKKDV | KGKPGKGKKK |
| 570 | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2663 | 1 | 659.3506 | -6.24 | 2 | 61.6 | 11.0 | 1 | 7-17 | K.SVEHSPKIHQR.N | | WUP:QUP 0.16<br>QU:MU 0.90 |

# Detailed Protein Report

## Protein 1571: receptor activity-modifying protein 3 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5032023 | **Score:** | 11.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 16.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 12.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 2.16 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
METGALRRPQ LLPLLLLLCG GCPRAGGCNE TGMLERLPLC GKAFADMMGK VDVWKWCNLS EFIVYYESFT NCTEMEANVV
        90        100        110        120        130        140        150
GCYWPNPLAQ GFITGIHRQF FSNCTVDRVH LEDPPDEVLI PLIVIPVVLT VAMAGLVVWR SKRTDTLL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1830 | 1 | 961.3217 | -133.49 | 2 | 53.2 | 11.0 | 1 | 25-42 | R.AGGCNETGMLERLPLCGK.A | Carbamidomethyl: 4;<br>Oxidation: 9 | WUP:QUP 2.16 |

# Detailed Protein Report

## Protein 1572: PREDICTED: serine/threonine-protein kinase Nek10 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578805707 | **Score:** | 11.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 132.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPDQDKKVKT | TEKSTDKQQE | ITIRDYSDLK | RLRCLLNVQS | SKQQLPAINF | DSAQNSMTKS | EPAIRAGGHR | ARGQWHESTE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AVELENFSIN | YKNERNFSKH | PQRKLFQEIF | TALVKNRLIS | REWVNRAPSI | HFLRVLICLR | LLMRDPCYQE | ILHSLGGIEN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LAQYMEIVAN | EYLGYGEEQH | TVDKLVNMTY | IFQKLAAVKD | QREWVTTSGA | HKTLVNLLGA | RDTNVLLGSL | LALASLAESQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ECREKISELN | IVENLLMILH | EYDLLSKRLT | AELLRLLCAE | PQVKEQVKLY | EGIPVLLSLL | HSDHLKLLWS | IVWILVQVCE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DPETSVEIRI | WGGIKQLLHI | LQGDRNFVSD | HSSIGSLSSA | NAAGRIQQLH | LSEDLSPREI | QENTFSLQAA | CCAALTELVL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NDTNAHQVVQ | ENGVYTIAKL | ILPNKQKNAA | KSNLLQCYAF | RALRFLFSME | RNRPLFKRLF | PTDLFEIFID | IGHYVRDISA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YEELVSKLNL | LVEDELKQIA | ENIESINQNK | APLKYIGNYA | ILDHLGSGAF | GCVYKVRKHS | GQNLLAMKEV | NLHNPAFGKD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KKDRDSSVRN | IVSELTIIKE | QLYHPNIVRY | YKTFLENDRL | YIVMELIEGA | PLGEHFSSLK | EKHHHFTEER | LWKIFIQLCL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ALRYLHKEKR | IVHRDLTPNN | IMLGDKDKVT | VTDFGLAKQK | QENSKLTSVV | GTILYSCPEV | LKSEPYGEKA | DVWAVGCILY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| QMATLSPPFY | STNMLSLATK | IVEAVYEPVP | EGIYSEKVTD | TISRCLTPDA | EARPDIVEVS | SMISDVMMKY | LDNLSTSQLS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LEKKLERERR | RTQRYFMEAN | RNTVTCHHEL | AVLSHETFEK | ASLSSSSSGA | ASLKSELSES | ADLPPEGFQA | SYGKDEDRAC |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DEILSDDNFN | LENAEKDTYS | EVDDELDISD | NSSSSSSSPL | KESTFNILKR | SFSASGGERQ | SQTRDFTGGT | GSRPRPALLP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LDLLLKVPPH | MLRAHIKEIE | AELVTGWQSH | SLPAVILRNL | KDHASAGIAV | SQRKVRQISD | PIQQILIQLH | KIIYITQLPP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ALHHNLKRRV | IERFKKSLFS | QQSNPCNLKS | EIKKLSQGSP | EPIEPNFFTA | DYHLLHRSSG | GNSLSPNDPT | GLPTSIELEE |
| 1130 | 1140 | 1150 | 1160 | 1170 | | | |
| GITYEQMQTV | IEEVLEESGY | YNFTSNRYHS | YPWGTKNHPT | KR | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1938 | 1 | 847.8278 | -165.90 | 2 | 54.6 | 11.0 | 2 | 999-1014 | R.NLKDHASAGIAVSQRK.V | |

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# Detailed Protein Report

## Protein 1573: RIMS-binding protein 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|140561070 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 116.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| | | **Sequence Coverage [%]:** | 1.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.30 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MREAAERRQQ | LQLEHDQALA | VLSAKQQEID | LLQKSKVREL | EEKCRTQSEQ | FNLLSRDLEK | FRQHAGKIDL | LGGSAVAPLD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ISTAPSKPFP | QFMNGLATSL | GKGQESAIGG | SSAIGEYIRP | LPQPGDRPEP | LSAKPTFLSR | SGSARCRSES | DMENERNSNT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SKQRYSGKVH | LCVARYSYNP | FDGPNENPEA | ELPLTAGKYL | YVYGDMDEDG | FYEGELLDGQ | RGLVPSNFVD | FVQDNESRLA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| STLGNEQDQN | FINHSGIGLE | GEHILDLHSP | THIDAGITDN | SAGTLDVNID | DIGEDIVPYP | RKITLIKQLA | KSVIVGWEPP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AVPPGWGTVS | SYNVLVDKET | RMNLTLGSRT | KALIEKLNMA | ACTYRISVQC | VTSRGSSDEL | QCTLLVGKDV | VVAPSHLRVD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NITQISAQLS | WLPTNSNYSH | VIFLNEEEFD | IVKAARYKYQ | FFNLRPNMAY | KVKVLAKPHQ | MPWQLPLEQR | EKKEAFVEFS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TLPAGPPAPP | QDVTVQAGVT | PATIRVSWRP | PVLTPTGLSN | GANVTGYGVY | AKGQRVAEVI | FPTADSTAVE | LVRLRSLEAK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GVTVRTLSAQ | GESVDSAVAA | VPPELLVPPT | PHPRPAPQSK | PLASSGVPET | KDEHLGPHAR | MDEAWEQSRA | PGPVHGHMLE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PPVGPGRRSP | SPSRILPQPQ | GTPVSTTVAK | AMAREAAQRV | AESSRLEKRS | VFLERSSAGQ | YAASDEEDAY | DSPDFKRRGA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SVDDFLKGSE | LGKQPHCCHG | DEYHTESSRG | SDLSDIMEED | EEELYSEMQL | EDGGRRRPSG | TSHNALKILG | NPASAGRVDH |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| MGRRFPRGSA | GPQRSRPVTV | PSIDDYGRDR | LSPDFYEESE | TDPGAEELPA | RIFVALFDYD | PLTMSPNPDA | AEEELPFKEG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| QIIKVYGDKD | ADGFYRGETC | ARLGLIPCNM | VSEIQADDEE | MMDQLLRQGF | LPLNTPVEKI | ERSRRSGRRH | SVSTRRMVAL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| YDYDPRESSP | NVDVEAELTF | CTGDIITVFG | EIDEDGFYYG | ELNGQKGLVP | SNFLEEVPDD | VEVYLSDAPS | HYSQDTPMRS |
| 1050 | 1060 | | | | | | |
| KAKRKKSVHF | TP | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 665 | 1 | 639.3437 | 13.28 | 2 | 37.9 | 10.9 | 1 | 339-349 | K.ETRMNLTLGSR.T | | WUP:QUP 0.30 |

# Detailed Protein Report

## Protein 1574: PREDICTED: probable phospholipid-transporting ATPase IG isoform X3 [Homo sapiens]

**Accession:** gi|578838665
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 10.9
**MW [kDa]:** 126.6
**pI:** 6.4
**Sequence Coverage [%]:** 2.1
**No. of unique Peptides:** 1

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.49 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.15 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578838667 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: probable phospholipid-transporting ATPase IG isoform X4 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFRRSLNRFC | AGEEKRVGTR | TVFVGNHPVS | ETEAYIAQRF | CDNRIVSSKY | TLWNFLPKNL | FEQFRRIANF | YFLIIFLVQV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TVDTPTSPVT | SGLPLFFVIT | VTAIKQGYED | CLRHRADNEV | NKSTVYIIEN | AKRVRKESEK | IKVGDVVEVQ | ADETFPCDLI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLSSCTTDGT | CYVTTASLDG | ESNCKTHYAV | RDTIALCTAE | SIDTLRAAIE | CEQPQPDLYK | FVGRINIYSN | SLEAVARSLG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PENLLLKGAT | LKNTEKIYGV | AVYTGMETKM | ALNYQGKSQK | RSAVEKSINA | FLIVYLFILL | TKAAVCTTLK | YVWQSTPYND |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EPWYNQKTQK | ERETLKVLKM | FTDFLSFMVL | FNFIIPVSMY | VTVEMQKFLG | SFFISWDKDF | YDEEINEGAL | VNTSDLNEEL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GQVDYVFTDK | TGTLTENSME | FIECCIDGHK | YKGVTQEVDG | LSQTDGTLTY | FDKVDKNREE | LFLRALCLCH | TVEIKTNDAV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DGATESAELT | YISSSPDEIA | LVKGAKRYGF | TFLGNRNGYM | RVENQRKEIE | EYELLHTLNF | DAVRRRMSVI | VKTQEGDILL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FCKGADSAVF | PRVQNHEIEL | TKVHVERNAM | DGYRTLCVAF | KEIAPDDYER | INRQLIEAKM | ALQDREEKME | KVFDDIETNM |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NLIGATAVED | KLQDQAAETI | EALHAAGLKV | WVLTGDKMET | AKSTCYACRL | FQTNTELLEL | TTKTIEESER | KEDRLHELLI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EYRKKLLHEF | PKSTRSFKKA | WTEHQEYGLI | IDGSTLSLIL | NSSQDSSSNN | YKSIFLQICM | KCTAVLCCRM | APLQKAQIVR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| MVKNLKGSPI | TLSIGDGAND | VSMILESHVG | IGIKGKEGRQ | AARNSDYSVP | KFKHLKKLLL | AHGHLYYVRI | AHLVQYFFYK |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| NLCFILPQFL | YQFFCGFSQQ | PLYDAAYLTM | YNICFTSLPI | LAYSLLEQHI | NIDTLTSDPR | LYMKISGNAM | LQLGPFLYWT |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FLAAFEGTVF | FFGTYFLFQT | ASLEENGKVY | GNWTFGTIVF | TVLVFTVTLK | LALDTRFWTW | INHFVIWGSL | AFYVFFSFFW |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | |
| GGIIWPFLKQ | QRMYFVFAQM | LSSVSTWLAI | ILLIFISLFP | EILLIVLKNV | RRRSARVHHL | ISSSA | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 237 | 1 | 898.4036 | -13.81 | 3 | 33.0 | 10.9 | 2 | 588-610 | R.<br>NAMDGYRTLCVAFKEIAPDDYER.<br>I | Oxidation: 3 | WUP:QUP 1.15<br>QU:MU 1.49 |

# Detailed Protein Report

## Protein 1575: PREDICTED: phosphatidate phosphatase PPAPDC1A isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578819062 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRELAIEIGV | RALLFGVFVF | TEFLDPFQRV | IQPEEIWLYK | NPLVQSDNIP | TRLMFAISFL | TPLAVICVVK | IIRRTDKTEI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KEAFLAVSLA | LALNGVCTNT | IKLIVGSCLF | GPWLHDVLLG | GQAALLHREW | AGKELAALCC | HPALVLRHDD | CPVPHVRLQA |
| 170 | 180 | 190 | 200 | | | | |
| SLARFLCGWS | HRPHFCIHLL | QTALSSSGQH | SLP | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1787 | 1 | 901.3035 | -281.98 | 1 | 50.7 | 10.9 | 2 | 71-77 | K.IIRRTDK.T | |

# Detailed Protein Report

## Protein 1576: ubiquitin-like protein 7 isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|14249682 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| | | **Sequence Coverage [%]:** | 5.3 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|557948089 | refseq_human (refseq_human_20140103.fasta) | ubiquitin-like protein 7 isoform a [Homo sapiens] |
| gi\|557947994 | refseq_human (refseq_human_20140103.fasta) | ubiquitin-like protein 7 isoform a [Homo sapiens] |
| gi\|41152107 | refseq_human (refseq_human_20140103.fasta) | ubiquitin-like protein 7 isoform a [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MSLSDWHLAV KLADQPLTPK SILRLPETEL GEYSLGGYSI SFLKQLIAGK LQESVPDPEL IDLIYCGRKL KDDQTLDFYG
        90        100        110        120        130        140        150        160
IQPGSTVHVL RKSWPEPDQK PEPVDKVAAM REFRVLHTAL HSSSSYREAV FKMLSNKESL DQIIVATPGL SSDPIALGVL
       170        180        190        200        210        220        230        240
QDKDLFSVFA DPNMLDTLVP AHPALVNAIV LVLHSVAGSA PMPGTDSSSR SMPSSSYRDM PGGFLFEGLS DDEDDFHPNT
       250        260        270        280        290        300        310        320
RSTPSSSTPS SRPASLGYSG AAGPRPITQS ELATALALAS TPESSSHTPT PGTQGHSSGT SPMSSGVQSG TPITNDLFSQ
       330        340        350        360        370        380        390
ALQHALQASG QPSLQSQWQP QLQQLRDMGI QDDELSLRAL QATGGDIQAA LELIFAGGAP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2456 | 1 | 754.4649 | 115.07 | 3 | 59.0 | 10.9 | 0 | 72-91 | K.DDQTLDFYGIQPGSTVHVLR.K | |

# Detailed Protein Report

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## Protein 1577: disintegrin and metalloproteinase domain-containing protein 18 isoform 1 preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|7656861 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 82.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFLLLALLTE | LGRLQAHEGS | EGIFLHVTVP | RKIKSNDSEV | SERKMIYIIT | IDGQPYTLHL | GKQSFLPQNF | LVYTYNETGS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LHSVSPYFMM | HCHYQGYAAE | FPNSFVTLSI | CSGLRGFLQF | ENISYGIEPV | ESSARFEHII | YQMKNNDPNV | SILAVNYSHI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WQKDQPYKVP | LNSQIKNLSK | LLPQYLEIYI | IVEKALYDYM | GSEMMAVTQK | IVQVIGLVNT | MFTQFKLTVI | LSSLELWSNE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NQISTSGDAD | DILQRFLAWK | RDYLILRPHD | IAYLLVYRKH | PKYVGATFPG | TVCNKSYDAG | IAMYPDAIGL | EGFSVIIAQL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LGLNVGLTYD | DITQCFCLRA | TCIMNHEAVS | ASGRKIFSNC | SMHDYRYFVS | KFETKCLQKL | SNLQPLHQNQ | PVCGNGILES |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NEECDCGNKN | ECQFKKCCDY | NTCKLKGSVK | CGSGPCCTSK | CELSIAGTPC | RKSIDPECDF | TEYCNGTSSN | CVPDTYALNG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| RLCKLGTAYC | YNGQCQTTDN | QCAKIFGKGA | QGAPFACFKE | VNSLHERSEN | CGFKNSQPLP | CERKDVLCGK | LACVQPHKNA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| NKSDAQSTVY | SYIQDHVCVS | IATGSSMRSD | GTDNAYVADG | TMCGPEMYCV | NKTCRKVHLM | GYNCNATTKC | KGKGICNNFG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NCQCFPGHRP | PDCKFQFGSP | GGSIDDGNFQ | KSGDFYTEKG | YNTHWNNWFI | LSFCIFLPFF | IVFTTVIFKR | NEISKSCNRE |
| 730 | 740 | | | | | | |
| NAEYNRNSSV | VSESDDVGH | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2129 | 1 | 734.3188 | -28.32 | 2 | 55.0 | 10.9 | 0 | 617-629 | K.VHLMGYNCNATTK.C | Oxidation: 4 |

# Detailed Protein Report

## Protein 1578: coiled-coil domain-containing protein 142 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|217416372 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 80.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAQASRSGSL | PPLVIVPPLR | AQPGGTGEEQ | WERSRTGGLR | WEVHCWPSGT | SGGTPWWPTP | ADVSEDYEAD | AAAWRRGPAG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GGPIPPALQR | LRAVLLRLHR | EREQLLQARD | CAYHLQSAVR | LMKTLSPGSP | SGGPSPLPQW | CRDLQLHPSQ | GAVLRIGPGE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TLEPLLLARP | IGLAAQCLEA | VIEMQLRALG | REPASPGLSS | QLAELLFALP | AYHTLQRKAL | SHVPGAARPF | PTSRVLRLLT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GERGCQVASR | LDEALQGSAL | RDQLRRRCQE | EGDLLPGLLG | LVGGVAGSAS | CGLGLGGAGA | LWSQYWTLLW | AACAQSLDLN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LGPWRDPRAT | AQQLSQALGQ | ASLPQECEKE | LASLCHRLLH | QSLIWSWDQG | FCQALGSALG | GQSSLPTSSG | TAELLQQLFP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PLLDALREPR | LRRIFCQPAG | LCTLQTTLLW | FLGRAQQYLA | AWDPASFLLL | IQKDLPPLLH | EAEALYSLAS | EESLALEVEQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QLGLEIQKLT | AQIQLLPEES | LSVFSQECHK | QAMQGFKLYM | PRGRYWRLRL | CPEPPSAPSE | YAGLVVRTVL | EPVLQGLQGL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PPQAQAPALG | QALTAIVGAW | LDHILTHGIR | FSLQGALQLK | QDFGVVRELL | EEEQWSLSPD | LRQTLLMLSI | FQQLDGALLC |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LLQQPLPKSQ | VHRRPPCCCA | CQEVQTTKLP | SSCLNSLESL | EPPLQPGTSP | AQTGQLQSTL | GGRGPSPEGY | LVGNQQAWLA |
| 730 | 740 | 750 | | | | | |
| LRQHQRPRWH | LPFFSCLGTS | PES | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1711 | 1 | 1044.9814 | -114.61 | 2 | 51.2 | 10.9 | 1 | 1-20 | -.MAQASRSGSLPPLVIVPPLR.A | |

## Protein 1579: polycystic kidney disease protein 1-like 2 isoform d [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|509155833 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 197.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 0.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MGEDSPVAMF SWYLDNTPTE QAEPLLDACR LRGFWPRSLT LLQSNTSTLL LNSSFLQSRG EVIRIRATAL TRHAYGEDTY
        90        100        110        120        130        140        150        160
VISTVPPREV PACTIAPEEG TVLTSFAIFC NASTALGPLE FCFCLESGSC LHCGPEPALP SVYLPLGEEN NDFVLTVVIS
       170        180        190        200        210        220        230        240
ATNRAGDTQQ TQAMAKVALG DTCVEDVAFQ AAVSEKIPTA LQGEGGPEQL LQLAKAVSSM LNQEHESQGS GQSLSIDVRQ
       250        260        270        280        290        300        310        320
KVREHVLGSL SAVTTGLEDV QRVQELAEVL REVTCRSKEL TPSAQWEASL ALQHASEALL TVSAKARPED QRRQAATRDL
       330        340        350        360        370        380        390        400
FQAVGSVLEA SLSNRPEEPA EASSSQIATV LRLLRVMEHV QTTLLLGKLP GGLPAMLATP SISVYTNRIQ PWSWQGSSLR
       410        420        430        440        450        460        470        480
PDAADSATFM LPAASSLSSL EGGQEPVDIK IMSFPKSPFP ARSHFDVSGT VGGLRVTSPS GQLIPVKNLS ENIEILLPRH
       490        500        510        520        530        540        550        560
SQRHSQPTVL NLTSPEALWV NVTSGEATLG IQLHWRPDIA LTLSLGYGYH PNKSSYDAQT HLVPMVAPDE LPTWILSPQD
       570        580        590        600        610        620        630        640
LRFGEGVYYL TVVPESDLEP APGRDLTVGI TTFLSHCVFW DEVQETWDDS GCQVGPRTSP YQTHCLCNHL TFFGSTFLVM
       650        660        670        680        690        700        710        720
SNAINIHQTA ELFATFEDNP VVVTTVGCLC VVYVLVVIWA RRKDAQDQAK VKVTVLEDND PFAQYHYLVT VYTGHRRGAA
       730        740        750        760        770        780        790        800
TSSKVTVTLY GLDGEREPHH LADPDTPVFE RGAVDAFLLS TLFPLGELRS LRLWHDNSGD RPSWYVSRVL VYDLVMDRKW
       810        820        830        840        850        860        870        880
YFLCNSWLSI NVGDCVLDKV FPVATEQDRK QFSHLFFMKT SAGFQDGHIW YSIFSRCARS SFTRVQRVSC CFSLLLCTML
       890        900        910        920        930        940        950        960
TSIMFWGVPK DPAEQKMDLG KIEFTWQEVM IGLESSILMF PINLLIVQIF QNTRPRVAKE QNTGKWDRGS PNLTPSPQPM
       970        980        990       1000       1010       1020       1030       1040
EDGLLTPEAV TKDVSRIVSS LFKALKVPSP ALGWDSVNLM DINSLLALVE DVIYPQNTSG QVFWEEAKKR EDPVTLTLGS
      1050       1060       1070       1080       1090       1100       1110       1120
SEMKEKSQCP KPKAARSGPW KDSAYRQCLY LQLEHVEQEL RLVGPRGFSQ PHSHAQALRQ LQTLKGGLGV QPGTWAPAHA
      1130       1140       1150       1160       1170       1180       1190       1200
SALQVSKPPQ GLPWWCILVG WLLVAATSGV AAFFTMLYGL HYGRASSLRW LISMAVSFVE SMFVTQPLKV LGFAAFFALV
      1210       1220       1230       1240       1250       1260       1270       1280
LKRVDDEEDT VAPLPGHLLG PDPYALFRAR RNSSRDVYQP PLTAAIEKMK TTHLKEQKAF ALIREILAYL GFLWMLLLVA
      1290       1300       1310       1320       1330       1340       1350       1360
YGQRDPSAYH LNRHLQHSFT RGFSGVLGFR EFFKWANTTL VSNLYGHPPG FITDGNSKLV GSAQIRQVRV QESSCPLAQQ
      1370       1380       1390       1400       1410       1420       1430       1440
PQAYLNGCRA PYSLDAEDMA DYGEGWNATT LSEWQYQSQD QRQGYPIWGK LTVYRGGGYV VPLGTDRQST SRILRYLFDN
      1450       1460       1470       1480       1490       1500       1510       1520
TWLDALTRAV FVESTVYNAN VNLFCIVTLT LETSALGTFF THAALQSLRL YPFTDGWHPF VVAAELIYFL FLLYYMVVQG
      1530       1540       1550       1560       1570       1580       1590       1600
KRMSKETWGY FCSKWNLLEL AIILASWSAL AVFVKRAVLA ERDLQRCRNH REEGISFSET AAADAALGYI IAFLVLLSTV
      1610       1620       1630       1640       1650       1660       1670       1680
KLWHLLRLNP KMNMITAALR RAWGDISGFM IVILTMLLAY SIASNLIFGW KLRSYKTLFD AAETMVSLQL GIFNYEEVLD
      1690       1700       1710       1720       1730       1740       1750       1760
YSPVLGSFLI GSCIVFMTFV VLNLFISVIL VAFSEEQKYY QLSEEGEIVD LLLMKILSFL GIKSKREEPG SSREQPGSLS
      1770       1780
QTRHSRPAQA LPKD
```

| Cmpd. | No. of | m/z meas. | Δ m/z | z | Rt | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

|  | Cmpds. |  | [ppm] |  | [min] |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|
| 2032 | 2 | 616.2737 | -47.55 | 2 | 55.3 | 10.9 | 1 | 891-901 | K.DPAEQKMDLGK.I |  |

# Detailed Protein Report

## Protein 1580: thioredoxin domain-containing protein 5 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|224493972 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 36.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MEDAKVYVAK VDCTAHSDVC SAQGVRGYPT LKLFKPGQEA VKYQGPRDFQ TLENWMLQTL NEEPVTPEPE VEPPSAPELK
        90        100        110        120        130        140        150        160
QGLYELSASN FELHVAQGDH FIKFFAPWCG HCKALAPTWE QLALGLEHSE TVKIGKVDCT QHYELCSGNQ VRGYPTLLWF
       170        180        190        200        210        220        230        240
RDGKKVDQYK GKRDLESLRE YVESQLQRTE TGATETVTPS EAPVLAAEPE ADKGTVLALT ENNFDDTIAE GITFIKFYAP
       250        260        270        280        290        300        310        320
WCGHCKTLAP TWEELSKKEF PGLAGVKIAE VDCTAERNIC SKYSVRGYPT LLLFRGGKKV SEHSGGRDLD SLHRFVLSQA
       330
KDEL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1785 | 1 | 582.1343 | -236.00 | 2 | 50.7 | 10.9 | 0 | 268-277 | K.IAEVDCTAER.N | Carbamidomethyl: 6 |

# Detailed Protein Report

## Protein 1581: zinc finger CCHC domain-containing protein 24 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|223633947 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 26.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 7.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSLLSAIDTS | AASVYQPAQL | LNWVYLSLQD | THQASAFDAF | RPEPTAGAAP | PELAFGKGRP | EQLGSPLHSS | YLNSFFQLQR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GEALSNSVYK | GASPYGSLNN | IADGLSSLTE | HFSDLTLTSE | ARKPSKRPPP | NYLCHLCFNK | GHYIKDCPQA | RPKGEGLTPY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QGKKRCFGEY | KCPKCKRKWM | SGNSWANMGQ | ECIKCHINVY | PHKQRPLEKP | DGLDVSDQSK | EHPQHLCEKC | KVLGYYCRRV |
| 250 | | | | | | | |
| Q | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2518 | 1 | 1013.8383 | -110.40 | 2 | 61.4 | 10.9 | 1 | 178-194 | R.KWMSGNSWANMGQECIK.C | Carbamidomethyl: 15 |

# Detailed Protein Report

## Protein 1582: endoribonuclease Dicer isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|307133775 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 208.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.24 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.51 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKSPALQPLS | MAGLQLMTPA | SSPMGPFFGL | PWQQEAIHDN | IYTPRKYQVE | LLEAALDHNT | IVCLNTGSGK | TFIAVLLTKE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LSYQIRGDFS | RNGKRTVFLV | NSANQVAQQV | SAVRTHSDLK | VGEYSNLEVN | ASWTKERWNQ | EFTKHQVLIM | TCYVALNVLK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NGYLSLSDIN | LLVFDECHLA | ILDHPYREIM | KLCENCPSCP | RILGLTASIL | NGKCDPEELE | EKIQKLEKIL | KSNAETATDL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VVLDRYTSQP | CEIVVDCGPF | TDRSGLYERL | LMELEEALNF | INDCNISVHS | KERDSTLISK | QILSDCRAVL | VVLGPWCADK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VAGMMVRELQ | KYIKHEQEEL | HRKFLLFTDT | FLRKIHALCE | EHFSPASLDL | KFVTPKVIKL | LEILRKYKPY | ERQQFESVEW |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YNNRNQDNYV | SWSDSEDDDE | DEEIEEKEKP | ETNFPSPFTN | ILCGIIFVER | RYTAVVLNRL | IKEAGKQDPE | LAYISSNFIT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GHGIGKNQPR | NKQMEAEFRK | QEEVLRKFRA | HETNLLIATS | IVEEGVDIPK | CNLVVRFDLP | TEYRSYVQSK | GRARAPISNY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IMLADTDKIK | SFEEDLKTYK | AIEKILRNKC | SKSVDTGETD | IDPVMDDDDV | FPPYVLRPDD | GGPRVTINTA | IGHINRYCAR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LPSDPFTHLA | PKCRTRELPD | GTFYSTLYLP | INSPLRASIV | GPPMSCVRLA | ERVVALICCE | KLHKIGELDD | HLMPVGKETV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KYEEELDLHD | EEETSVPGRP | GSTKRRQCYP | KAIPECLRDS | YPRPDQPCYL | YVIGMVLTTP | LPDELNFRRR | KLYPPEDTTR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| CFGILTAKPI | PQIPHFPVYT | RSGEVTISIE | LKKSGFMLSL | QMLELITRLH | QYIFSHILRL | EKPALEFKPT | DADSAYCVLP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LNVVNDSSTL | DIDFKFMEDI | EKSEARIGIP | STKYTKETPF | VFKLEDYQDA | VIIPRYRNFD | QPHRFYVADV | YTDLTPLSKF |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PSPEYETFAE | YYKTKYNLDL | TNLNQPLLDV | DHTSSRLNLL | TPRHLNQKGK | ALPLSSAEKR | KAKWESLQNK | QILVPELCAI |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| HPIPASLWRK | AVCLPSILYR | LHCLLTAEEL | RAQTASDAGV | GVRSLPADFR | YPNLDFGWKK | SIDSKSFISI | SNSSSAENDN |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| YCKHSTIVPE | NAAHQGANRT | SSLENHDQMS | VNCRTLLSES | PGKLHVEVSA | DLTAINGLSY | NQNLANGSYD | LANRDFCQGN |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| QLNYYKQEIP | VQPTTSYSIQ | NLYSYENQPQ | PSDECTLLSN | KYLDGNANKS | TSDGSPVMAV | MPGTTDTIQV | LKGRMDSEQS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PSIGYSSRTL | GPNPGLILQA | LTLSNASDGF | NLERLEMLGD | SFLKHAITTY | LFCTYPDAHE | GRLSYMRSKK | VSNCNLYRLG |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| KKKGLPSRMV | VSIFDPPVNW | LPPGYVVNQD | KSNTDKWEKD | EMTKDCMLAN | GKLDEDYEEE | DEEEESLMWR | APKEEADYED |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DFLEYDQEHI | RFIDNMLMGS | GAFVKKISLS | PFSTTDSAYE | WKMPKKSSLG | SMPFSSDFED | FDYSSWDAMC | YLDPSKAVEE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| DDFVVGFWNP | SEENCGVDTG | KQSISYDLHT | EQCIADKSIA | DCVEALLGCY | LTSCGERAAQ | LFLCSLGLKV | LPVIKRTDRE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| KALCPTRENF | NSQQKNLSVS | CAAASVASSR | SSVLKDSEYG | CLKIPPRCMF | DHPDADKTLN | HLISGFENFE | KKINYRFKNK |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| AYLLQAFTHA | SYHYNTITDC | YQRLEFLGDA | ILDYLITKHL | YEDPRQHSPG | VLTDLRSALV | NNTIFASLAV | KYDYHKYFKA |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | |
| VSPELFHVID | DFVQFQLEKN | EMQGMDSEKS | FLQMYPVPLC | ENCLKWNQKL | PNLARLRELT | TGRSESLWK | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 894 | 1 | 848.9522 | 46.83 | 2 | 41.2 | 10.9 | 0 | 121-135 | K.VGEYSNLEVNASWTK.E | | QU:MU 1.24<br>WUP:QUP 0.51 |

# Detailed Protein Report

## Protein 1583: PREDICTED: ubiquitin-conjugating enzyme E2 variant 1-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578805476 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 13.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 10.1 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MDITDIPEKS SEGQSSSNSN ARWQPPWAQA IYESQIYSLK IECGPKYPEE LPFVRFVTKI NMSRVNSSNG MVNPRAISAL
        90        100        110        120
AKWQNSYIIK VILQELQRLM MSKENVKHPQ PSEGQCYSN
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2510 | 1 | 673.8533 | 115.98 | 2 | 62.0 | 10.9 | 0 | 108-119 | K.HPQPSEGQCYSN.- | |

# Detailed Protein Report

## Protein 1584: zinc finger protein 679 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|224586910 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 47.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 6.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAKRPGSPGS | REMGLLTFRD | VVIEFSLEEW | QCLDHAQQNL | YRDVMLENYR | NLVSLGIAVS | KPDLITCLEQ | NKEPWNIKRN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EMVTKHPVMC | SHFTQDLPPE | LGIKDSLQKV | IPRRYGKSGH | DNLQVKTCKS | MGECEVQKGG | CNEVNQCLST | TQNKIFQTHK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CVKVFGKFSN | SNRHKTRHTG | KKHFKCKKYG | KSFCMVSQLH | QHQIIHTREN | SYQCEECGKP | FNCSSTLSKH | KRIHTGEKPY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RCEECGKAFT | WSSTLTKHRR | IHTGEKPYTC | EECGQAFSRS | STLANHKRIH | TGEKPYTCEE | CGKAFSLSSS | LTYHKRIHTG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EKPYTCEECG | KAFNCSSTLK | KHKIIHTGEK | PYKCKECGKA | FAFSSTLNTH | KRIHTGEEPY | KCEECDKAFK | WSSSLANHKS |
| 410 | 420 | | | | | | |
| MHTGEKPYKC | E | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 980 | 1 | 946.4851 | 32.32 | 3 | 42.3 | 10.9 | 2 | 139-163 | K.GGCNEVNQCLSTTQNKIFQTHKCVK.V | Carbamidomethyl: 23 |

# Detailed Protein Report

## Protein 1585: nucleoside diphosphate kinase 3 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|37693993 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 19.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MICLVLTIFA | NLFPAACTGA | HERTFLAVKP | DGVQRRLVGE | IVRRFERKGF | KLVALKLVQA | SEELLREHYA | ELRERPFYGR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LVKYMASGPV | VAMVWQGLDV | VRTSRALIGA | TNPADAPPGT | IRGDFCIEVG | KNLIHGSDSV | ESARREIALW | FRADELLCWE |
| 170 | | | | | | | |
| DSAGHWLYE | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 739 | 1 | 512.6267 | -224.89 | 2 | 38.8 | 10.9 | 0 | 123-131 | R.GDFCIEVGK.N | Carbamidomethyl: 4 |

# Detailed Protein Report

## Protein 1586: OTU domain-containing protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|223941923 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 51.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.86 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MQLYSSVCTH | YPAGAPGPTA | AAPAPPAAAT | PFKVSLQPPG | AAGAAPEPET | GECQPAAAAE | HREAAAVPAA | KMPAFSSCFE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VVSGAAAPAS | AAAGPPGASC | KPPLPPHYTS | TAQITVRALG | ADRLLLHGPD | PVPGAAGSAA | APRGRCLLLA | PAPAAPVPPR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RGSSAWLLEE | LLRPDCPEPA | GLDATREGPD | RNFRLSEHRQ | ALAAAKHRGP | AATPGSPDPG | PGPWGEEHLA | ERGPRGWERG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GDRCDAPGGD | AARRPDPEAE | APPAGSIEAA | PSSAAEPVIV | SRSDPRDEKL | ALYLAEVEKQ | DKYLRQRNKY | RFHIIPDGNC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LYRAVSKTVY | GDQSLHRELR | EQTVHYIADH | LDHFSPLIEG | DVGEFIIAAA | QDGAWAGYPE | LLAMGQMLNV | NIHLTTGGRL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ESPTVSTMIH | YLGPEDSLRP | SIWLSWLSNG | HYDAVFDHSY | PNPEYDNWCK | QTQVQRKRDE | ELAKSMAISL | SKMYIEQNAC |
| 490 | | | | | | | |
| S | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 364 | 1 | 529.8113 | 176.64 | 2 | 34.5 | 10.9 | 0 | 473-481 | K.MYIEQNACS.- | | WUP:QUP 0.86 |

# Detailed Protein Report

## Protein 1587: immunoglobulin superfamily member 10 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|296011049 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 66.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 4.3 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578807304 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: immunoglobulin superfamily member 10 isoform X6 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGDDLILMHV | SLRLKPAKID | HKQYFRKQVL | HGKDFQVDCK | ASGSPVPEIS | WSLPDGTMIN | NAMQADDSGH | RTRRYTLFNN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GTLYFNKVGV | AEEGDYTCYA | QNTLGKDEMK | VHLTVITAAP | RIRQSNKTNK | RIKAGDTAVL | DCEVTGDPKP | KIFWLLPSND |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MISFSIDRYT | FHANGSLTIN | KVKLLDSGEY | VCVARNPSGD | DTKMYKLDVV | SKPPLINGLY | TNRTVIKATA | VRHSKKHFDC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RAEGTPSPEV | MWIMPDNIFL | TAPYYGSRIT | VHKNGTLEIR | NVRLSDSADF | ICVARNEGGE | SVLVVQLEVL | EMLRRPTFRN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PFNEKIVAQL | GKSTALNCSV | DGNPPPEIIW | ILPNGTRFSN | GPQSYQYLIA | SNGSFIISKT | TREDAGKYRC | AARNKVGYIE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KLVILEIGQK | PVILTYAPGT | VKGISGESLS | LHCVSDGIPK | PNIKWTMPSG | YVVDRPQING | KYILHDNGTL | VIKEATAYDR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GNYICKAQNS | VGHTLITVPV | MIVAYPPRIT | NRPPRSIVTR | TGAAFQLHCV | ALGVPKPEIT | WEMPDHSLLS | TASKERTHGS |
| 570 | 580 | 590 | 600 | 610 | | | |
| EQLHLQGTLV | IQNPQTSDSG | IYKCTAKNPL | GSDYAATYIQ | VI | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2141 | 1 | 946.8637 | -28.07 | 3 | 57.2 | 10.9 | 2 | 207-232 | K.LDVVSKPPLINGLYTNRTVIKATAVR.H | |

# Detailed Protein Report

## Protein 1588: amphiregulin preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4502199 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| | | **Sequence Coverage [%]:** | 6.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MRAPLLPPAP | VVLSLLILGS | GHYAAGLDLN | DTYSGKREPF | SGDHSADGFE | VTSRSEMSSG | SEISPVSEMP | SSSEPSSGAD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YDYSEEYDNE | PQIPGYIVDD | SVRVEQVVKP | PQNKTESENT | SDKPKRKKKG | GKNGKNRRNR | KKKNPCNAEF | QNFCIHGECK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YIEHLEAVTC | KCQQEYFGER | CGEKSMKTHS | MIDSSLSKIA | LAAIAAFMSA | VILTAVAVIT | VQLRRQYVRK | YEGEAEERKK |
| 250 | 260 | | | | | | |
| LRQENGNVHA | IA | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1180 | 1 | 977.2721 | -136.69 | 2 | 44.3 | 10.9 | 0 | 144-160 | K.NPCNAEFQNFCIHGECK.Y | |

# Detailed Protein Report

## Protein 1589: PREDICTED: eukaryotic translation initiation factor 2D isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578800618 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 48.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.1 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSTAEMLTSG | LKGRGFSVLH | TYQDHLWRSG | NKSSPPSIAP | LALDSADLSE | EKGSVQMDST | LQGDMRHMTL | EGEEENGEVH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QAREDKSLSE | APEDTSTRGL | NQDSTDSKTL | QEQMDELLQQ | CFLHALKCRV | KKADLPLLTS | TFLGSHMFSC | CPEGRQLDIK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KSSYKKLSKF | LQQMQQEQII | QVKELSKGVE | SIVAVDWKHP | RITSFVIPEP | SPTSQTIQEG | SREQPYHPPD | IKPLYCVPAS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MTLLFQESGH | KKGSFLEGSE | VRTIVINYAK | KNDLVDADNK | NLVRLDPILC | DCILEKNEQH | TVMKLPWDSL | LTRCLEKLQP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AYQVTLPGQE | PIVKKGRICP | IDITLAQRAS | NKKVTVVRNL | EAYGLDPYSV | AAILQQRCQA | STTVNPAPGA | KDSLQVQIQG |
| 410 | 420 | 430 | 440 | | | | |
| NQVHHLGWLL | LEEYQLPRKH | IQGLEKALKP | GKKK | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 753 | 1 | 787.4122 | -14.92 | 2 | 39.4 | 10.9 | 1 | 305-317 | K.LPWDSLLTRCLEK.L | |

# Detailed Protein Report

## Protein 1590: desmin [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|55749932 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 53.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| | | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSQAYSSSQR | VSSYRRTFGG | APGFPLGSPL | SSPVFPRAGF | GSKGSSSSVT | SRVYQVSRTS | GGAGGLGSLR | ASRLGTTRTP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SSYGAGELLD | FSLADAVNQE | FLTTRTNEKV | ELQELNDRFA | NYIEKVRFLE | QQNAALAAEV | NRLKGREPTR | VAELYEEELR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ELRRQVEVLT | NQRARVDVER | DNLLDDLQRL | KAKLQEEIQL | KEEAENNLAA | FRADVDAATL | ARIDLERRIE | SLNEEIAFLK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KVHEEEIREL | QAQLQEQQVQ | VEMDMSKPDL | TAALRDIRAQ | YETIAAKNIS | EAEEWYKSKV | SDLTQAANKN | NDALRQAKQE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MMEYRHQIQS | YTCEIDALKG | TNDSLMRQMR | ELEDRFASEA | SGYQDNIARL | EEEIRHLKDE | MARHLREYQD | LLNVKMALDV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EIATYRKLLE | GEESRINLPI | QTYSALNFRE | TSPEQRGSEV | HTKKTVMIKT | IETRDGEVVS | EATQQQHEVL | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 80 | 1 | 707.7702 | -112.32 | 2 | 29.9 | 10.9 | 1 | 38-52 | R.AGFGSKGSSSSVTSR.V | |

# Detailed Protein Report

## Protein 1591: dnaJ homolog subfamily C member 27 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|310616728 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 20.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| | | **Sequence Coverage [%]:** | 9.6 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEANMPKRKE | PGRSLRIKVI | SMGNAEVGKS | CIIKRYCEKR | FVSKYLATIG | IDYGVTKVHV | RDREIKVNIF | DMAGHPFFYE |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| VRNEFYKDTQ | GVILVYDVGQ | KDSFDALDAW | LAEMKQELGP | HGNMENIIFV | VCANKIDCTK | HRCVDESEGR | LWAESKGFLY |
| **170** | **180** | | | | | | |
| FETSAQTGEG | INEMFQG | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2209 | 1 | 953.1391 | 111.03 | 2 | 58.0 | 10.9 | 1 | 45-61 | K.YLATIGIDYGVTKVHVR.D | |

# Detailed Protein Report

**Protein 1592:** **PREDICTED: type II inositol 3,4-bisphosphate 4-phosphatase isoform X9 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578809595 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 66.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 3.19 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEIKEEGASE | EGQHFLPTAQ | ANDPGDCQFT | SIQKTPNEPQ | LEFILACKDL | VAPVRDRKLN | TLVQISVIHP | VEQSLTRYSS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TEIVEGTRDP | LFLTGVTFPS | EYPIYEETKI | KLTVYDVKDK | SHDTVRTSVL | PEHKDPPPEV | GRSFLGYASF | KVGELLKSKE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QLLVLSLRTS | DGGKVVGTIE | VSVVKMGEIE | DGEADHITTD | VQGQKCALVC | ECTAPESVSG | KDNLPFLNSV | LKNPVCKLYR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FPTSDNKWMR | IREQMSESIL | SFHIPKELIS | LHIKEDLCRN | QEIKELGELS | PHWDNLRKNV | LTHCDQMVNM | YQDILTELSK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ETGSSFKSSS | SKGEKTLEFV | PINLHLQRMQ | VHSPHLKDIS | SGIPQIDALY | DVITVGAPAA | HFQGFKNGGL | RKLLHRFETE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RRNTGYQFIY | YSPENTAKAK | EVLSNINQLQ | PLIATHADLL | LNSASQHSPD | SLKNSLKMLS | EKTELFVHAF | KDQLVRSALL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ALYTARPGGI | LKKPPSPKSS | TEESSPQDQP | PVMRGQDSIP | HHSDYDEEEW | DRVWANVGKS | LNCIIAMVDK | LIERDGGSEG |
| 570 | 580 | 590 | 600 | | | | |
| SGGNNDGEKE | PSLTDAIPSH | PRGCDNGNNN | SYKLL | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2038 | 1 | 945.8225 | -108.23 | 2 | 55.4 | 10.9 | 1 | 551-569 | K.LIERDGGSEGSGGNNDGEK.E | | WUP:QUP 3.19 |

# Detailed Protein Report

## Protein 1593: PREDICTED: WD repeat-containing protein 60 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530387279 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 64.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRSTKLLRLI | DLDFSFTFSL | LDLPPVNEYD | MYIRNFGKKN | TKQAYVQCNE | DNVERDIQTE | EIETREVWTQ | HPGESTVVSG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GSEQRDTSDA | VVMPKIDTPR | LCSFLRAACQ | VMAVLLEEDR | LAAEPSWNLR | AQDRALYFSD | SSSQLNTSLP | FLQNRKVSSL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HTSRVQRQMV | VSVHDLPEKS | FVPLLDSKYV | LCVWDIWQPS | GPQKVLICES | QVTCCCLSPL | KAFLLFAGTA | HGSVVVWDLR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EDSRLHYSVT | LSDGFWTFRT | ATFSTDGILT | SVNHRSPLQA | VEPISTSVHK | KQSFVLSPFS | TQEEMSGLSF | HIASLDESGV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LNVWVVVELP | KADIAGSISD | LGLMPGGRVK | LVHSALIQLG | DSLSHKGNEF | WGTTQTLNVK | FLPSDPNHFI | IGTDMGLISH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GTRQDLRVAP | KLFKPQQHGI | RPVKVNVIDF | SPFGEPIFLA | GCSDGSIRLH | QLSSAFPLLQ | WDSSTDSHAV | TGLQWSPTRP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AVFLVQDDTS | NIYIWDLLQS | DLGPVAKQQV | SPNRLVAMAA | VGEPEKAGGS | FLALVLARAS | GSIDIQHLKR | RWAAPEVDEC |
| 570 | 580 | | | | | | |
| NRLRLLLQEA | LWPEGKLHK | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 102 | 1 | 619.6363 | -51.30 | 3 | 30.2 | 10.9 | 1 | 332-350 | K.ADIAGSISDLGLMPGGRVK.L | |

# Detailed Protein Report

## Protein 1594: divergent paired-related homeobox [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|61969664 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MPGSEDLRKG KDQMHSHRKR TMFTKKQLED LNILFNENPY PNPSLQKEMA SKIDIHPTVL QVWFKNHRAK LKKAKCKHIH
        90        100        110        120        130        140        150        160
QKQETPQPPI PEGGVSTSVG LRNADTLPRL PNAAHPIGLV YTGHRVPSFQ LILYPNLKVP ANDFIGHRIV HFGCCRDPNI
       170        180        190        200
YCLYPILESQ VCAPSFHSGS PACSSNQSRE R
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1658 | 1 | 524.8093 | 123.74 | 2 | 51.0 | 10.9 | 0 | 149-156 | R.IVHFGCCR.D | Carbamidomethyl: 6, 7 |

# Detailed Protein Report

## Protein 1595: protein Wnt-10a precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|16936520 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.7 |
| | | **Sequence Coverage [%]:** | 3.1 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGSAHPRPWL | RLRPQPQPRP | ALWVLLFFLL | LLAAAMPRSA | PNDILDLRLP | PEPVLNANTV | CLTLPGLSRR | QMEVCVRHPD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VAASAIQGIQ | IAIHECQHQF | RDQRWNCSSL | ETRNKIPYES | PIFSRGFRES | AFAYAIAAAG | VVHAVSNACA | LGKLKACGCD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ASRRGDEEAF | RRKLHRLQLD | ALQRGKGLSH | GVPEHPALPT | ASPGLQDSWE | WGGCSPDMGF | GERFSKDFLD | SREPHRDIHA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RMRLHNNRVG | RQAVMENMRR | KCKCHGTSGS | CQLKTCWQVT | PEFRTVGALL | RSRFHRATLI | RPHNRNGGQL | EPGPAGAPSP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| APGAPGPRRR | ASPADLVYFE | KSPDFCEREP | RLDSAGTVGR | LCNKSSAGSD | GCGSMCCGRG | HNILRQTRSE | RCHCRFHWCC |
| 410 | 420 | | | | | | |
| FVVCEECRIT | EWVSVCK | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2462 | 1 | 676.2569 | -62.81 | 2 | 61.3 | 10.9 | 1 | 262-274 | K.CKCHGTSGSCQLK.T | |

# Detailed Protein Report

**Protein 1596:** **PREDICTED: SH3 domain-containing RING finger protein 3 isoform X2 [Homo sapiens]**

**Accession:** gi|578804249
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 10.9
**MW [kDa]:** 63.9
**pI:** 9.8
**Sequence Coverage [%]:** 1.8
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLLGASWLCA | SKAAAAAAQS | EGDEDRPGER | RRRRAAATAA | GAGEDMDESS | LLDLLECSVC | LERLDTTAKV | LPCQHTFCRR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CLESIVCSRH | ELRCPECRIL | VGCGVDELPA | NILLVRLLDG | IRQRPRAGTS | PGGSPPARPI | PGQSAAPTLA | GGGGGAAGST |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PGSPVFLSAA | AGSTAGSLRE | LATSRTAPAA | KNPCLLPYGK | ALYSYEGKEP | GDLKFNKGDI | IVLRRKVDEQ | WYHGELHGTQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GFLPASYIQC | IQPLPHAPPQ | GKALYDFEMK | DKDQDKDCLT | FTKDEILTVL | RRVDENWAEG | MLGDKIGIFP | LLYVELNDSA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KQLIEMDKPC | PAAASSCNAS | LPSDSGAVAS | VAPSPTLSSS | GAVSAFQRRV | DGKKNTKKRH | SFTALSVTHR | SSQAASHRHS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MEISAPVLIS | SSDPRAAARI | GDLAHLSCAA | PTQDVSSSAG | STPTAVPRAA | SVSGEQGTPP | KVQLPLNVYL | ALYAYKPQKS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DELELHKGEM | YRVLEKCQDG | WFKGASLRTG | VSGVFPGNYV | TPVSRVPAGG | AGPPRNNVVG | GSPLAKGITT | TMHPGSGSLS |
| 570 | 580 | 590 | 600 | 610 | 620 | | |
| SLATATRPAL | PITTPQAHAQ | HPTASPPTGS | CLRHSAQPTA | SQARSTISTG | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 447 | 1 | 705.2428 | -148.77 | 2 | 34.1 | 10.9 | 1 | 493-503 | R.VLEKCQDGWFK.G | Carbamidomethyl: 5 |

# Detailed Protein Report

## Protein 1597: sorting nexin-18 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|157057543 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 68.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MALRARALYD | FRSENPGEIS | LREHEVLSLC | SEQDIEGWLE | GVNSRGDRGL | FPASYVQVIR | APEPGPAGDG | GPGAPARYAN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VPPGGFEPLP | VAPPASFKPP | PDAFQALLQP | QQAPPPSTFQ | PPGAGFPYGG | GALQPSPQQL | YGGYQASQGS | DDDWDDEWDD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SSTVADEPGA | LGSGAYPDLD | GSSSAGVGAA | GRYRLSTRSD | LSLGSRGGSV | PPQHHPSGPK | SSATVSRNLN | RFSTFVKSGG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EAFVLGEASG | FVKDGDKLCV | VLGPYGPEWQ | ENPYPFQCTI | DDPTKQTKFK | GMKSYISYKL | VPTHTQVPVH | RRYKHFDWLY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ARLAEKFPVI | SVPHLPEKQA | TGRFEEDFIS | KRRKGLIWWM | NHMASHPVLA | QCDVFQHFLT | CPSSTDEKAW | KQGKRKAEKD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EMVGANFFLT | LSTPPAAALD | LQEVESKIDG | FKCFTKKMDD | SALQLNHTAN | EFARKQVTGF | KKEYQKVGQS | FRGLSQAFEL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DQQAFSVGLN | QAIAFTGDAY | DAIGELFAEQ | PRQDLDPVMD | LLALYQGHLA | NFPDIIHVQK | GKAWPLEQVI | WSVLCRLKGA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| TLTAVPLWVS | ESYSTGEEAS | RDVDAWVFSL | ECKLDCSTGS | FLLEYLALGN | EYSFSKVQRV | PLMTVLSF | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1470 | 1 | 1022.6762 | 114.58 | 1 | 46.8 | 10.9 | 0 | 620-628 | R.VPLMTVLSF.- | Oxidation: 4 |

# Detailed Protein Report

## Protein 1598: PREDICTED: bromodomain adjacent to zinc finger domain protein 2B isoform X27 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578804191 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 215.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MESGERLPSS | AASSTTPTSS | STPSVASVVS | KGGLSTGVAS | LSSTINPCGH | LFRTAGDQPF | NLSTVSSAFP | MVSHPVFGLH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SASSGHSEFG | GLGTLGTPTA | LAAHPQLASF | PGAEWWRTTD | AHTRTGATFF | PPLLGIPPLF | APPAQNHDSS | SFHSRTSGKS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NRNGPEKGVN | GSINGSNTSS | VIGINTSVLS | TTASSSMGQT | KSTSSGGGNR | KCNQEQSKNQ | PLDARVDKIK | DKKPRKKAME |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SSSNSDSDSG | TSSDTSSEGI | SSSDSDDLEE | DEEEEDQSIE | ESEDDDSDSE | SEAQHKSNNQ | VLLHGISDPK | ADGQKATEKA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QEKRIHQPLP | LASESQTHSF | QSQQKQPQVL | SQQLPFIFQS | SQAKEESVNK | HTSVIQSTGL | VSNVKPLSLV | NQAKKETYMK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LIVPSPDVLK | AGNKNTSEES | SLLTSELRSK | REQYKQAFPS | QLKKQESSKS | LKKVIAALSN | PKATSSSPAH | PKQTLENNHP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NPFLTNALLG | NHQPNGVIQS | VIQEAPLALT | TKTKMQSKIN | ENIAAASSTP | FSSPVNLSTS | GRRTPGNQTP | VMPSASPILH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SQGKEKAVSN | NVNPVKTQHH | SHPAKSLVEQ | FRGTDSDIPS | SKDSEDSNED | EEEDDEEEDE | EDDEDDESDD | SQSESDSNSE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SDTEGSEEED | DDDKDQDESD | SDTEGEKTSM | KLNKTTSSVK | SPSMSLTGHS | TPRNLHIAKA | PGSAPAALCS | ESQSPAFLGT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SSSTLTSSPH | SGTSKRRRVT | DERELRIPLE | YGWQRETRIR | NFGGRLQGEV | AYYAPCGKKL | RQYPEVIKYL | SRNGIMDISR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DNFSFSAKIR | VGDFYEARDG | PQGMQWCLLK | EEDVIPRIRA | MEGRRGRPPN | PDRQRAREES | RMRRRKGRPP | NVGNAEFLDN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ADAKLLRKLQ | AQEIARQAAQ | IKLLRKLQKQ | EQARVAKEAK | KQQAIMAAEE | KRKQKEQIKI | MKQQEKIKRI | QQIRMEKELR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| AQQILEAKKK | KKEEAANAKL | LEAEKRIKEK | EMRRQQAVLL | KHQELERHRL | DMVWERERRR | QHMMLMKAME | ARKKAEEKER |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LKQEKRDEKR | LNKERKLEQR | RLELEMAKEL | KKPNEDMCLA | DQKPLPELPR | IPGLVLSGST | FSDCLMVVQF | LRNFGKVLGF |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DVNIDVPNLS | VLQEGLLNIG | DSMGEVQDLL | VRLLSAAVCD | PGLITGYKAK | TALGEHLLNV | GVNRDNVSEI | LQIFMEAHCG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| QTELTESLKT | KAFQAHTPAQ | KASVLAFLIN | ELACSKSVVS | EIDKNIDYMS | NLRRDKWVVE | GKLRKLRIIH | AKKTGKRDTS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| GGIDLGEEQH | PLGTPTPGRK | RRRKGGDSDY | DDDDDDDSDD | QGDEDDEDEE | DKEDKKGKKT | DICEDEDEGD | QAASVEELEK |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| QIEKLSKQQS | QYRRKLFDAS | HSLRSVMFGQ | DRYRRRYWIL | PQCGGIFVEG | MESGEGLEEI | AKEREKLKKA | ESVQIKEEMF |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| ETSGDSLNCS | NTDHCEQKED | LKEKDNTNLF | LQKPGSFSKL | SKLLEVAKMP | PESEVMTPKP | NAGANGCTLS | YQNSGKHSLG |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| SVQSTATQSN | VEKADSNNLF | NTGSSGPGKF | YSPLPNDQLL | KTLTEKNRQW | FSLLPRTPCD | DTSLTHADMS | TASLVTPQSQ |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| PPSKSPSPTP | APLGSSAQNP | VGLNPFALSP | LQVKGGVSMM | GLQFCGWPTG | VVTSNIPFTS | SVPSLGSGLG | LSEGNGNSFL |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| TSNVASSKSE | SPVPQNEKAT | SAQPAAVEVA | KPVDFPSPKP | IPEEMQFGWW | RIIDPEDLKA | LLKVLHLRGI | REKALQKQIQ |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| KHLDYITQAC | LKNKDVAIIE | LNENEENQVT | RDIVENWSVE | EQAMEMDLSV | LQQVEDLERR | VASASLQVKG | WMCPEPASER |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| EDLVYFEHKS | FTKLCKEHDG | EFTGEDESSA | HALERKSDNP | LDIAVTRLAD | LERNIERSTA | KSVEREIMKN | CFFFVMAVTK |
| 1930 | 1940 | 1950 | 1960 | | | | |
| AVIPTAIDPR | LQQSQMETGF | VQLALLRQVV | KL | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1818 | 1 | 1273.0889 | -96.81 | 2 | 51.1 | 10.9 | 2 | 1931-1952 | R.LQQSQMETGFVQLALLRQVVKL.- | Oxidation: 6 |

# Detailed Protein Report

**Protein 1599:** **TFIIH basal transcription factor complex helicase XPD subunit isoform 2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|195947407 | **Score:** | 10.9 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 4.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRELKRTLDA | KGHGVLEMPS | GTGKTVSLLA | LIMAYQRAYP | LEVTKLIYCS | RTVPEIEKVI | EELRKLLNFY | EKQEGEKLPF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LGLALSSRKN | LCIHPEVTPL | RFGKDVDGKC | HSLTASYVRA | QYQHDTSLPH | CRFYEEFDAH | GREVPLPAGI | YNLDDLKALG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RRQGWCPYFL | ARYSILHANV | VVYSYHYLLD | PKIADLVSKE | LARKAVVVFD | EAHNIDNVCI | DSMSVNLTRR | TLDRCQGNLE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TLQKTVLRIK | ETDEQRLRDE | YRRLVEGLRE | ASAARETDAH | LANPVLPDEV | LQEAVPGSIR | TAEHFLGFLR | RLLEYVKWRL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RVQHVVQESP | PAFLSGLAQR | VCIQRKPLRF | CAERLRSLLH | TLEITDLADF | SPLTLLANFA | TLVSTYAKGQ | AQHCGSSRNQ |
| 410 | | | | | | | |
| KRSHP | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1633 | 1 | 977.4534 | -60.37 | 2 | 48.7 | 10.9 | 2 | 6-24 | K.RTLDAKGHGVLEMPSGTGK.T | |

# Detailed Protein Report

**Protein 1600:** **PREDICTED: TGF-beta-activated kinase 1 and MAP3K7-binding protein 3 isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578837866 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 75.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MAQSSPQLDI QVLHDLRQRF PEIPEGVVSQ CMLQNNNNLE ACCRALSQES SKYLYMEYHS PDDNRMNRNR LLHINLGIHS

        90        100        110        120        130        140        150        160
PSSYHPGDGA QLNGGRTLVH SSSDGHIDPQ HAAGKQLICL VQEPHSAPAV VAATPNYNPF FMNEQNRSAA TPPSQPPQQP

       170        180        190        200        210        220        230        240
SSMQTGMNPS AMQGPSPPPP PPSYMHIPRY STNPITVTVS QNLPSGQTVP RALQILPQIP SNLYGSPGSI YIRQTSQSSS

       250        260        270        280        290        300        310        320
GRQTPQSTPW QSSPQGPVPH YSQRPLPVYP HQQNYQPSQY SPKQQQIPQS AYHSPPPSQC PSPFSSPQHQ VQPSQLGHIF

       330        340        350        360        370        380        390        400
MPPSPSTTPP HPYQQGPPSY QKQGSHSVAY LPYTASSLSK GSMKKIEITV EPSQRPGTAI NRSPSPISNQ PSPRNQHSLY

       410        420        430        440        450        460        470        480
TATTPPSSSP SRGISSQPKP PFSVNPVYIT YTQPTGPSCT PSPSPRVIPN PTTVFKITVG RATTENLLNL VDQEERSAAP

       490        500        510        520        530        540        550        560
EPIQPISVIP GSGGEKGSHK YQRSSSSGSD DYAYTQALLL HQRARMERLA KQLKLEKEEL ERLKSEVNGM EHDLMQRRLR

       570        580        590        600        610        620        630        640
RVSCTTAIPT PEEMTRLRSM NRQLQINVDC TLKEVDLLQS RGNFDPKAMN NFYDNIEPGP VVPPKPSKKE HRTGSTQSPR

       650        660        670        680
TQPRDEDYEG APWNCDSCTF LNHPALNRCE QCEMPRYT
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2667 | 1 | 821.4359 | -63.35 | 2 | 63.5 | 10.8 | 1 | 447-461 | R.VIPNPTTVFKITVGR.A | |

# Detailed Protein Report

## Protein 1601: arylsulfatase A isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|146229327 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 44.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGMYPGVLVP | SSRGGLPLEE | VTVAEVLAAR | GYLTGMAGKW | HLGVGPEGAF | LPPHQGFHRF | LGIPYSHDQG | PCQNLTCFPP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ATPCDGGCDQ | GLVPIPLLAN | LSVEAQPPWL | PGLEARYMAF | AHDLMADAQR | QDRPFFLYYA | SHHTHYPQFS | GQSFAERSGR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GPFGDSLMEL | DAAVGTLMTA | IGDLGLLEET | LVIFTADNGP | ETMRMSRGGC | SGLLRCGKGT | TYEGGVREPA | LAFWPGHIAP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GVTHELASSL | DLLPTLAALA | GAPLPNVTLD | GFDLSPLLLG | TGKSPRQSLF | FYPSYPDEVR | GVFAVRTGKY | KAHFFTQGSA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HSDTTADPAC | HASSSLTAHE | PPLLYDLSKD | PGENYNLLGG | VAGATPEVLQ | ALKQLQLLKA | QLDAAVTFGP | SQVARGEDPA |
| 410 | 420 | 430 | | | | | |
| LQICCHPGCT | PRPACCHCPD | PHA | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2659 | 1 | 741.3515 | -11.91 | 2 | 63.3 | 10.8 | 2 | 205-218 | R.MSRGGCSGLLRCGK.G | Carbamidomethyl: 6 |

# Detailed Protein Report

## Protein 1602: platelet-derived growth factor D isoform 2 precursor [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|15451921 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 42.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
|  |  | **Sequence Coverage [%]:** | 3.0 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MHRLIFVYTL | ICANFCSCRD | TSATPQSASI | KALRNANLRR | DDLYRRDETI | QVKGNGYVQS | PRFPNSYPRN | LLLTWRLHSQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ENTRIQLVFD | NQFGLEEAEN | DICRYDFVEV | EDISETSTII | RGRWCGHKEV | PPRIKSRTNQ | IKITFKSDDY | FVAKPGFKIY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YSLLEDFQPA | AASETNWESV | TSSISGVSYN | SPSVTDPTLI | ADALDKKIAE | FDTVEDLLKY | FNPESWQEDL | ENMYLDTPRY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RGRSYHDRKS | KVDLDRLNDD | AKRYSCTPRN | YSVNIREELK | LANVVFFPRC | LLVQRCGGNC | GCGTVNWRSC | TCNSGKTVKK |
| 330 | 340 | 350 | 360 | 370 |  |  |  |
| YHEVLQFEPG | HIKRRGRAKT | MALVDIQLDH | HERCDCICSS | RPPR |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2901 | 1 | 682.8331 | -42.36 | 2 | 65.0 | 10.8 | 1 | 270-280 | R.NYSVNIREELK.L |  |

BRUKER

# Detailed Protein Report

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**Protein 1603:** **uncharacterized protein C17orf80 isoform d [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|571026655 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 60.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSDNPPRMEV | CPYCKKPFKR | LKSHLPYCKM | IGPTIPTDQK | VYQSKPATLP | RAKKMKGPIK | DLIKAKGKEL | ETENEERNSK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LVVDKPEQTV | KTFPLPAVGL | ERAATTKADK | DIKNPIQPSF | KMLKNTKPMT | TFQEETKAQF | YASEKTSPKR | ELAKDLPKSG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ESRCNPSEAG | ASLLVGSIEP | SLSNQDRKYS | STLPNDVQTT | SGDLKLDKID | PQRQELLVKL | LDVPTGDCHI | SPKNVSDGVK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RVRTLLSNER | DSKGRDHLSG | VPTDVTVTET | PEKNTESLIL | SLKMSSLGKI | QVMEKQEKGL | TLGVETCGSK | GNAEKSMSAT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EKQERTVMSH | GCENFNTRDS | VTGKESQGER | PHLSLFIPRE | TTYQFHSVSQ | SSSQSLASLA | TTFLQEKKAE | AQNHNCVPDV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KALMESPEGQ | LSLEPKSDSQ | FQASHTGCQS | PLCSAQRHTP | QSPFTNHAAA | AGRKTLRSCM | GLEWFPELYP | GYLGLGVLPG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | |
| KPQCWNAMTQ | KPQLISPQGE | RLSQGWIRCN | TTIRKSGFGG | ITMLFTGYFV | LCCSWSFRRL | KLQRWRK | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 555 | 1 | 712.9189 | 120.57 | 2 | 35.4 | 10.8 | 0 | 389-401 | K.AEAQNHNCVPDVK.A | |

# Detailed Protein Report

## Protein 1604: thromboxane-A synthase isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|195972900 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 52.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.96 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.29 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMEALGFLKL | EVNGPMVTVA | LSVALLALLK | WYSTSAFSRL | EKLGLRHPKP | SPFIGNLTFF | RQGFWESQME | LRKLYGPLCG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YYLGRRMFIV | ISEPDMIKQV | LVENFSNFTN | RMASGLEFKS | VADSVLFLRD | KRWEEVRGAL | MSAFSPEKLN | EMVPLISQAC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DLLLAHLKRY | AESGDAFDIQ | RCYCNYTTDV | VASVAFGTPV | DSWQAPEDPF | VKHCKRFFEF | CIPRPILVLL | LSFPSIMVPL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ARILPNKNRD | ELNGFFNKLI | RNVIALRDQQ | AAEERRRDFL | QMVLDARHSA | SPMGVQDFDI | VRDVFSSTGC | KPNPSRQHQP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SPMARPLTVD | EIVGQAFIFL | IAGYEIITNT | LSFATYLLAT | NPDCQEKLLR | EVDVFKEKHM | APEFCSLEEG | LPYLDMVIAE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | |
| TLRMYPPAFR | FTREAAQDCE | VLGQRIPAGA | VLEMAVGALH | HDPEHWPSPE | TFNPERYRCS | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 168 | 1 | 688.1793 | -200.32 | 2 | 32.1 | 10.8 | 0 | 414-425 | R.EAAQDCEVLGQR.I | Carbamidomethyl: 6 | WUP:QUP 1.29<br>QU:MU 0.96 |

# Detailed Protein Report

**Protein 1605:** **calcium-binding and coiled-coil domain-containing protein 1 isoform 2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|219521893 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 67.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.5 |
| | | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEESPLSRAP | SRGGVNFLNV | ARTYIPNTKV | ECHYTLPPGT | MPSASDWIGI | FKVEAACVRD | YHTFVWSSVP | ESTTDGSPIH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TSVQFQEPRP | MDELVTLEEA | DGGSDILLVV | PKATVLQNQL | DESQQERNDL | MQLKLQLEGQ | VTELRSRVQE | LERALATARQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EHTELMEQYK | GISRSHGEIT | EERDILSRQQ | GDHVARILEL | EDDIQTISEK | VLTKEVELDR | LRDTVKALTR | EQEKLLGQLK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EVQADKEQSE | AELEPLKEQL | RGAQELAASS | QQKATLLGEE | LASAAAARDR | TIAELHRSRL | EVAEVNGRLA | ELGLHLKEEK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CQWSKERAGL | LQSVEAEKDK | ILKLSAEILR | LEKAVQEERT | QNQVFKTELA | REKDSSLVQL | SESKRELTEL | RSALRVLQKE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KEQLQEEKQE | LLEYMRKLEA | RLEKVADEKW | NEDATTEDEE | AAVGLSCPAA | LTDSEDESPE | DMRLPPYGLC | ERGDPGSSPA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GPREASPLVV | ISQPAPISPH | LSGPAEDSSS | DSEAEDEKSV | LMAAVQSGGE | EANLLLPELG | SAFYDMASGF | TVGTLSETST |
| 570 | 580 | 590 | 600 | 610 | | | |
| GGPATPTWKE | CPICKERFPA | ESDKDALEDH | MDGHFFFSTQ | DPFTFE | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 903 | 1 | 678.9131 | 43.92 | 2 | 40.8 | 10.8 | 1 | 148-159 | R.VQELERALATAR.Q | |

# Detailed Protein Report

**Protein 1606:** **PREDICTED: zinc finger protein 682 isoform X2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530415345 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 36.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| | | **Sequence Coverage [%]:** | 3.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGKMWIIHTE | EKLCICEECG | KTFKWFSYLT | KHKRIHTGEK | PYKCEECGKA | FNWCSSLTKH | KRIHTGEKPY | KCEECGKAFH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| WCSPFVRHKK | IHTGEKPYTC | EDCGRAFNRH | SHLTKHKTIH | TGKKPYKCKE | CGKAFNHCSL | LTIHERTHTG | EKPYKCEECG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KAFNSSSILT | EHKVIHSGEK | PYKCEKCDKV | FKRFSYLTKH | KRIHTGEKPY | KCEECGKAFN | WSSILTEHKR | IHTGEKPYNC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EECGKAFNRC | SHLTRHKKIH | TAVKRYKCEE | CGKAFKRCSH | LNEHKRVQRG | EKSCKYKKCG | EAFNHCSNLT | T |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2669 | 2 | 625.3264 | 41.56 | 2 | 64.4 | 10.8 | 0 | 78-87 | K.AFHWCSPFVR.H | |

# Detailed Protein Report

## Protein 1607: septin-9 isoform f [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|164698504 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| | | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 1.55 **CV:** 0.00 % **No. of Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578830273 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: septin-9 isoform X7 [Homo sapiens] |
| gi\|530411385 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: septin-9 isoform X5 [Homo sapiens] |
| gi\|530411383 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: septin-9 isoform X4 [Homo sapiens] |
| gi\|530411381 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: septin-9 isoform X3 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MADTPRDAGL | KQAPASRNEK | APVDFGYVGI | DSILEQMRRK | AMKQGFEFNI | MVVGQSGLGK | STLINTLFKS | KISRKSVQPT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SEERIPKTIE | IKSITHDIEE | KGVRMKLTVI | DTPGFGDHIN | NENCWQPIMK | FINDQYEKYL | QEEVNINRKK | RIPDTRVHCC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LYFIPATGHS | LRPLDIEFMK | RLSKVVNIVP | VIAKADTLTL | EERVHFKQRI | TADLLSNGID | VYPQKEFDED | SEDRLVNEKF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| REMIPFAVVG | SDHEYQVNGK | RILGRKTKWG | TIEVENTTHC | EFAYLRDLLI | RTHMQNIKDI | TSSIHFEAYR | VKRLNEGSSA |
| 330 | 340 | | | | | | |
| MANGMEEKEP | EAPEM | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2038 | 1 | 719.7894 | -86.50 | 2 | 53.9 | 10.8 | 0 | 299-310 | K.DITSSIHFEAYR.V | | QU:MU 1.55 |

# Detailed Protein Report

## Protein 1608: sister chromatid cohesion protein PDS5 homolog A isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|155030220 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| | | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDFTAQPKPA | TALCGVVSAD | GKIAYPPGVK | EITDKITTDE | MIKRLKMVVK | TFMDMDQDSE | DEKQQYLPLA | LHLASEFFLR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NPNKDVRLLV | ACCLADIFRI | YAPEAPYTSH | DKLKDIFLFI | TRQLKGLEDT | KSPQFNRYFY | LLENLAWVKS | YNICFELEDC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NEIFIQLFRT | LFSVINNSHN | KKVQMHMLDL | MSSIIMEGDG | VTQELLDSIL | INLIPAHKNL | NKQSFDLAKV | LLKRTVQTIE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ACIANFFNQV | LVLGRSSVSD | LSEHVFDLIQ | ELFAIDPHLL | LSVMPQLEFK | LKSNDGEERL | AVVRLLAKLF | GSKDSDLATQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NRPLWQCFLG | RFNDIHVPVR | LESVKFASHC | LMNHPDLAKD | LTEYLKVRSH | DPEEAIRHDV | IVTIITAAKR | DLALVNDQLL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GFVRERTLDK | RWRVRKEAMM | GLAQLYKKYC | LHGEAGKEAA | EKVSWIKDKL | LHIYYQNSID | DKLLVEKIFA | QYLVPHNLET |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EERMKCLYYL | YASLDPNAVK | ALNEMWKCQN | MLRSHVRELL | DLHKQPTSEA | NCSAMFGKLM | TIAKNLPDPG | KAQDFVKKFN |
| 570 | 580 | 590 | 600 | 610 | | | |
| QVLGDDEKLR | SQLELLISPT | CSCKQADICV | VSKSYFTLFL | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2709 | 1 | 735.9193 | 133.23 | 2 | 64.2 | 10.8 | 0 | 525-538 | K.QPTSEANCSAMFGK.L | |

# Detailed Protein Report

## Protein 1609: mediator of RNA polymerase II transcription subunit 17 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|28558975 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 72.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSGVRAVRIS | IESACEKQVH | EVGLDGTETY | LPPLSMSQNL | ARLAQRIDFS | QGSGSEEEEA | AGTEGDAQEW | PGAGSSADQD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DEEGVVKFQP | SLWPWDSVRN | NLRSALTEMC | VLYDVLSIVR | DKKFMTLDPV | SQDALPPKQN | PQTLQLISKK | KSLAGAAQIL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LKGAERLTKS | VTENQENKLQ | RDFNSELLRL | RQHWKLRKVG | DKILGDLSYR | SAGSLFPHHG | TFEVIKNTDL | DLDKKIPEDY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CPLDVQIPSD | LEGSAYIKVS | IQKQAPDIGD | LGTVNLFKRP | LPKSKPGSPH | WQTKLEAAQN | VLLCKEIFAQ | LSREAVQIKS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QVPHIVVKNQ | IISQPFPSLQ | LSISLCHSSN | DKKSQKFATE | KQCPEDHLYV | LEHNLHLLIR | EFHKQTLSSI | MMPHPASAPF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GHKRMRLSGP | QAFDKNEINS | LQSSEGLLEK | IIKQAKHIFL | RSRAAATIDS | LASRIEDPQI | QAHWSNINDV | YESSVKVLIT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SQGYEQICKS | IQLQLNIGVE | QIRVVHRDGR | VITLSYQEQE | LQDFLLSQMS | QHQVHAVQQL | AKVMGWQVLS | FSNHVGLGPI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ESIGNASAIT | VASPSGDYAI | SVRNGPESGS | KIMVQFPRNQ | CKDLPKSDVL | QDNKWSHLRG | PFKEVQWNKM | EGRNFVYKME |
| 650 | 660 | | | | | | |
| LLMSALSPCL | L | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1453 | 1 | 1023.6455 | 110.49 | 2 | 48.4 | 10.8 | 2 | 121-138 | R.DKKFMTLDPVSQDALPPK.Q | Oxidation: 5 |

# Detailed Protein Report

## Protein 1610: M-phase inducer phosphatase 2 isoform 7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|566559982 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 53.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| | | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 1.45 **CV:** 0.00 % **No. of Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|566559984 | refseq_human (refseq_human_20140103.fasta) | M-phase inducer phosphatase 2 isoform 7 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDSPSPMDPH | MAEQTFEQAI | QAASRIIRNE | QFAIRRFQSM | PVRLLGHSPV | LRNITNSQAP | DGRRKSEAGS | GAASSSGEDK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ENDGFVFKMP | WKPTHPSSTH | ALAEWASRRE | AFAQRPSSAP | DLMCLSPDRK | MEVEELSPLA | LGRFSLTPAE | GDTEEDDGFV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DILESDLKDD | DAVPPGMESL | ISAPLVKTLE | KEEEKDLVMY | SKCQRLFRSP | SMPCSVIRPI | LKRLERPQDR | DTPVQNKRRR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SVTPPEEQQE | AEEPKARVLR | SKSLCHDEIE | NLLDSDHREL | IGDYSKAFLL | QTVDGKHQDL | KYISPETMVA | LLTGKFSNIV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DKFVIVDCRY | PYEYEGGHIK | TAVNLPLERD | AESFLLKSPI | APCSLDKRVI | LIFHCEFSSE | RGPRMCRFIR | ERDRAVNDYP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | |
| SLYYPEMYIL | KGGYKEFFPQ | HPNFCEPQDY | RPMNHEAFKD | ELKTFRLKTR | SWAGERSRRE | LCSRLQDQ | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2473 | 1 | 812.2434 | -170.71 | 2 | 60.8 | 10.8 | 2 | 64-80 | R.RKSEAGSGAASSSGEDK.E | | QU:MU 1.45 |

# Detailed Protein Report

## Protein 1611: PREDICTED: uncharacterized protein LOC101928352 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578796908 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.8 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 13.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578845616 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: uncharacterized protein LOC101928352 [Homo sapiens] |
| gi\|578826487 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: uncharacterized protein LOC101928352 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MARGGWRVVR AGTAKSFVGA LKRPTGGPAL GGTRAARPEP RVRAPTPAGL ARLLHLRASS LCLQPSEGDP DGFIFGNLPR
        90        100        110        120        130        140        150        160
LFRLFYPHQA PSSEGQLSPL ITGEGARNSS NTHFGTGKPA GGERAARGIN PCGAGGGAGL TQALVGQMAP ATTGTLGRLS
       170        180        190        200        210        220        230        240
PALGKFELQT CPESFSRPSP QGPSLDRGTQ AAALQPKGLD QQGCPWHICT AYFPERQSEG AGMWAPVHNL PHHTKDKPR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2465 | 1 | 938.4759 | 3.50 | 3 | 59.1 | 10.8 | 0 | 128-158 | R.GINPCGAGGGAGLTQALVGQMAPATTGTLGR.L | Oxidation: 21 |

# Detailed Protein Report

## Protein 1612: decorin isoform c precursor [Homo sapiens]

**Accession:** gi|19743850
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 10.8
**MW [kDa]:** 23.3
**pI:** 6.8
**Sequence Coverage [%]:** 5.7
**No. of unique Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKATIILLLL | AQVSWAGPFQ | QRGLFDFMLE | DEASGIGPEV | PDDRDFEPSL | GPVCPFRCQC | HLRVVQCSDL | GLPPSLTELH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LDGNKISRVD | AASLKGLNNL | AKLGLSFNSI | SAVDNGSLAN | TPHLRELHLD | NNKLTRVPGG | LAEHKYIQVV | YLHNNNISVV |
| 170 | 180 | 190 | 200 | 210 | 220 | | |
| GSSDFCPPGH | NTKKASYSGV | SLFSNPVQYW | EIQPSTFRCV | YVRSAIQLGN | YK | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2807 | 1 | 639.3549 | -23.37 | 2 | 63.7 | 10.8 | 1 | 134-145 | K.LTRVPGGLAEHK.Y | |

# Detailed Protein Report

## Protein 1613: PREDICTED: brain mitochondrial carrier protein 1 isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578838760 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 8.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSFGRGGVEM | AAPRLPKQRF | GYFRWFQCFR | VGAAVAFPTV | GASASQSSDE | PEQHQKSTTV | SHEMSGLNWK | PFVYGGLASI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VAEFGTFPVD | LTKTRLQVQG | QSIDARFKEI | KYRGMFHALF | RICKEEGVLA | LYSGIAPALL | RQASYGTIKI | GIYQSLKRLF |
| 170 | 180 | 190 | 200 | 210 | 220 | | |
| VERLEDSNAG | SRKLVPREHD | WKLYRYIPTR | RHQGSVEGCG | SNCSACCHRC | RSRATSL | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 867 | 1 | 631.1419 | -155.18 | 3 | 39.3 | 10.8 | 0 | 192-209 | R.HQGSVEGCGSNCSACCHR.C | Carbamidomethyl: 16 |

# Detailed Protein Report

## Protein 1614: interphotoreceptor matrix proteoglycan 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|57242793 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 138.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.4 |
| | | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.66 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MIMFPLFGKI | SLGILIFVLI | EGDFPSLTAQ | TYLSIEEIQE | PKSAVSFLLP | EESTDLSLAT | KKKQPLDRRE | TERQWLIRRR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RSILFPNGVK | ICPDESVAEA | VANHVKYFKV | RVCQEAVWEA | FRTFWDRLPG | REEYHYWMNL | CEDGVTSIFE | MGTNFSESVE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HRSLIMKKLT | YAKETVSSSE | LSSPVPVGDT | STLGDTTLSV | PHPEVDAYEG | ASESSLERPE | ESISNEIENV | IEEATKPAGE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QIAEFSIHLL | GKQYREELQD | SSSFHHQHLE | EEFISEVENA | FTGLPGYKEI | RVLEFRSPKE | NDSGVDVYYA | VTFNGEAISN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TTWDLISLHS | NKVENHGLVE | LDDKPTVVYT | ISNFRDYIAE | TLQQNFLLGN | SSLNPDPDSL | QLINVRGVLR | HQTEDLVWNT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QSSSLQATPS | SILDNTFQAA | WPSADESITS | SIPPLDFSSG | PPSATGRELW | SESPLGDLVS | THKLAFPSKM | GLSSSPEVLE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VSSLTLHSVT | PAVLQTGLPV | ASEERTSGSH | LVEDGLANVE | ESEDFLSIDS | LPSSSFTQPV | PKETIPSMED | SDVSLTSSPY |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LTSSIPFGLD | SLTSKVKDQL | KVSPFLPDAS | MEKELIFDGG | LGSGSGQKVD | LITWPWSETS | SEKSAEPLSK | PWLEDDDSLL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PAEIEDKKLV | LVDKMDSTDQ | ISKHSKYEHD | DRSTHFPEEE | PLSGPAVPIF | ADTAAESASL | TLPKHISEVP | GVDDYSVTKA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PLILTSVAIS | ASTDKSDQAD | AILREDMEQI | TESSNYEWFD | SEVSMVKPDM | QTLWTILPES | ERVWTRTSSL | EKLSRDILAS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TPQSADRLWL | SVTQSTKLPP | TTISTLLEDE | VIMGVQDISL | ELDRIGTDYY | QPEQVQEQNG | KVGSYVEMST | SVHSTEMVSV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| AWPTEGGDDL | SYTQTSGALV | VFFSLRVTNM | MFSEDLFNKN | SLEYKALEQR | FLELLVPYLQ | SNLTGFQNLE | ILNFRNGSIV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VNSRMKFANS | VPPNVNNAVY | MILEDFCTTA | YNTMNLAIDK | YSLDVESGDE | ANPCKFQACN | EFSECLVNPW | SGEAKCRCFP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GYLSVEERPC | QSLCDLQPDF | CLNDGKCDIM | PGHGAICRCR | VGENWWYRGK | HCEEFVSEPV | IIGITIASVV | GLLVIFSAII |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| YFFIRTLQAH | HDRSERESPF | SGSSRQPDSL | SSIENAVKYN | PVYESHRAGC | EKYEGPYPQH | PFYSSASGDV | IGGLSREEIR |
| 1210 | 1220 | 1230 | 1240 | 1250 | | | |
| QMYESSELSR | EEIQERMRVL | ELYANDPEFA | AFVREQQVEE | V | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1972 | 1 | 766.2672 | -96.45 | 2 | 55.0 | 10.8 | 1 | 1067-1080 | K.CDIMPGHGAICRCR.V | | WUP:QUP 0.66 |

# Detailed Protein Report

## Protein 1615: PREDICTED: growth/differentiation factor 9 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530379837 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578810283 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: growth/differentiation factor 9 isoform X2 [Homo sapiens] |
| gi\|572153064 | refseq_human (refseq_human_20140103.fasta) | growth/differentiation factor 9 isoform 2 [Homo sapiens] |
| gi\|572153044 | refseq_human (refseq_human_20140103.fasta) | growth/differentiation factor 9 isoform 2 [Homo sapiens] |
| gi\|572152931 | refseq_human (refseq_human_20140103.fasta) | growth/differentiation factor 9 isoform 2 [Homo sapiens] |
| gi\|572152923 | refseq_human (refseq_human_20140103.fasta) | growth/differentiation factor 9 isoform 2 [Homo sapiens] |
| gi\|572152852 | refseq_human (refseq_human_20140103.fasta) | growth/differentiation factor 9 isoform 2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKKLYKTYAT | KEGIPKSNRS | HLYNTVRLFT | PCTRHKQAPG | DQVTGILPSV | ELLFNLDRIT | TVEHLLKSVL | LYNINNSVSF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SSAVKCVCNL | MIKEPKSSSR | TLGRAPYSFT | FNSQFEFGKK | HKWIQIDVTS | LLQPLVASNK | RSIHMSINFT | CMKDQLEHPS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AQNGLFNMTL | VSPSLILYLN | DTSAQAYHSW | YSLHYKRRPS | QGPDQERSLS | AYPVGEEAAE | DGRSSHHRHR | RGQETVSSEL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KKPLGPASFN | LSEYFRQFLL | PQNECELHDF | RLSFSQLKWD | NWIVAPHRYN | PRYCKGDCPR | AVGHRYGSPV | HTMVQNIIYE |
| 330 | 340 | 350 | 360 | 370 | | | |
| KLDSSVPRPS | CVPAKYSPLS | VLTIEPDGSI | AYKEYEDMIA | TKCTCR | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1385 | 1 | 905.0891 | 159.82 | 2 | 46.9 | 10.8 | 2 | 86-100 | K.CVCNLMIKEPKSSSR.T | Carbamidomethyl: 1, 3 |

# Detailed Protein Report

## Protein 1616: 4-trimethylaminobutyraldehyde dehydrogenase [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|115387104 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 56.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFLRAGLAAL | SPLLRSLRPS | PVAAMSTGTF | VVSQPLNYRG | GARVEPADAS | GTEKAFEPAT | GRVIATFTCS | GEKEVNLAVQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NAKAAFKIWS | QKSGMERCRI | LLEAARIIRE | REDEIATMEC | INNGKSIFEA | RLDIDISWQC | LEYYAGLAAS | MAGEHIQLPG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GSFGYTRREP | LGVCVGIGAW | NYPFQIASWK | SAPALACGNA | MVFKPSPFTP | VSALLLAEIY | SEAGVPPGLF | NVVQGGAATG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QFLCQHPDVA | KVSFTGSVPT | GMKIMEMSAK | GIKPVTLELG | GKSPLIIFSD | CDMNNAVKGA | LMANFLTQGQ | VCCNGTRVFV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QKEILDKFTE | EVVKQTQRIK | IGDPLLEDTR | MGPLINRPHL | ERVLGFVKVA | KEQGAKVLCG | GDIYVPEDPK | LKDGYYMRPC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VLTNCRDDMT | CVKEEIFGPV | MSILSFDTEA | EVLERANDTT | FGLAAGVFTR | DIQRAHRVVA | ELQAGTCFIN | NYNVSPVELP |
| 490 | 500 | 510 | 520 | | | | |
| FGGYKKSGFG | RENGRVTIEY | YSQLKTVCVE | MGDVESAF | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2653 | 1 | 701.8506 | 76.61 | 2 | 63.2 | 10.8 | 0 | 506-518 | K.TVCVEMGDVESAF.- | Oxidation: 6 |

# Detailed Protein Report

## Protein 1617: zinc finger protein 182 isoform 2 [Homo sapiens]

**Accession:** gi|55769561
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 10.8
**MW [kDa]:** 71.5
**pI:** 10.0
**Sequence Coverage [%]:** 2.1
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAKPQGLVTF | EDVAVDFTQE | EWQYLNPPQR | TLYRDVMLET | YSNLVFVGQQ | VTKPNLILKL | EVEECPAEGK | IPFWNFPEVC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QVDEQIERQH | QDDQDKCLLM | QVGFSDKKTI | ITKSARDCHE | FGNILHLSTN | LVASIQRPDK | HESFGNNMVD | NLDLFSRSSA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ENKYDNGCAK | LFFHTEYEKT | NPGMKPYGYK | ECGKGLRRKK | GLSLHQRIKN | GEKPFECTAC | RKTFSKKSHL | IVHWRTHTGE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KPFGCTECGK | AFSQKSQLII | HLRTHTGERP | FECPECGKAF | REKSTVIIHY | RTHTGEKPYE | CNECGKAFTQ | KSNLIVHQKT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HTGEKTYECT | KCGESFIQKL | DLIIHHSTHT | GKKPHECNEC | KKTFSDKSTL | IIHQRTHTGE | KPHKCTECGK | SFNEKSTLIV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HQRTHTGEKP | YECDVCGKTF | TQKSNLGVHQ | RTHSGEKPFE | CNECEKAFSQ | KSYLMLHQRG | HTGEKPYECN | ECEKAFSQKS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YLIIHQRTHT | EEKPYKCNEC | GKAFREKSKL | IIHQRIHTGE | KPYECPVCWK | AFSQKSQLII | HQRTHTGEKP | YACTECGKAF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| REKSTFTVHQ | RTHTGEKPYK | CTECGKAFTQ | KSNLIVHQRT | HAGKKAHGRG | HTRKSKFMAH | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2287 | 1 | 820.0989 | 163.30 | 2 | 58.5 | 10.8 | 2 | 223-235 | K.TFSKKSHLIVHWR.T | |

# Detailed Protein Report

## Protein 1618: protein FAM65B isoform 2 [Homo sapiens]

**Accession:** gi|14277690
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl, Oxidation

**Score:** 10.8
**MW [kDa]:** 65.7
**pI:** 5.1
**Sequence Coverage [%]:** 4.7
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLVGSQSFSP | GGPNGIIRSQ | SFAGFSGLQE | RRSRCNSFIE | NSSALKKPQA | KLKKMHNLGH | KNNNPPKEPQ | PKRVEEVYRA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LKNGLDEYLE | VHQTELDKLT | AQLKDMKRNS | RLGVLYDLDK | QIKTIERYMR | RLEFHISKVD | ELYEAYCIQR | RLQDGASKMK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QAFATSPASK | AARESLTEIN | RSFKEYTENM | CTIEVELENL | LGEFSIKMKG | LAGFARLCPG | DQYEIFMKYG | RQRWKLKGKI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EVNGKQSWDG | EETVFLPLIV | GFISIKVTEL | KGLATHILVG | SVTCETKELF | AARPQVVAVD | INDLGTIKLN | LEITWYPFDV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EDMTASSGAG | NKAAALQRRM | SMYSQGTPET | PTFKDHSFFS | NLPDDIFENG | KAAEEKMPLS | LSFSDLPNGD | CALTSHSTGS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PSNSTNPEIT | ITPAEFNLSS | LASQNEGMDD | TSSASSRNSL | GEGQEPKSHL | KEEDPEEPRK | PASAPSEACR | RQSSGAGAEH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LFLENDVAEA | LLQESEEASE | LKPVELDTSE | GNITKQLVKR | LTSAEVPMAT | DRLLSEGSVG | GESEGCRSFL | DGSLEDAFNG |
| 570 | 580 | 590 | 600 | | | | |
| LLLALEPHKE | QYKEFQDLNQ | EVMNLDDILK | K | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1567 | 1 | 994.1375 | -4.03 | 3 | 47.9 | 10.8 | 2 | 520-547 | K.RLTSAEVPMATDRLLSEGSVGGESEGCR.S | Carbamidomethyl: 27;<br>Oxidation: 9 |

# Detailed Protein Report

## Protein 1619: SH2 domain-containing adapter protein B [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|106879210 | **Score:** | 10.8 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 55.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAKWLNKYFS | LGNSKTKSPP | QPPRPDYREQ | RRRGERPSQP | PQAVPQASSA | ASASCGPATA | SCFSASSGSL | PDDSGSTSDL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IRAYRAQKER | DFEDPYNGPG | SSLRKLRAMC | RLDYCGGSGE | PGGVQRAFSA | SSASGAAGCC | CASSGAGAAA | SSSSSSGSPH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LYRSSSERRP | ATPAEVRYIS | PKHRLIKVES | AAGGGAGDPL | GGACAGGRTW | SPTACGGKKL | LNKCAASAAE | ESGAGKKDKV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TIADDYSDPF | DAKNDLKSKA | GKGESAGYME | PYEAQRIMTE | FQRQESVRSQ | HKGIQLYDTP | YEPEGQSVDS | DSESTVSPRL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RESKLPQDDD | RPADEYDQPW | EWNRVTIPAL | AAQFNGNEKR | QSSPSPSRDR | RRQLRAPGGG | FKPIKHGSPE | FCGILGERVD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PAVPLEKQIW | YHGAISRGDA | ENLLRLCKEC | SYLVRNSQTS | KHDYSLSLRS | NQGFMHMKLA | KTKEKYVLGQ | NSPPFDSVPE |
| 490 | 500 | 510 | | | | | |
| VIHYYTTRKL | PIKGAEHLSL | LYPVAVRTL | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 167 | 1 | 930.2673 | -158.81 | 2 | 32.1 | 10.8 | 1 | 260-276 | K.AGKGESAGYMEPYEAQR.I | Oxidation: 10 |

# Detailed Protein Report

## Protein 1620: tristetraprolin [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|393539038 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MANRYTMDLT | AIYESLLSLS | PDVPVPSDHG | GTESSPGWGS | SGPWSLSPSD | SSPSGVTSRL | PGRSTSLVEG | RSCGWVPPPP |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| GFAPLAPRLG | PELSPSPTSP | TATSTTPSRY | KTELCRTFSE | SGRCRYGAKC | QFAHGLGELR | QANRHPKYKT | ELCHKFYLQG |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| RCPYGSRCHF | IHNPSEDLAA | PGHPPVLRQS | ISFSGLPSGR | RTSPPPPGLA | GPSLSSSSFS | PSSSPPPPGD | LPLSPSAFSA |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| APGTPLARRD | PTPVCCPSCR | RATPISVWGP | LGGLVRTPSV | QSLGSDPDEY | ASSGSSLGGS | DSPVFEAGVF | APPQPVAAPR |
| **330** | **340** | | | | | | |
| RLPIFNRISV | SE | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 373 | 1 | 644.3883 | 111.01 | 2 | 34.3 | 10.7 | 0 | 130-140 | K.CQFAHGLGELR.Q | Carbamidomethyl: 1 |

## Protein 1621: dynactin subunit 5 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|312261189 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 9.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 15.5 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MELGELLYNK SEYIETASGN KVSRQSVLCG SQNIVLNGKN FVISVFLSPY IRCHSACRDR KRSDESVRLS VNNREWWGLV
        90
NWRM
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2098 | 1 | 766.3104 | -117.44 | 2 | 54.6 | 10.7 | 2 | 62-74 | K.RSDESVRLSVNNR.E | |

# Detailed Protein Report

## Protein 1622: centromere protein S [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|41327703 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 15.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| | | **Sequence Coverage [%]:** | 15.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|395394019 | refseq_human (refseq_human_20140103.fasta) | APITD1-CORT protein isoform 4 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MEEEAETEEQ QRFSYQQRLK AAVHYTVGCL CEEVALDKEM QFSKQTIAAI SELTFRQCEN FAKDLEMFAR HAKRTTINTE
        90        100        110        120        130        140
DVKLLARRSN SLLKYITDKS EEIAQINLER KAQKKKSED GSKNSRQPAE AGVVESEN
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1455 | 1 | 1095.6408 | 129.54 | 2 | 48.4 | 10.7 | 2 | 118-138 | K.SEDGSKNSRQPAEAGVVESEN.- | |

# Detailed Protein Report

## Protein 1623: tRNA (cytosine(34)-C(5))-methyltransferase isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|301336155 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 82.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGRRSRGRRL | QQQQRPEDAE | DGAEGGGKRG | EAGWEGGYPE | IVKENKLFEH | YYQELKIVPE | GEWGQFMDAL | REPLPATLRI |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TGYKRYPEEL | AWHTNLSRKI | LRKSPHLEKF | HQFLVSETES | GNISRQEAVS | MIPPLLLNVR | PHHKILDMCA | APGSKTTQLI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EMLHADMNVP | FPEGFVIAND | VDNKRCYLLV | HQAKRLSSPC | IMVVNHDASS | IPRLQIDVDG | RKEILFYDRI | LCDVPCSGDG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TMRKNIDVWK | KWTTLNSLQL | HGLQLRIATR | GAEQLAEGGR | MVYSTCSLNP | IEDEAVIASL | LEKSEGALEL | ADVSNELPGL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KWMPGITQWK | VMTKDGQWFT | DWDAVPHSRH | TQIRPTMFPP | KDPEKLQAMH | LERCLRILPH | HQNTGGFFVA | VLVKKSSMPW |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NKRQPKLQGK | SAETRESTQL | SPADLTEGKP | TDPSKLESPS | FTGTGDTEIA | HATEDLENNG | SKKDGVCGPP | PSKKMKLFGF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KEDPFVFIPE | DDPLFPPIEK | FYALDPSFPR | MNLLTRTTEG | KKRQLYMVSK | ELRNVLLNNS | EKMKVINTGI | KVWCRNNSGE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EFDCAFRLAQ | EGIYTLYPFI | NSRIITVSME | DVKILLTQEN | PFFRKLSSET | YSQAKDLAKG | SIVLKYEPDS | ANPDALQCPI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VLCGWRGKAS | IRTFVPKNER | LHYLRMMGLE | VLGEKKKEGV | ILTNESAAST | GQPDNDVTEG | QRAGEPNSPD | AEEANSPDVT |
| 730 | 740 | | | | | | |
| AGCDPAGVHP | PR | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2775 | 1 | 927.9938 | 26.39 | 2 | 65.8 | 10.7 | 2 | 362-376 | K.DPEKLQAMHLERCLR.I | Oxidation: 8 |

# Detailed Protein Report

## Protein 1624: PREDICTED: mucin-19-like isoform X15 [Homo sapiens]

**Accession:** gi|578797289
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 10.7
**MW [kDa]:** 49.8
**pI:** 10.3
**Sequence Coverage [%]:** 3.7
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEVGAQGLQV | NGGVEHRNYR | SMEVGAHGLQ | VNGGVEHRDY | KSMDVGPQGL | QVNGGGGTGT | SGQWRWGTWT | KGQWRWDRET |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TGQWRWGHRD | YRSMEVGAQG | LHVSGDGVTG | TTGQWRWGHR | DYSSMEVGAQ | GLQVNGGGAQ | GLQVSGSGVT | GTTGQWRWGH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RDYRSLEVGA | QELQVNGGGG | TGTTGQWRWG | TGTTRQWRWS | HRDYRSMEVE | SQGLQVNGGG | GTGTAGQWRW | STGTTGQWRW |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| STGTTGQWRW | GTGTTGQWRC | STETTGQWRC | STETTGQWRW | GTGTTGQWRW | STETTGQWTW | STGTTGQWRW | GHRDYRSMEV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EHRDYRSMEV | EHRDYRSMEV | ESQGLQVNGG | GAERLQVNGR | GVQGLQVNGG | GAQRLQVNGG | GAQGLQVNGG | GAQRLQVNGG |
| 410 | 420 | 430 | 440 | 450 | 460 | | |
| GVTGTTGQWT | WSIGTTGQWR | WGHRDYRSME | VGAEGLHVSG | GGAQRLGNGQ | LAGLGQ | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1877 | 1 | 599.5609 | -112.71 | 3 | 53.3 | 10.7 | 0 | 1-17 | -.MEVGAQGLQVNGGVEHR.N | Oxidation: 1 |

## Protein 1625: PREDICTED: cyclin-dependent kinase 12 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530412415 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 139.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPNSERHGGK | KDGSGGASGT | LQPSSGGGSS | NSRERHRLVS | KHKRHKSKHS | KDMGLVTPEA | ASLGTVIKPL | VEYDDISSDS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DTFSDDMAFK | LDRRENDERR | GSDRSDRLHK | HRHHQHRRSR | DLLKAKQTEK | EKSQEVSSKS | GSMKDRISGS | SKRSNEETDD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YGKAQVAKSS | SKESRSSKLH | KEKTRKEREL | KSGHKDRSKS | HRKRETPKSY | KTVDSPKRRS | RSPHRKWSDS | SKQDDSPSGA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SYGQDYDLSP | SRSHTSSNYD | SYKKSPGSTS | RRQSVSPPYK | EPSAYQSSTR | SPSPYSRRQR | SVSPYSRRRS | SSYERSGSYS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GRSPSPYGRR | RSSSPFLSKR | SLSRSPLPSR | KSMKSRSRSP | AYSRHSSSHS | KKKRSSSRSR | HSSISPVRLP | LNSSLGAELS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RKKKERAAAA | AAAKMDGKES | KGSPVFLPRK | ENSSVEAKDS | GLESKKLPRS | VKLEKSAPDT | ELVNVTHLNT | EVKNSSDTGK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VKLDENSEKH | LVKDLKAQGT | RDSKPIALKE | EIVTPKETET | SEKETPPPLP | TIASPPPPLP | TTTPPPQTPP | LPPLPPIPAL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PQQPPLPPSQ | PAFSQVPASS | TSTLPPSTHS | KTSAVSSQAN | SQPPVQVSVK | TQVSVTAAIP | HLKTSTLPPL | PLPPLLPGDD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| DMDSPKETLP | SKPVKKEKEQ | RTRHLLTDLP | LPPELPGGDL | SPPDSPEPKA | ITPPQQPYKK | RPKICCPRYG | ERRQTESDWG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KRCVDKFDII | GIIGEGTYGQ | VYKAKDKDTG | ELVALKKVRL | DNEKEGFPIT | AIREIKILRQ | LIHRSVVNMK | EIVTDKQDAL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DFKKDKGAFY | LVFEYMDHDL | MGLLESGLVH | FSEDHIKSFM | KQLMEGLEYC | HKKNFLHRDI | KCSNILLNNS | GQIKLADFGL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ARLYNSEESR | PYTNKVITLW | YRPPELLLGE | ERYTPAIDVW | SCGCILGELF | TKKPIFQANL | ELAQLELISR | LCGSPCPAVW |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| PDVIKLPYFN | TMKPKKQYRR | RLREEFSFIP | SAALDLLDHM | LTLDPSKRCT | AEQTLQSDFL | KDVELSKMAP | PDLPHWQDCH |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ELWSKKRRRQ | RQSGVVVEEP | PPSKTSRKET | TSGTSTEPVK | NSSPAPPQPA | PGKVESGAGD | AIGLADITQQ | LNQSELAVLL |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| NLLQSQTDLS | IPQMAQLLNI | HSNPEMQQQL | EALNQSISAL | TEATSQQQDS | ETMAPEESLK | EAPSAPVILP | SAEQTTLEAS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | | |
| STPADMQNIL | AVLLSQLMKT | QEPAGSLEEN | NSDKNSGPQG | PRRTPTMPQE | EAADGV | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1432 | 1 | 959.7733 | -9.76 | 3 | 47.5 | 10.7 | 1 | 1022-1045 | K.DVELSKMAPPDLPHWQDCHELWSK.K | Oxidation: 7 |

## Protein 1626: PREDICTED: putative protein FAM157B-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578813822 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.2 |
| | | **Sequence Coverage [%]:** | 6.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578844171 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: putative protein FAM157B-like [Homo sapiens] |
| gi\|578840953 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: putative protein FAM157B-like [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGGGQRPMGL | GSEFFRLLHD | LHLLAFAMKR | IWTSEIHRRG | EATARPRAPE | HPAPPATAVR | GRDAASQNLK | RRPGSGTDGL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RLQGAEPSRL | LRTYARGAVI | PTGTPERAQP | PPPQDPLGRR | RWLSRNTWGP | WPGTTQPPSP | QLLRNDWGSC | GFMVPEAARG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KVFQDSQEGA | HIRRETVSKS | VCAEPWRHQR | ARDPAPTNFP | LKCQKQRGAS | TSSGQHGGRV | NLVFFIGCWN | VIRVNVWSLL |
| 250 | | | | | | | |
| QCPETER | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1583 | 1 | 798.3796 | -14.25 | 2 | 49.5 | 10.7 | 0 | 2-16 | M.GGGQRPMGLGSEFFR.L | |

# Detailed Protein Report

## Protein 1627: stromal interaction molecule 2 isoform 2 precursor [Homo sapiens]

**Accession:** gi|281182822
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 10.7
**MW [kDa]:** 83.9
**pI:** 6.3
**Sequence Coverage [%]:** 2.3
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLVLGLLVAG | AADGCELVPR | HLRGRRATGS | AATAASSPAA | AAGDSPALMT | DPCMSLSPPC | FTEEDRFSLE | ALQTIHKQMD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DDKDGGIEVE | ESDEFIREDM | KYKDATNKHS | HLHREDKHIT | IEDLWKRWKT | SEVHNWTLED | TLQWLIEFVE | LPQYEKNFRD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NNVKGTTLPR | IAVHEPSFMI | SQLKISDRSH | RQKLQLKALD | VVLFGPLTRP | PHNWMKDFIL | TVSIVIGVGG | CWFAYTQNKT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SKEHVAKMMK | DLESLQTAEQ | SLMDLQERLE | KAQEENRNVA | VEKQNLERKM | MDEINYAKEE | ACRLRELREG | AECELSRRQY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AEQELEQVRM | ALKKAEKEFE | LRSSWSVPDA | LQKWLQLTHE | VEVQYYNIKR | QNAEMQLAIA | KDEAEKIKKK | RSTVFGTLHV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AHSSSLDEVD | HKILEAKKAL | SELTTCLRER | LFRWQQIEKI | CGFQIAHNSG | LPSLTSSLYS | DHSWVVMPRV | SIPPYPIAGG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VDDLDEDTPP | IVSQFPGTMA | KPPGSLARSS | SLCRSRRSIV | PSSPQPQRAQ | LAPHAPHPSH | PRHPHHPQHT | PHSLPSPDPD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ILSVSSCPAL | YRNEEEEEAI | YFSAEKQWEV | PDTASECDSL | NSSIGRKQSP | PLSLEIYQTL | SPRKISRDEV | SLEDSSRGDS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PVTVDVSWGS | PDCVGLTETK | SMIFSPASKV | YNGILEKSCS | MNQLSSGIPV | PKPRHTSCSS | AGNDSKPVQE | APSVARISSI |
| 730 | 740 | 750 | | | | | |
| PHDLCHNGEK | SKKPSKIKSL | FKKKSK | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1467 | 1 | 619.9415 | -65.11 | 3 | 46.7 | 10.7 | 0 | 678-694 | K.SCSMNQLSSGIPVPKPR.H | Carbamidomethyl: 2 |

# Detailed Protein Report

## Protein 1628: testis-specific serine/threonine-protein kinase 6 [Homo sapiens]

**Accession:** gi|14042966
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 10.7
**MW [kDa]:** 30.3
**pI:** 9.9
**Sequence Coverage [%]:** 6.6
**No. of unique Peptides:** 1

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.68 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.80 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSGDKLLSEL GYKLGRTIGE GSYSKVKVAT SKKYKGTVAI KVVDRRRAPP DFVNKFLPRE LSILRGVRHP HIVHVFEFIE
        90        100        110        120        130        140        150        160
VCNGKLYIVM EAAATDLLQA VQRNGRIPGV QARDLFAQIA GAVRYLHDHH LVHRDLKCEN VLLSPDERRV KLTDFGFGRQ
       170        180        190        200        210        220        230        240
AHGYPDLSTT YCGSAAYASP EVLLGIPYDP KKYDVWSMGV VLYVMVTGCM PFDDSDIAGL PRRQKRGVLY PEGLELSERC
       250        260        270        280
KALIAELLQF SPSARPSAGQ VARNCWLRAG DSG
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1140 | 1 | 941.4544 | -87.18 | 2 | 44.4 | 10.7 | 1 | 107-124 | R.IPGVQARDLFAQIAGAVR.Y | | QU:MU 0.68<br>WUP:QUP 2.80 |

# Detailed Protein Report

## Protein 1629: uncharacterized protein C15orf65 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|311771669 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 13.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 10.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.99 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MTDRNRDKKS TSPSNSDTEM KSEQLPPCVN PGNPVFSCML DPKTLQTATS LSKPQMIMYK TNSSHYGEFL PIPQFFPCNY
         90        100        110        120        130
TPKEQVFSSH IRATGFYQNN TLNTAPDRTR TLDFPNIQHT L
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 835 | 1 | 706.2186 | -146.50 | 2 | 38.8 | 10.7 | 1 | 9-21 | K.KSTSPSNSDTEMK.S | | WUP:QUP 0.99 |

# Detailed Protein Report

## Protein 1630: adipogenesis regulatory factor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|5802976 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 7.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| | | **Sequence Coverage [%]:** | 18.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.32 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MASKGLQDLK QQVEGTAQEA VSAAGAAAQQ VVDQATEAGQ KAMDQLAKTT QETIDKTANQ ASDTFSGIGK KFGLLK
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1543 | 2 | 698.7028 | -194.58 | 2 | 49.5 | 10.7 | 0 | 57-70 | K.TANQASDTFSGIGK.K | | QU:MU 0.32 |

# Detailed Protein Report

## Protein 1631: uncharacterized protein C17orf98 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|122937325 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 17.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 7.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.56 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 5.69 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MAYLSECRLR LEKGFILDGV AVSTAARAYG RSRPKLWSAI PPYNAQQDYH ARSYFQSHVV PPLLRKTDQD HGGTGRDGWI
        90        100        110        120        130        140        150        160
VDYIHIFGQG QRYLNRRNWA GTGHSLQQVT GHDHYNADLK PIDGFNGRFG YRRNTPALRQ STSVFGEVTH FPLF
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 372 | 1 | 675.8993 | 38.72 | 2 | 34.3 | 10.7 | 2 | 129-139 | R.FGYRRNTPALR.Q | | WUP:QUP 5.69<br>QU:MU 0.56 |

# Detailed Protein Report

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## Protein 1632: mediator of RNA polymerase II transcription subunit 23 isoform c [Homo sapiens]

**Accession:** gi|395455064
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 10.7
**MW [kDa]:** 155.5
**pI:** 7.2
**Sequence Coverage [%]:** 0.6
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| METQLQSIFE | EVVKTEVIEE | AFPGMFMDTP | EDEKTKLISC | LGAFRQFWGG | LSQESHEQCI | QWIVKFIHGQ | HSPKRISFLY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DCLAMAVETG | LLPPRLVCES | LINSDTLEWE | RTQLWALTFK | LVRKIIGGVD | YKGVRDLLKV | ILEKILTIPN | TVSSAVVQQL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LAAREVIAYI | LERNACLLPA | YFAVTEIRKL | YPEGKLPHWL | LGNLVSDFVD | TFRPTARINS | ICGRCSLLPV | VNNSGAICNS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| WKLDPATLRF | PLKGLLPYDK | DLFEPQTALL | RYVLEQPYSR | DMVCNMLGLN | KQHKQRCPVL | EDQLVDLVVY | AMERSETEEK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FDDGGTSQLL | WQHLSSQLIF | FVLFQFASFP | HMVLSLHQKL | AGRGLIKGRD | HLMWVLLQFI | SGSIQKNALA | DFLPVMKLFD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LLYPEKEYIP | VPDINKPQST | HAFAMTCIWI | HLNRKAQNDN | SKLQIPIPHS | LRLHHEFLQQ | SLRNKSLQMN | DYKIALLCNA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YSTNSECFTL | PMGALVETIY | GNGIMRIPLP | GTNCMASGSI | TPLPMNLLDS | LTVHAKMSLI | HSIATRVIKL | AHAKSSVALA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PALVETYSRL | LVYMEIESLG | IKGFISQLLP | TVFKSHAWGI | LHTLLEMFSY | RMHHIQPHYR | VQLLSHLHTL | AAVAQTNQNQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LHLCVESTAL | RLITALGSSE | VQPQFTRFLS | DPKTVLSAES | EELNRALILT | LARATHVTDF | FTGSDSIQGT | WCKDILQTIM |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SFTPHNWASH | TLSCFPGPLQ | AFFKQNNVPQ | ESRFNLKKNV | EEEYRKWKSM | SNENDIITHF | SMQGSPPLFL | CLLWKMLLET |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| DHINQIGYRV | LERIGARALV | AHVRTFADFL | VYEFSTSAGG | QQLNKCIEIL | NDMVWKYNIV | TLDRLILCLA | MRSHEGNEAQ |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VCYFIIQLLL | LKPNDFRNRV | SDFVKENSPE | HWLQNDWHTK | HMNYHKKYPE | KLYFEGLAEQ | VDPPVQIQSP | YLPIYFGNVC |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LRFLPVFDIV | IHRFLELLPV | SKSLETLLDH | LGGLYKFHDR | PVTYLYNTLH | YYEMHLRDRA | FLKRKLVHAI | IGSLKDNRPQ |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| GWCLSDTYLK | CAMNAREENP | WVPDDTYYCR | LIGRLVDTMA | GKSPGPFPNC | DWRFNEFPNP | AAHALHVTCV | ELMALAVSGK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EVGNALLNVV | LKSQPLVPRE | NITAWMNAIG | LIITALPEPY | WIVLHDRIVS | VISSPSLTSE | TEWVGYPFRL | FDFTACHQSY |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SEMSCSYTLA | LAHAVWHHSS | IGQLSLIPKF | LTEVLLPIVK | TEFQLLYVYH | LVGPFLQRFQ | QERTRCMIEI | GVAFYDMLLN |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| VDQCSTHLNY | MDPICDFLYH | MKYMFTGDSV | KEQVEKIICN | LKPALKLRLR | FITHISKMEP | AAVPPQAMNS | GSPAPQSNQ |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2623 | 1 | 964.2392 | -292.20 | 1 | 61.1 | 10.7 | 1 | 898-905 | R.NRVSDFVK.E | |

# Detailed Protein Report

## Protein 1633: SH3 and multiple ankyrin repeat domains protein 2 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|254911082 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 135.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

*QU:MU* **Median:** 4.63 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MMMNVPGGGA | AAVMMTGYNN | GRCPRNSLYS | DCIIEEKTVV | LQKKDNEGFG | FVLRGAKADT | PIEEFTPTPA | FPALQYLESV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DEGGVAWQAG | LRTGDFLIEV | NNENVVKVGH | RQVVNMIRQG | GNHLVLKVVT | VTRNLDPDDT | ARKKAPPPPK | RAPTTALTLR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SKSMTSELEE | LVDKASVRKK | KDKPEEIVPA | SKPSRAAENM | AVEPRVATIK | QRPSSRCFPA | GSDMNSVYER | QGIAVMTPTV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PGSPKAPFLG | IPRGTMRRQK | SIDSRIFLSG | ITEEERQFLA | PPMLKFTRSL | SMPDTSEDIP | PPPQSVPPSP | PPPSPTTYNC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PKSPTPRVYG | TIKPAFNQNS | AAKVSPATRS | DTVATMMREK | GMYFRRELDR | YSLDSEDLYS | RNAGPQANFR | NKRGQMPENP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YSEVGKIASK | AVYVPAKPAR | RKGMLVKQSN | VEDSPEKTCS | IPIPTIIVKE | PSTSSSGKSS | QGSSMEIDPQ | APEPPSQLRP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DESLTVSSPF | AAAIAGAVRD | REKRLEARRN | SPAFLSTDLG | DEDVGLGPPA | PRTRPSMFPE | EGDFADEDSA | EQLSSPMPSA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TPREPENHFV | GGAEASAPGE | AGRPLNSTSK | AQGPESSPAV | PSASSGTAGP | GNYVHPLTGR | LLDPSSPLAL | ALSARDRAMK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ESQQGPKGEA | PKADLNKPLY | IDTKMRPSLD | AGFPTVTRQN | TRGPLRRQET | ENKYETDLGR | DRKGDDKKNM | LIDIMDTSQQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KSAGLLMVHT | VDATKLDNAL | QEEDEKAEVE | MKPDSSPSEV | PEGVSETEGA | LQISAAPEPT | TVPGRTIVAV | GSMEEAVILP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| FRIPPPPLAS | VDLDEDFIFT | EPLPPPLEFA | NSFDIPDDRA | ASVPALSDLV | KQKKSDTPQS | PSLNSSQPTN | SADSKKPASL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| SNCLPASFLP | PPESFDAVAD | SGIEEVDSRS | SSDHHLETTS | TISTVSSIST | LSSEGGENVD | TCTVYADGQA | FMVDKPPVPP |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KPKMKPIIHK | SNALYQDALV | EEDVDSFVIP | PPAPPPPPGS | AQPGMAKVLQ | PRTSKLWGDV | TEIKSPILSG | PKANVISELN |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SILQQMNREK | LAKPGEGLDS | PMGAKSASLA | PRSPEIMSTI | SGTRSTTVTF | TVRPGTSQPI | TLQSRPPDYE | SRTSGTRRAP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SPVVSPTEMN | KETLPAPLSA | ATASPSPALS | DVFSLPSQPP | SGDLFGLNPA | GRSRSPSPSI | LQQPISNKPF | TTKPVHLWTK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | |
| PDVADWLESL | NLGEHKEAFM | DNEIDGSHLP | NLQKEDLIDL | GVTRVGHRMN | IERALKQLLD | R | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2084 | 2 | 840.7946 | -147.22 | 2 | 55.9 | 10.7 | 1 | 708-721 | K.KNMLIDIMDTSQQK.S | Oxidation: 3 | QU:MU 4.63 |

# Detailed Protein Report

## Protein 1634: PREDICTED: protein unc-80 homolog isoform X8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578804137 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 278.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVKRKSSEGQ | EQDGGRGIPL | PIQTFLWRQT | SAFLRPKLGK | QYEASCVSFE | RVLVENKLHG | LSPALSEAIQ | SISRWELVQA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ALPHVLHCTA | TLLSNRNKLG | HQDKLGVAET | KLLHTLHWML | LEAPQDCNNE | RFGGTDRGSS | WGGSSSAFIH | QVENQGSPGQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PCQSSSNDEE | ENNRRKIFQN | SMATVELFVF | LFAPLVHRIK | ESDLTFRLAS | GLVIWQPMWE | HRQPGVSGFT | ALVKPIRNII |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TAKRSSPINS | QSRTCESPNQ | DARHLEGLQV | VCETFQSDSI | SPKATISGCH | RGNSFDGSLS | SQTSQERGPS | HSRASLVIPP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CQRSRYATYF | DVAVLRCLLQ | PHWSEEGTQW | SLMYYLQRLR | HMLEEKPEKP | PEPDIPLLPR | PRSSSMVAAA | PSLVNTHKTQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DLTMKCNEEE | KSLSSEAFSK | VSLTNLRRSA | VPDLSSDLGM | NIFKKFKSRK | EDRERKGSIP | FHHTGKRRPR | RMGVPFLLHE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DHLDVSPTRS | TFSFGSFSGL | GEDRRGIEKG | GWQTTILGKL | TRRGSSDAAT | EMESLSARHS | HSHHTLVSDL | PDPSNSHGEN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TVKEVRSQIS | TITVATFNTT | LASFNVGYAD | FFNEHMRKLC | NQVPIPEMPH | EPLACANLPR | SLTDSCINYS | YLEDTEHIDG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TNNFVHKNGM | LDLSVVLKAV | YLVLNHDISS | RICDVALNIV | ECLLQLGVVP | CVEKNRKKSE | NKENETLEKR | PSEGAFQFKG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VSGSSTCGFG | GPAVSGAGDG | GGEEGGGGDG | GGGGGDGGGG | GGGGGGPYEK | NDKNQEKDES | TPVSNHRLAL | TMLIKIVKSL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GCAYGCGEGH | RGLSGDRLRH | QVFRENAQNC | LTKLYKLDKM | QFRQTMRDYV | NKDSLNNVVD | FLHALLGFCM | EPVTDNKAGF |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GNNFTTVDNK | STAQNVEGII | VSAMFKSLIT | RCASTTHELH | SPENLGLYCD | IRQLVQFIKE | AHGNVFRRVA | LSALLDSAEK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| LAPGKKVEEN | EQESKPAGSK | RSEAGSIVDK | GQVSSAPEEC | RSFMSGRPSQ | TPEHDEQMQG | ANLGRKDFWR | KMFKSQSAAS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| DTSSQSEQDT | SECTTAHSGT | TSDRRARSRS | RRISLRKKLK | LPIGNWLKRS | SLSGLADGVE | DLLDISSVDR | LSFIRQSSKV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KFTSAVKLSE | GGPGSGMENG | RDEEENFFKR | LGCHSFDDHL | SPNQDGGKSK | NVVNLGAIRQ | GMKRFQFLLN | CCEPGTIPDA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SILAAALDLE | APVVARAALF | LECARFVHRC | NRGNWPEWMK | GHHVNITKKG | LSRGRSPIVG | NKRNQKLQWN | AAKLFYQWGD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| AIGVRLNELC | HGESESPANL | LGLIYDEETK | RRLRKEDEEE | DFLDDSTVNP | SKCGCPFALK | MAACQLLLEI | TTFLRETFSC |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LPRPRTEPLV | DLESCRLRLD | PELDRHRYER | KISFAGVLDE | NEDSKDSLHS | SSHTLKSDAG | VEEKKVPSRK | IRIGGSRLLQ |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| IKGTRSFQVK | KGGSLSSIRR | VGSLKSSKLS | RQDSESEAEE | LQLSQSRDTV | TDLEGSPWSA | SEPSIEPEGM | SNAGAEENYH |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| RNMSWLHVMI | LLCNQQSFIC | THVDYCHPHC | YLHHSRSCAR | LVRAIKLLYG | DSVDSLRESS | NISSVALRGK | KQKECSDKSC |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| LRTPSLKKRV | SDANLEGKKD | SGMLKYIRLQ | VMSLSPAPLS | LLIKAAPILT | EEMYGDIQPA | AWELLLSMDE | HMAGAAAAMF |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| LLCAVKVPEA | VSDMLMSEFH | HPETVQRLNA | VLKFHTLWRF | RYQVWPRMEE | GAQQIFKIPP | PSINFTLPSP | VLGMPSVPMF |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| DPPWVPQCSG | SVQDPINEDQ | SKSFSARAVS | RSHQRAEHIL | KNLQQEEEKK | RLGREASLIT | AIPITQEACY | EPTCTPNSEP |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| EEEVEEVTNL | ASRRLSVSPS | CTSSTSHRNY | SFRRGSVWSV | RSAVSAEDEE | HTTEHTPNHH | VPQPPQAVFP | ACICAAVLPI |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| VHLMEDGEVR | EDGVAVSAVA | QQVLWNCLIE | DPSTVLRHFL | EKLTISNRQD | ELMYMLRKLL | LNIGDFPAQT | SHILFNYLVG |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| LIMYFVRTPC | EWGMDAISAT | LTFLWEVVGY | VEGLFFKDLK | QTMKKEQCEV | KLLVTASMPG | TKTLVVHGQN | ECDIPTQLPV |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| HEDTQFEALL | KECLEFFNIP | ESQSTHYFLM | DKRWNLIHYN | KTYVRDIYPF | RRSVSPQLNL | VHMHPEKGQE | LIQKQVFTRK |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2444 | 1 | 754.6487 | -64.65 | 3 | 58.8 | 10.7 | 2 | 981-1001 | K.RSEAGSIVDKGQVSSAPEECR.S | Carbamidomethyl: 20 |

# Detailed Protein Report

## Protein 1635: protein FAM111B isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|218156273 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 81.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|218156275 | refseq_huma (refseq_human_20140103.fasta) | protein FAM111B isoform b [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKQTHADTPV | DHCLSGIRKC | SSTFKLKSEV | NKHETALEMQ | NPNLNNKECC | FTFTLNGNSR | KLDRSVFTAY | GKPSESIYSA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LSANDYFSER | IKNQFNKNII | VYEEKTIDGH | INLGMPLKCL | PSDSHFKITF | GQRKSSKEDG | HILRQCENPN | MECILFHVVA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IGRTRKKIVK | INELHEKGSK | LCIYALKGET | IEGALCKDGR | FRSDIGEFEW | KLKEGHKKIY | GKQSMVDEVS | GKVLEMDISK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KKALQQKDIH | KKIKQNESAT | DEINHQSLIQ | SKKKVHKPKK | DGETKDVEHS | REQILPPQDL | SHYIKDKTRQ | TIPRIRNYYF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CSLPRKYRQI | NSQVRRRPHL | GRRYAINLDV | QKEAINLLKN | YQTLNEAIMH | QYPNFKEEAQ | WVRKYFREEQ | KRMNLSPAKQ |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FNIYKKDFGK | MTANSVSVAT | CEQLTYYSKS | VGFMQWDNNG | NTGNATCFVF | NGGYIFTCRH | VVHLMVGKNT | HPSLWPDIIS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KCAKVTFTYT | EFCPTPDNWF | SIEPWLKVSN | ENLDYAILKL | KENGNAFPPG | LWRQISPQPS | TGLIYLIGHP | EGQIKKIDGC |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TVIPLNERLK | KYPNDCQDGL | VDLYDTTSNV | YCMFTQRSFL | SEVWNTHTLS | YDTCFSDGSS | GSPVFNASGK | LVALHTFGLF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | |
| YQRGFNVHAL | IEFGYSMDSI | LCDIKKTNES | LYKSLNDEKL | ETYDEEKGKQ | ESSLQDHQIE | PMEC | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2771 | 1 | 729.3742 | -25.36 | 2 | 65.8 | 10.7 | 1 | 556-568 | K.KIDGCTVIPLNER.L | |

# Detailed Protein Report

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**Protein 1636:** **disintegrin and metalloproteinase domain-containing protein 20 preproprotein [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|50845382 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 87.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530404802 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: disintegrin and metalloproteinase domain-containing protein 20 isoform X2 [Homo sapiens] |
| gi\|530404800 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: disintegrin and metalloproteinase domain-containing protein 20 isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MVQLHQDTDP | QIPKGQPCTL | NSSEGGARPA | VPHTLFSSAL | DRWLHNDSFI | MAVGEPLVHI | RVTLLLLWFG | MFLSISGHSQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ARPSQYFTSP | EVVIPLKVIS | RGRGAKAPGW | LSYSLRFGGQ | RYIVHMRVNK | LLFAAHLPVF | TYTEQHALLQ | DQPFIQDDCY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YHGYVEGVPE | SLVALSTCSG | GFLGMLQIND | LVYEIKPISV | SATFEHLVYK | IDSDDTQFPP | MRCGLTEEKI | AHQMELQLSY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NFTLKQSSFV | GWWTHQRFVE | LVVVVDNIRY | LFSQSNATTV | QHEVFNVVNI | VDSFYHPLEV | DVILTGIDIW | TASNPLPTSG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DLDNVLEDFS | IWKNYNLNNR | LQHDVAHLFI | KDTQGMKLGV | AYVKGICQNP | FNTGVDVFED | NRLVVFAITL | GHELGHNLGM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QHDTQWCVCE | LQWCIMHAYR | KVTTKFSNCS | YAQYWDSTIS | SGLCIQPPPY | PGNIFRLKYC | GNLVVEEGEE | CDCGTIRQCA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KDPCCLLNCT | LHPGAACAFG | ICCKDCKFLP | SGTLCRQQVG | ECDLPEWCNG | TSHQCPDDVY | VQDGISCNVN | AFCYEKTCNN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| HDIQCKEIFG | QDARSASQSC | YQEINTQGNR | FGHCGIVGTT | YVKCWTPDIM | CGRVQCENVG | VIPNLIEHST | VQQFHLNDTT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CWGTDYHLGM | AIPDIGEVKD | GTVCGPEKIC | IRKKCASMVH | LSQACQPKTC | NMRGICNNKQ | HCHCNHEWAP | PYCKDKGYGG |
| 730 | 740 | 750 | 760 | 770 | 780 | | |
| SADSGPPPKN | NMEGLNVMGK | LRYLSLLCLL | PLVAFLLFCL | HVLFKKRTKS | KEDEEG | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1299 | 1 | 727.3560 | 8.30 | 2 | 45.9 | 10.7 | 1 | 505-516 | K.DCKFLPSGTLCR.Q | Carbamidomethyl: 2, 11 |

# Detailed Protein Report

## Protein 1637: acyl-coenzyme A thioesterase 2, mitochondrial [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|148727286 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 53.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSNKLLSPHP | HSVVLRSEFK | MASSPAVLRA | SRLYQWSLKS | SAQFLGSPQL | RQVGQIIRVP | ARMAATLILE | PAGRCCWDEP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VRIAVRGLAP | EQPVTLRASL | RDEKGALFQA | HARYRADTLG | ELDLERAPAL | GGSFAGLEPM | GLLWALEPEK | PLVRLVKRDV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RTPLAVELEV | LDGHDPDPGR | LLCQTRHERY | FLPPGVRREP | VRVGRVRGTL | FLPPEPGPFP | GIVDMFGTGG | GLLEYRASLL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AGKGFAVMAL | AYYNYEDLPK | TMETLHLEYF | EEAMNYLLSH | PEVKGPGVGL | LGISKGGELC | LSMASFLKGI | TAAVVINGSV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ANVGGTLHYK | GETLPPVGVN | RNRIKVTKDG | YADIVDVLNS | PLEGPDQKSF | IPVERAESTF | LFLVGQDDHN | WKSEFYANEA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CKRLQAHGRR | KPQIICYPET | GHYIEPPYFP | LCRASLHALV | GSPIIWGGEP | RAHAMAQVDA | WKQLQTFFHK | HLGGHEGTIP |
| 490 | | | | | | | |
| SKV | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1526 | 1 | 719.8132 | -81.11 | 2 | 49.3 | 10.7 | 1 | 17-29 | R.SEFKMASSPAVLR.A | Oxidation: 5 |

# Detailed Protein Report

**Protein 1638:** **PREDICTED: alpha-(1,3)-fucosyltransferase 6 isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530425179 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDPLGPAKPQ | WSWRCCLTTL | LFQLLMAVCF | FSYLRVSQDD | PTVYPNGSRF | PDSTGTPAHS | IPLILLWTWP | FNKPIALPRC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SEMVPGTADC | NITADRKVYP | QADAVIVHHR | EVMYNPSAQL | PRSPRRQGQR | WIWFSMESPS | HCWQLKAMDG | YFNLTMSYRS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DSDIFTPYGW | LEPWSGQPAH | PPLNLSAKTE | LVAWAVSNWG | PNSARVRYYQ | SLQAHLKVDV | YGRSHKPLPQ | GTMMETLSRY |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KFYLAFENSL | HPDYITEKLW | RNALEAWAVP | VVLGPSRSNY | ERFLPPDAFI | HVDDFQSPKD | LARYLQELDK | DHARYLSYFR |
| 330 | 340 | 350 | 360 | | | | |
| WRETLRPRSF | SWALAFCKAC | WKLQEESRTR | LPEASPA | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2638 | 1 | 625.8207 | -14.87 | 2 | 63.8 | 10.7 | 0 | 208-217 | R.YYQSLQAHLK.V | |

# Detailed Protein Report

## Protein 1639: fibroblast growth factor 13 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4758366 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 27.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| | | **Sequence Coverage [%]:** | 5.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAAAIASSLI | RQKRQARERE | KSNACKCVSS | PSKGKTSCDK | NKLNVFSRVK | LFGSKKRRRR | RPEPQLKGIV | TKLYSRQGYH |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| LQLQADGTID | GTKDEDSTYT | LFNLIPVGLR | VVAIQGVQTK | LYLAMNSEGY | LYTSELFTPE | CKFKESVFEN | YYVTYSSMIY |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| RQQQSGRGWY | LGLNKEGEIM | KGNHVKKNKP | AAHFLPKPLK | VAMYKEPSLH | DLTEFSRSGS | GTPTKSRSVS | GVLNGGKSMS |
| **250** | | | | | | | |
| HNEST | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2152 | 1 | 698.2417 | -140.23 | 2 | 55.3 | 10.7 | 2 | 22-35 | K.SNACKCVSSPSKGK.T | |

# Detailed Protein Report

## Protein 1640: osteomodulin precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4826876 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| | | **Sequence Coverage [%]:** | 6.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGFLSPIYVI | FFFFGVKVHC | QYETYQWDED | YDQEPDDDYQ | TGFPFRQNVD | YGVPFHQYTL | GCVSECFCPT | NFPSSMYCDN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RKLKTIPNIP | MHIQQLYLQF | NEIEAVTANS | FINATHLKEI | NLSHNKIKSQ | KIDYGVFAKL | PNLLQLHLEH | NNLEEFPFPL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PKSLERLLLG | YNEISKLQTN | AMDGLVNLTM | LDLCYNYLHD | SLLKDKIFAK | MEKLMQLNLC | SNRLESMPPG | LPSSLMYLSL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ENNSISSIPE | KYFDKLPKLH | TLRMSHNKLQ | DIPYNIFNLP | NIVELSVGHN | KLKQAFYIPR | NLEHLYLQNN | EIEKMNLTVM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| CPSIDPLHYH | HLTYIRVDQN | KLKEPISSYI | FFCFPHIHTI | YYGEQRSTNG | QTIQLKTQVF | RRFPDDDDES | EDHDDPDNAH |
| 410 | 420 | 430 | | | | | |
| ESPEQEGAEG | HFDLHYYENQ | E | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1562 | 1 | 1011.7872 | -55.61 | 3 | 49.7 | 10.7 | 0 | 224-251 | R.LESMPPGLPSSLMYLSLENNSISSIPEK.Y | |

# Detailed Protein Report

**Protein 1641:** **carcinoembryonic antigen-related cell adhesion molecule 16 precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|291190766 | **Score:** | 10.7 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 3.3 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MALTGYSWLL LSATFLNVGA EISITLEPAQ PSEGDNVTLV VHGLSGELLA YSWYAGPTLS VSYLVASYIV STGDETPGPA

        90        100        110        120        130        140        150        160
HTGREAVRPD GSLDIQGILP RHSGTYILQT FNRQLQTEVG YGHVQVHEIL AQPTVLANST ALVERRDTLR LMCSSPSPTA

       170        180        190        200        210        220        230        240
EVRWFFNGGA LPVALRLGLS PDGRVLARHG IRREEAGAYQ CEVWNPVSVS RSEPINLTVY FGPERVAILQ DSTTRTGCTI

       250        260        270        280        290        300        310        320
KVDFNTSLTL WCVSRSCPEP EYVWTFNGQA LKNGQDHLNI SSMTAAQEGT YTCIAKNTKT LLSGSASVVV KLSAAAVATM

       330        340        350        360        370        380        390        400
IVPVPTKPTE GQDVTLTVQG YPKDLLVYAW YRGPASEPNR LLSQLPSGTW IAGPAHTGRE VGFPNCSLLV QKLNLTDTGR

       410        420        430
YTLKTVTVQG KTETLEVELQ VAPLG
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2150 | 1 | 820.7952 | -138.29 | 2 | 56.7 | 10.7 | 0 | 242-255 | K.VDFNTSLTLWCVSR.S | |

# Detailed Protein Report

## Protein 1642: beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|148539888 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 61.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.67 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 5.69 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530420099 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase isoform X2 [Homo sapiens] |
| gi\|148539890 | refseq_human (refseq_human_20140103.fasta) | beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKMRRYKLFL | MFCMAGLCLI | SFLHFFKTLS | YVTFPRELAS | LSPNLVSSFF | WNNAPVTPQA | SPEPGGPDLL | RTPLYSHSPL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LQPLPPSKAA | EELHRVDLVL | PEDTTEYFVR | TKAGGVCFKP | GTKMLERPPP | GRPEEKPEGA | NGSSARRPPR | YLLSARERTG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GRGARRKWVE | CVCLPGWHGP | SCGVPTVVQY | SNLPTKERLV | PREVPRRVIN | AINVNHEFDL | LDVRFHELGD | VVDAFVVCES |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NFTAYGEPRP | LKFREMLTNG | TFEYIRHKVL | YVFLDHFPPG | GRQDGWIADD | YLRTFLTQDG | VSRLRNLRPD | DVFIIDDADE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IPARDGVLFL | KLYDGWTEPF | AFHMRKSLYG | FFWKQPGTLE | VVSGCTVDML | QAVYGLDGIR | LRRRQYYTMP | NFRQYENRTG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HILVQWSLGS | PLHFAGWHCS | WCFTPEGIYF | KLVSAQNGDF | PRWGDYEDKR | DLNYIRGLIR | TGGWFDGTQQ | EYPPADPSEH |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| MYAPKYLLKN | YDRFHYLLDN | PYQEPRSTAA | GGWRHRGPEG | RPPARGKLDE | AEV | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 851 | 1 | 675.8655 | 2.82 | 2 | 40.7 | 10.6 | 1 | 111-123 | R.TKAGGVCFKPGTK.M | Carbamidomethyl: 7 | WUP:QUP 5.69<br>QU:MU 0.67 |

# Detailed Protein Report

## Protein 1643: zinc finger protein 99 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|339418230 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 100.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGSLTFWDVT | IEFALEEWQC | LDMAQQNLYR | NVMLENYRNL | VFLGIAVSKL | DLITCLKQGK | EPWNMKRHEM | VTKPPVISSH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FTQDFWPDQS | IKDSFQEIIL | RTYARCGHKN | LRLRKDCESV | NEGKMHEEAY | NKLNQCWTTT | QGKIFQCNKY | VKVFHKYSNS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NRYKIRHTKK | KTFKCMKCSK | SFFMLSHLIQ | HKRIHTRENI | YKCEERGKAF | KWFSTLIKHK | IIHTEDKPYK | YKKCGKAFNI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SSMFTKCKII | HTGKKPCKCE | ECGKVFNNSS | TLMKHKIIHT | GKKPYKCEEC | GKAFKQSSHL | TRHKAIHTGE | KPYKCEECGK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AFNHFSALRK | HQIIHTGKKP | YKCEECGKAF | SQSSTLRKHE | IIHTEEKPYK | YEECGKAFSN | LSALRKHEII | HTGQKPYKCE |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| ECGKAFKWSS | KLTVHKVIHT | AEKPCKCEEC | GKAFKRFSAL | RKHKIIHTGK | QPYKCEECSK | AFSNFSALRK | HEIIHTGEKP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| YKCEECGKAF | KWSSKLTVHK | VIHMEEKPCK | CEECGKAFKH | FSALRKHKII | HTGKKPYKCE | ECGKAFNNSS | TLMKHKIIHT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GKKPYKCEEC | GKAFKQSSHL | TRHKAIHTGE | KPYKCEECGK | AFNHFSALRK | HQIIHTGKKP | YKCEECGKAF | SQSSTLRKHE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| IIHTGEKPYK | CEECGKAFKW | SSHLTRHKVI | HTEEKPYKCE | ECGKAFNHFS | ALRKHKIIHT | GKKPYKCEEC | GKAFSQSSTL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RKHEIIHTGE | KPYKCEECGK | AFKWSSKLTV | HKVIHTAEKP | CKCEECGKAF | KHFSALRKHK | IIHTGKKPYK | CEECGKAFNN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | |
| SSTLRKHEII | HTGEKSYKCE | ECGKAFQWSS | KLTLHKVIHM | ERNPANVKNV | AKLLNISQPL | ENMR | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2579 | 1 | 822.4636 | 21.90 | 2 | 62.9 | 10.6 | 1 | 181-193 | K.SFFMLSHLIQHKR.I | |

# Detailed Protein Report

## Protein 1644: protein phosphatase 1 regulatory subunit 12B isoform f [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|268607514 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 43.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| | | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAELEHLGGK | RAESARMRRA | EQLRRWRGSL | TEQEPAERRG | AGRQPLTRRG | SPRVRFEDGA | VFLAACSSGD | TDEVRKLLAR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GADINTVNVD | GLTALHQACI | DENLDMVKFL | VENRANVNQQ | DNEGWTPLHA | AASCGYLNIA | EYFINHGASV | GIVNSEGEVP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SDLAEEPAMK | DLLLEQVKKQ | GVDLEQSRKE | EEQQMLQDAR | QWLNSGKIED | VRQARSGATA | LHVAAAKGYS | EVLRLLIQAG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YELNVQDYDG | WTPLHAAAHW | GVKEACSILA | EALCDMDIRN | KLGQTPFDVA | DEGLVEHLEL | LQKKQNVLRS | EKETRNKLIE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| SDLNSKIQSG | FFKNKEKMLY | EEETPKSQEM | EEENKESSSS | SSEEEEGEDE | ASESETEKEA | VLFWPF | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1674 | 1 | 900.4535 | -28.47 | 2 | 49.3 | 10.6 | 2 | 201-215 | R.QWLNSGKIEDVRQAR.S | |

# Detailed Protein Report

## Protein 1645: coiled-coil domain-containing protein 61 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|391353392 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 57.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.9 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.84 **CV:** 0.00 % **No. of Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530417117 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: coiled-coil domain-containing protein 61 isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDQPAGLQVD | YVFRGVEHAV | RVMVSGQVLE | LEVEDRMTAD | QWRGEFDAGF | IEDLTHKTGN | FKQFNIFCHM | LESALTQSSE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SVTLDLLTYT | DLESLRNRKM | GGRPGSLAPR | SAQLNSKRYL | ILIYSVEFDR | IHYPLPLPYQ | GKPDPVVLQG | IIRSLKEELG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RLQGLDGQNT | RDTRENEIWH | LREQVSRLAS | EKRELEAQLG | RSREEALAGR | AARQEAEALR | GLVRGLELEL | RQERGLGHRV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| AGRRGQDCRR | LAKELEEAKA | SERSLRARLK | TLTSELALYK | RGRRTPPVQP | PPTREDRASS | SRERSASRGR | GAARSSSRES |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GRGSRGRGRP | ARPSPSPTGG | RALRFDPTAF | VKAKERKQRE | IQMKQQQRNR | LGSGGSGDGP | SVSWSRQTQP | PAALTGRGDA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PNRSRNRSSS | VDSFRSRCSS | ASSCSDLEDF | SESLSRGGHR | RRGKPPSPTP | WSGSNMKSPP | VERSHHQKSL | ANSGGWVPIK |
| 490 | 500 | 510 | 520 | | | | |
| EYSSEHQAAD | MAEIDARLKA | LQEYMNRLDM | RS | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1920 | 2 | 785.8075 | -102.14 | 2 | 54.4 | 10.6 | 0 | 443-457 | R.GKPPSPTPWSGSNMK.S | | WUP:QUP 0.84 |

# Detailed Protein Report

## Protein 1646: PREDICTED: gamma-tubulin complex component 5 isoform X1 [Homo sapiens]

**Accession:** gi|578839948
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 10.6
**MW [kDa]:** 101.3
**pI:** 5.5
**Sequence Coverage [%]:** 2.5
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEDEEMDIGP | YMDTPNWSEE | SEEENDQQPL | SREDSGIQVD | RTPLEEQDQN | RKLDPCISWK | ADEPDDRSWL | EHHVVHQYWT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ARPSHFPHSL | HLHSNLAAVW | DQHLYSSDPL | YVPDDRVLVT | ETQVIRETLW | LLSGVKKLFI | FQLIDGKVTV | RNNIIVTHLT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HSCLRSVLEQ | IAAYGQVVFR | LQEFIDEVMG | HSSESMLPGS | GSVPKKSTEA | PFRTYQAFMW | ALYKYFISFK | EELAEIEKCI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| INNDTTITLA | IVVDKLAPRL | SQLKVLHKVF | STGVAEVPPD | TRNVVRASHL | LNTLYKAILE | YDNVGEASEQ | TVSLLFSLWV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ETVRPYLQTV | DEWIVHGHLW | DGAREFIIQR | NKNVPVNHRD | FWYATYTLYS | VSEKTENEEK | MSDNASASSG | SDQGPSSRQH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TMVSFLKPVL | KQIIMAGKSM | QLLKNLQCAE | STTCQAGARD | AERKSLYTLF | LESVQSRLRH | GEDSTPQVLT | EQQATKENLM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KMQSIAESHL | ELDDVHDPLL | AINFARMYLE | QSDFHEKFAG | GDVCVDRSSE | SVTCQTFELT | LRSCLYPHID | KQYLDCCGNL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| MQTLKKDYRL | VEYLQAMRNF | FLMEGGDTMY | DFYTSIFDKI | REKETWQNVS | FLNVQLQEAV | GQRYPEDSSR | LSISFENVDT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| AKKKLPVHIL | DGLTLSYKVP | WPVDIVISLE | CQKIYNQVFL | LLLQIKWAKY | SLDVLLFGEL | VSTAEKPRLK | EGLIHEQDTV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AQFGPQKEPV | RQQIHRMFLL | RVKLMHFVNS | LHNYIMTRIL | HSTGLEFQHQ | VEEAKDLDQL | IKIHYRYLST | IHDRCLLREK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VSFVKEAIMK | VLNLALMFAD | GWQAGLGTWR | MESIEKMESD | FKNCHMFLVT | ILNKAVCRGS | FPHLESLALS | LMAGMEQS |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1078 | 1 | 872.4298 | 5.61 | 3 | 43.6 | 10.6 | 2 | 837-858 | K.MESDFKNCHMFLVTILNKAVCR.G | Oxidation: 1 |

# Detailed Protein Report

## Protein 1647: PREDICTED: ankyrin repeat domain-containing protein 42 isoform X6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530396729 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.1 |
| | | **Sequence Coverage [%]:** | 11.1 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.65 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.44 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
         10         20         30         40         50         60         70         80
MPGVANSGPS TSSRETANPC SRKKVHFGSI HDAVRAGDVK QLSEIVVRGA SINELDVLHK FTPLHWAAHS GSLECLHWLL
         90        100        110        120        130        140        150        160
WHGADITHVT TRGWTASHIA AIRGQDACVQ ALIMNGANLT AQDDRGCTPL HLAATHGHSF TLQIMLRSGV DPSVTDKREW
        170        180        190        200
RPVHYAAFHG RLGCLQLLVK WGCSIEDVDY NGNLPEPP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 28 | 1 | 1103.5007 | -1.58 | 2 | 30.0 | 10.6 | 1 | 1-22 | -.MPGVANSGPSTSSRETANPCSR.K | | WUP:QUP 0.44<br>QU:MU 1.65 |

## Protein 1648: cadherin-15 preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4826669 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 88.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDAAFLLVLG | LLAQSLCLSL | GVPGWRRPTT | LYPWRRAPAL | SRVRRAWVIP | PISVSENHKR | LPYPLVQIKS | DKQQLGSVIY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SIQGPGVDEE | PRGVFSIDKF | TGKVFLNAML | DREKTDRFRL | RAFALDLGGS | TLEDPTDLEI | VVVDQNDNRP | AFLQEAFTGR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VLEGAVPGTY | VTRAEATDAD | DPETDNAALR | FSILQQGSPE | LFSIDELTGE | IRTVQVGLDR | EVVAVYNLTL | QVADMSGDGL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TATASAIITL | DDINDNAPEF | TRDEFFMEAI | EAVSGVDVGR | LEVEDRDLPG | SPNWVARFTI | LEGDPDGQFT | IRTDPKTNEG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VLSIVKALDY | ESCEHYELKV | SVQNEAPLQA | AALRAERGQA | KVRVHVQDTN | EPPVFQENPL | RTSLAEGAPP | GTLVATFSAR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DPDTEQLQRL | SYSKDYDPED | WLQVDAATGR | IQTQHVLSPA | SPFLKGGWYR | AIVLAQDDAS | QPRTATGTLS | IEILEVNDHA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PVLAPPPPGS | LCSEPHQGPG | LLLGATDEDL | PPHGAPFHFQ | LSPRLPELGR | NWSLSQVNVS | HARLRPRHQV | PEGLHRLSLL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LRDSGQPPQQ | REQPLNVTVC | RCGKDGVCLP | GAAALLAGGT | GLSLGALVIV | LASALLLLVL | VLLVALRARF | WKQSRGKGLL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| HGPQDDLRDN | VLNYDEQGGG | EEDQDAYDIS | QLRHPTALSL | PLGPPPLRRD | APQGRLHPQP | PRVLPTSPLD | IADFINDGLE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| AADSDPSVPP | YDTALIYDYE | GDGSVAGTLS | SILSSQGDED | QDYDYLRDWG | PRFARLADMY | GHPCGLEYGA | RWDHQAREGL |
| 810 | 820 | | | | | | |
| SPGALLPRHR | GRTA | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 851 | 1 | 578.2825 | -67.04 | 3 | 39.0 | 10.6 | 1 | 45-59 | R.RAWVIPPISVSENHK.R | |

# Detailed Protein Report

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## Protein 1649: ATPase ASNA1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|50428938 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAGVAGWGV | EAEEFEDAPD | VEPLEPTLSN | IIEQRSLKWI | FVGGKGGVGK | TTCSCSLAVQ | LSKGRESVLI | ISTDPAHNIS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DAFDQKFSKV | PTKVKGYDNL | FAMEIDPSLG | VAELPDEFFE | EDNMLSMGKK | MMQEAMSAFP | GIDEAMSYAE | VMRLVKGMNF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SVVVFDTAPT | GHTLRLLNFP | TIVERGLGRL | MQIKNQISPF | ISQMCNMLGL | GDMNADQLAS | KLEETLPVIR | SVSEQFKDPE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QTTFICVCIA | EFLSLYETER | LIQELAKCKI | DTHNIIVNQL | VFPDPEKPCK | MCEARHKIQA | KYLDQMEDLY | EDFHIVKLPL |
| 330 | 340 | 350 | | | | | |
| LPHEVRGADK | VNTFSALLLE | PYKPPSAQ | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1356 | 1 | 699.4617 | 171.51 | 2 | 45.3 | 10.6 | 0 | 51-63 | K.TTCSCSLAVQLSK.G | Carbamidomethyl: 5 |

# Detailed Protein Report

## Protein 1650: PREDICTED: uncharacterized protein LOC102724147 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|578824644 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 38.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.8 |
|  |  | **Sequence Coverage [%]:** | 3.0 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGVGDDLQEP | SAIIGASPVQ | SGFLGGRKEQ | DLGKRCHKGK | AAGPGSRGSK | ALMCSTGVSK | APLTYLMSYG | FELGWRKGNR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AVACREDRGG | ESVGMGQESI | LSQCESSEYK | TTVETIPAFK | AFTMDRRAYV | VCGVRSVAGR | KSFMCDGGAG | RLSDWLRRRP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LRIARPPPRA | QPAPSRRLRA | AARRRQDAQG | WDRRPSPSPG | PGRAGTPGPA | ASRVRRGGAA | RCRPAACAPS | RGPGSGSGAP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RARAHGGQSA | EAVPSACNER | NPGEPPGASE | ELGCCVQGCC | CRRGCLKLLK | VESRLEGAAR | REPEGKEVGR | CKSDRHGQTD |
| 330 | 340 | 350 | 360 | 370 |  |  |  |
| AQTFGRHCVG | SLPGAHEAPQ | HRLTQERGKN | TFNSEEATQS | SLL |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2833 | 1 | 616.3620 | 86.61 | 2 | 64.0 | 10.6 | 2 | 302-312 | R.EPEGKEVGRCK.S |  |

# Detailed Protein Report

**Protein 1651:** **PREDICTED: EF-hand calcium-binding domain-containing protein 7 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530363476 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAISPRSDAT | FSSQKSTPSE | SPRTKKFPLT | EEEIFYMNCR | AAYLTVFKSS | LENIISKDQL | YLALQHAGRN | PSQKTINKYW |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| TPQTAKLNFD | DFCIILRKEK | PTSKAELLKS | FKQLDVNDDG | CILHTDLYKF | LTKRGEKMTR | EEVNAIINLA | DVNADGKFDY |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| IKFCKLYMTT | NEQCLKTTLE | KLEVDSKLMR | HQFGNHIEGS | PERDPSPVPK | PSPKITRKTD | PETFLNKGDT | RSSLLSATRK |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| FKTSVSFTVT | MGANGNRNSK | LMEPNLIKDW | QHMQSKGCFF | LEEDGEIISH | QYRMQIAQRS | MVYLTIKPLN | LSQVEGKPSP |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| WLSVDTALYI | LKENESQANL | QLVCFTELRN | REVFGWTGEL | GPGIYWLIPS | TTGCRLRKKI | KPVTDEAQLV | YRDETGELFL |
| **410** | **420** | **430** | **440** | **450** | **460** | **470** | **480** |
| TKEFKSTLSD | IFEVIDLDGN | GLLSLEEYNF | FELRTSGEKC | DEDAWAVCRE | NFDTKRNELT | RQGFMDLNLM | EANDREGDPC |
| **490** | **500** | **510** | **520** | **530** | **540** | **550** | **560** |
| DLWVTLHSMG | YNKALELTEA | CPFVIDIYAE | KCKPKIKAVH | MEACSGQLEK | AICKSVLSNG | DAKVMDGYEN | IIVHTYSCDT |
| **570** | **580** | **590** | **600** | **610** | | | |
| WITSVIENKS | DEKVIIHISN | ELSKNCINNR | GLNIFAVEVG | PKSTMP | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1835 | 1 | 835.2818 | -104.41 | 2 | 52.8 | 10.6 | 0 | 462-475 | R.QGFMDLNLMEANDR.E | Oxidation: 4 |

# Detailed Protein Report

## Protein 1652: PREDICTED: inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 1-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578798047 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 90.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.0 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRIHGFFVSL | SRNTIMRELA | PQFQIPWSIP | TEAEDIPIVP | TTSGTMMELR | CVIAIIRHGD | RTPKQKMKME | VKHPRFFALF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EKHGGYKTGK | LKLKRPEQLQ | EVLDITRLLL | AELEKEPGGE | IEEKTGKLEQ | LKSVLEMYGH | FSGINRKVQL | TYYPHGVKAS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NEGQDPQRET | LAPSLLLVLK | WGGELTPAGR | VQAEELGRAF | RCMYPGGQGD | YAGFPGCGLL | RLHSTFRHDL | KIYASDEGRV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QMTAAAFAKG | LLALEGELTP | ILVQMVKSAN | MNGLLDSDGD | SLSSCQHRVK | ARLHHILQQD | APFGPEDYDQ | LAPTRSTSLL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NSMTIIQNPV | KVCDQVFALI | ENLTHQIRER | MQDPRSVDLQ | LYHSETLELM | LQRWSKLERD | FRQKSGRYDI | SKIPDIYDCV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KYDVQHNGSL | GLQGTAELLR | LSKALADVVI | PQEYGISREE | KLEIAVGFCL | PLLRKILLDL | QRTHEDESVN | KLHPLYSRGV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LSPGRHVRTR | LYFTSESHVH | SLLSVFRYGG | LLDETQDAQW | QRALDYLSAI | SELNYMTQIV | IMLYEDNTQD | PLSEERFHVE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LHFSPGVKGV | EEEGSARLAV | DSNEEMKTNQ | GSMENLCPGK | ASDEPDRALQ | TSPQPPEGPG | LPRRSPLIRN | RKAGSMEVLS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ETSSSRPGGY | RLFSSSRPPT | EMKQSGLGSQ | CTGLFSTTVL | GGSSSAPNLQ | DYARSHGKKL | PPASLKHRDE | LLFVPAVKRF |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SVSFAKHPTN | ELLDDQHPVV | RLLRSFSSDC | TGGRPVSLDA | TLAHHLHQCS | YHLRLFRNWL | RSGQDDPECL | YGTPCHQTGC |
| 810 | | | | | | | |
| CHYPGWV | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2855 | 1 | 626.8538 | 4.88 | 2 | 64.4 | 10.6 | 1 | 51-61 | R.CVIAIIRHGDR.T | |

# Detailed Protein Report

## Protein 1653: lysine-specific demethylase 5A [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|110618244 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 192.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| | | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

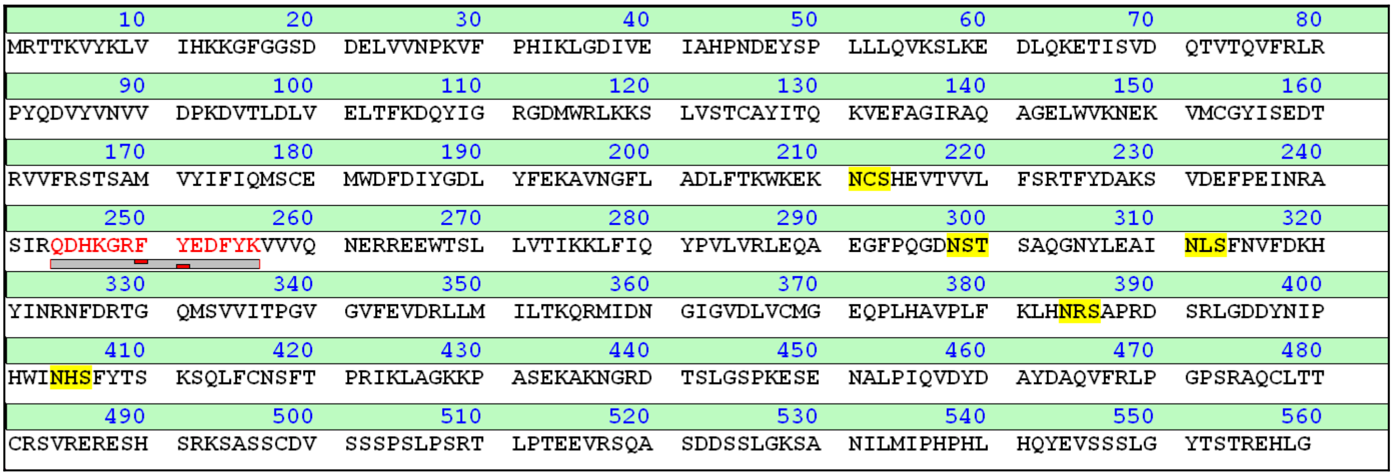
| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAGVGPGGYA | AEFVPPPECP | VFEPSWEEFT | DPLSFIGRIR | PLAEKTGICK | IRPPKDWQPP | FACEVKSFRF | TPRVQRLNEL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EAMTRVRLDF | LDQLAKFWEL | QGSTLKIPVV | ERKILDLYAL | SKIVASKGGF | EMVTKEKKWS | KVGSRLGYLP | GKGTGSLLKS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| HYERILYPYE | LFQSGVSLMG | VQMPNLDLKE | KVEPEVLSTD | TQTSPEPGTR | MNILPKRTRR | VKTQSESGDV | SRNTELKKLQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IFGAGPKVVG | LAMGTKDKED | EVTRRRKVTN | RSDAFNMQMR | QRKGTLSVNF | VDLYVCMFCG | RGNNEDKLLL | CDGCDDSYHT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FCLIPPLPDV | PKGDWRCPKC | VAEECSKPRE | AFGFEQAVRE | YTLQSFGEMA | DNFKSDYFNM | PVHMVPTELV | EKEFWRLVSS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IEEDVIVEYG | ADISSKDFGS | GFPVKDGRRK | ILPEEEEYAL | SGWNLNNMPV | LEQSVLAHIN | VDISGMKVPW | LYVGMCFSSF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CWHIEDHWSY | SINYLHWGEP | KTWYGVPSHA | AEQLEEVMRE | LAPELFESQP | DLLHQLVTIM | NPNVLMEHGV | PVYRTNQCAG |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| EFVVTFPRAY | HSGFNQGYNF | AEAVNFCTAD | WLPIGRQCVN | HYRRLRRHCV | FSHEELIFKM | AADPECLDVG | LAAMVCKELT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LMTEEETRLR | ESVVQMGVLM | SEEEVFELVP | DDERQCSACR | TTCFLSALTC | SCNPERLVCL | YHPTDLCPCP | MQKKCLRYRY |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PLEDLPSLLY | GVKVRAQSYD | TWVSRVTEAL | SANFNHKKDL | IELRVMLEDA | EDRKYPENDL | FRKLRDAVKE | AETCASVAQL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LLSKKQKHRQ | SPDSGRTRTK | LTVEELKAFV | QQLFSLPCVI | SQARQVKNLL | DDVEEFHERA | QEAMMDETPD | SSKLQMLIDM |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GSSLYVELPE | LPRLKQELQQ | ARWLDEVRLT | LSDPQQVTLD | VMKKLIDSGV | GLAPHHAVEK | AMAELQELLT | VSERWEEKAK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VCLQARPRHS | VASLESIVNE | AKNIPAFLPN | VLSLKEALQK | AREWTAKVEA | IQSGSNYAYL | EQLESLSAKG | RPIPVRLEAL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PQVESQVAAA | RAWRERTGRT | FLKKNSSHTL | LQVLSPRTDI | GVYGSGKNRR | KKVKELIEKE | KEKDLDLEPL | SDLEEGLEET |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RDTAMVVAVF | KEREQKEIEA | MHSLRAANLA | KMTMVDRIEE | VKFCICRKTA | SGFMLQCELC | KDWFHNSCVP | LPKSSSQKKG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SSWQAKEVKF | LCPLCMRSRR | PRLETILSLL | VSLQKLPVRL | PEGEALQCLT | ERAMSWQDRA | RQALATDELS | SALAKLSVLS |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| QRMVEQAARE | KTEKIISAEL | QKAAANPDLQ | GHLPSFQQSA | FNRVVSSVSS | SPRQTMDYDD | EETDSDEDIR | ETYGYDMKDT |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ASVKSSSSLE | PNLFCDEEIP | IKSEEVVTHM | WTAPSFCAEH | AYSSASKSCS | QGSSTPRKQP | RKSPLVPRSL | EPPVLELSPG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| AKAQLEELMM | VGDLLEVSLD | ETQHIWRILQ | ATHPPSEDRF | LHIMEDDSME | EKPLKVKGKD | SSEKKRKRKL | EKVEQLFGEG |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| KQKSKELKKM | DKPRKKKLKL | GADKSKELNK | LAKKLAKEEE | RKKKKEKAAA | AKVELVKEST | EKKREKKVLD | IPSKYDWSGA |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| EESDDENAVC | AAQNCQRPCK | DKVDWVQCDG | GCDEWFHQVC | VGVSPEMAEN | EDYICINCAK | KQGPVSPGPA | PPPSFIMSYK |
| 1690 | 1700 | | | | | | |
| LPMEDLKETS | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 305 | 1 | 741.5254 | 116.78 | 3 | 33.8 | 10.6 | 2 | 983-1002 | K.NIPAFLPNVLSLKEALQKAR.E | |

# Detailed Protein Report

## Protein 1654: DEP domain-containing protein 5 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|55749924 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 63.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.2 |
| | | **Sequence Coverage [%]:** | 2.3 |
| | | **No. of unique Peptides:** | 1 |



| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRTTKVYKLV | IHKKGFGGSD | DELVVNPKVF | PHIKLGDIVE | IAHPNDEYSP | LLLQVKSLKE | DLQKETISVD | QTVTQVFRLR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PYQDVYVNVV | DPKDVTLDLV | ELTFKDQYIG | RGDMWRLKKS | LVSTCAYITQ | KVEFAGIRAQ | AGELWVKNEK | VMCGYISEDT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RVVFRSTSAM | VYIFIQMSCE | MWDFDIYGDL | YFEKAVNGFL | ADLFTKWKEK | NCSHEVTVVL | FSRTFYDAKS | VDEFPEINRA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SIRQDHKGRF | YEDFYKVVVQ | NERREEWTSL | LVTIKKLFIQ | YPVLVRLEQA | EGFPQGDNST | SAQGNYLEAI | NLSFNVFDKH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YINRNFDRTG | QMSVVITPGV | GVFEVDRLLM | ILTKQRMIDN | GIGVDLVCMG | EQPLHAVPLF | KLHNRSAPRD | SRLGDDYNIP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HWINHSFYTS | KSQLFCNSFT | PRIKLAGKKP | ASEKAKNGRD | TSLGSPKESE | NALPIQVDYD | AYDAQVFRLP | GPSRAQCLTT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| CRSVRERESH | SRKSASSCDV | SSSPSLPSRT | LPTEEVRSQA | SDDSSLGKSA | NILMIPHPHL | HQYEVSSSLG | YTSTREHLG |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 853 | 1 | 866.9126 | 5.90 | 2 | 39.1 | 10.6 | 2 | 244-256 | R.QDHKGRFYEDFYK.V | |

# Detailed Protein Report

## Protein 1655: E3 ubiquitin-protein ligase HECTD3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|157738609 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 97.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAGPGPGAVL | ESPRQLLGRV | RFLAEAARSL | RAGRPLPAAL | AFVPREVLYK | LYKDPAGPSR | VLLPVWEAEG | LGLRVGAAGP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| APGTGSGPLR | AARDSIELRR | GACVRTTGEE | LCNGHGLWVK | LTKEQLAEHL | GDCGLQEGWL | LVCRPAEGGA | RLVPIDTPNH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LQRQQQLFGV | DYRPVLRWEQ | VVDLTYSHRL | GSRPQPAEAY | AEAVQRLLYV | PPTWTYECDE | DLIHFLYDHL | GKEDENLGSV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KQYVESIDVS | SYTEEFNVSC | LTDSNADTYW | ESDGSQCQHW | VRLTMKKGTI | VKKLLLTVDT | TDDNFMPKRV | VVYGGEGDNL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KKLSDVSIDE | TLIGDVCVLE | DMTVHLPIIE | IRIVECRDDG | IDVRLRGVKI | KSSRQRELGL | NADLFQPTSL | VRYPRLEGTD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PEVLYRRAVL | LQRFIKILDS | VLHHLVPAWD | HTLGTFSEIK | QVKQFLLLSR | QRPGLVAQCL | RDSESSKPSF | MPRLYINRRL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AMEHRACPSR | DPACKNAVFT | QVYEGLKPSD | KYEKPLDYRW | PMRYDQWWEC | KFIAEGIIDQ | GGGFRDSLAD | MSEELCPSSA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DTPVPLPFFV | RTANQGNGTG | EARDMYVPNP | SCRDFAKYEW | IGQLMGAALR | GKEFLVLALP | GFVWKQLSGE | EVSWSKDFPA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VDSVLVKLLE | VMEGMDKETF | EFKFGKELTF | TTVLSDQQVV | ELIPGGAGIV | VGYGDRSRFI | QLVQKARLEE | SKEQVAAMQA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GLLKVVPQAV | LDLLTWQELE | KKVCGDPEVT | VDALRKLTRF | EDFEPSDSRV | QYFWEALNNF | TNEDRSRFLR | FVTGRSRLPA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | |
| RIYIYPDKLG | YETTDALPES | STCSSTLFLP | HYASAKVCEE | KLRYAAYNCV | AIDTDMSPWE | E | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2262 | 1 | 682.8045 | -92.58 | 2 | 58.2 | 10.6 | 0 | 75-90 | R.VGAAGPAPGTGSGPLR.A | |

# Detailed Protein Report

## Protein 1656: nudC domain-containing protein 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|122939165 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| | | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| METGAAELYD | QALLGILQHV | GNVQDFLRVL | FGFLYRKTDF | YRLLRHPSDR | MGFPPGAAQA | LVLQVFKTFD | HMARQDDEKR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RQELEEKIRR | KEEEEAKTVS | AAAAEKEPVP | VPVQEIEIDS | TTELDGHQEV | EKVQPPGPVK | EMAHGSQEAE | APGAVAGAAE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VPREPPILPR | IQEQFQKNPD | SYNGAVRENY | TWSQDYTDLE | VRVPVPKHVV | KGKQVSVALS | SSSIRVAMLE | ENGERVLMEG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KLTHKINTES | SLWSLEPGKC | VLVNLSKVGE | YWWNAILEGE | EPIDIDKINK | ERSMATVDEE | EQAVLDRLTF | DYHQKLQGKP |
| 330 | 340 | 350 | 360 | 370 | | | |
| QSHELKVHEM | LKKGWDAEGS | PFRGQRFDPA | MFNISPGAVQ | F | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 102 | 1 | 709.7874 | -161.04 | 2 | 31.2 | 10.6 | 1 | 212-225 | K.GKQVSVALSSSSIR.V | |

# Detailed Protein Report

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## Protein 1657: ubiquitin-like-conjugating enzyme ATG3 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|523704487 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 35.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| | | **Sequence Coverage [%]:** | 5.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MQNVINTVKG | KALEVAEYLT | PVLKESKFKE | TGVITPEEFV | AAGDHLVHHC | PTWQWATGEE | LKVKAYLPTG | KQFLVTKNVP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CYKRCKQMEY | SDELEAIIEE | DDGDGGWVDT | YHNTGITGIT | EAVKEITLEN | KDNIRLQDCS | ALCEEEEDED | EGEAADMEEY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EESGLLETDE | ATLDTRKIVE | ACKAKTDAGG | EDAILQTRTY | DLYITYDKYY | QTPRLWLFGY | DEQRQPLTVE | HMYEDISQDH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VKKTVTIENH | PHLPPPPMCS | VHPCRHAEVM | KKIIETVAEG | GGELGVHMYP | SLYVRLVAKW | LLTIFFLRNL | V |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2808 | 1 | 973.5062 | -99.59 | 2 | 65.5 | 10.6 | 2 | 296-311 | R.LVAKWLLTIFFLRNLV.- | |

# Detailed Protein Report

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**Protein 1658:** **PREDICTED: zinc finger protein 207 isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530411140 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 4.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAVSSLGCLC | ALTVLIRYCN | RDFDDEKILI | QHQKAKHFKC | HICHKKLYTG | PGLAIHCMQV | HKETIDAVPN | AIPGRTDIEL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EIYGMEGIPE | KDMDERRRLL | EQKTQESQKK | KQQDDSDEYD | DDDSAASTSF | QPQPVQPQQG | YIPPMAQPGL | PPVPGAPGMP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PGIPPLMPGV | PPLMPGMPPV | MPGMPPGLHH | QRKYTQSFCG | ENIMMPMGGM | MPPGPGIPPL | MPGMPPGMPP | PVPRPGIPPM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TQAQAVSAPG | ILNRPPAPTA | TVPAPQPPVT | KPLFPSAGQA | QAAVQGPVGT | DFKPLNSTPA | TTTEPPKPTF | PAYTQSTAST |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| TSTTNSTAAK | PAASITSKPA | TLTTTSATSK | LIHPDEDISL | EERRAQLPKY | QRNLPRPGQA | PIGNPPVGPI | GGMMPPQPGI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | |
| PQQQGMRPPM | PPHGQYGGHH | QGMPGYLPGA | MPPYGQGPPM | VPPYQGGPPR | PPMGMRPPVM | SQGGRY | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2193 | 1 | 1130.1787 | 62.33 | 2 | 57.8 | 10.6 | 2 | 351-369 | K.LIHPDEDISLEERRAQLPK.Y | |

# Detailed Protein Report

## Protein 1659: PREDICTED: glycine--tRNA ligase isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578813403 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MEDTLKRRFF YDQAFAIYGG VSGLYDFGPV GCALKNNIIQ TWRQHFIQEE QILEIDCTML TPEPVLKTSG HVDKFADFMV
        90        100        110        120        130        140        150        160
KDVKNGECFR ADHLLKAHLQ KLMSDKKCSV EKKSEMESVL AQLDNYGQQE LADLFVNYNV KSPITGNDLS PPVSFNLMFK
       170        180        190        200        210        220        230        240
TFIGPGGNMP GYLRPETAQG IFLNFKRLLE FNQGKLPFAA AQIGNSFRNE ISPRSGLIRV REFTMAEIEH FVDPSEKDHP
       250        260        270        280        290        300        310        320
KFQNVADLHL YLYSAKAQVS GQSARKMRLG DAVEQGVINN TVLGYFIGRI YLYLTKVGIS PDKLRFRQHM ENEMAHYACD
       330        340        350        360        370        380        390        400
CWDAESKTSY GWIEIVGCAD RSCYDLSCHA RATKVPLVAE KPLKEPKTVN VVQFEPSKGA IGKAYKKDAK LVMEYLAICD
       410        420        430        440        450        460        470        480
ECYITEMEML LNEKGEFTIE TEGKTFQLTK DMINVKRFQK TLYVEEVVPN VIEPSFGLGR IMYTVFEHTF HVREGDEQRT
       490        500        510        520        530        540        550        560
FFSFPAVVAP FKCSVLPLSQ NQEFMPFVKE LSEALTRHGV SHKVDDSSGS IGRRYARTDE IGVAFGVTID FDTVNKTPHT
       570        580        590        600        610        620
ATLRDRDSMR QIRAEISELP SIVQDLANGN ITWADVEARY PLFEGQETGK KETIEE
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1178 | 1 | 660.7641 | 128.35 | 3 | 43.0 | 10.6 | 2 | 85-101 | K.NGECFRADHLLKAHLQK.L | |

# Detailed Protein Report

## Protein 1660: plastin-2 [Homo sapiens]

**Accession:** gi|167614506
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 10.6
**MW [kDa]:** 70.2
**pI:** 5.2
**Sequence Coverage [%]:** 2.4
**No. of unique Peptides:** 1

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530402335 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: plastin-2 isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MARGSVSDEE | MMELREAFAK | VDTDGNGYIS | FNELNDLFKA | ACLPLPGYRV | REITENLMAT | GDLDQDGRIS | FDEFIKIFHG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LKSTDVAKTF | RKAINKKEGI | CAIGGTSEQS | SVGTQHSYSE | EEKYAFVNWI | NKALENDPDC | RHVIPMNPNT | NDLFNAVGDG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IVLCKMINLS | VPDTIDERTI | NKKKLTPFTI | QENLNLALNS | ASAIGCHVVN | IGAEDLKEGK | PYLVLGLLWQ | VIKIGLFADI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ELSRNEALIA | LLREGESLED | LMKLSPEELL | LRWANYHLEN | AGCNKIGNFS | TDIKDSKAYY | HLLEQVAPKG | DEEGVPAVVI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DMSGLREKDD | IQRAECMLQQ | AERLGCRQFV | TATDVVRGNP | KLNLAFIANL | FNRYPALHKP | ENQDIDWGAL | EGETREERTF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RNWMNSLGVN | PRVNHLYSDL | SDALVIFQLY | EKIKVPVDWN | RVNKPPYPKL | GGNMKKLENC | NYAVELGKNQ | AKFSLVGIGG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| QDLNEGNRTL | TLALIWQLMR | RYTLNILEEI | GGGQKVNDDI | IVNWVNETLR | EAKKSSSISS | FKDPKISTSL | PVLDLIDAIQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| PGSINYDLLK | TENLNDDEKL | NNAKYAISMA | RKIGARVYAL | PEDLVEVNPK | MVMTVFACLM | GKGMKRV | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2352 | 1 | 836.1191 | 173.33 | 2 | 59.3 | 10.6 | 2 | 442-456 | R.VNKPPYPKLGGNMKK.L | |

# Detailed Protein Report

## Protein 1661: 26S proteasome non-ATPase regulatory subunit 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|25777612 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 60.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 1.17 | **CV:** 0.00 % | **No. of Peptides:** 1 |
| ***WUP:QUP*** | **Median:** 1.48 | **CV:** 0.00 % | **No. of Peptides:** 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKQEGSARRR | GADKAKPPPG | GGEQEPPPPP | APQDVEMKEE | AATGGGSTGE | ADGKTAAAAA | EHSQRELDTV | TLEDIKEHVK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QLEKAVSGKE | PRFVLRALRM | LPSTSRRLNH | YVLYKAVQGF | FTSNNATRDF | LLPFLEEPMD | TEADLQFRPR | TGKAASTPLL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PEVEAYLQLL | VVIFMMNSKR | YKEAQKISDD | LMQKISTQNR | RALDLVAAKC | YYYHARVYEF | LDKLDVVRSF | LHARLRTATL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RHDADGQATL | LNLLLRNYLH | YSLYDQAEKL | VSKSVFPEQA | NNNEWARYLY | YTGRIKAIQL | EYSEARRTMT | NALRKAPQHT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AVGFKQTVHK | LLIVVELLLG | EIPDRLQFRQ | PSLKRSLMPY | FLLTQAVRTG | NLAKFNQVLD | QFGEKFQADG | TYTLIIRLRH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NVIKTGVRMI | SLSYSRISLA | DIAQKLQLDS | PEDAEFIVAK | AIRDGVIEAS | INHEKGYVQS | KEMIDIYSTR | EPQLAFHQRI |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| SFCLDIHNMS | VKAMRFPPKS | YNKDLESAEE | RREREQQDLE | FAKEMAEDDD | DSFP | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1059 | 1 | 644.3242 | -69.99 | 2 | 41.5 | 10.6 | 2 | 97-107 | R.ALRMLPSTSRR.L | | QU:MU 1.17<br>WUP:QUP 1.48 |

# Detailed Protein Report

## Protein 1662: mitochondrial ribonuclease P protein 1 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|117647226 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 47.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.42 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 2.94 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MAAFLKMSVS VNFFRPFTRF LVPFTLHRKR NNLTILQRYM SSKIPAVTYP KNESTPPSEE LELDKWKTTM KSSVQEECVS
        90        100        110        120        130        140        150        160
TISSSKDEDP LAATREFIEM WRLLGREVPE HITEEELKTL MECVSNTAKK KYLKYLYTKE KVKKARQIKK EMKAAAREEA
       170        180        190        200        210        220        230        240
KNIKLLETTE EDKQKNFLFL RLWDRNMDIA MGWKGAQAMQ FGQPLVFDMA YENYMKRKEL QNTVSQLLES EGWNRRNVDP
       250        260        270        280        290        300        310        320
FHIYFCNLKI DGALHRELVK RYQEKWDKLL LTSTEKSHVD LFPKDSIIYL TADSPNVMTT FRHDKVYVIG SFVDKSMQPG
       330        340        350        360        370        380        390        400
TSLAKAKRLN LATECLPLDK YLQWEIGNKN LTLDQMIRIL LCLKNNGNWQ EALQFVPKRK HTGFLEISQH SQEFINRLKK
       410
AKT
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1651 | 1 | 494.2802 | 79.88 | 2 | 50.4 | 10.6 | 0 | 87-95 | K.DEDPLAATR.E | | WUP:QUP 2.94<br>QU:MU 0.42 |

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# Detailed Protein Report

## Protein 1663: heparan sulfate 2-O-sulfotransferase 1 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|6912420 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 1.02 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGLLRIMMPP | KLQLLAVVAF | AVAMLFLENQ | IQKLEESRSK | LERAIARHEV | REIEQRHTMD | GPRQDATLDE | EEDMVIIYNR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VPKTASTSFT | NIAYDLCAKN | KYHVLHINTT | KNNPVMSLQD | QVRFVKNITS | WKEMKPGFYH | GHVSYLDFAK | FGVKKKPIYI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| NVIRDPIERL | VSYYYFLRFG | DDYRPGLRRR | KQGDKKTFDE | CVAEGGSDCA | PEKLWLQIPF | FCGHSSECWN | VGSRWAMDQA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KYNLINEYFL | VGVTEELEDF | IMLLEAALPR | FFRGATELYR | TGKKSHLRKT | TEKKLPTKQT | IAKLQQSDIW | KMENEFYEFA |
| 330 | 340 | 350 | 360 | | | | |
| LEQFQFIRAH | AVREKDGDLY | ILAQNFFYEK | IYPKSN | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1976 | 1 | 918.3749 | -77.62 | 2 | 55.1 | 10.6 | 0 | 336-350 | K.DGDLYILAQNFFYEK.I | | QU:MU 1.02 |

## Protein 1664: PREDICTED: transcription factor E2F3 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530381501 | **Score:** | 10.6 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.1 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 8.9 |
| | | **No. of unique Peptides:** | 1 |

```
         10         20         30         40         50         60         70         80
MGCSLSEDGG MLAQCQGLSK EVTELSQEEK KLDELIQSCT LDLKLLTEDS ENQRLAYVTY QDIRKISGLK DQTVIVVKAP
         90        100        110        120        130        140        150        160
PETRLEVPDS IESLQIHLAS TQGPIEVYLC PEETETHSPM KTNNQDHNGN IPKPASKDLA STNSGHSDCS VSMGNLSPLA
        170        180        190        200        210        220        230
SPANLLQQTE DQIPSNLEGP FVNLLPPLLQ EDYLLSLGEE EGISDLFDAY DLEKLPLVED FMCS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1643 | 2 | 715.5471 | -131.04 | 3 | 48.9 | 10.6 | 0 | 1-20 | -.MGCSLSEDGGMLAQCQGLSK.E | Carbamidomethyl: 3, 15;<br>Oxidation: 11 |

## Protein 1665: PREDICTED: myotubularin-related protein 13 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530395847 | **Score:** | 10.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 207.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.9 |
| | | **Sequence Coverage [%]:** | 0.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 2.31 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MARLADYFIV | VGYDHEKPGS | GEGLGKIIQR | FPQKDWDDTP | FPQGIELFCQ | PGGWQLSRER | KQPTFFVVVL | TDIDSDRHYC |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SCLTFYEAEI | NLQGTKKEEI | EGEAKVSGLI | QPAEVFAPKS | LVLVSRLYYP | EIFRACLGLI | YTVYVDSLNV | SLESLIANLC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ACLVPAAGGS | QKLFSLGAGD | RQLIQTPLHD | SLPITGTSVA | LLFQQLGIQN | VLSLFCAVLT | ENKVLFHSAS | FQRLSDACRA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LESLMFPLKY | SYPYIPILPA | QLLEVLSSPT | PFIIGVHSVF | KTDVHELLDV | IIADLDGGTI | KIPECIHLSS | LPEPLLHQTQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SALSLILHPD | LEVADHAFPP | PRTALSHSKM | LDKEVRAVFL | RLFAQLFQGY | RSCLQLIRIH | AEPVIHFHKL | VAFEVERIKV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| EENNPVKMIK | HVRELAEQLF | KNENPNPHMA | FQKVPRPTEG | SHLRVHILPF | PEINEARVQE | LIQENVAKNQ | NAPPATRIEK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KCVVPAGPPV | VSIMDKVTTV | FNSAQRLEVV | RNCISFIFEN | KILETEKTLP | AALRALKGKA | ARQCLTDELG | LHVQQNRAIL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DHQQFDYIIR | MMNCTLQDCS | SLEEYNIAAA | LLPLTSAFYR | KLAPGVSQFA | YTCVQDHPIW | TNQQFWETTF | YNAVQEQVRS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LYLSAKEDNH | APHLKQKDKL | PDDHYQEKTA | MDLAAEQLRL | WPTLSKSTQQ | ELVQHEESTV | FSQAIHFANL | MVNLLVPLDT |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SKNKLLRTSA | PGDWESGSNS | IVTNSIAGSV | AESYDTESGF | EDSENTDIAN | SVVRFITRFI | DKVCTESGVT | QDHIKSLHCM |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IPGIVAMHIE | TLEAVHRESR | RLPPIQKPKI | LRPALLPGEE | IVCEGLRVLL | DPDGREEATG | GLLGGPQLLP | AEGALFLTTY |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| RILFRGTPHD | QLVGEQTVVR | SFPIASITKE | KKITMQNQLQ | QNMQEGLQIT | SASFQLIKVA | FDEEVSPEVV | EIFKKQLMKF |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RYPQSIFSTF | AFAAGQTTPQ | IILPKQKEKN | TSFRTFSKTI | VKGAKRAGKM | TIGRQYLLKK | KTGTIVEERV | NRPGWNEDDD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VSVSDESELP | TSTTLKASEK | STMEQLVEKA | CFRDYQRLGL | GTISGSSSRS | RPEYFRITAS | NRMYSLCRSY | PGLLVVPQAV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| QDSSLPRVAR | CYRHNRLPVV | CWKNSRSGTL | LLRSGGFHGK | GVVGLFKSQN | SPQAAPTSSL | ESSSSIEQEK | YLQALLNAVS |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VHQKLRGNST | LTVRPAFALS | PGTERRTSRM | STVLKQVVPG | HLDVNPSNSF | AQGGVWASLR | SSTRLISSPT | SFIDVGARLA |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| GKDHSASFSN | SSYLQNQLLK | RQAALYIFGE | KSQLRNFKVE | FALNCEFVPV | EFHEIRQVKA | SFKKLMRACI | PSTIPTDSEV |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| TFLKALGDSE | WFPQLHRIMQ | LAVVVSEVLE | NGSSVLVCLE | EGWDITAQVT | SLVQLLSDPF | YRTLEGFQML | VEKEWLSFGH |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KFSQRSSLTL | NCQGSGFAPV | FLQFLDCVHQ | VHNQYPTEFE | FNLYYLKFLA | FHYVSNRFKT | FLLDSDYERL | EHGTLFDDKG |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| EKHAKKGVCI | WECIDRMHKR | SPIFFNYLYS | PLEIEALKPN | VNVSSLKKWD | YYIEETLSTG | PSYDWMMLTP | KHFPSEDSDL |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| AGEAGPRSQR | RTVWPCYDDV | SCTQPDALTS | LFSEIEKLEH | KLNQAPEKWQ | QLWERVTVDL | KEEPRTDRSQ | RHLSRSPGIV |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| STNLPSYQKR | SLLHLPDSSM | GEEQNSSISP | SNGVERRAAT | LYSQYTSKND | ENRSFEGTLY | KRGALLKGWK | PRWFVLDVTK |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| HQLRYYDSGE | DTSCKGHIDL | AEVEMVIPAG | PSMGAPKHTS | DKAFFDLKTS | KRVYNFCAQD | GQSAQQWMDK | IQSCISDA |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|

| | | | [ppm] | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 196 | 1 | 795.3885 | 19.62 | 2 | 31.3 | 10.5 | 1 | 1527-1539 | K.GVCIWECIDRMHK.R | | QU:MU 2.31 |

# Detailed Protein Report

## Protein 1666: uncharacterized protein C14orf105 isoform 5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|545687738 | **Score:** | 10.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 17.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| | | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MYFDIPLEHR | ETSIIKRHPP | QRLQKLEPID | LPRVITSGRL | LSQREARTMH | KAKVLEKKMQ | TPMYTSENRQ | YLHKMQVLEM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | |
| IRKRQEAQME | LKKSLHGEAR | INKQSPRDHK | AKKTLQSTPR | NDDHDLLTML | PDEILNRGPG | QTHS | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 128 | 1 | 930.2523 | -305.66 | 1 | 31.3 | 10.5 | 1 | 113-120 | K.KTLQSTPR.N | |

# Detailed Protein Report

**Protein 1667:** **PREDICTED: pleckstrin homology domain-containing family H member 1 isoform X9 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578826005 | **Score:** | 10.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 99.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNVDKRATQI | SNMPFMDESS | GSDDDCSSQA | SFRISVPSSE | SRKTSGLGSP | RAIKRGVSMS | SLSSEGDYAI | PPDACSLDSD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YSEPEHKLQR | TSSYSTDGLG | LGGESLEKSG | YLLKMGSQVK | TWKRRWFVLR | QGQIMYYKSP | SDVIRKPQGQ | VDLNSRCQIV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RGEGSQTFQL | ISEKKTYYLT | ADSPSLLEEW | IRVLQSLLKV | QATGPPALLR | GGTKPTVKGW | LTKVKHGHSK | VVWCALVGKI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FYYYRSHEDK | RPLGCLPVRD | AHIEEVDRSC | DSDEDYEAGG | TRRLLSSHCT | LVIHPTEHSP | TYLLIGTKHE | KDTWLYHLTV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AAGGSSAKVG | TAYEQLIGKL | MDGEGDPDSP | LWRHPMLCYS | KDGLYASLTT | LPSEALQTEA | LKLFKSCQLF | INVPVEAASV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DYHVSLAQTA | LQVCLVHPEL | QSEIYCQLMK | QTSCRPPQKY | SLMQCWQLLA | LCAPLFLPQH | HFLWYVKQQL | QRHADPRSET |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GQYATYCQRA | VERTLRTGER | EARPSRMEVV | SILLRNPFHH | SLPFSIPVHF | TNGTYHVVGF | DGSSTVDEFL | QRLNQEIGMR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KPSHSGFALF | TDDPSGRDLE | HCLQGSVKIC | DAISKWEQAM | KELHPGKSEG | GTRVVKLMYK | NRLYFRSQVK | GETDRERLLL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ASQTSREIVA | GRFPINKELA | LEMAALMAQV | EYGDLEKPAL | PGPGGTSPAK | AQHLLQQVLD | RFHPRRYRHG | APAEQLRHLA |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| DMLTTKWATL | QGCSPPECIR | IYLTVARKWP | FFGAKLFAAQ | PAQLSSKENA | LVWIAVNEDG | VSILDHNTMQ | VHITYPYSSV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TTFGGCRDDF | MLVIRSIPDK | SSGKSHIEKL | IFRMAAPKIA | EATFIMASYM | NHCTTTVNPP | TNPPGACQLW | ELDGRQFFSS |
| 890 | 900 | | | | | | |
| VSCATKGPTL | L | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 636 | 1 | 891.1482 | 34.85 | 3 | 37.9 | 10.5 | 2 | 246-268 | R.SHEDKRPLGCLPVRDAHIEEVDR.S | |

# Detailed Protein Report

## Protein 1668: calcium-activated potassium channel subunit alpha-1 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|238624130 | **Score:** | 10.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 137.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.7 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MANGGGGGGG | SSGGGGGGGG | SSLRMSSNIH | ANHLSLDASS | SSSSSSSSSS | SSSSSSSSSS | VHEPKMDALI | IPVTMEVPCD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SRGQRMWWAF | LASSMVTFFG | GLFIILLWRT | LKYLWTVCCH | CGGKTKEAQK | INNGSSQADG | TLKPVDEKEE | AVAAEVGWMT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SVKDWAGVMI | SAQTLTGRVL | VVLVFALSIG | ALVIYFIDSS | NPIESCQNFY | KDFTLQIDMA | FNVFFLLYFG | LRFIAANDKL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| WFWLEVNSVV | DFFTVPPVFV | SVYLNRSWLG | LRFLRALRLI | QFSEILQFLN | ILKTSNSIKL | VNLLSIFIST | WLTAAGFIHL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VENSGDPWEN | FQNNQALTYW | ECVYLLMVTM | STVGYGDVYA | KTTLGRLFMV | FFILGGLAMF | ASYVPEIIEL | IGNRKKYGGS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YSAVSGRKHI | VVCGHITLES | VSNFLKDFLH | KDRDDVNVEI | VFLHNISPNL | ELEALFKRHF | TQVEFYQGSV | LNPHDLARVK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IESADACLIL | ANKYCADPDA | EDASNIMRVI | SIKNYHPKIR | IITQMLQYHN | KAHLLNIPSW | NWKEGDDAIC | LAELKLGFIA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| QSCLAQGLST | MLANLFSMRS | FIKIEEDTWQ | KYYLEGVSNE | MYTEYLSSAF | VGLSFPTVCE | LCFVKLKLLM | IAIEYKSANR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ESRILINPGN | HLKIQEGTLG | FFIASDAKEV | KRAFFYCKAC | HDDITDPKRI | KKCGCKRPKM | SIYKRMRRAC | CFDCGRSERD |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CSCMSGRVRG | NVDTLERAFP | LSSVSVNDCS | TSFRAFEDEQ | PSTLSPKKKQ | RNGGMRNSPN | TSPKLMRHDP | LLIPGNDQID |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| NMDSNVKKYD | STGMFHWCAP | KEIEKVILTR | SEAAMTVLSG | HVVVCIFGDV | SSALIGLRNL | VMPLRASNFH | YHELKHIVFV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GSIEYLKREW | ETLHNFPKVS | ILPGTPLSRA | DLRAVNINLC | DMCVILSANQ | NNIDDTSLQD | KECILASLNI | KSMQFDDSIG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VLQANSQGFT | PPGMDRSSPD | NSPVHGMLRQ | PSITTGVNIP | IITELVNDTN | VQFLDQDDDD | DPDTELYLTQ | PFACGTAFAV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SVLDSLMSAT | YFNDNILTLI | RTLVTGGATP | ELEALIAEEN | ALRGGYSTPQ | TLANRDRCRV | AQLALLDGPF | ADLGDGGCYG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DLFCKALKTY | NMLCFGIYRL | RDAHLSTPSQ | CTKRYVITNP | PYEFELVPTD | LIFCLMQFDH | NAGQSRASLS | HSSHSSQSSS |
| 1210 | 1220 | 1230 | 1240 | | | | |
| KKSSSVHSIP | STANRQNRPK | SRESRDKQKY | VQEERL | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2635 | 1 | 644.1226 | -193.67 | 2 | 61.2 | 10.5 | 1 | 717-727 | R.SERDCSCMSGR.V | Carbamidomethyl: 5 |

# Detailed Protein Report

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**Protein 1669:** **succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|11321583 | **Score:** | 10.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 50.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.7 |
| | | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.84 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAASMFYGRL | VAVATLRNHR | PRTAQRAAAQ | VLGSSGLFNN | HGLQVQQQQQ | RNLSLHEYMS | MELLQEAGVS | VPKGYVAKSP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DEAYAIAKKL | GSKDVVIKAQ | VLAGGRGKGT | FESGLKGGVK | IVFSPEEAKA | VSSQMIGKKL | FTKQTGEKGR | ICNQVLVCER |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KYPRREYYFA | ITMERSFQGP | VLIGSSHGGV | NIEDVAAESP | EAIIKEPIDI | EEGIKKEQAL | QLAQKMGFPP | NIVESAAENM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VKLYSLFLKY | DATMIEINPM | VEDSDGAVLC | MDAKINFDSN | SAYRQKKIFD | LQDWTQEDER | DKDAAKANLN | YIGLDGNIGC |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LVNGAGLAMA | TMDIIKLHGG | TPANFLDVGG | GATVHQVTEA | FKLITSDKKV | LAILVNIFGG | IMRCDVIAQG | IVMAVKDLEI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | |
| KIPVVVRLQG | TRVDDAKALI | ADSGLKILAC | DDLDEAARMV | VKLSEIVTLA | KQAHVDVKFQ | LPI | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1749 | 1 | 785.8811 | -26.88 | 2 | 51.7 | 10.5 | 2 | 275-287 | K.INFDSNSAYRQKK.I | | WUP:QUP 0.84 |

# Detailed Protein Report

## Protein 1670: protein FAM194B [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|210147567 | **Score:** | 10.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 81.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSAENNQLSG | ASPPHPPTTP | QYSTQNLPSE | KEDTEVELDE | ESLQDESPFS | PEGESLEDKE | YLEEEEDLEE | EEYLGKEEYL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KEEEYLGKEE | HLEEEEYLEK | AGYLEEEEYI | EEEEYLGKEG | YLEEEEYLGK | EEHLEEEEYL | GKEGYLEKED | YIEEVDYLGK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KAYLEEEEYL | GKKSYLEEEK | ALEKEENLEE | EEALEKEENL | DGKENLYKKY | LKEPKASYSS | QTMLLRDARS | PDAGPSQVTT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FLTVPLTFAT | PSPVSESATE | SSELLLTLYR | RSQASQTDWC | YDRTAVKSLK | SKSETEQETT | TKLAPEEHVN | TKVQQKKEEN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VLEFASKENF | WDGITDESID | KLEVEDLDEN | FLNSSYQTVF | KTIIKEMAAH | NELEEDFDIP | LTKLLESENR | WKLVIMLKKN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| YEKFKETILR | IKRRREAQKL | TEMTSFTFHL | MSKPTPEKPE | TEEIQKPQRV | VHHRKKLERD | KEWIQKKTVV | HQGDGKLILY |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PNKNVYQILF | PDGTGQIHYP | SGNLAMLILY | AKMKKFTYII | LEDSLEGRIR | ALINNSGNAT | FYDENSDIWL | NLSSNLGYYF |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| PKDKRQKAWN | WWNLNIHVHA | PPVQPISLKI | NEYIQVQIRS | QDKIIFCFTY | EQKQICLNLG | TRYKFVIPEV | LSEMKKKTIL |
| 650 | 660 | 670 | 680 | 690 | 700 | | |
| EAEPGPTAQK | IRVLLGKMNR | LLNYATTPDL | ENFIEAVSIS | LMDNKYLKKM | LSKLWF | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2059 | 1 | 1051.4459 | -42.83 | 2 | 56.1 | 10.5 | 0 | 366-383 | K.EMAAHNELEEDFDIPLTK.L | |

# Detailed Protein Report

## Protein 1671: sterile alpha motif domain-containing protein 9-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|51339291 | **Score:** | 10.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 184.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578814011 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: sterile alpha motif domain-containing protein 9-like isoform X6 [Homo sapiens] |
| gi\|578814009 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: sterile alpha motif domain-containing protein 9-like isoform X5 [Homo sapiens] |
| gi\|578814007 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: sterile alpha motif domain-containing protein 9-like isoform X4 [Homo sapiens] |
| gi\|530385585 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: sterile alpha motif domain-containing protein 9-like isoform X3 [Homo sapiens] |
| gi\|530385581 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: sterile alpha motif domain-containing protein 9-like isoform X1 [Homo sapiens] |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSKQVSLPEM | IKDWTKEHVK | KWVNEDLKIN | EQYGQILLSE | EVTGLVLQEL | TEKDLVEMGL | PWGPALLIKR | SYNKLNSKSP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ESDNHDPGQL | DNSKPSKTEH | QKNPKHTKKE | EENSMSSNID | YDPREIRDIK | QEESILMKEN | VLDEVANAKH | KKKGKLKPEQ |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LTCMPYPFDQ | FHDSHRYIEH | YTLQPETGAL | NLIDPIHEFK | ALTNTETATE | VDIKMKFSNE | VFRFASACMN | SRTNGTIHFG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VKDKPHGEIV | GVKITSKAAF | IDHFNVMIKK | YFEESEINEA | KKCIREPRFV | EVLLQNNTPS | DRFVIEVDTI | PKHSICNDKY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FYIQMQICKD | KIWKQNQNLS | LFVREGASSR | DILANSKQRD | VDFKAFLQNL | KSLVASRKEA | EEEYGMKAMK | KESEGLKLVK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LLIGNRDSLD | NSYYDWYILV | TNKCHPNQIK | HLDFLKEIKW | FAVLEFDPES | MINGVVKAYK | ESRVANLHFP | NQYEDKTTNM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| WEKISTLNLY | QQPSWIFCNG | RSDLKSETYK | PLEPHLWQRE | RASEVRKLIL | FLTDENIMTR | GKFLVVFLLL | SSVESPGDPL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IETFWAFYQA | LKGMENMLCI | SVNSHIYQRW | KDLLQTRMKM | EDELTNHSIS | TLNIELVNST | ILKLKSVTRS | SRRFLPARGS |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SSVILEKKKE | DVLTALEILC | ENECTETDIE | KDKSKFLEFK | KSKEEHFYRG | GKVSWWNFYF | SSENYSSDFV | KRDSYEKLKD |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LIHCWAESPK | PIFAKIINLY | HHPGCGGTTL | AMHVLWDLKK | NFRCAVLKNK | TTDFAEIAEQ | VINLVTYRAK | SHQDYIPVLL |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LVDDFEEQEN | VYFLQNAIHS | VLAEKDLRYE | KTLVIILNCM | RSRNPDESAK | LADSIALNYQ | LSSKEQRAFG | AKLKEIEKQH |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KNCENFYSFM | IMKSNFDETY | IENVVRNILK | GQDVDSKEAQ | LISFLALLSS | YVTDSTISVS | QCEIFLGIIY | TSTPWEPESL |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| EDKMGTYSTL | LIKTEVAEYG | RYTGVRIIHP | LIALYCLKEL | ERSYHLDKCQ | IALNILEENL | FYDSGIGRDK | FQHDVQTLLL |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| TRQRKVYGDE | TDTLFSPLME | ALQNKDIEKV | LSAGSRRFPQ | NAFICQALAR | HFYIKEKDFN | TALDWARQAK | MKAPKNSYIS |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DTLGQVYKSE | IKWWLDGNKN | CRSITVNDLT | HLLEAAEKAS | RAFKESQRQT | DSKNYETENW | SPQKSQRRYD | MYNTACFLGE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| IEVGLYTIQI | LQLTPFFHKE | NELSKKHMVQ | FLSGKWTIPP | DPRNECYLAL | SKFTSHLKNL | QSDLKRCFDF | FIDYMVLLKM |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| RYTQKEIAEI | MLSKKVSRCF | RKYTELFCHL | DPCLLQSKES | QLLQEENCRK | KLEALRADRF | AGLLEYLNPN | YKDATTMESI |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| VNEYAFLLQQ | NSKKPMTNEK | QNSILANIIL | SCLKPNSKLI | QPLTTLKKQL | REVLQFVGLS | HQYPGPYFLA | CLLFWPENQE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| LDQDSKLIEK | YVSSLNRSFR | GQYKRMCRSK | QASTLFYLGK | RKGLNSIVHK | AKIEQYFDKA | QNTNSLWHSG | DVWKKNEVKD |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | |
| LLRRLTGQAE | GKLISVEYGT | EEKIKIPVIS | VYSGPLRSGR | NIERVSFYLG | FSIEGPLAYD | IEVI | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 372 | 1 | 699.2836 | -142.88 | 3 | 33.3 | 10.5 | 1 | 718-735 | K.LKDLIHCWAESPKPIFAK.I | |

# Detailed Protein Report

## Protein 1672: ral GTPase-activating protein subunit beta isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|544711150 | **Score:** | 10.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 166.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.1 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MYSEWRSLHL | VIQNDQGHTS | VLHSYPESVG | REVANAVVRP | LGQVLGTPSV | AGSENLLKTD | KEVKWTMEVI | CYGLTLPLDG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ETVKYCVDVY | TDWIMALVLP | KDSIPLPVIK | EPNQYVQTIL | KHLQNLFVPR | QEQGSSQIRL | CLQVLRAIQK | LARESSLMAR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| ETWEVLLLFL | LQINDILLAP | PTVQGGIAEN | LAEKLIGVLF | EVWLLACTRC | FPTPPYWKTA | KEMVANWRHH | PAVVEQWSKV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ICALTSRLLR | FTYGPSFPAF | KVPDEDASLI | PPEMDNECVA | QTWFRFLHML | SNPVDLSNPA | IISSTPKFQE | QFLNVSGMPQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ELNQYPCLKH | LPQIFFRAMR | GISCLVDAFL | GISRPRSDSA | PPTPVNRLSM | PQSAAVSTTP | PHNRRHRAVT | VNKATMKTST |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VSTAHASKVQ | HQTSSTSPLS | SPNQTSSEPR | PLPAPRRPKV | NSILNLFGSW | LFDAAFVHCK | LHNGINRDSS | MTAITTQASM |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EFRRKGSQMS | TDTMVSNPMF | DASEFPDNYE | AGRAEACGTL | CRIFCSKKTG | EEILPAYLSR | FYMLLIQGLQ | INDYVCHPVL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| ASVILNSPPL | FCCDLKGIDV | VVPYFISALE | TILPDRELSK | FKSYVNPTEL | RRSSINILLS | LLPLPHHFGT | VKSEVVLEGK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| FSNDDSSSYD | KPITFLSLKL | RLVNILIGAL | QTETDPNNTQ | MILGAMLNIV | QDSALLEAIG | CQMEMGGGEN | NLKSHSRTNS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GISSASGGST | EPTTPDSERP | AQALLRDYDS | AAGLLIRSIH | LVTQRLNSQW | RQDMSISLAA | LELLSGLAKV | KVMVDSGDRK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| RAISSVCTYI | VYQCSRPAPL | HSRDLHSMIV | AAFQCLCVWL | TEHPDMLDEK | DCLKEVLEIV | ELGISGSKSK | NNEQEVKYKG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| DKEPNPASMR | VKDAAEATLT | CIMQLLGAFP | SPSGPASPCS | LVNETTLIKY | SRLPTINKHS | FRYFVLDNSV | ILAMLEQPLG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NEQNDFFPSV | TVLVRGMSGR | LAWAQQLCLL | PRGAKANQKL | FVPEPRPVPK | NDVGFKYSVK | HRPFPEEVDK | IPFVKADLSI |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| PDLHEIVTEE | LEERHEKLRS | GMAQQIAYEI | HLEQQSEEEL | QKRSFPDPVT | DCKPPPPAQE | FQTARLFLSH | FGFLSLEALK |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| EPANSRLPPH | LIALDSTIPG | FFDDIGYLDL | LPCRPFDTVF | IFYMKPGQKT | NQEILKNVES | SRTVQPHFLE | FLLSLGWSVD |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VGRHPGWTGH | VSTSWSINCC | DDGEGSQQEE | VISSEDIGAS | IFNGQKKVLY | YADALTEIAF | VVPSPVESLT | DSLESNISDQ |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DSDSNMDLMP | GILKQPSLTL | ELFPNHTDNL | NSSQRLSPSS | RMRKLPQGRP | VPPLGPETRV | SVVWVERYDD | IENFPLSELM |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| TEISTGVETT | ANSSTSLRST | TLEKEVPVIF | IHPLNTGLFR | IKIQGATGKF | NMVIPLVDGM | IVSRRALGFL | VRQTVINICR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | | |
| RKRLESDSYS | PPHVRRKQKI | TDIVNKYRNK | QLEPEFYTSL | FQEVGLKNCS | S | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2029 | 1 | 682.2615 | -118.35 | 3 | 55.3 | 10.5 | 0 | 85-101 | K.YCVDVYTDWIMALVLPK.D | Oxidation: 11 |

# Detailed Protein Report

## Protein 1673: PREDICTED: zinc finger protein 37A isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530392431 | **Score:** | 10.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 54.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 5.3 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530392433 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 37A isoform X6 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKFNEFNKGG | KCFCDEKHEI | IHSEEEPSEY | NKNGNSFWLN | EDLIWHQKIK | NWEQSFEYNE | CGKAFPENSL | FLVHKRGYTG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QKTCKYTEHG | KTCDMSFFIT | HQQTHPRENH | YGNECGENIF | EESILLEHQS | VYPFSQKLNL | TPIQRTHSIN | NIIEYNECGT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FFSEKLVLHL | QQRTHTGEKP | YECHECGKTF | TQKSAHTRHQ | RTHTGGKPYE | CHECGKTFYK | NSDLIKHQRI | HTGERPYGCH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ECGKSFSEKS | TLTQHQRTHT | GEKPYECHEC | GKTFSFKSVL | TVHQKTHTGE | KPYECYACGK | AFLRKSDLIK | HQRIHTGEKP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YECNECGKSF | SEKSTLTKHL | RTHTGEKPYE | CIQCGKFFCY | YSGFTEHLRR | HTGEKPFGCN | ECGKTFRQKS | ALIVHQRTHI |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RQKPYGCNQC | GKSFCVKSKL | IAHHRTHTGE | KPYECNVCGK | SFYVKSKLTV | HQRIHLGRNP | INVVNEGNYS | G |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2269 | 1 | 1023.8465 | 48.31 | 3 | 58.8 | 10.5 | 2 | 83-107 | K.TCKYTEHGKTCDMSFFITHQQTHPR.E | Carbamidomethyl: 2;<br>Oxidation: 13 |

# Detailed Protein Report

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## Protein 1674: zinc finger protein 668 isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|289547677 | **Score:** | 10.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 67.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.5 |
| | | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|289547684 | refseq_human (refseq_human_20140103.fasta) | zinc finger protein 668 isoform a [Homo sapiens] |
| gi\|289547680 | refseq_human (refseq_human_20140103.fasta) | zinc finger protein 668 isoform a [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEVEAAEARS | PAPGYKRSGR | RYKCLSCTKT | FPNAPRAARH | AATHGPADCS | EEVAEVKPKP | ETEAKAEEAS | GEKVSGSAAK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PRPYACPLCP | KAYKTAPELR | SHGRSHTGEK | PFPCPECGRR | FMQPVCLRVH | LASHAGELPF | RCAHCPKAYG | ALSKLKIHQR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GHTGERPYAC | ADCGKSFADP | SVFRKHRRTH | AGLRPYSCER | CGKAYAELKD | LRNHERSHTG | ERPFLCSECG | KSFSRSSSLT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CHQRIHAAQK | PYRCPACGKG | FTQLSSYQSH | ERTHSGEKPF | LCPRCGRMFS | DPSSFRRHQR | AHEGVKPYHC | EKCGKDFRQP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ADLAMHRRVH | TGDRPFKCLQ | CDKTFVASWD | LKRHALVHSG | QRPFRCEECG | RAFAERASLT | KHSRVHSGER | PFHCNACGKS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FVVSSSLRKH | ERTHRSSEAA | GVPPAQELVV | GLALPVGVAG | ESSAAPAAGA | GLGDPPAGLL | GLPPESGGVM | ATQWQVVGMT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VEHVECQDAG | VREAPGPLEG | AGEAGGEEAD | EKPPQFVCRE | CKETFSTMTL | LRRHERSHPE | LRPFPCTQCG | KSFSDRAGLR |
| 570 | 580 | 590 | 600 | 610 | 620 | | |
| KHSRTHSSVR | PYTCPHCPKA | FLSASDLRKH | ERTHPVPMGT | PTPLEPLVAL | LGMPEEGPA | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2114 | 1 | 900.3727 | -52.43 | 3 | 56.3 | 10.5 | 2 | 161-185 | R.GHTGERPYACADCGKSFADPSVFRK.H | |

# Detailed Protein Report

## Protein 1675: PREDICTED: putative uncharacterized protein LOC388900 isoform X1 [Homo sapiens]

**Accession:** gi|530420293
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 10.5
**MW [kDa]:** 55.6
**pI:** 10.1
**Sequence Coverage [%]:** 1.9
**No. of unique Peptides:** 1

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.11 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.98 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MLFSWVKRQR KSQYSCKGSE LRHARSSVIK RKTADKNLLA ELYQYSNFNS SKPNKLPNGV DFCDMVGNVV RAERDCLSGK
        90        100        110        120        130        140        150        160
HFCSGRELEK FLSSSSPRAI WLDSFWWIFH ERYQPNKELQ NNLFDRIAQH YALLLFRVPK SHSEEALLKR LPSLLSKAVY
       170        180        190        200        210        220        230        240
TSFCCCFPQS WFDTHEFKSD ICNTMSLWIS GTYPSPQSYD SWDYSELDPE RFRREELMLY RRRLTKGREF SLFAGKRAFS
       250        260        270        280        290        300        310        320
QKPAQSRKFY HPQSSSANSP SEKTSSAKQN SEKSLRMQNT AKEHHCQTLV LKKPTQEVKR ISEARECENM FPKKSCAACK
       330        340        350        360        370        380        390        400
SPELTSNLFN IYGKSPLIVY FLQNYASLQQ HGKNVLIVRR EKTTSTPDCT PTYTDVISET LCSMKKRKDN LNQLYQHHWT
       410        420        430        440        450        460        470        480
EWNYFDKHLK ELQDNFSREM KNIDPKAADT KKANHMFIPP SAVNEESPDK KTKEGKGGEG KRRETEVEHF FPLTSKP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1201 | 2 | 507.1525 | -225.20 | 2 | 43.3 | 10.5 | 0 | 141-149 | K.SHSEEALLK.R | | WUP:QUP 0.98<br>QU:MU 1.11 |

# Detailed Protein Report

## Protein 1676: transcription factor Sp8 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|39812501 | **Score:** | 10.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 48.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLAATCNKIG | SPSPSPSSLS | DSSSSFGKGF | HPWKRSSSSS | SASCNVVGSS | LSSFGVSGAS | RNGGSSSAAA | AAAAAAAAAA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ALVSDSFSCG | GSPGSSAFSL | TSSSAAAAAA | AAAAAASSSP | FANDYSVFQA | PGVSGGSGGG | GGGGGGGSSA | HSQDGSHQPV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FISKVHTSVD | GLQGIYPRVG | MAHPYESWFK | PSHPGLGAAG | EVGSAGASSW | WDVGAGWIDV | QNPNSAAALP | GSLHPAAGGL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QTSLHSPLGG | YNSDYSGLSH | SAFSSGASSH | LLSPAGQHLM | DGFKPVLPGS | YPDSAPSPLA | GAGGSMLSAG | PSAPLGGSPR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SSARRYSGRA | TCDCPNCQEA | ERLGPAGASL | RRKGLHSCHI | PGCGKVYGKT | SHLKAHLRWH | TGERPFVCNW | LFCGKRFTRS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DELQRHLRTH | TGEKRFACPV | CNKRFMRSDH | LSKHVKTHSG | GGGGGGSAGS | GSGGKKGSDT | DSEHSAAGSP | PCHSPELLQP |
| 490 | 500 | | | | | | |
| PEPGHRNGLE | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2670 | 1 | 980.4483 | 58.67 | 2 | 61.7 | 10.5 | 1 | 326-342 | R.YSGRATCDCPNCQEAER.L | Carbamidomethyl: 12 |

# Detailed Protein Report

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## Protein 1677: PREDICTED: GDP-mannose 4,6 dehydratase isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578811609 | **Score:** | 10.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 32.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.40 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 3.37 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MAHAPARCPS | ARGSGDGEMG | KPRNVALITG | ITGQDGSYLA | EFLLEKGYEV | HGIVRRSSSF | NTGRIEHLYK | NPQAHIEGNM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| KLHYGDLTDS | TCLVKIINEV | KPTEIYNLGA | QSHVKISFDL | AEYTADVDGV | GTLRLLDAVK | TCGLINSVKF | YQASTSELYG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KVQEIPQKET | TPFYPRSPYG | AAKLYAYWIV | VNFREAYNLF | AVNGILFNHE | SPRRGANFVT | RKISRSVAKI | YLGQLECFSL |
| 250 | 260 | 270 | 280 | 290 | 300 | | |
| GNLDAKRDWG | HAKDYVEHTS | SQMSHSSGLW | ILIGSLLSYT | RNPIFKNHCS | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1480 | 1 | 428.0689 | -309.31 | 2 | 46.9 | 10.5 | 0 | 57-64 | R.SSSFNTGR.I | | QU:MU 0.40<br>WUP:QUP 3.37 |

# Detailed Protein Report

## Protein 1678: dual specificity tyrosine-phosphorylation-regulated kinase 2 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4503427 | **Score:** | 10.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNDHLHVGSH | AHGQIQVQQL | FEDNSNKRTV | LTTQPNGLTT | VGKTGLPVVP | ERQLDSIHRR | QGSSTSLKSM | EGMGKVKATP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MTPEQAMKQY | MQKLTAFEHH | EIFSYPEIYF | LGLNAKKRQG | MTGGPNNGGY | DDDQGSYVQV | PHDHVAYRYE | VLKVIGKGSF |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GQVVKAYDHK | VHQHVALKMV | RNEKRFHRQA | AEEIRILEHL | RKQDKDNTMN | VIHMLENFTF | RNHICMTFEL | LSMNLYELIK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KNKFQGFSLP | LVRKFAHSIL | QCLDALHKNR | IIHCDLKPEN | ILLKQQGRSG | IKVIDFGSSC | YEHQRVYTYI | QSRFYRAPEV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ILGARYGMPI | DMWSLGCILA | ELLTGYPLLP | GEDEGDQLAC | MIELLGMPSQ | KLLDASKRAK | NFVSSKGYPR | YCTVTTLSDG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SVVLNGGRSR | RGKLRGPPES | REWGNALKGC | DDPLFLDFLK | QCLEWDPAVR | MTPGQALRHP | WLRRRLPKPP | TGEKTSVKRI |
| 490 | 500 | 510 | 520 | 530 | | | |
| TESTGAITSI | SKLPPPSSSA | SKLRTNLAQM | TDANGNIQQR | TVLPKLVS | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 959 | 1 | 546.7312 | -52.04 | 4 | 40.3 | 10.5 | 2 | 69-88 | K.SMEGMGKVKATPMTPEQAMK.Q | Oxidation: 2, 5 |

# Detailed Protein Report

## Protein 1679: solute carrier family 15 member 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|21717816 | **Score:** | 10.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 62.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***WUP:QUP*** | **Median:** | 1.44 | **CV:** | 0.00 % | **No. of Peptides:** | 1 | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEGSGGGAGE | RAPLLGARRA | AAAAAAAGAF | AGRRAACGAV | LLTELLERAA | FYGITSNLVL | FLNGAPFCWE | GAQASEALLL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FMGLTYLGSP | FGGWLADARL | GRARAILLSL | ALYLLGMLAF | PLLAAPATRA | ALCGSARLLN | CTAPGPDAAA | RCCSPATFAG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LVLVGLGVAT | VKANITPFGA | DQVKDRGPEA | TRRFFNWFYW | SINLGAILSL | GGIAYIQQNV | SFVTGYAIPT | VCVGLAFVVF |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LCGQSVFITK | PPDGSAFTDM | FKILTYSCCS | QKRSGERQSN | GEGIGVFQQS | SKQSLFDSCK | MSHGGPFTEE | KVEDVKALVK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IVPVFLALIP | YWTVYFQMQT | TYVLQSLHLR | IPEISNITTT | PHTLPAAWLT | MFDAVLILLL | IPLKDKLVDP | ILRRHGLLPS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SLKRIAVGMF | FVMCSAFAAG | ILESKRLNLV | KEKTINQTIG | NVVYHAADLS | LWWQVPQYLL | IGISEIFASI | AGLEFAYSAA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PKSMQSAIMG | LFFFFSGVGS | FVGSGLLALV | SIKAIGWMSS | HTDFGNINGC | YLNYYFFLLA | AIQGATLLLF | LIISVKYDHH |
| 570 | 580 | | | | | | |
| RDHQRSRANG | VPTSRRA | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 549 | 1 | 766.5243 | 166.36 | 2 | 36.8 | 10.5 | 1 | 173-186 | K.ANITPFGADQVKDR.G | | WUP:QUP 1.44 |

# Detailed Protein Report

## Protein 1680: kinetochore-associated protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|7661960 | **Score:** | 10.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 250.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 0.7 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578824490 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: kinetochore-associated protein 1 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWNDIELLTN | DDTGSGYLSV | GSRKEHGTAL | YQVDLLVKIS | SEKASLNPKI | QACSLSDGFI | IVADQSVILL | DSICRSLQLH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LVFDTEVDVV | GLCQEGKFLL | VGERSGNLHL | IHVTSKQTLL | TNAFVQKAND | ENRRTYQNLV | IEKDGSNEGT | YYMLLLTYSG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FFCITNLQLL | KIQQAIENVD | FSTAKKLQGQ | IKSSFISTEN | YHTLGCLSLV | AGDLASEVPV | IIGGTGNCAF | SKWEPDSSKK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GMTVKNLIDA | EIIKGAKKFQ | LIDNLLFVLD | TDNVLSLWDI | YTLTPVWNWP | SLHVEEFLLT | TEADSPSSVT | WQGITNLKLI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ALTASANKKM | KNLMVYSLPT | MEILYSLEVS | SVSSLVQTGI | STDTIYLLEG | VCKNDPKLSE | DSVSVLVLRC | LTEALPENRL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SRLLHKHRFA | EAESFAIQFG | LDVELVYKVK | SNHILEKLAL | SSVDASEQTE | WQQLVDDAKE | NLHKIQDDEF | VVNYCLKAQW |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ITYETTQEML | NYAKTRLLKK | EDKTALIYSD | GLKEVLRAHA | KLTTFYGAFG | PEKFSGSSWI | EFLNNEDDLK | DIFLQLKEGN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LVCAQYLWLR | HRANFESRFD | VKMLESLLNS | MSASVSLQKL | CPWFKNDVIP | FVRRTVPEGQ | IILAKWLEQA | ARNLELTDKA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NWPENGLQLA | EIFFTAEKTD | ELGLASSWHW | ISLKDYQNTE | EVCQLRTLVN | NLRELITLHR | KYNCKLALSD | FEKENTTTIV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| FRMFDKVLAP | ELIPSILEKF | IRVYMREHDL | QEEELLLLYI | EDLLNRCSSK | STSLFETAWE | AKAMAVIACL | SDTDLIFDAV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LKIMYAAVVP | WSAAVEQLVK | QHLEMDHPKV | KLLQESYKLM | EMKKLLRGYG | IREVNLLNKE | IMRVVRYILK | QDVPSSLEDA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LKVAQAFMLS | DDEIYSLRII | DLIDREQGED | CLLLLKSLPP | AEAEKTAERV | IIWARLALQE | EPDHSKEGKA | WRMSVAKTSV |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DILKILCDIQ | KDNLQKKDEC | EEMLKLFKEV | ASLQENFEVF | LSFEDYSNSS | LVADLREQHI | KAHEVAQAKH | KPGSTPEPIA |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AEVRSPSMES | KLHRQALALQ | MSKQELEAEL | TLRALKDGNI | KTALKKCSDL | FKYHCNADTG | KLLFLTCQKL | CQMLADNVPV |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TVPVGLNLPS | MIHDLASQAA | TICSPDFLLD | ALELCKHTLM | AVELSRQCQM | DDCGILMKAS | FGTHKDPYEE | WSYSDFFSED |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| GIVLESQMVL | PVIYELISSL | VPLAESKRYP | LESTSLPYCS | LNEGDGLVLP | VINSISALLQ | NLQESSQWEL | ALRFVVGSFG |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| TCLQHSVSNF | MNATLSEKLF | GETTLVKSRH | VVMELKEKAV | IFIRENATTL | LHKVFNCRLV | DLDLALGYCT | LLPQKDVFEN |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LWKLIDKAWQ | NYDKILAISL | VGSELASLYQ | EIEMGLKFRE | LSTDAQWGIR | LGKLGISFQP | VFRQHFLTKK | DLIKALVENI |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DMDTSLILEY | CSTFQLDCDA | VLQLFIETLL | HNTNAGQGQG | DASMDSAKRR | HPKLLAKALE | MVPLLTSTKD | LVISLSGILH |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| KLDPYDYEMI | EVVLKVIERA | DEKITNININ | QALSILKHLK | SYRRISPPVD | LEYQYMLEHV | ITLPSAAQTR | LPFHLIFFGT |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| AQNFWKILST | ELSEESFPTL | LLISKLMKFS | LDTLYVSTAK | HVFEKKLKPK | LLKLTQAKSS | TLINKEITKI | TQTIESCLLS |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| IVNPEWAVAI | AISLAQDIPE | GSFKISALKF | CLYLAERWLQ | NIPSQDEKRE | KAEALLKKLH | IQYRRSGTEA | VLIAHKLNTE |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| EYLRVIGKPA | HLIVSLYEHP | SINQRIQNSS | GTDYPDIHAA | AKEIAEVNEI | NLEKVWDMLL | EKWLCPSTKP | GEKPSELFEL |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| QEDEALRRVQ | YLLLSRPIDY | SSRMLFVFAT | STTTTLGMHQ | LTFAHRTRAL | QCLFYLADKE | TIESLFKKPI | EEVKSYLRCI |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| TFLASFETLN | IPITYELFCS | SPKEGMIKGL | WKNHSHESMA | VRLVTELCLE | YKIYDLQLWN | GLLQKLLGFN | MIPYLRKVLK |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| AISSIHSLWQ | VPYFSKAWQR | VIQIPLLSAS | CPLSPDQLSD | CSESLIAVLE | CPVSGDLDLI | GVARQYIQLE | LPAFALACLM |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| LMPHSEKRHQ | QIKNFLGSCD | PQVILKQLEE | HMNTGQLAGF | SHQIRSLILN | NIINKKEFGI | LAKTKYFQML | KMHAMNTNNI |
| 2170 | 2180 | 2190 | 2200 | 2210 | | | |
| TELVNYLAND | LSLDEASVLI | TEYSKHCGKP | VPPDTAPCEI | LKMFLSGLS | | | |

| Cmpd. | No. of | m/z meas. | Δ m/z | z | Rt | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|

| | Cmpds. | | [ppm] | | [min] | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 1494 | 1 | 981.9243 | -80.41 | 2 | 47.0 | 10.5 | 2 | 128-143 | K.ANDENRRTYQNLVIEK.D | |

# Detailed Protein Report

## Protein 1681: PREDICTED: THO complex subunit 4 isoform X1 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|530413446 | **Score:** | 10.5 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 20.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
|  |  | **Sequence Coverage [%]:** | 5.6 |
|  |  | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.80 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MPDSAPAMAD | KMDMSLDDII | KLNRSQRGGR | GGGRGRGRAG | SQGGRGGGAQ | AAARVNRGGG | PIRNRPAIAR | GAAGGGGRNR |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| PAPYSRPKQL | PDKWQHDLFD | SGFGGGAGVE | TGGKLLVSNL | DFGVSDADIQ | ELFAEFGTLK | KAAVHYDRSG | RSLGTADVHF |
| **170** | **180** | **190** | **200** |  |  |  |  |
| ERKADALKAM | KQYNGVPLDA | SYIPPLLQLL | PEDSLL |  |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1036 | 1 | 567.1165 | -238.74 | 2 | 43.0 | 10.5 | 0 | 1-11 | -.MPDSAPAMADK.M |  | QU:MU 0.80 |

# Detailed Protein Report

## Protein 1682: PREDICTED: putative methyltransferase NSUN5 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530432553 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 41.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.6 |
| | | **Sequence Coverage [%]:** | 4.5 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.88 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.63 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGLYAAAAGV | LAGVESRQGS | IKGLVYSSNF | QNVKQLYALV | CETQRYSAVL | DAVIASAGLL | RAEKKLRPHL | AKVLVYELLL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GKGFRGGGGR | WKALLGRHQA | RLKAELARLK | VHRGVSRNED | LLEVGSRPGP | ASQLPRFVRV | NTLKTCSDDV | VDYFKRQGFS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YQGRASSLDD | LRALKGKHFL | LDPLMPELLV | FPAQTDLHEH | PLYRAGHLIL | QDRASCLPAM | LLDPPPGSHV | IDACAAPGNK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TSHLAALLKN | QGSLPLTWMP | SGWHPWPRCW | PGLASLAVNW | LRRTSWRSPP | RIHATMRSTT | SCWILPAVAR | VCRADSWRSP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| GQAHLARCVC | MPWQGSSSEP | CATHSLSLPC | SGSSTPRAPS | ARRRMKTWCE | MRCSRTRAPS | G | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 31 | 1 | 668.3030 | -47.78 | 3 | 30.2 | 10.4 | 2 | 140-156 | R.VNTLKTCSDDVVDYFKR.Q | | WUP:QUP 0.63<br>QU:MU 0.88 |

# Detailed Protein Report

## Protein 1683: PREDICTED: filamin-B isoform X7 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578805877 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 225.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 0.6 |
| | | **No. of unique Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPVTEKDLAE | DAPWKKIQQN | TFTRWCNEHL | KCVNKRIGNL | QTDLSDGLRL | IALLEVLSQK | RMYRKYHQRP | TFRQMQLENV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SVALEFLDRE | SIKLVSIDSK | AIVDGNLKLI | LGLVWTLILH | YSISMPVWED | EGDDDAKKQT | PKQRLLGWIQ | NKIPYLPITN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FNQNWQDGKA | LGALVDSCAP | GLCPDWESWD | PQKPVDNARE | AMQQADDWLG | VPQVITPEEI | IHPDVDEHSV | MTYLSQFPKA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KLKPGAPLKP | KLNPKKARAY | GRGIEPTGNM | VKQPAKFTVD | TISAGQGDVM | VFVEDPEGNK | EEAQVTPDSD | KNKTYSVEYL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PKVTGLHKVT | VLFAGQHISK | SPFEVSVDKA | QGDASKVTAK | GPGLEAVGNI | ANKPTYFDIY | TAGAGVGDIG | VEVEDPQGKN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TVELLVEDKG | NQVYRCVYKP | MQPGPHVVKI | FFAGDTIPKS | PFVVQVGEAC | NPNACRASGR | GLQPKGVRIR | ETTDFKVDTK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| AAGSGELGVT | MKGPKGLEEL | VKQKDFLDGV | YAFEYYPSTP | GRYSIAITWG | GHHIPKSPFE | VQVGPEAGMQ | KVRAWGPGLH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GGIVGRSADF | VVESIGSEVG | SLGFAIEGPS | QAKIEYNDQN | DGSCDVKYWP | KEPGEYAVHI | MCDDEDIKDS | PYMAFIHPAT |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GGYNPDLVRA | YGPGLEKSGC | IVNNLAEFTV | DPKDAGKAPL | KIFAQDGEGQ | RIDIQMKNRM | DGTYACSYTP | VKAIKHTIAV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VWGGVNIPHS | PYRVNIGQGS | HPQKVKVFGP | GVERSGLKAN | EPTHFTVDCT | EAGEGDVSVG | IKCDARVLSE | DEEDVDFDII |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| HNANDTFTVK | YVPPAAGRYT | IKVLFASQEI | PASPFRVKVD | PSHDASKVKA | EGPGLSKAGV | ENGKPTHFTV | YTKGAGKAPL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| NVQFNSPLPG | DAVKDLDIID | NYDYSHTVKY | TPTQQGNMQV | LVTYGGDPIP | KSPFTVGVAA | PLDLSKIKLN | GLENRVEVGK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DQEFTVDTRG | AGGQGKLDVT | ILSPSRKVVP | CLVTPVTGRE | NSTAKFIPRE | EGLYAVDVTY | DGHPVPGSPY | TVEASLPPDP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| SKVKAHGPGL | EGGLVGKPAE | FTIDTKGAGT | GGLGLTVEGP | CEAKIECSDN | GDGTCSVSYL | PTKPGEYFVN | ILFEEVHIPG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| SPFKADIEMP | FDPSKVVASG | PGLEHGKVGE | AGLLSVDCSE | AGPGALGLEA | VSDSGTKAEV | SIQNNKDGTY | AVTYVPLTAG |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| MYTLTMKYGG | ELVPHFPARV | KVEPAVDTSR | IKVFGPGIEG | KDVFREATTD | FTVDSRPLTQ | VGGDHIKAHI | ANPSGASTEC |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| FVTDNADGTY | QVEYTPFEKG | LHVVEVTYDD | VPIPNSPFKV | AVTEGCQPSR | VQAQGPGLKE | AFTNKPNVFT | VVTRGAGIGG |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LGITVEGPSE | SKINCRDNKD | GSCSAEYIPF | APGDYDVNIT | YGGAHIPGSP | FTAKITDDSR | RCSQVKLGSA | ADFLLDISET |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| DLSSLTASIK | APSGRDEPCL | LKRLPNNHIG | ISFIPREVGE | HLVSIKKNGN | HVANSPVSIM | VVQSEIGDAR | RAKVYGRGLS |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| EGRTFEMSDF | IVDTRDAGYG | GISLAVEGPS | KVDIQTEDLE | DGTCKVSYFP | TVPGVYIVST | KFADEHVPGS | PFTVKISGEG |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| RVKESITRTS | RAPSVATVGS | ICDLNLKIPE | INSSDMSAHV | TSPSGRVTEA | EIVPMGKNSH | CVRFVPQEMG | VHTVSVKYRG |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| QHVTGSPFQF | TVGPLGEGGA | HKVRAGGPGL | ERGEAGVPAE | FSIWTREAGA | GGLSIAVEGP | SKAEITFDDH | KNGSCGVSYI |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| AQEPGNYEVS | IKFNDEHIPE | SPYLVPVIAP | SDDARRLTVM | SLQESGLKVN | QPASFAIRLN | GAKGKIDAKV | HSPSGAVEEC |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| HVSELEPDKY | AVRFIPHENG | VHTIDVKFNG | SHVVGSPFKV | RVGEPGQAGN | PALVSAYGTG | LEGGTTGIQS | EFFINTTRAG |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| PGTLSVTIEG | PSKVKMDCQE | TPEGYKVMYT | PMAPGNYLIS | VKYGGPNHIV | GSPFKAKVTG | QRLVSPGSAN | ETSSILVESV |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| TRSSTETCYS | AIPKASSDAS | KVTSKGAGLS | KAFVGQKSSF | LVDCSKAGSN | MLLIGVHGPT | TPCEEVSMKH | VGNQQYNVTY |
| 2090 | 2100 | 2110 | | | | | |
| VVKERGDYVL | AVKWGEEHIP | GSPFHVTVP | | | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 224 | 1 | 575.6716 | -248.03 | 2 | 31.6 | 10.4 | 0 | 1136-1147 | K.VVASGPGLEHGK.V | |

# Detailed Protein Report

## Protein 1684: exocyst complex component 4 isoform a [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|82546830 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 110.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAEAAGGKY | RSTVSKSKDP | SGLLISVIRT | LSTSDDVEDR | ENEKGRLEEA | YEKCDRDLDE | LIVQHYTELT | TAIRTYQSIT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ERITNSRNKI | KQVKENLLSC | KMLLHCKRDE | LRKLWIEGIE | HKHVLNLLDE | IENIKQVPQK | LEQCMASKHY | LSATDMLVSA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VESLEGPLLQ | VEGLSDLRLE | LHSKKMNLHL | VLIDELHRHL | YIKSTSRVVQ | RNKEKGKISS | LVKDASVPLI | DVTNLPTPRK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FLDTSHYSTA | GSSSVREINL | QDIKEDLELD | PEENSTLFMG | ILIKGLAKLK | KIPETVKAII | ERLEQELKQI | VKRSTTQVAD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SGYQRGENVT | VENQPRLLLE | LLELLFDKFN | AVAAAHSVVL | GYLQDTVVTP | LTQQEDIKLY | DMADVWVKIQ | DVLQMLLTEY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| LDMKNTRTAS | EPSAQLSYAS | TGREFAAFFA | KKKPQRPKNS | LFKFESSSHA | ISMSAYLREQ | RRELYSRSGE | LQGGPDDNLI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EGGGTKFVCK | PGARNITVIF | HPLLRFIQEI | EHALGLGPAK | QCPLREFLTV | YIKNIFLNQV | LAEINKEIEG | VTKTSDPLKI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LANADTMKVL | GVQRPLLQST | IIVEKTVQDL | LNLMHDLSAY | SDQFLNMVCV | KLQEYKDTCT | AAYRGIVQSE | EKLVISASWA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KDDDISRLLK | SLPNWMNMAQ | PKQLRPKREE | EEDFIRAAFG | KESEVLIGNL | GDKLIPPQDI | LRDVSDLKAL | ANMHESLEWL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| ASRTKSAFSN | LSTSQMLSPA | QDSHTNTDLP | PVSEQIMQTL | SELAKSFQDM | ADRCLLVLHL | EVRVHCFHYL | IPLAKEGNYA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IVANVESMDY | DPLVVKLNKD | ISAIEEAMSA | SLQQHKFQYI | FEGLGHLISC | ILINGAQYFR | RISESGIKKM | CRNIFVLQQN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LTNITMSREA | DLDFARQYYE | MLYNTADELL | NLVVDQGVKY | TELEYIHALT | LLHRSQTGVG | ELTTQNTRLQ | RLKEIICEQA |
| 970 | 980 | | | | | | |
| AIKQATKDKK | ITTV | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2395 | 1 | 724.8481 | 15.80 | 2 | 59.8 | 10.4 | 0 | 651-662 | K.SLPNWMNMAQPK.Q | Oxidation: 6, 8 |

# Detailed Protein Report

## Protein 1685: ATP-dependent DNA helicase PIF1 isoform b [Homo sapiens]

**Accession:** gi|557357747
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 10.4
**MW [kDa]:** 77.1
**pI:** 11.7
**Sequence Coverage [%]:** 1.7
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLSGIEAAAG | EYEDSELRCR | VAVEELSPGG | QPRRRQALRT | AELSLGRNER | RELMLRLQAP | GPAGRPRCFP | LRAARLFTRF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AEAGRSTLRL | PAHDTPGAGA | VQLLLSDCPP | DRLRRFLRTL | RLKLAAAPGP | GPASARAQLL | GPRPRDFVTI | SPVQPEERRL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RAATRVPDTT | LVKRPVEPQA | GAEPSTEAPR | WPLPVKRLSL | PSTKPQLSEE | QAAVLRAVLK | GQSIFFTGSA | GTGKSYLLKR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ILGSLPPTGT | VATASTGVAA | CHIGGTTLHA | FAGIGSGQAP | LAQCVALAQR | PGVRQGWLNC | QRLVIDEISM | VEADLFDKLE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AVARAVRQQN | KPFGGIQLII | CGDFLQLPPV | TKGSQPPRFC | FQSKSWKRCV | PVTLELTKVW | RQADQTFISL | LQAVRLGRCS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DEVTRQLQAT | ASHKVGRDGI | VATRLCTHQD | DVALTNERRL | QELPGKVHRF | EAMDSNPELA | STLDAQCPVS | QLLQLKLGAQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VMLVKNLSVS | RGLVNGARGV | VVGFEAEGRG | LPQVRFLCGV | TEVIHADRWT | VQATGGQLLS | RQQLPLQLAW | AMSIHKSQGM |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TLDCVEISLG | RVFASGQAYV | ALSRARSLQG | LRVLDFDPMA | VRCDPRVLHF | YATLRRGRSL | SLAAEGRGNE | DRCSGSSIRA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | |
| LGGDWWGLRL | GAASKQRTEL | RCVSTARPSL | AQPRTNTLQS | LTKEHKLQNV | HPYFKLLFQG | INSVWGH | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1593 | 1 | 685.8528 | -16.87 | 2 | 49.6 | 10.4 | 0 | 696-707 | K.LLFQGINSVWGH.- | |

# Detailed Protein Report

## Protein 1686: zinc/RING finger protein 4 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|150170725 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPLCRPEHLM | PRASRVPVAA | SLPLSHAVIP | TQLPSRPGHR | PPGRPRRCPK | ASCLPPPVGP | SSTQTAKRVT | MGWPRPGRAL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VAVKALLVLS | LLQVPAQAVV | RAVLEDNSSS | VDFADLPALF | GVPLAPEGIR | GYLMEVKPAN | ACHPIEAPRL | GNRSLGAIVL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IRRYDCTFDL | KVLNAQRAGF | EAAIVHNVHS | DDLVSMTHVY | EDLRGQIAIP | SVFVSEAASQ | DLRVILGCNK | SAHALLLPDD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PPCHDLGCHP | VLTVSWVLGC | TLALVVSAFF | VLNHLWLWAQ | ACCSHRRPVK | TSTCQKAQVR | TFTWHNDLCA | ICLDEYEEGD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QLKILPCSHT | YHCKCIDPWF | SQAPRRSCPV | CKQSVAATED | SFDSTTYSFR | DEDPSLPGHR | PPIWAIQVQL | RSRRLELLGR |
| 410 | 420 | 430 | | | | | |
| ASPHCHCSTT | SLEAEYTTVS | SAPPEAPGQ | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1567 | 1 | 502.6240 | -197.50 | 2 | 49.8 | 10.4 | 0 | 164-171 | R.YDCTFDLK.V | |

# Detailed Protein Report

## Protein 1687: PREDICTED: protein CROC-4 isoform X6 [Homo sapiens]

**Accession:** gi|578800428

**Database:** refseq_human(refseq_human_20140103.fasta)

**Database Date:** 2015-11-30

**Modification(s):** Oxidation

**Score:** 10.4

**MW [kDa]:** 14.5

**pI:** 11.0

**Sequence Coverage [%]:** 14.6

**No. of unique Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLRSLRNFQV | LAFISPQDAP | PPTLSLHLPT | VTVSFTRRAA | RERKREASEI | PEWIDRCYVI | GAASSTPQEA | RSWGERGSPA |
| 90 | 100 | 110 | 120 | 130 | 140 | | |
| AGATRTVSPP | HRSLELGIQE | EAASFVFWCH | RRWPPMAFGL | SAPDFGLLQL | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2797 | 1 | 711.3592 | -17.14 | 3 | 66.1 | 10.4 | 1 | 112-130 | R.RWPPMAFGLSAPDFGLLQL.- | Oxidation: 5 |

# Detailed Protein Report

## Protein 1688: apolipoprotein L1 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|211938442 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 42.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| | | **Sequence Coverage [%]:** | 4.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530420490 | refseq_human(refseq_human_20140103.fasta) | PREDICTED: apolipoprotein L1 isoform X2 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEGAALLRVS | VLCIWVQQNV | PSGTDTGDPQ | SKPLGDWAAG | TMDPESSIFI | EDAIKYFKEK | VSTQNLLLLL | TDNEAWNGFV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AAAELPRNEA | DELRKALDNL | ARQMIMKDKN | WHDKGQQYRN | WFLKEFPRLK | SELEDNIRRL | RALADGVQKV | HKGTTIANVV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SGSLSISSGI | LTLVGMGLAP | FTEGGSLVLL | EPGMELGITA | ALTGITSSTM | DYGKKWWTQA | QAHDLVIKSL | DKLKEVREFL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GENISNFLSL | AGNTYQLTRG | IGKDIRALRR | ARANLQSVPH | ASASRPRVTE | PISAESGEQV | ERVNEPSILE | MSRGVKLTDV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| APVSFFLVLD | VVYLVYESKH | LHEGAKSETA | EELKKVAQEL | EEKLNILNNN | YKILQADQEL | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 39 | 1 | 909.4150 | -88.72 | 2 | 30.3 | 10.4 | 1 | 271-287 | R.ARANLQSVPHASASRPR.V | |

## Protein 1689: ubiquitin-like modifier-activating enzyme 5 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|13376212 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 44.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 2.40 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MAESVERLQQ RVQELERELA QERSLQVPRS GDGGGGRVRI EKMSSEVVDS NPYSRLMALK RMGIVSDYEK IRTFAVAIVG
        90        100        110        120        130        140        150        160
VGGVGSVTAE MLTRCGIGKL LLFDYDKVEL ANMNRLFFQP HQAGLSKVQA AEHTLRNINP DVLFEVHNYN ITTVENFQHF
       170        180        190        200        210        220        230        240
MDRISNGGLE EGKPVDLVLS CVDNFEARMT INTACNELGQ TWMESGVSEN AVSGHIQLII PGESACFACA PPLVVAANID
       250        260        270        280        290        300        310        320
EKTLKREGVC AASLPTTMGV VAGILVQNVL KFLLNFGTVS FYLGYNAMQD FFPTMSMKPN PQCDDRNCRK QQEEYKKKVA
       330        340        350        360        370        380        390        400
ALPKQEVIQE EEIIHEDNE  WGIELVSEVS EEELKNFSGP VPDLPEGITV AYTIPKKQED SVTELTVEDS GESLEDLMAK
       410
MKNM
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 676 | 1 | 733.6504 | -69.47 | 3 | 38.5 | 10.4 | 2 | 43-61 | K.MSSEVVDSNPYSRLMALKR.M | Oxidation: 15 | QU:MU 2.40 |

# Detailed Protein Report

## Protein 1690: PREDICTED: serine/threonine-protein kinase tousled-like 1 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578805282 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 45.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.36 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.06 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSVQSSSGSL | EGPPSWSQLS | TSPTPGSAAA | ARSLLNHTPP | SGRPREGAMD | ELHSLDPRRQ | ELLEARFTGV | ASGSTGSTGS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CSVGAKASTN | NESSNHSFGS | LGSLSDKESE | TPEKKQSESS | RGRKRKAENQ | NESSQGKSIG | GRGHKISDYF | EYQGGNGSSP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VRGIPPAIRS | PQNSHSHSTP | SSSVRPNSPS | PTALAFGDHP | IVQPKQLSFK | IIQTDLTMLK | LAALESNKIQ | DLEKKEGRID |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DLLRANCDLR | RQIDEQQKLL | EKYKERLNKC | ISMSKKLLIE | KSTQEKLSSR | EKSMQDRLRL | GHFTTVRHGA | SFTEQWTDGF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AFQNLVKQQE | WVNQQREDIE | RQRKLLAKRK | PPTANNSQAP | STNSEPKQRK | NKAVNGAEND | PFVRPNLPQL | LTLAEYHEQE |
| 410 | 420 | | | | | | |
| EIFKLRLGHL | KKR | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1076 | 1 | 540.6516 | -238.63 | 2 | 41.7 | 10.4 | 1 | 267-275 | R.LNKCISMSK.K | Carbamidomethyl: 4 | QU:MU 2.36<br>WUP:QUP 0.06 |

# Detailed Protein Report

## Protein 1691: guanine nucleotide-binding protein-like 3 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|45643127 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 60.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.46 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.75 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|45643129 | refseq_huma (refseq_human_20140103.fasta) | guanine nucleotide-binding protein-like 3 isoform 2 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTCHKRYKIQ | KKVREHHRKL | RKEAKKRGHK | KPRKDPGVPN | SAPFKEALLR | EAELRKQRLE | ELKQQQKLDR | QKELEKKRKL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ETNPDIKPSN | VEPMEKEFGL | CKTENKAKSG | KQNSKKLYCQ | ELKKVIEASD | VVLEVLDARD | PLGCRCPQVE | EAIVQSGQKK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LVLILNKSDL | VPKENLESWL | NYLKKELPTV | VFRASTKPKD | KGKITKRVKA | KKNAAPFRSE | VCFGKEGLWK | LLGGFQETCS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KAIRVGVIGF | PNVGKSSIIN | SLKQEQMCNV | GVSMGLTRSM | QVVPLDKQIT | IIDSPSFIVS | PLNSSSALAL | RSPASIEVVK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PMEAASAILS | QADARQVVLK | YTVPGYRNSL | EFFTVLAQRR | GMHQKGGIPN | VEGAAKLLWS | EWTGASLAYY | CHPPTSWTPP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PYFNESIVVD | MKSGFNLEEL | EKNNAQSIRA | IKGPHLANSI | LFQSSGLTNG | IIEEKDIHEE | LPKRKERKQE | EREDDKDSDQ |
| 490 | 500 | 510 | 520 | 530 | 540 | | |
| ETVDEEVDEN | SSGMFAAEET | GEALSEETTA | GEQSTRSFIL | DKIIEEDDAY | DFSTDYV | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 107 | 1 | 591.7687 | -44.15 | 2 | 31.1 | 10.4 | 0 | 231-241 | K.LLGGFQETCSK.A | | QU:MU 0.46<br>WUP:QUP 1.75 |

# Detailed Protein Report

## Protein 1692: G-protein coupled receptor 64 isoform 6 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|296317297 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 106.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MVFSVRQCGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEE DTDNSSLSPP PAKLSVVSFA PSSNGTPEVE TTSLNDVTLS
        90        100        110        120        130        140        150        160
LLPSNETEKT KITIVKTFNA SGVKPQRNIC NLSSICNDSA FFRGEIMFQY DKESTVPQNQ HITNGTLTGV LSLSELKRSE
       170        180        190        200        210        220        230        240
LNKTLQTLSE TYFIMCATAE AQSTLNCTFT IKLNNTMNAC AVIAALERVK IRPMEHCCCS VRIPCPSSPE ELEKLQCDLQ
       250        260        270        280        290        300        310        320
DPIVCLADHP RGPPFSSSQS IPVVPRATVL SQVPKATSFA EPPDYSPVTH NVPSPIGEIQ PLSPQPSAPI ASSPAIDMPP
       330        340        350        360        370        380        390        400
QSETISSPMP QTHVSGTPPP VKASFSSPTV SAPANVNTTS APPVQTDIVN TSSISDLENQ VLQMEKALSL GSLEPNLAGE
       410        420        430        440        450        460        470        480
MINQVSRLLH SPPDMLAPLA QRLLKVVDDI GLQLNFSNTT ISLTSPSLAL AVIRVNASSF NTTTFVAQDP ANLQVSLETQ
       490        500        510        520        530        540        550        560
APENSIGTIT LPSSLMNNLP AHDMELASRV QFNFFETPAL FQDPSLENLS LISYVISSSV ANLTVRNLTR NVTVTLKHIN
       570        580        590        600        610        620        630        640
PSQDELTVRC VFWDLGRNGG RGGWSDNGCS VKDRRLNETI CTCSHLTSFG VLLDLSRTSV LPAQMMALTF ITYIGCGLSS
       650        660        670        680        690        700        710        720
IFLSVTLVTY IAFEKIRRDY PSKILIQLCA ALLLLNLVFL LDSWIALYKM QGLCISVAVF LHYFLLVSFT WMGLEAFHMY
       730        740        750        760        770        780        790        800
LALVKVFNTY IRKYILKFCI VGWGVPAVVV TIILTISPDN YGLGSYGKFP NGSPDDFCWI NNNAVFYITV VGYFCVIFLL
       810        820        830        840        850        860        870        880
NVSMFIVVLV QLCRIKKKKQ LGAQRKTSIQ DLRSIAGLTF LLGITWGFAF FAWGPVNVTF MYLFAIFNTL QGFFIFIFYC
       890        900        910        920        930        940        950        960
VAKENVRKQW RRYLCCGKLR LAENSGNAST ERNGVSFSVQ NGDVCLHDFT GKQHMFNEKE DSCNGKGRMA LRRTSKRGSL
       970
HFIEQM
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1967 | 1 | 862.3053 | -65.50 | 2 | 54.5 | 10.4 | 1 | 933-946 | K.QHMFNEKEDSCNGK.G | Carbamidomethyl: 11 |

# Detailed Protein Report

## Protein 1693: uncharacterized protein LOC89758 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|343183327 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 13.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.8 |
| | | **Sequence Coverage [%]:** | 10.8 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.51 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.79 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSISTSAIIS SAMKWSFSED KLEDLVPSMK NSSFQVPVCP ECIPSSGFLV SLTSRMKPWT LVICAHPSLL SSVPGRLTST
        90        100        110        120        130
NCITRLPPSG FQMDLANGQH QWERRGQEER QAEASLLLCP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1711 | 1 | 648.2267 | -186.12 | 2 | 51.7 | 10.4 | 0 | 2-14 | M.SISTSAIISSAMK.W | | QU:MU 0.51<br>WUP:QUP 1.79 |

# Detailed Protein Report

## Protein 1694: secretin preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|11345450 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 13.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.0 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 10.7 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MAPRPLLLLL LLLGGSAARP APPRARRHSD GTFTSELSRL REGARLQRLL QGLVGKRSEQ DAENSMAWTR LSAGLLCPSG
        90        100        110        120        130
SNMPILQAWM PLDGTWSPWL PPGPMVSEPA GAAAEGTLRP R
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 918 | 1 | 770.6818 | -179.60 | 2 | 39.9 | 10.4 | 0 | 58-70 | R.SEQDAENSMAWTR.L | Oxidation: 9 |

# Detailed Protein Report

## Protein 1695: PREDICTED: probable cation-transporting ATPase 13A3 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578807712 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 120.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 2.0 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

***WUP:QUP*** **Median:** 7.96 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MHAYRKLLYG VNEIAVKVPS VFKLLIKEVL NPFYIFQLFS VILWSTDEYY YYALAIVVMS IVSIVSSLYS IRKQYVMLHD
        90        100        110        120        130        140        150        160
MVATHSTVRV SVCRVNEEIE EIFSTDLVPG DVMVIPLNGT IMPCDAVLIN GTCIVNESML TGESVPVTKT NLPNPSVDVK
       170        180        190        200        210        220        230        240
GIGDELYNPE THKRHTLFCG TTVIQTRFYT GELVKAIVVR TGFSTSKGQL VRSILYPKPT DFKLYRDAYL FLLCLVAVAG
       250        260        270        280        290        300        310        320
IGFIYTIINS ILNEVQVGVI IIESLDIITI TVPPALPAAM TAGIVYAQRR LKKIGIFCIS PQRINICGQL NLVCFDKTGT
       330        340        350        360        370        380        390        400
LTEDGLDLWG IQRVENARFL SPEENVCNEM LVKSQFVACM ATCHSLTKIE GVLSGDPLDL KMFEAIGWIL EEATEEETAL
       410        420        430        440        450        460        470        480
HNRIMPTVVR PPKQLLPEST PAGNQEMELF ELPATYEIGI VRQFPFSSAL QRMSVVARVL GDRKMDAYMK GAPEAIAGLC
       490        500        510        520        530        540        550        560
KPETVPVDFQ NVLEDFTKQG FRVIALAHRK LESKLTWHKV QNISRDAIEN NMDFMGLIIM QNKLKQETPA VLEDLHKANI
       570        580        590        600        610        620        630        640
RTVMVTGDSM LTAVSVARDC GMILPQDKVI IAEALPPKDG KVAKINWHYA DSLTQCSHPS AIDPEAIPVK LVHDSLEDLQ
       650        660        670        680        690        700        710        720
MTRYHFAMNG KSFSVILEHF QDLVPKLMLH GTVFARMAPD QKTQLIEALQ NVDYFVGMCG DGANDCGALK RAHGGISLSE
       730        740        750        760        770        780        790        800
LEASVASPFT SKTPSISCVP NLIREGRAAL ITSFCVFKFM ALYSIIQYFS VTLLYSILSN LGDFQFLFID LAIILVVVFT
       810        820        830        840        850        860        870        880
MSLNPAWKEL VAQRPPSGLI SGALLFSVLS QIIICIGFQS LGFFWVKQQP WYEVWHPKSD ACNTTGSGFW NSSHVDNETE
       890        900        910        920        930        940        950        960
LDEHNIQNYE NTTVFFISSF QYLIVAIAFS KGKPFRQPCY KNYFFVFSVI FLYIFILFIM LYPVASVDQV LQIVCVPYQW
       970        980        990       1000       1010       1020       1030       1040
RVTMLIIVLV NAFVSITVEN FFLDMVLWKV VFNRDKQGEY RFSTTQPPQE SVDRWGKCCL PWALGCRKKT PKAKYMYLAQ
      1050       1060       1070       1080
ELLVDPEWPP KPQTTTEAKA LVKENGSCQI ITIT
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2025 | 1 | 1044.3877 | -140.05 | 2 | 55.2 | 10.4 | 0 | 712-732 | R.AHGGISLSELEASVASPFTSK.T | | WUP:QUP 7.96 |

# Detailed Protein Report

## Protein 1696: collagen triple helix repeat-containing protein 1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|368711292 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 7.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWPPGRSITV | KLREKTVSRK | LEMNGPSAFQ | GLICGKYNGM | CLQGPAGVPG | RDGSPGANGI | PGTPGIPGRD | GFKGEKGECL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RESFEESWTP | NYKQCSWSSL | NYGIDLGKIA | ECTFTKMRSN | SALRVLFSGS | LRLKCRNACC | QRWYFTFNGA | ECSGPLPIEA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | |
| IIYLDQGSPE | MNSTINIHRT | SSVEGLCEGI | GAGLVDVAIW | VGTCSDYPKG | DASTGWNSVS | RIIIEELPK | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1904 | 1 | 840.7997 | -128.54 | 2 | 53.7 | 10.4 | 0 | 21-36 | K.LEMNGPSAFQGLICGK.Y | Oxidation: 3 |

# Detailed Protein Report

## Protein 1697: CD27 antigen precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4507587 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 29.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 10.8 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MARPHPWWLC VLGTLVGLSA TPAPKSCPER HYWAQGKLCC QMCEPGTFLV KDCDQHRKAA QCDPCIPGVS FSPDHHTRPH
        90        100        110        120        130        140        150        160
CESCRHCNSG LLVRNCTITA NAECACRNGW QCRDKECTEC DPLPNPSLTA RSSQALSPHP QPTHLPYVSE MLEARTAGHM
       170        180        190        200        210        220        230        240
QTLADFRQLP ARTLSTHWPP QRSLCSSDFI RILVIFSGMF LVFTLAGALF LHQRRKYRSN KGESPVEPAE PCRYSCPREE
       250        260        270
EGSTIPIQED YRKPEPACSP
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1812 | 1 | 1045.8095 | 11.98 | 3 | 51.0 | 10.4 | 1 | 58-85 | R.KAAQCDPCIPGVSFSPDHHTRPHCESCR.H | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 1698: PREDICTED: triadin isoform X4 [Homo sapiens]

**Accession:** gi|578812314
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 10.4
**MW [kDa]:** 81.5
**pI:** 9.9
**Sequence Coverage [%]:** 1.9
**No. of unique Peptides:** 1

## Quantitation

***QU:MU*** **Median:** 0.94 **CV:** 0.00 % **No. of Peptides:** 1
***WUP:QUP*** **Median:** 0.78 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MTEITAEGNA | STTTTVIDSK | NGSVPKSPGK | VLKRTVTEDI | VTTFSSPAAW | LLVIALIITW | SAVAIVMFDL | VDYKNFSASS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IAKIGSDPLK | LVRDAMEETT | DWIYGFFSLL | SDIISSEDEE | DDDGDEDTDK | GEIDEPPLRK | KEIHKDKTEK | QEKPERKIQT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KVTHKEKEKG | KEKVREKEKP | EKKATHKEKI | EKKEKPETKT | LAKEQKKAKT | AEKSEEKTKK | EVKGGKQEKV | KQTAAKVKEV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QKTPSKPKEK | EDKEKAAVSK | HEQKDQYAFC | RYMIDIFVHG | DLKPGQSPAI | PPPLPTEQAS | RPTPASPALE | EKEGEKKKAE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KKVTSETKKK | AEKEDIKKKS | EKETAIDVEK | KEPGKASETK | QGTVKIAAQA | AAKKDEKKED | SKKTKKPAEV | EQPKGKKQEK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| KEKHVEPAKS | PKKEHSVPSD | KQVKAKTERA | KEEIGAVSIK | KAVPGKKEEK | TTKTVEQEIR | KEKSGKTSSI | LKDKEPIKGK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EEKVPASLKE | KEPETKKDEK | MSKAGKEVKP | KPPQLQGKKE | EKPEPQIKKE | AKPAISEKVQ | IHKQDIVKPE | KTVSHGKPEE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KVLKQVKAVT | IEKTAKPKPT | KKAEHREREP | PSIKTDKPKP | TPKGTSEVTE | SGKKKTEISE | KESKEKADMK | HLREEKVSTR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KESLQLHNVT | KAEKPARVSN | VEDVPASKKA | KEGTEDVSPT | KQKSPISFFQ | CVYLDGYNGY | GFQFPFTPAD | RPGESSGQAN |
| 730 | | | | | | | |
| SPGQKQQGQ | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1230 | 1 | 736.3924 | -23.04 | 2 | 45.5 | 10.4 | 2 | 658-671 | R.VSNVEDVPASKKAK.E | | WUP:QUP 0.78<br>QU:MU 0.94 |

# Detailed Protein Report

**Protein 1699:** **deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial isoform 3 [Homo sapiens]**

**Accession:** gi|70906444

**Database:** refseq_human(refseq_human_20140103.fasta)

**Database Date:** 2015-11-30

**Score:** 10.4

**MW [kDa]:** 15.4

**pI:** 6.2

**Sequence Coverage [%]:** 12.8

**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MQLRFARLSE HATAPTRGSA RAAGYDLYSA YDYTIPPMEK AVVKTDIQIA LPSGCYGRVA PRSGLAAKHF IDVGAGVIDE
        90        100        110        120        130        140        150
DYRGNVGVVL FNFGKEKFEV KKGDRIAQLI CERIFYPEIE EVQALDDTER GSGGFGSTGK N
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1576 | 1 | 671.0938 | 82.25 | 3 | 48.0 | 10.4 | 2 | 84-101 | R.GNVGVVLFNFGKEKFEVK.K | |

# Detailed Protein Report

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## Protein 1700: melanopsin isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|15150803 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 52.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 3.22 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MNPPSGPRVP | PSPTQEPSCM | ATPAPPSWWD | SSQSSISSLG | RLPSISPTAP | GTWAAAWVPL | PTVDVPDHAH | YTLGTVILLV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GLTGMLGNLT | VIYTFCRSRS | LRTPANMFII | NLAVSDFLMS | FTQAPVFFTS | SLYKQWLFGE | TGCEFYAFCG | ALFGISSMIT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LTAIALDRYL | VITRPLATFG | VASKRRAAFV | LLGVWLYALA | WSLPPFFGWS | AYVPEGLLTS | CSWDYMSFTP | AVRAYTMLLC |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CFVFFLPLLI | IIYCYIFIFR | AIRETGRALQ | TFGACKGNGE | SLWQRQRLQS | ECKMAKIMLL | VILLFVLSWA | PYSAVALVAF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AGYAHVLTPY | MSSVPAVIAK | ASAIHNPIIY | AITHPKYRVA | IAQHLPCLGV | LLGVSRRHSR | PYPSYRSTHR | STLTSHTSNL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SWISIRRRQE | SLGSESEVGW | THMEAAAVWG | AAQQANGRSL | YGQGLEDLEA | KAPPRPQGHE | AETPGKTKGL | IPSQDPRM |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 831 | 1 | 711.9280 | 96.72 | 2 | 39.9 | 10.4 | 0 | 439-451 | R.SLYGQGLEDLEAK.A | | QU:MU 3.22 |

# Detailed Protein Report

## Protein 1701: PREDICTED: vacuolar protein sorting-associated protein 53 homolog isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530410472 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 72.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578829979 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: vacuolar protein sorting-associated protein 53 homolog isoform X3 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGIPQIRQLS | ERVKAAQTEL | GQQILADFEE | AFPSQGTKRP | GGPSNVLRDA | CLVANILDPR | IKQEIIKKFI | KQHLSEYLVL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FQENQDVAWL | DKIDRRYAWI | KRQLVDYEEK | YGRMFPREWC | MAERIAVEFC | HVTRAELAKI | MRTRAKEIEV | KLLLFAIQRT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TNFEGFLAKR | FSGCTLTDGT | LKKLESPPPS | TNPFLEDEPT | PEMEELATEK | GDLDQPKKPK | APDNPFHGIV | SKCFEPHLYV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YIESQDKNLG | ELIDRFVADF | KAQGPPKPNT | DEGGAVLPSC | ADLFVYYKKC | MVQCSQLSTG | EPMIALTTIF | QKYLREYAWK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ILSGNLPKTT | TSSGGLTISS | LLKEKEGSEV | AKFTLEELCL | ICNILSTAEY | CLATTQQLEE | KLKEKVDVSL | IERINLTGEM |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DTFSTVISSS | IQLLVQDLDA | ACDPALTAMS | KMQWQNVEHV | GDQSPYVTSV | ILHIKQNVPI | IRDNLASTRK | YFTQFCVKFA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| NSFIPKFITH | LFKCKPISMV | GAEQLLLDTH | SLKMVLLDLP | SISSQVVRKA | PASYTKIVVK | GMTRAEMILK | VVMAPHEPLV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VFVDNYIKLL | TDCNTETFQK | ILDMKGLKRS | EQSSMLELLR | QRLPAPPSGA | ESSGSLSLTA | PTPEQESSRI | RKLEKLIKKR |
| 650 | | | | | | | |
| L | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2698 | 1 | 946.5530 | 92.66 | 3 | 62.2 | 10.4 | 0 | 262-288 | K.AQGPPKPNTDEGGAVLPSCADLFVYYK.K | |

# Detailed Protein Report

## Protein 1702: PREDICTED: histone H2A deubiquitinase MYSM1 isoform X4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578798291 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 94.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| | | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAEEADVDI | EGDVVAAAGA | QPGSGENTAS | VLQKDHYLDS | SWRTENGLIP | WTLDNTISEE | NRAVIEKMLL | EEEYYLSKKS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QPEKVWLDQK | EDDKKYMKSL | QKTAKIMVHS | PTKPASYSVK | WTIEEKELFE | QGLAKFGRRW | TKISKLIGSR | TVLQVKSYAR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QYFKNKVKCG | LDKETPNQKT | GHNLQVKNED | KGTKAWTPSC | LRGRADPNLN | AVKIEKLSDD | EEVDITDEVD | ELSSQTPQKN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SSSDLLLDFP | NSKMHETNQG | EFITSDSQEA | LFSKSSRGCL | QNEKQDETLS | SSEITLWTEK | QSNGDKKSIE | LNDQKFNELI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KNCNKHDGRG | IIVDARQLPS | PEPCEIQKNL | NDNEMLFHSC | QMVEESHEEE | ELKPPEQEIE | IDRNIIQEEE | KQAIPEFFEG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RQAKTPERYL | KIRNYILDQW | EICKPKYLNK | TSVRPGLKNC | GDVNCIGRIH | TYLELIGAIN | FGCEQAVYNR | PQTVDKVRIR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DRKDAVEAYQ | LAQRLQSMRT | RRRRVRDPWG | NWCDAKDLEG | QTFEHLSAEE | LAKRREEEKG | RPVKSLKVPR | PTKSSFDPFQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LIPCNFFSEE | KQEPFQVKVA | SEALLIMDLH | AHVSMAEVIG | LLGGRYSEVD | KVVEVCAAEP | CNSLSTGLQC | EMDPVSQTQA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SETLAVRGFS | VIGWYHSHPA | FDPNPSLRDI | DTQAKYQSYF | SRGGAKFIGM | IVSPYNRNNP | LPYSQITCLV | ISEEISPDGS |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YRLPYKFEVQ | QMLEEPQWGL | VFEKTRWIIE | KYRLSHSVPM | DKIFRRDSDL | TCLQKLLECM | RKTLSKVTNC | FMAEEFLTEI |
| 810 | 820 | 830 | | | | | |
| ENLFLSNYKS | NQENGVTEEN | CTKELLM | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 189 | 1 | 614.3478 | 6.42 | 2 | 32.1 | 10.4 | 2 | 535-544 | R.REEEKGRPVK.S | |

# Detailed Protein Report

## Protein 1703: lysine-specific demethylase 4C isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|226442893 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 91.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEVAEVESPL | NPSCKIMTFR | PSMEEFREFN | KYLAYMESKG | AHRAGLAKVI | PPKEWKPRQC | YDDIDNLLIP | APIQQMVTGQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SGLFTQYNIQ | KKAMTVKEFR | QLANSGKYCT | PRYLDYEDLE | RKYWKNLTFV | APIYGADING | SIYDEGVDEW | NIARLNTVLD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VVEEECGISI | EGVNTPYLYF | GMWKTTFAWH | TEDMDLYSIN | YLHFGEPKSW | YAIPPEHGKR | LERLAQGFFP | SSSQGCDAFL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RHKMTLISPS | VLKKYGIPFD | KITQEAGEFM | ITFPYGYHAG | FNHGFNCAES | TNFATVRWID | YGKVAKLCTC | RKDMVKISMD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| IFVRKFQPDR | YQLWKQGKDI | YTIDHTKPTP | ASTPEVKAWL | QRRRKVRKAS | RSFQCARSTS | KRPKADEEEE | VSDEVDGAEV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PNPDSVTDDL | KVSEKSEAAV | KLRNTEASSE | EESSASRMQV | EQNLSDHIKL | SGNSCLSTSV | TEDIKTEDDK | AYAYRSVPSI |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SSEADDSIPL | SSGYEKPEKS | DPSELSWPKS | PESCSSVAES | NGVLTEGEES | DVESHGNGLE | PGEIPAVPSG | ERNSFKVPSI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AEGENKTSKS | WRHPLSRPPA | RSPMTLVKQQ | APSDEELPEV | LSIEEEVEET | ESWAKPLIHL | WQTKSPNFAA | EQEYNATVAR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| MKPHCAICTL | LMPYHKPDSS | NEENDARWET | KLDEVVTSEG | KTKPLIPEMC | FIYSEENIEY | SPPNAFLEED | GTSLLISCAK |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| CCVRVHASCY | GIPSHEICDG | WLCARCKRNA | WTAECCLCNL | RGGALKQTKN | NKWAHVMCAV | AVPEVRFTNV | PERTQIDVGR |
| 810 | 820 | | | | | | |
| IPLQRLKLGR | LGI | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 168 | 1 | 855.2417 | -169.95 | 2 | 31.8 | 10.4 | 1 | 748-761 | K.RNAWTAECCLCNLR.G | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 1704: PREDICTED: zinc finger protein 225 isoform X2 [Homo sapiens]

**Accession:** gi|530417182
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 10.4
**MW [kDa]:** 72.6
**pI:** 10.4
**Sequence Coverage [%]:** 2.9
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEMETVSESG | THEGLFSHQT | WEQISSDLTR | FQDSMVNSFQ | FSKQDDMPCQ | VDAGLSIIHV | RQKPSEGRTC | KKSFSDVSVL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DLHQQLQSRE | KSHTCDECGK | SFCYSSALRI | HQRVHMGEKL | YNCDVCGKEF | NQSSHLQIHQ | RIHTGEKPFK | CEQCGKGFSR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RSGLYVHRKL | HTGVKPHICE | KCGKAFIHDS | QLQEHQRIHT | GEKPFKCDIC | CKSFRSRANL | NRHSMVHMRE | KPFRCDTCGK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SFGLKSALNS | HRMVHTGEKR | YKCEECGKRF | IYRQDLYKHQ | IDHTGEKPYN | CKECGKSFRW | ASGLSRHVRV | HSGETTFKCE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ECGKGFYTNS | QRYSHQRAHS | GEKPYRCEEC | GKGYKRRLDL | DFHQRVHRGE | KPYNCKECGK | SFGWASCLLN | HQRIHSGEKP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FKCEECGKRF | TQNSQLYTHR | RVHSGEKPFK | CEECGKRFTQ | NSQLYSHRRV | HTGVKPYKCE | ECGKGFNSKF | NLDMHQRVHT |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GERPYNCKEC | GKSFSRASSI | LNHKRLHGDE | KPFKCEECGK | RFTENSQLHS | HQRVHTGEKP | YKCEKCGKSF | RWASTHLTHQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| RLHSREKLLQ | CEDCGKSIVH | SSCLKDQQRD | QSGEKTSKCE | DCGKRYKRRL | NLDTLLSLFL | NDT | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1688 | 1 | 682.9670 | -30.19 | 3 | 51.4 | 10.4 | 2 | 307-324 | R.HVRVHSGETTFKCEECGK.G | |

## Protein 1705: PREDICTED: SAYSvFN domain-containing protein 1 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530382235 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 13.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.5 |
| | | **Sequence Coverage [%]:** | 24.1 |
| | | **No. of unique Peptides:** | 1 |

```
         10         20         30         40         50         60         70         80
MLEAAQPQGS TSETPWNTAI PLPSCWDQSF LTNITFLKVL LWLVLLGLFV ELEFGLAYFV LSLFYWMYVG TRGPEEKKEG
         90        100        110        120
EKSAYSVFNP GCEAIQGTLT AEQLERELQL RPLAGR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2378 | 1 | 1009.8372 | 20.04 | 3 | 60.2 | 10.4 | 1 | 79-106 | K.EGEKSAYSVFNPGCEAIQGTLTAEQLER.E | |

## Protein 1706: PREDICTED: melanoma inhibitory activity protein 3 isoform X3 [Homo sapiens]

**Accession:** gi|578800895
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 10.4
**MW [kDa]:** 209.3
**pI:** 4.6
**Sequence Coverage [%]:** 0.6
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAAAPGLLVW | LLVLRLPWRV | PGQLDPSTGR | RFSEHKLCAD | DECSMLMYRG | EALEDFTGPD | CRFVNFKKGD | PVYVYYKLAR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GWPEVWAGSV | GRTFGYFPKD | LIQVVHEYTK | EELQVPTDET | DFVCFDGGRD | DFHNYNVEEL | LGFLELYNSA | ATDSEKAVEK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TLQDMEKNPE | LSKEREPEPE | PVEANSEESD | SVFSENTEDL | QEQFTTQKHH | SHANSQANHA | QGEQASFESF | EEMLQDKLKV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PESENNKTSN | SSQVSNEQDK | IDAYKLLKKE | MTLDLKTKFG | STADALVSDD | ETTRLVTSLE | DDFDEELDTE | YYAVGKEDEE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NQEDFDELPL | LTFTDGEDMK | TPAKSGVEKY | PTDKEQNSNE | EDKVQLTVPP | GIKNDDKNIL | TTWGDTIFSI | VTGGEETRDT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MDLESSSSEE | EKEDDDDALV | PDSKQGKPQS | ATDYSDPDNV | DDGLFIVDIP | KTNNDKEVNA | EHHIKGKGRG | VQESKRGLVQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DKTELEDENQ | EGMTVHSSVH | SNNLNSMPAA | EKGKDTLKSA | YDDTENDLKG | AAIHISKGML | HEEKPGEQIL | EGGSESESAQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| KAAGNQMNDR | KIQQESLGSA | PLMGDDHPNA | SRDSVEGDAL | VNGAKLHTLS | VEHQREELKE | ELVLKTQNQP | RFSSPDEIDL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PRELEDEVPI | LGRNLPWQQE | RDVAATASKQ | MSEKIRLSEG | EAKEDSLDEE | FFHHKAMQGT | EVGQTDQTDS | TGGPAFLSKV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EEDDYPSEEL | LEDENAINAK | RSKEKNPGNQ | GRQFDVNLQV | PDRAVLGTIH | PDPEIEESKQ | ETSMILDSEK | TSETAAKGVN |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TGGREPNTMV | EKERPLADKK | AQRPFERSDF | SDSIKIQTPE | LGEVFQNKDS | DYLKNDNPEE | HLKTSGLAGE | PEGELSKEDH |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| ENTEKYMGTE | SQGSAAAEPE | DDSFHWTPHT | SVEPGHSDKR | EDLLIISSFF | KEQQSLQRFQ | KYFNVHELEA | LLQEMSSKLK |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| SAQQESLPYN | MEKVLDKVFR | ASESQILSIA | EKMLDTRVAE | NRDLGMNENN | IFEEAAVLDD | IQDLIYFVRY | KHSTAEETAT |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| LVMAPPLEEG | LGGAMEEMQP | LHEDNFSREK | TAELNVQVPE | EPTHLDQRVI | GDTHASEVSQ | KPNTEKDLDP | GPVTTEDTPM |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| DAIDANKQPE | TAAEEPASVT | PLENAILLIY | SFMFYLTKSL | VATLPDDVQP | GPDFYGLPWK | PVFITAFLGI | ASFAIFLWRT |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| VLVVKDRVYQ | VTEQQISEKL | KTIMKENTEL | VQKLSNYEQK | IKESKKHVQE | TRKQNMILSD | EAIKYKDKIK | TLEKNQEILD |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| DTAKNLRVML | ESEREQNVKN | QDLLQQEIED | WSKLHAELSE | QIKSFEKSQK | DLEVALTHKD | DNINALTNCI | TQLNLLECES |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| ESEGQNKGGN | DSDELANGEV | GGDRNEKMKN | QIKQMMDVSR | TQTAISVVEE | DLKLLQLKLR | ASVSTKCNLE | DQVKKLEDDR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| NSLQAAKAGL | EDECKTLRQK | VEILNELYQQ | KEMALQKKLS | QEEYERQERE | HRLSAADEKA | VSAAEEVKTY | KRRIEEMEDE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| LQKTERSFKN | QIATHEKKAH | ENWLKARAAE | RAIAEEKREA | ANLRHKLLEL | TQKMAMLQEE | PVIVKPMPGK | PNTQNPPRRG |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| PLSQNGSFGP | SPVSGGECSP | PLTVEPPVRP | LSATLNRRDM | PRSEFGSVDG | PLPHPRWSAE | ASGKPSPSDP | GSGTATMMNS |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| SSRGSSPTRV | LDEGKQTVLQ | EPEVPSVPSI | TSLAERPVAV | NMAPKGPPPF | PGVPLMSTPM | GGPVPPPIRY | GPPPQLCGPF |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| GPRPLPPPFG | PGMRPPLGLR | EFAPGVPPGR | RDLPLHPRGF | LPGHAPFRPL | GSLGPREYFI | PGTRLPPPTH | GPQEYPPPPA |
| 1850 | 1860 | 1870 | 1880 | | | | |
| VRDLLPSGSR | DEPPPASQST | SQDCSQALKQ | SP | | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2077 | 1 | 734.3308 | -113.16 | 2 | 54.4 | 10.4 | 1 | 920-931 | K.REDLLIISSFFK.E | |

# Detailed Protein Report

## Protein 1707: PREDICTED: collagen alpha-4(IV) chain isoform X9 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|578803629 | **Score:** | 10.4 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 135.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 0.8 |
|  |  | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 1.54 **CV:** 0.00 % **No. of Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MWSLHIVLMR | CSFRLTKSLA | TGPWSLILIL | FSVQYVYGSG | KKYIGPCGGR | DCSVCHCVPE | KGSRGPPGPP | GPQGPIGPLG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| APGPIGLSGE | KGMRGDRGPP | GAAGDKGDKG | PTGVPGFPGL | DGIPGHPGPP | GPRGKPGMSG | HNGSRGDPGF | PGGRGALGPG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GPLGHPGEKG | EKGNSVFILG | AVKGIQGDRG | DPGLPGLPGS | WGAGGPAGPT | GYPGEPGLVG | PPGQPGRPGL | KGNPGVGVKG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QMGDPGEVGQ | QGSPGPTLLV | EPPDFCLYKG | EKGIKGIPGM | VGLPGPPGRK | GESGIGAKGE | KGIPGFPGPR | GDPGSYGSPG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FPGLKGELGL | VGDPGLFGLI | GPKGDPGNRG | HPGPPGVLVT | PPLPLKGPPG | DPGFPGRYGE | TGDVGPPGPP | GLLGRPGEAC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| AGMIGPPGPQ | GFPGLPGLPG | EAGIPGRPDS | APGKPGKPGS | PGLPGAPGLQ | GLPGSSVIYC | SVGNPGPQGI | KGKVGPPGGR |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GPKGEKGNEG | LCACEPGPMG | PPGPPGLPGR | QGSKGDLGLP | GWLGTKGDPG | PPGAEGPPGL | PGKHGASGPP | GNKGAKGDMV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| VSRVKGHKGE | RGPDGPPGFP | GQPGSHGRDG | HAGEKGDPGP | PGDHEDATPG | GKGFPGPLGP | PGKAGPVGPP | GLGFPGPPGE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| RGHPGVPGHP | GVRGPDGLKG | QKGDTISCNV | TYPGRHGPPG | FDGPPGPKGF | PGPQGAPGLS | GSDGHKGRPG | TPGTAEIPGP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| PGFRGDMGDP | GFGGEKGSSP | VGPPGPPGSP | GVNGQKGIPG | DPAFGHLGPP | GKRGLSGVPG | IKGPRGDPGC | PGAEGPAGIP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| GFLGLKGPKG | REGHAGFPGV | PGPPGHSCER | GAPGIPGQPG | LPGYPGSPGA | PGGKGQPGDV | GPPGPAGMKG | LPGLPGRPGA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| HGPPGLPGIP | GPFGDDGLPG | PPGPKGPRGL | PGFPGFPGER | GKPGAEGCPG | AKGEPGEKGM | SGLPGDRGLR | GAKGAIGPPG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| DEGEMAIISQ | KGTPGEPGPP | GDDGFPGERG | DKGTPGMQGR | RGEPGRYGPP | GFHRGEPGEK | GQPGPPGPPG | PPGSTGLRGF |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| IGFPGLPGDQ | GEPGSPGPPG | FSGIDGARGP | KGNKGDPASH | FGPPGPKGEP | GSPGCPGHFG | ASGEQGLPGI | QGPRGSPGRP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| GPPGSSGPPG | CPGDHGMPGL | RGQPGEMGDP | GPRGLQGDPG | IPGPPGIKGP | SGSPGLNGLH | GLKGQKGTKG | ASGLHDVGPP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| GPVGIPGLKG | ERGDPGSPGI | SPPGPRGKKG | PPGPPGSSGP | PGPAGATGRA | PKDIPDPGPP | GDQGPPGPDG | PRGAPGPPGL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| PGSVDLLRGE | PGDCGLPGPP | GPPGPPGPPG | YKGFPGCDGK | DGQKGPVGFP | GPQGPHGFPG | PPGEKGLPGP | PGRKGPTGLP |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 |  |
| GPRGEPGPPA | DVDDCPRIPG | LPGAPGMRGP | EGAMGLPGMR | GPSGPGGTRG | RQTALRKTCN |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 383 | 1 | 607.1372 | -213.64 | 2 | 33.4 | 10.4 | 0 | 1142-1153 | R.GQPGEMGDPGPR.G | Oxidation: 6 | WUP:QUP 1.54 |

# Detailed Protein Report

## Protein 1708: eukaryotic translation initiation factor 4B [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|50053795 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.4 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAASAKKKNK | KGKTISLTDF | LAEDGGTGGG | STYVSKPVSW | ADETDDLEGD | VSTTWHSNDD | DVYRAPPIDR | SILPTAPRAA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| REPNIDRSRL | PKSPPYTAFL | GNLPYDVTEE | SIKEFFRGLN | ISAVRLPREP | SNPERLKGFG | YAEFEDLDSL | LSALSLNEES |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LGNRRIRVDV | ADQAQDKDRD | DRSFGRDRNR | DSDKTDTDWR | ARPATDSFDD | YPPRRGDDSF | GDKYRDRYDS | DRYRDGYRDG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YRDGPRRDMD | RYGGRDRYDD | RGSRDYDRGY | DSRIGSGRRA | FGSGYRRDDD | YRGGGDRYED | RYDRRDDRSW | SSRDDYSRDD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YRRDDRGPPQ | RPKLNLKPRS | TPKEDDSSAS | TSQSTRAASI | FGGAKPVDTA | AREREVEERL | QKEQEKLQRQ | LDEPKLERRP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RERHPSWRSE | ETQERERSRT | GSESSQTGTS | TTSSRNARRR | ESEKSLENET | LNKEEDCHSP | TSKPPKPDQP | LKVMPAPPPK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ENAWVKRSSN | PPARSQSSDT | EQQSPTSGGG | KVAPAQPSEE | GPGRKDENKV | DGMNAPKGQT | GNSSRGPGDG | GNRDHWKESD |
| 570 | 580 | 590 | 600 | 610 | 620 | | |
| RKDGKKDQDS | RSAPEPKKPE | ENPASKFSSA | SKYAALSVDG | EDENEGEDYA | E | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 450 | 1 | 658.3852 | 121.93 | 2 | 35.3 | 10.3 | 2 | 215-225 | R.RGDDSFGDKYR.D | |

# Detailed Protein Report

---

**Protein 1709:** **porphobilinogen deaminase isoform 4 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|384551656 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 33.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 5.6 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MRVIRVGTRK | SQLARIQTDS | VVATLKASYP | GLQFEIIAMS | TTGDKILDTA | LSKIGEKSLF | TKELEHALEK | NEVDLVVHSL |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| KDLPTVLPPG | FTIGAICKRE | NPHDAVVFHP | KFVGKTLETL | PEKSVVGTSS | LRRAAQLQRK | FPHLEFRSIR | GNLNTRLRKL |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| DEQQEFSAII | LATAGLQRMG | WHNRVGQILH | PEECMYAVGQ | EGGCSVPVAV | HTAMKDGQLY | LTGGVWSLDG | SDSIQETMQA |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | |
| TIHVPAQHED | GPEDDPQLVG | ITARNIPRGP | QLAAQNLGIS | LANLLLSKGA | KNILDVARQL | NDAH | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1460 | 1 | 620.0760 | 74.02 | 3 | 47.9 | 10.3 | 2 | 10-26 | R.KSQLARIQTDSVVATLK.A | |

# Detailed Protein Report

## Protein 1710: PREDICTED: SH3 and PX domain-containing protein 2A isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530394650 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 106.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.5 |
| | | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MILEQYVVVS | NYKKQENSEL | SLQAGEVVDV | IEKNESGWWF | VSTSEEQGWV | PATYLEAQNG | TRDDSDINTS | KTGEVSKRRK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AHLRRLDRRW | TLGGMVNRQH | SREEKYVTVQ | PYTSQSKDEI | GFEKGVTVEV | IRKNLEGWWY | IRYLGKEGWA | PASYLKKAKD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DLPTRKKNLA | GPVEIIGNIM | EISNLLNKKA | SGDKETPPAE | GEGHEAPIAK | KEISLPILCN | ASNGSAVGVP | DRTVSRLAQG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SPAVARIAPQ | RAQISSPNLR | TRPPPRRESS | LGFQLPKPPE | PPSVEVEYYT | IAEFQSCISD | GISFRGGQKA | EVIDKNSGGW |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WYVQIGEKEG | WAPASYIDKR | KKPNLSRRTS | TLTRPKVPPP | APPSKPKEAE | EGPTGASESQ | DSPRKLKYEE | PEYDIPAFGF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DSEPELSEEP | VEDRASGERR | PAQPHRPSPA | SSLQRARFKV | GESSEDVALE | EETIYENEGF | RPYAEDTLSA | RGSSGDSDSP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GSSSLSLTRK | NSPKSGSPKS | SSLLKLKAEK | NAQAEMGKNH | SSASFSSSIT | INTTCCSSSS | SSSSSLSKTS | GDLKPRSASD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AGIRGTPKVR | AKKDADANAG | LTSCPRAKPS | VRPKPFLNRA | ESQSQEKMDI | STLRRQLRPT | GQLRGGLKGS | KSEDSELPPQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| TASEAPSEGS | RRSSSDLITL | PATTPPCPTK | KEWEGPATSY | MTCSAYQKVQ | DSEISFPAGV | EVQVLEKQES | GWWYVRFGEL |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| EGWAPSHYLV | LDENEQPDPS | GKELDTVPAK | GRQNEGKSDS | LEKIERRVQA | LNTVNQSKKA | TPPIPSKPPG | GFGKTSGTPA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VKMRNGVRQV | AVRPQSVFVS | PPPKDNNLSC | ALRRNESLTA | TDGLRGVRRN | SSFSTARSAA | AEAKGRLAER | AASQGSDSPL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LPAQRNSIPV | SPVRPKPIEK | SQFIHNNLKD | VYVSIADYEG | DEETAGFQEG | VSMEVLERNP | NGWWYCQILD | GVKPFKGWVP |
| 970 | | | | | | | |
| SNYLEKKN | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2762 | 1 | 665.3756 | -3.39 | 2 | 64.9 | 10.3 | 1 | 768-779 | R.VQALNTVNQSKK.A | |

# Detailed Protein Report

## Protein 1711: PREDICTED: ubiquitin carboxyl-terminal hydrolase 15 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530401067 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 74.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRGEIAKSYA | ELIKQMWSGK | FSYVTPRAFK | TQVGRFAPQF | SGYQQQDCQE | LLAFLLDGLH | EDLNRIRKKP | YIQLKDADGR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PDKVVAEEAW | ENHLKRNDSI | IVDIFHGLFK | STLVCPECAK | ISVTFDPFCY | LTLPLPMKKE | RTLEVYLVRM | DPLTKPMQYK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VVVPKIGNIL | DLCTALSALS | GIPADKMIVT | DIYNHRFHRI | FAMDENLSSI | MERDDIYVFE | ININRTEDTE | HVIIPVCLRE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KFRHSSYTHH | TGSSLFGQPF | LMAVPRNNTE | DKLYNLLLLR | MCRYVKISTE | TEETEGSLHC | CKDQNINGNG | PNGIHEEGSP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| SEMETDEPDD | ESSQDQELPS | ENENSQSEDS | VGGDNDSENG | LCTEDTCKGQ | LTGHKKRLFT | FQFNNLGNTD | INYIKDDTRH |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| IRFDDRQLRL | DERSFLALDW | DPDLKKRYFD | ENAAEDFEKH | ESVEYKPPKK | PFVKLKDCIE | LFTTKEKLGA | EDPWYCPNCK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EHQQATKKLD | LWSLPPVLVV | HLKRFSYSRY | MRDKLDTLVD | FPINDLDMSE | FLINPNAGPC | RYNLIAVSNH | YGGMGGGHYT |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AFAKNKDDGK | WYYFDDSSVS | TASEDQIVSK | AAYVLFYQRQ | DTFSGTGFFP | LDRETKGASA | ATGIPLESDE | DSNDNDNDIE |
| 650 | | | | | | | |
| NENCMHTN | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1496 | 1 | 619.7680 | 82.44 | 3 | 47.1 | 10.3 | 1 | 488-503 | K.KLDLWSLPPVLVVHLK.R | |

# Detailed Protein Report

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## Protein 1712: transcription factor HIVEP2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|110347463 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 268.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.5 |
| | | **Sequence Coverage [%]:** | 0.7 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | |
|---|---|---|---|
| ***QU:MU*** | **Median:** 1.21 | **CV:** 0.00 % | **No. of Peptides:** 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530383649 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: transcription factor HIVEP2 isoform X2 [Homo sapiens] |

# Detailed Protein Report

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDTGDTALGQ | KATSRSGETD | KASGRWRQEQ | SAVIKMSTFG | SHEGQRQPQI | EPEQIGNTAS | AQLFGSGKLA | SPSEVVQQVA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EKQYPPHRPS | PYSCQHSLSF | PQHSLPQGVM | HSTKPHQSLE | GPPWLFPGPL | PSVASEDLFP | FPIHGHSGGY | PRKKISSLNP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AYSQYSQKSI | EQAEEAHKKE | HKPKKPGKYI | CPYCSRACAK | PSVLKKHIRS | HTGERPYPCI | PCGFSFKTKS | NLYKHRKSHA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| HAIKAGLVPF | TESAVSKLDL | EAGFIDVEAE | IHSDGEQSTD | TDEESSLFAE | ASDKMSPGPP | IPLDIASRGG | YHGSLEESLG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GPMKVPILII | PKSGIPLPNE | SSQYIGPDML | PNPSLNTKAD | DSHTVKQKLA | LRLSEKKGQD | SEPSLNLLSP | HSKGSTDSGY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FSRSESAEQQ | ISPPNTNAKS | YEEIIFGKYC | RLSPRNALSV | TTTSQERAAM | GRKGIMEPLP | HVNTRLDVKM | FEDPVSQLIP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SKGDVDPSQT | SMLKSTKFNS | ESRQPQIIPS | SIRNEGKLYP | ANFQGSNPVL | LEAPVDSSPL | IRSNSVPTSS | ATNLTIPPSL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| RGSHSFDERM | TGSDDVFYPG | TVGIPPQRML | RRQAAFELPS | VQEGHVEVEH | HGRMLKGISS | SSLKEKKLSP | GDRVGYDYDV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CRKPYKKWED | SETPKQNYRD | ISCLSSLKHG | GEYFMDPVVP | LQGVPSMFGT | TCENRKRRKE | KSVGDEEDTP | MICSSIVSTP |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VGIMASDYDP | KLQMQEGVRS | GFAMAGHENL | SHGHTERFDP | CRPQLQPGSP | SLVSEESPSA | IDSDKMSDLG | GRKPPGNVIS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| VIQHTNSLSR | PNSFERSESA | ELVACTQDKA | PSPSETCDSE | ISEAPVSPEW | APPGDGAESG | GKPSPSQQVQ | QQSYHTQPRL |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VRQHNIQVPE | IRVTEEPDKP | EKEKEAQSKE | PEKPVEEFQW | PQRSETLSQL | PAEKLPPKKK | RLRLADMEHS | SGESSFESTG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| TGLSRSPSQE | SNLSHSSSFS | MSFEREETSK | LSALPKQDEF | GKHSEFLTVP | AGSYSLSVPG | HHHQKEMRRC | SSEQMPCPHP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AEVPEVRSKS | FDYGNLSHAP | VSGAAASTVS | PSRERKKCFL | VRQASFSGSP | EISQGEVGMD | QSVKQEQLEH | LHAGLRSGWH |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| HGPPAVLPPL | QQEDPGKQVA | GPCPPLSSGP | LHLAQPQIMH | MDSQESLRNP | LIQPTSYMTS | KHLPEQPHLF | PHQETIPFSP |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| IQNALFQFQY | PTVCMVHLPA | QQPPWWQAHF | PHPFAQHPQK | SYGKPSFQTE | IHSSYPLEHV | AEHTGKKPAE | YAHTKEQTYP |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| CYSGASGLHP | KNLLPKFPSD | QSSKSTETPS | EQVLQEDFAS | ANAGSLQSLP | GTVVPVRIQT | HVPSYGSVMY | TSISQILGQN |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| SPAIVICKVD | ENMTQRTLVT | NAAMQGIGFN | IAQVLGQHAG | LEKYPIWKAP | QTLPLGLESS | IPLCLPSTSD | SVATLGGSKR |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| MLSPASSLEL | FMETKQQKRV | KEEKMYGQIV | EELSAVELTN | SDIKKDLSRP | QKPQLVRQGC | ASEPKDGLQS | GSSSFSSLSP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| SSSQDYPSVS | PSSREPFLPS | KEMLSGSRAP | LPGQKSSGPS | ESKESSDELD | IDETASDMSM | SPQSSSLPAG | DGQLEEEGKG |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| HKRPVGMLVR | MASAPSGNVA | DSTLLLTDMA | DFQQILQFPS | LRTTTTVSWC | FLNYTKPNYV | QQATFKSSVY | ASWCISSCNP |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| NPSGLNTKTT | LALLRSKQKI | TAEIYTLAAM | HRPGTGKLTS | SSAWKQFTQM | KPDASFLFGS | KLERKLVGNI | LKERGKGDIH |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| GDKDIGSKQT | EPIRIKIFEG | GYKSNEDYVY | VRGRGRGKYI | CEECGIRCKK | PSMLKKHIRT | HTDVRPYVCK | LCNFAFKTKG |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| NLTKHMKSKA | HMKKCLELGV | SMTSVDDTET | EEAENLEDLH | KAAEKHSMSS | ISTDHQFSDA | EESDGEDGDD | NDDDDEDEDD |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | 1990 | 2000 |
| FDDQGDLTPK | TRSRSTSPQP | PRFSSLPVNV | GAVPHGVPSD | SSLGHSSLIS | YLVTLPSIRV | TQLMTPSDSC | EDTQMTEYQR |
| 2010 | 2020 | 2030 | 2040 | 2050 | 2060 | 2070 | 2080 |
| LFQSKSTDSE | PDKDRLDIPS | CMDEECMLPS | EPSSSPRDFS | PSSHHSSPGY | DSSPCRDNSP | KRYLIPKGDL | SPRRHLSPRR |
| 2090 | 2100 | 2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
| DLSPMRHLSP | RKEAALRREM | SQRDVSPRRH | LSPRRPVSPG | KDITARRDLS | PRRERRYMTT | IRAPSPRRAL | YHNPPLSMGQ |
| 2170 | 2180 | 2190 | 2200 | 2210 | 2220 | 2230 | 2240 |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2332 | 1 | 869.4368 | 43.79 | 2 | 59.0 | 10.3 | 0 | 1276-1291 | K.EQTYPCYSGASGLHPK.N | | QU:MU 1.21 |

# Detailed Protein Report

## Protein 1713: TBC1 domain family member 16 isoform d [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|427918115 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 32.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 4.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MKVAPDKTCM | QFSIRRPKLP | SSETHPEESM | YKRLGVSAWL | NHLNELGQVE | EEYKLRKAIF | FGGIDVSIRG | EVWPFLLRYY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SHESTSEERE | ALRLQKRKEY | SEIQQKRLSM | TPEEHRAFWR | NVQFTVDKDV | VRTDRNNQFF | RGEDNPNVES | MRRILLNYAV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YNPAVGYSQG | MSDLVAPILA | EVLDESDTFW | CFVGLMQNTI | FVSSPRDEDM | EKQLLYLREL | LRLTHVRFYQ | HLVSLGEDGL |
| 250 | 260 | 270 | 280 | | | | |
| QMLFCHRWLL | LCFKREFPEA | EALRIWEACW | AHYQGADV | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 944 | 1 | 756.2363 | -177.88 | 2 | 40.2 | 10.3 | 1 | 3-15 | K.VAPDKTCMQFSIR.R | Oxidation: 8 |

# Detailed Protein Report

**Protein 1714:** **PREDICTED: serine/threonine-protein phosphatase 6 regulatory subunit 1 isoform X3 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578834138 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 82.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGILINRKTD | QLVSFLRKKD | DFVDLLLQHI | GTSAIMDLLL | RLLTCVERPQ | LRQDVVNWLN | EEKIVQRLIE | QIHPSKDENQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HSNASQSLCD | IIRLSREQMI | QVQDSPEPDQ | LLATLEKQET | IEQLLSNMFE | GEQSQSVIVS | GIQVLLTLLE | PRRPRSESVT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VNSFFSSVDG | QLELLAQGAL | ESTVSSVGAL | HALRPRLSCF | HQLLLEPPKL | EPLQMTWGML | APPLGNTRLH | VVKLLASALS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ANDAALTHEL | LALDVPNTML | DLFFHYVFNN | FLHAQVEGCV | STMLSLGPPP | DSSPETPIQN | PVVKHLLQQC | RLVERILTSW |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EENDRVQCAG | GPRKGYMGHL | TRVAGALVQN | TEKGPNAEQL | RQLLKELPSE | QQEQWEAFVS | GPLAETNKKN | MVDLVNTHHL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| HSSSDDEDDR | LKEFNFPEEA | VLQQAFMDFQ | MQRMTSAFID | HFGFNDEEFG | EQEESVNAPF | DKTANITFSL | NADDENPNAN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LLEICYKDRI | QQFDDDEEEE | DEEEAQGSGE | SDGEDGAWQG | SQLARGARLG | QPPGVRSGGS | TDSEDEEEED | EEEEEDEEGI |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GCAARGGATP | LSYPSPGPQP | PGPSWTATFD | PVPTDAPTSP | RVSGEEELHT | GPPAPQGPLS | VPQGLPTQSL | ASPPARDALQ |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| LRSQDPTPPS | APQEATEGSK | VTEPSAPCQA | LVSIGDLQAT | FHGIRSAPSS | SDSATRDPST | SVPASGAHQP | PQTTEGEKSP |
| 730 | 740 | 750 | 760 | | | | |
| EPLGLPQSQS | AQALTPPPIP | NGSAPEGPAS | PGSQ | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2205 | 1 | 714.4428 | 105.24 | 3 | 58.0 | 10.3 | 0 | 210-228 | K.LEPLQMTWGMLAPPLGNTR.L | Oxidation: 10 |

# Detailed Protein Report

## Protein 1715: PREDICTED: small G protein signaling modulator 3 isoform X6 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530420028 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 71.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

*QU:MU* **Median:** 1.30 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MSGSHTPACG PFSALTPSIW PQEILAKYTQ KEESAEQPEF YYDEFGFRVY KEEGDEPGSS LLANSPLMED APQRLRWQAH

        90        100        110        120        130        140        150        160
LEFTHNHDVG DLTWDKIAVS LPRSEKLRSL VLAGIPHGMR PQLWMRLSGA LQKKRNSELS YREIVKNSSN DETIAAKQIE

       170        180        190        200        210        220        230        240
KDLLRTMPSN ACFASMGSIG VPRLRRVLRA LAWLYPEIGY CQGTGMVAAC LLLFLEEEDA FWMMSAIIED LLPASYFSTT

       250        260        270        280        290        300        310        320
LLGVQTDQRV LRHLIVQYLP RLDKLLQEHD IELSLITLHW FLTAFASVVD IKLLLRIWDL FFYEGSRVLF QLTLGMLHLK

       330        340        350        360        370        380        390        400
EEELIQSENS ASIFNTLSDI PSQMEDAELL LGVAMRLAGS LTDVAVETQR RKHLAYLIAD QGQLLGAGTL TNLSQVVRRR

       410        420        430        440        450        460        470        480
TQRRKSTITA LLFGEDDLEA LKAKNIKQTE LVADLREAIL RVARHFQCTD PKNCSVELTP DYSMESHQRD HENYVACSRS

       490        500        510        520        530        540        550        560
HRRRAKALLD FERHDDDELG FRKNDIITIV SQKDEHCWVG ELNGLRGWFP AKFVEVLDER SKEYSIAGDD SVTEGVTDLV

       570        580        590        600        610        620        630        640
RGTLCPALKA LFEHGLKKPS LLGGACHPWL FIEEAAGREV ERDFASVYSR LVLCKTFRSF GVPSGWMKMA KS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 563 | 1 | 756.9503 | 105.42 | 2 | 35.5 | 10.3 | 2 | 619-632 | R.SFGVPSGWMKMAKS.- | | QU:MU 1.30 |

# Detailed Protein Report

**Protein 1716:** **ATP synthase F(0) complex subunit C3, mitochondrial isoform B precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|298358756 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 10.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 14.3 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MFACAKLACT PSLIRAGSRV AYRPISASVL SRPEASRTGE GSTVFNGAQN GVSQLIQREF QTSAISRDID TAAKFIGAGA
        90        100        110
ATVGVAGSGA GIGTVFGSLI IGYAR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 115 | 1 | 849.4132 | -20.25 | 2 | 30.4 | 10.3 | 1 | 1-15 | -.MFACAKLACTPSLIR.A | Carbamidomethyl: 9;<br>Oxidation: 1 |

# Detailed Protein Report

## Protein 1717: ubiquitin-associated protein 1 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|8394499 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 55.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578816520 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: ubiquitin-associated protein 1 isoform X1 [Homo sapiens] |
| gi\|283945566 | refseq_human (refseq_human_20140103.fasta) | ubiquitin-associated protein 1 isoform 1 [Homo sapiens] |
| gi\|283945562 | refseq_human (refseq_human_20140103.fasta) | ubiquitin-associated protein 1 isoform 1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MASKKLGADF | HGTFSYLDDV | PFKTGDKFKT | PAKVGLPIGF | SLPDCLQVVR | EVQYDFSLEK | KTIEWAEEIK | KIEEAEREAE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CKIAEAEAKV | NSKSGPEGDS | KMSFSKTHST | ATMPPPINPI | LASLQHNSIL | TPTRVSSSAT | KQKVLSPPHI | KADFNLADFE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CEEDPFDNLE | LKTIDEKEEL | RNILVGTTGP | IMAQLLDNNL | PRGGSGSVLQ | DEEVLASLER | ATLDFKPLHK | PNGFITLPQL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GNCEKMSLSS | KVSLPPIPAV | SNIKSLSFPK | LDSDDSNQKT | AKLASTFHST | SCLRNGTFQN | SLKPSTQSSA | SELNGHHTLG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LSALNLDSGT | EMPALTSSQM | PSLSVLSVCT | EESSPPNTGP | TVTPPNFSVS | QVPNMPSCPQ | AYSELQMLSP | SERQCVETVV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NMGYSYECVL | RAMKKKGENI | EQILDYLFAH | GQLCEKGFDP | LLVEEALEMH | QCSEEKMMEF | LQLMSKFKEM | GFELKDIKEV |
| 490 | 500 | 510 | | | | | |
| LLLHNNDQDN | ALEDLMARAG | AS | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 317 | 1 | 782.7456 | -174.52 | 2 | 34.0 | 10.3 | 1 | 457-468 | K.MMEFLQLMSKFK.E | Oxidation: 1, 2 |

# Detailed Protein Report

## Protein 1718: tectonin beta-propeller repeat-containing protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|32698704 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 129.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530385707 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: tectonin beta-propeller repeat-containing protein 1 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPNSVLWAVD | LFGRVYTLST | AGQYWEMCKD | SQLEFKRVSA | TTQCCWGIAC | DNQVYVYVCA | SDVPIRRREE | AYENQRWNPM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GGFCEKLLLS | DRWGWSDVSG | LQHRPLDRVA | LPSPHWEWES | DWYVDENFGG | EPTEKGGWTY | AIDFPATYTK | DKKWNSCVRR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RKWIRYRRYK | SRDIWAKIPS | KDDPKELPDP | FNDLSVGGWE | ITEEPVGRLS | VWAVSLQGKV | WYREDVSHSN | PEGSSWSLLD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TPGEVVQISC | GPHDLLWATL | WEGQALVREG | INRSNPKGSS | WSIVEPPGSE | NGVMHISVGV | SVVWAVTKDW | KVWFRRGVNS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| HNPCGTSWIE | MVGEMTMVNV | GMNDQVWGIG | CEDRAVYFRQ | GVTPSELSGK | TWKAIIAARE | CDRSHSGSSS | SLLSAGCFFG |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DEVRGSGESA | PSDTDASSEV | ERPGPGQILP | AEPLDDSKNA | TGNSASGLGA | GRTAEDTVED | ACPAEGSREA | RPNTHPGPAP |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| TPAELPWTNI | DLKEAKKVPS | HSAAGFPETT | SLSSLGLLPL | GLEEPYGVDD | HPLWAWVSGG | GCVVEACAMP | RWFTVQAGLS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SSVHMLSLSI | TPAQTAAWRK | QIFQQLTERT | KRELENFRHY | EQAVEQSVWV | KTGALQWWCD | WKPHKWVDVR | LALEQFTGHD |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GVRDSILFIY | YVVHEEKKYI | HIFLNEVVAL | VPVLNETKHS | FALYTPERTR | QRWPVRLAAA | TEQDMNDWLA | LLSLSCCESR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KVQGRPSPQA | IWSITCKGDI | FVSEPSPDLE | AHEHPLPCDQ | MFWRQMGGHL | RMVEANSRGV | VWGIGYDHTA | WVYTGGYGGG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| CFQGLASSTS | NIYTQSDVKC | VHIYENQRWN | PVTGYTSRGL | PTDRYMWSDA | SGLQECTKAG | TKPPSLQWAW | VSDWFVDFSV |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PGGTDQEGWQ | YASDFPASYH | GSKTMKDFVR | RRCWARKCKL | VTSGPWLEVP | PIALRDVSII | PESPGAEGSG | HSIALWAVSD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| KGDVLCRLGV | SELNPAGSSW | LHVGTDQPFA | SISIGACYQV | WAVARDGSAF | YRGSVYPSQP | AGDCWYHIPS | PPRQRLKQVS |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| AGQTSVYALD | ENGNLWYRQG | ITPSYPQGSS | WEHVSNNVCR | VSVGPLDQVW | VIANKVQGSH | SLSRGTVCHR | TGVQPHEPKG |
| 1130 | 1140 | 1150 | 1160 | 1170 | | | |
| HGWDYGIGGG | WDHISVRANA | TRAPRSSSQE | QEPSAPPEAH | GPVCC | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2289 | 1 | 840.8066 | -136.06 | 2 | 58.5 | 10.3 | 1 | 1096-1110 | K.VQGSHSLSRGTVCHR.T | Carbamidomethyl: 13 |

# Detailed Protein Report

## Protein 1719: heterogeneous nuclear ribonucleoprotein D0 isoform c [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|14110414 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 32.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| | | **Sequence Coverage [%]:** | 4.2 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

***WUP:QUP*** **Median:** 1.51 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSEEQFGGDG | AAAAATAAVG | GSAGEQEGAM | VAATQGAAAA | AGSGAGTGGG | TASGGTEGGS | AESEGAKIDA | SKNEEDEGHS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NSSPRHSEAA | TAQREEWKMF | IGGLSWDTTK | KDLKDYFSKF | GEVVDCTLKL | DPITGRSRGF | GFVLFKESES | VDKVMDQKEH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KLNGKVIDPK | RAKAMKTKEP | VKKIFVGGLS | PDTPEEKIRE | YFGGFGEVES | IELPMDNKTN | KRRGFCFITF | KEEEPVKKIM |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | |
| EKKYHNVGLS | KCEIKVAMSK | EQYQQQQQWG | SRGGFAGRAR | GRGGDQQSGY | GKVSRRGGHQ | NSYKPY | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2535 | 1 | 729.3445 | 63.67 | 2 | 60.0 | 10.3 | 0 | 73-85 | K.NEEDEGHSNSSPR.H | | WUP:QUP 1.51 |

# Detailed Protein Report

## Protein 1720: PREDICTED: exophilin-5 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578822067 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 201.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MREESGMPPP | WDASLLENEF | FQVLDDLDSK | LAQEQSASSV | NTRTPLNYGS | RTQFGHFYSS | GNRHGNITER | HKKHYNETSN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MSIYDILRPG | TPREGFKTFS | PRTSTIYDMY | RTREPRVFKE | DYVQKNTFGS | TSLCFDSRQR | SALPATGHFT | ARSLHFPATT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QSKSGFIPPR | HQQSPKRTPL | SSIIWNRSDS | SRDRENQEEF | LRAPSPMEID | PADKYVYPRG | FQENKRYESY | HSQNVYQRVS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LNAPMENAMS | PDTFENSENM | PFYHQSNTFT | RSFFSNTFGR | SGEQRRFGQG | PFWGQEKGHS | FWSDFHRSRK | SFSSSDRDFE |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MISMEANSVS | AIHGHNVSSE | HWESFSSGYG | TDVSRGQEEP | HPWQFDFQRS | TLDSMVVSHG | NETQLTPHFG | TPNVCSMTGS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SYHVKSSELV | SQQDSSPVEV | HINKEASSFG | IAQTLASSFK | TSFSQISDDR | RNPQSPNLQN | PTVTLQKIFP | NKPASHPMRS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| HTEVTVTSSN | SVDSLPLAKS | QPNILVTEVN | NEKDLNESIS | EEDKQLSKMD | QTNKAGEIPQ | PVSQTGISNS | LPDFQNPLSQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| DSAKSNGFGF | NASTIISSKK | SPRVFSRKDT | SKMYIPHTDK | SNDIKQDKRF | TENRKLGSTA | SLPFIQEHRT | PPSFPRTDQG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| CHQELTVNNE | DISRIITNNH | WSSALTDTQN | AQYSKCKLTP | GHKTSCDSLD | LSSAALPDSS | PSKNSSLDAP | VVPSTTVFSR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RSPSDKDPSL | GEREEKDNAG | KNQKNQFIVS | HSENQERNDS | PVPTHDEVVD | VKCHSHSPFR | NERGKGKIRH | HISCIEKLSK |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| TESISVPTSD | HRSLIEANQS | NSKVSELDTI | YCTLPRKSSS | FLIHGRQSGS | KIMAASLRNG | PPPFQIKNNV | EDAMGNYMLN |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| KFSPSSPESA | NECSKVLSDS | ALEAPEATER | MTNVKSSGST | SVRKGPLPFL | INRAMSCPSG | EPHASTGREG | RKKPLTSGMD |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ASELTPRAWE | RIISPVESDS | SVRDCSLTKR | QHQKENFQEY | TEKEGKMAAS | RRSVFALSNE | DPLPFCSDLS | GKERGKTLHK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| VKTTSTFSVS | GDEDNVKCLE | VVSIYYTLPR | KPSKKFCNLL | QQYTQNTNLL | IESPQVETET | FPNALEKDKQ | NYSTREQSGT |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| PSCENLKMSV | NSDQTLTTEN | MTAFRLSNRG | PLAPTLQEMA | SVEAAVSLPE | EESKAREIFS | DNLAKTPLGD | SENKKERGKK |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| LQSETLHTSL | MLQRKNVSEE | KSENCQQSIN | SSNSGPSSLP | ALSEVNIGNS | QTRRSSWECT | GSGRAIPFTG | SGKCPQKDHT |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| STAVGDGSSG | SQPREGRGDI | GTNCQKMTNK | TLSHSESQVF | ALTPALHKLQ | LGEETQSDEP | NLESLQSEPR | ELPQRSQEAN |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| MTESRKAEDE | MQKSAWDQPS | LPEGNKNKTN | LDDLVKGENR | SSVKHRLAAM | SKASRKFPAK | DVSPRRHVAT | IFPQSGSRSG |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| FDHLSLGTVE | CNPLFPEPTP | KSAESIGESR | LSENGKHVKK | SENLLPITVL | PNREPSTHVS | NQKSNSISQR | HQNEFKNVSE |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| SPSKHENSKD | VTAAQNLVRE | SGAPSPITFT | SLREAEFSDN | QRRLSPPFPL | EPAQKSRVSS | PLASFLQQQR | SASSLEWEPE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| PHLYRSKSLK | SINVHGDLLR | KSHPPKVRER | HFSESTSIDN | ALSRLTLGNE | FSVNNGYSRR | FRSFSELPSC | DGNESWAYRS |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| GTKTGPRSAI | SIYRPIDYGI | FGKEQQLAFL | ENVKRSLTQG | RLWKPSFLKN | PGFLKDDLRN | PPNPSESLSS | NSPSSQVPED |
| 1770 | 1780 | 1790 | 1800 | 1810 | | | |
| GLSPSEPLNI | YEDDPVDSDC | DTDTTTDDEY | YLDENDKESE | L | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2720 | 1 | 1086.5521 | 56.79 | 2 | 64.3 | 10.3 | 1 | 1274-1294 | K.CPQKDHTSTAVGDGSSGSQPR.E | Carbamidomethyl: 1 |

# Detailed Protein Report

## Protein 1721: diphthine--ammonia ligase isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|18087809 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 30.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRVAALISGG | KDSCYNMMQC | IAAGHQIVAL | ANLRPAENQV | GSDELDSYMY | QTVGHHAIDL | YAEAMALPLY | RRTIRGRSLD |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TRQVYTKCEG | DEVEDLYELL | KLVKEKEEVE | GISVGAILSD | YQRIRVENVC | KRLNLQPLAY | LWQRNQEDLL | REMISSNIQA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MIIKVAALGL | DPDKHLGKTL | DQMEPYLIEL | SKKYGVHVCG | EGGEYETFTL | DCPLFKKKII | VDSSEVVIHS | ADAFAPVAYL |
| 250 | 260 | 270 | | | | | |
| RFLELHLEDK | VSSVPDNYRT | SNYIYNF | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1742 | 1 | 480.7260 | -88.12 | 2 | 50.1 | 10.3 | 1 | 124-131 | R.IRVENVCK.R | |

# Detailed Protein Report

## Protein 1722: protein FAM26F isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|451172090 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 16.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 9.1 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 0.83 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MFPVLGWILI AVVIIILLIF TSVTRCLSPV SFLQLKFWKI YLEQEQQILK SKATEHATEL AKENIKCFFE GSHPKEYNTP
         90        100        110        120        130        140        150
SMKEWQQISS LYTFNPKGQY YSMLHKYVNR KEKTHSIRST EGDTVIPVLG FVDSSGINST PEL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 842 | 1 | 837.9031 | -3.98 | 2 | 40.6 | 10.3 | 1 | 98-110 | K.GQYYSMLHKYVNR.K | Oxidation: 6 | QU:MU | 0.83 |

# Detailed Protein Report

## Protein 1723: active regulator of SIRT1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|34996527 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 15.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.5 |
| | | **Sequence Coverage [%]:** | 11.0 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSAALLRRGL ELLAASEAPR DPPGQAKPRG APVKRPRKTK AIQAQKLRNS AKGKVPKSAL DEYRKRECRD HLRVNLKFLT
        90        100        110        120        130        140
RTRSTVAESV SQQILRQNRG RKACDRPVAK TKKKKAEGTV FTEEDFQKFQ QEYFGS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 216 | 1 | 838.0958 | 161.69 | 2 | 32.7 | 10.3 | 1 | 82-96 | R.TRSTVAESVSQQILR.Q | |

# Detailed Protein Report

## Protein 1724: AP-2 complex subunit alpha-1 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|19913416 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 105.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| | | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPAVSKGDGM | RGLAVFISDI | RNCKSKEAEI | KRINKELANI | RSKFKGDKAL | DGYSKKKYVC | KLLFIFLLGH | DIDFGHMEAV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NLLSSNKYTE | KQIGYLFISV | LVNSNSELIR | LINNAIKNDL | ASRNPTFMCL | ALHCIANVGS | REMGEAFAAD | IPRILVAGDS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MDSVKQSAAL | CLLRLYKASP | DLVPMGEWTA | RVVHLLNDQH | MGVVTAAVSL | ITCLCKKNPD | DFKTCVSLAV | SRLSRIVSSA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| STDLQDYTYY | FVPAPWLSVK | LLRLLQCYPP | PEDAAVKGRL | VECLETVLNK | AQEPPKSKKV | QHSNAKNAIL | FETISLIIHY |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DSEPNLLVRA | CNQLGQFLQH | RETNLRYLAL | ESMCTLASSE | FSHEAVKTHI | DTVINALKTE | RDVSVRQRAA | DLLYAMCDRS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NAKQIVSEML | RYLETADYAI | REEIVLKVAI | LAEKYAVDYS | WYVDTILNLI | RIAGDYVSEE | VWYRVLQIVT | NRDDVQGYAA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KTVFEALQAP | ACHENMVKVG | GYILGEFGNL | IAGDPRSSPP | VQFSLLHSKF | HLCSVATRAL | LLSTYIKFIN | LFPETKATIQ |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GVLRAGSQLR | NADVELQQRA | VEYLTLSSVA | STDVLATVLE | EMPPFPERES | SILAKLKRKK | GPGAGSALDD | GRRDPSSNDI |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| NGGMEPTPST | VSTPSPSADL | LGLRAAPPPA | APPASAGAGN | LLVDVFDGPA | AQPSLGPTPE | EAFLSPGPED | IGPPIPEADE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| LLNKFVCKNN | GVLFENQLLQ | IGVKSEFRQN | LGRMYLFYGN | KTSVQFQNFS | PTVVHPGDLQ | TQLAVQTKRV | AAQVDGGAQV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| QQVLNIECLR | DFLTPPLLSV | RFRYGGAPQA | LTLKLPVTIN | KFFQPTEMAA | QDFFQRWKQL | SLPQQEAQKI | FKANHPMDAE |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VTKAKLLGFG | SALLDNVDPN | PENFVGAGII | QTKALQVGCL | LRLEPNAQAQ | MYRLTLRTSK | EPVSRHLCEL | LAQQF |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2708 | 1 | 974.0860 | 30.01 | 2 | 62.3 | 10.3 | 1 | 548-564 | K.FINLFPETKATIQGVLR.A | |

# Detailed Protein Report

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**Protein 1725:** **desmoglein-1 preproprotein [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|119703744 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 113.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MDWSFFRVVA | MLFIFLVVVE | VNSEFRIQVR | DYNTKNGTIK | WHSIRRQKRE | WIKFAAACRE | GEDNSKRNPI | AKIHSDCAAN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QQVTYRISGV | GIDQPPYGIF | VINQKTGEIN | ITSIVDREVT | PFFIIYCRAL | NSMGQDLERP | LELRVRVLDI | NDNPPVFSMA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TFAGQIEENS | NANTLVMILN | ATDADEPNNL | NSKIAFKIIR | QEPSDSPMFI | INRNTGEIRT | MNNFLDREQY | GQYALAVRGS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DRDGGADGMS | AECECNIKIL | DVNDNIPYME | QSSYTIEIQE | NTLNSNLLEI | RVIDLDEEFS | ANWMAVIFFI | SGNEGNWFEI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EMNERTNVGI | LKVVKPLDYE | AMQSLQLSIG | VRNKAEFHHS | IMSQYKLKAS | AISVTVLNVI | EGPVFRPGSK | TYVVTGNMGS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NDKVGDFVAT | DLDTGRPSTT | VRYVMGNNPA | DLLAVDSRTG | KLTLKNKVTK | EQYNMLGGKY | QGTILSIDDN | LQRTCTGTIN |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| INIQSFGNDD | RTNTEPNTKI | TTNTGRQEST | SSTNYDTSTT | STDSSQVYSS | EPGNGAKDLL | SDNVHFGPAG | IGLLIMGFLV |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LGLVPFLMIC | CDCGGAPRSA | AGFEPVPECS | DGAIHSWAVE | GPQPEPRDIT | TVIPQIPPDN | ANIIECIDNS | GVYTNEYGGR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| EMQDLGGGER | MTGFELTEGV | KTSGMPEICQ | EYSGTLRRNS | MRECREGGLN | MNFMESYFCQ | KAYAYADEDE | GRPSNDCLLI |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| YDIEGVGSPA | GSVGCCSFIG | EDLDDSFLDT | LGPKFKKLAD | ISLGKESYPD | LDPSWPPQST | EPVCLPQETE | PVVSGHPPIS |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| PHFGTTTVIS | ESTYPSGPGV | LHPKPILDPL | GYGNVTVTES | YTTSDTLKPS | VHVHDNRPAS | NVVVTERVVG | PISGADLHGM |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LEMPDLRDGS | NVIVTERVIA | PSSSLPTSLT | IHHPRESSNV | VVTERVIQPT | SGMIGSLSMH | PELANAHNVI | VTERVVSGAG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| VTGISGTTGI | SGGIGSSGLV | GTSMGAGSGA | LSGAGISGGG | IGLSSLGGTA | SIGHMRSSSD | HHFNQTIGSA | SPSTARSRIT |
| 1050 | | | | | | | |
| KYSTVQYSK | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1256 | 1 | 1018.4750 | 6.63 | 3 | 45.3 | 10.3 | 1 | 651-677 | R.MTGFELTEGVKTSGMPEICQEYSGTLR.R | Carbamidomethyl: 19;<br>Oxidation: 1, 15 |

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# Detailed Protein Report

## Protein 1726: A disintegrin and metalloproteinase with thrombospondin motifs 8 preproprotein [Homo sapiens]

**Accession:** gi|153792351
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 10.3
**MW [kDa]:** 96.4
**pI:** 5.8
**Sequence Coverage [%]:** 1.3
**No. of unique Peptides:** 1

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578821961 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: A disintegrin and metalloproteinase with thrombospondin motifs 8 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLPAPAAPRW | PPLLLLLLLL | LPLARGAPAR | PAAGGQASEL | VVPTRLPGSA | GELALHLSAF | GKGFVLRLAP | DDSFLAPEFK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IERLGGSGRA | TGGERGLRGC | FFSGTVNGEP | ESLAAVSLCR | GLSGSFLLDG | EEFTIQPQGA | GGSLAQPHRL | QRWGPAGARP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LPRGPEWEVE | TGEGQRQERG | DHQEDSEEES | QEEEAEGASE | PPPPLGATSR | TKRFVSEARF | VETLLVADAS | MAAFYGADLQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NHILTLMSVA | ARIYKHPSIK | NSINLMVVKV | LIVEDEKWGP | EVSDNGGLTL | RNFCNWQRRF | NQPSDRHPEH | YDTAILLTRQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| NFCGQEGLCD | TLGVADIGTI | CDPNKSCSVI | EDEGLQAAHT | LAHELGHVLS | MPHDDSKPCT | RLFGPMGKHH | VMAPLFVHLN |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QTLPWSPCSA | MYLTELLDGG | HGDCLLDAPA | AALPLPTGLP | GRMALYQLDQ | QCRQIFGPDF | RHCPNTSAQD | VCAQLWCHTD |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GAEPLCHTKN | GSLPWADGTP | CGPGHLCSEG | SCLPEEEVER | PKPVADGGWA | PWGPWGECSR | TCGGGVQFSH | RECKDPEPQN |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GGRYCLGRRA | KYQSCHTEEC | PPDGKSFREQ | QCEKYNAYNY | TDMDGNLLQW | VPKYAGVSPR | DRCKLFCRAR | GRSEFKVFEA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KVIDGTLCGP | ETLAICVRGQ | CVKAGCDHVV | DSPRKLDKCG | VCGGKGNSCR | KVSGSLTPTN | YGYNDIVTIP | AGATNIDVKQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RSHPGVQNDG | NYLALKTADG | QYLLNGNLAI | SAIEQDILVK | GTILKYSGSI | ATLERLQSFR | PLPEPLTVQL | LTVPGEVFPP |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| KVKYTFFVPN | DVDFSMQSSK | ERATTNIIQP | LLHAQWVLGD | WSECSSTCGA | GWQRRTVECR | DPSGQASATC | NKALKPEDAK |
| 890 | | | | | | | |
| PCESQLCPL | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 661 | 1 | 670.6764 | -217.65 | 2 | 38.3 | 10.3 | 1 | 664-675 | K.AGCDHVVDSPRK.L | Carbamidomethyl: 3 |

## Protein 1727: gamma-sarcoglycan [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4557847 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 32.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 6.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVREQYTTAT | EGICIERPEN | QYVYKIGIYG | WRKRCLYLFV | LLLLIILVVN | LALTIWILKV | MWFSPAGMGH | LCVTKDGLRL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EGESEFLFPL | YAKEIHSRVD | SSLLLQSTQN | VTVNARNSEG | EVTGRLKVGP | KMVEVQNQQF | QINSNDGKPL | FTVDEKEVVV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GTDKLRVTGP | EGALFEHSVE | TPLVRADPFQ | DLRLESPTRS | LSMDAPRGVH | IQAHAGKIEA | LSQMDILFHS | SDGMLVLDAE |
| 250 | 260 | 270 | 280 | 290 | 300 | | |
| TVCLPKLVQG | TWGPSGSSQS | LYEICVCPDG | KLYLSVAGVS | TTCQEHSHIC | L | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2456 | 1 | 973.1644 | 147.25 | 2 | 61.2 | 10.3 | 0 | 99-116 | R.VDSSLLLQSTQNVTVNAR.N | |

# Detailed Protein Report

**Protein 1728:** UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|111160385 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 43.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 6.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MRRRLRLRRD | ALLTLLLGAS | LGLLLYAQRD | GAAPTASAPR | GRGRAAPRPT | PGPRAFQLPD | AGAAPPAYEG | DTPAPPTPTG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PFDFARYLRA | KDQRRFPLLI | NQPHKCRGDG | APGGRPDLLI | AVKSVAEDFE | RRQAVRQTWG | AEGRVQGALV | RRVFLLGVPR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GAGSGGADEV | GEGARTHWRA | LLRAESLAYA | DILLWAFDDT | FFNLTLKEIH | FLAWASAFCP | DVRFVFKGDA | DVFVNVGNLL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| EFLAPRDPAQ | DLLAGDVIVH | ARPIRTRASK | YYIPEAVYGL | PAYPAYAGGG | GFVLSGATLH | RLAGACAQVE | LFPIDDVFLG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MCLQRLRLTP | EPHPAFRTFG | IPQPSAAPHL | STFDPCFYRE | LVVVHGLSAA | DIWLMWRLLH | GPHGPACAHP | QPVAAGPFQW |
| 410 | | | | | | | |
| DS | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1444 | 1 | 960.1132 | -52.99 | 3 | 47.7 | 10.3 | 1 | 302-327 | R.LAGACAQVELFPIDDVFLGMCLQRLR.L | |

# Detailed Protein Report

## Protein 1729: neuroendocrine convertase 1 isoform 3 [Homo sapiens]

|  |  |  |  |
|---|---|---|---|
| **Accession:** | gi\|295424145 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 49.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.3 |
|  |  | **Sequence Coverage [%]:** | 2.3 |
|  |  | **No. of unique Peptides:** | 1 |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLDGIVTDAI | EASSIGFNPG | HVDIYSASWG | PNDDGKTVEG | PGRLAQKAFE | YGVKQTSADL | HNDCTETHTG | TSASAPLAAG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| IFALALEANP | NLTWRDMQHL | VVWTSEYDPL | ANNPGWKKNG | AGLMVNSRFG | FGLLNAKALV | DLADPRTWRS | VPEKKECVVK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DNDFEPRALK | ANGEVIIEIP | TRACEGQENA | IKSLEHVQFE | ATIEYSRRGD | LHVTLTSAAG | TSTVLLAERE | RDTSPNGFKN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| WDFMSVHTWG | ENPIGTWTLR | ITDMSGRIQN | EGRIVNWKLI | LHGTSSQPEH | MKQPRVYTSY | NTVQNDRRGV | EKMVDPGEEQ |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PTQENPKENT | LVSKSPSSSS | VGGRRDELEE | GAPSQAMLRL | LQSAFSKNSP | PKQSPKKSPS | AKLNIPYENF | YEALEKLNKP |
| 410 | 420 | 430 | 440 | 450 |  |  |  |
| SQLKDSEDSL | YNDYVDVFYN | TKPYKHRDDR | LLQALVDILN | EEN |  |  |  |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1440 | 1 | 1018.7851 | 270.23 | 1 | 47.7 | 10.3 | 0 | 119-128 | K.NGAGLMVNSR.F |  |

# Detailed Protein Report

## Protein 1730: PREDICTED: cytochrome P450 2F1 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578834042 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 50.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.8 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDSISTAILL | LLLALVCLLL | TLSSRDKGKL | PPGPRPLSIL | GNLLLLCSQD | MLTSLTKLSK | EYGSMYTVHL | GPRRVVVLSG |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| YQAVKEALVD | QGEEFSGRGD | YPAFFNFTKG | NGIAFSSGDR | WKVLRQFSIQ | ILRNFGMGKR | SIEERILEEG | SFLLAELRKT |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| EGEPFDPTFV | LSRSVSNIIC | SVLFGSRFDY | DDERLLTIIR | LINDNFQIMS | SPWGELYDIF | PSLLDWVPGP | HQRIFQNFKC |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| LRDLIAHSVH | DHQASLDPRS | PRDFIQCFLT | KMAEEKEDPL | SHFHMDTLLM | TTHNLLFGGT | KTVSTTLHHA | FLALMKYPKV |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| QARVQEEIDL | VVGRARLPAL | KDRAAMPYTD | AVIHEVQRFA | DIIPMNLPHR | VTRDTAFRGF | LIPKGTDVIT | LLNTVHYDPS |
| **410** | **420** | **430** | **440** | **450** | | | |
| QFLTPQEFNP | EHFLDANQSF | KKSPAFMPFS | AALDAQRHSF | LLSTLLL | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 868 | 1 | 697.7757 | -98.23 | 2 | 40.4 | 10.3 | 1 | 110-122 | K.GNGIAFSSGDRWK.V | |

# Detailed Protein Report

## Protein 1731: PREDICTED: TANK-binding kinase 1-binding protein 1 isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578831704 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 67.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.5 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MESMFEDDIS | ILTQEALGPS | EVWLDSPGDP | SLGGDMCSAS | HFALITAYGD | IKERLGGLER | ENATLRRRLK | VYEIKYPLIS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DFGEEHGFSL | YEIKDGSLLE | VEKVSLQQRL | NQFQHELQKN | KEQEEQLGEM | IQAYEKLCVE | KSDLETELRE | MRALVETHLR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| QICGLEQQLR | QQQGLQDAAF | SNLSPPPAPA | PPCTDLDLHY | LALRGGSGLS | HGWPGSTPSV | SDLERRRLEE | ALEAAQGEAR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GAQLREEQLQ | AECERLQGEL | KQLQETRAQD | LASNQSERDM | AWVKRVGDDQ | VNLALAYTEL | TEELGRLREL | SSLQGRILRT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LLQEQARSGG | QRHSPLSQRH | SPAPQCPSPS | PPARAAPPCP | PCQSPVPQRR | SPVPPCPSPQ | QRRSPASPSC | PSPVPQRRSP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VPPSCQSPSP | QRRSPVPPSC | PAPQPRPPPP | PPPGERTLAE | RAYAKPPSHH | VKAGFQGRRS | YSELAEGAAY | AGASPPWLQA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| EAATLPKPRA | YGSELYGPGR | PLSPRRAFEG | IRLRFEKQPS | EEDEWAVPTS | PPSPEVGTIR | CASFCAGFPI | PESPAATAYA |
| 570 | 580 | 590 | 600 | 610 | 620 | | |
| HAEHAQSWPS | INLLMETVGS | DIRSCPLCQL | GFPVGYPDDA | LIKHIDSHLE | NSKI | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2713 | 1 | 840.4021 | -18.66 | 2 | 64.2 | 10.3 | 1 | 398-412 | R.RSPVPPSCQSPSPQR.R | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 1732: PREDICTED: sorting nexin-31 isoform X11 [Homo sapiens]

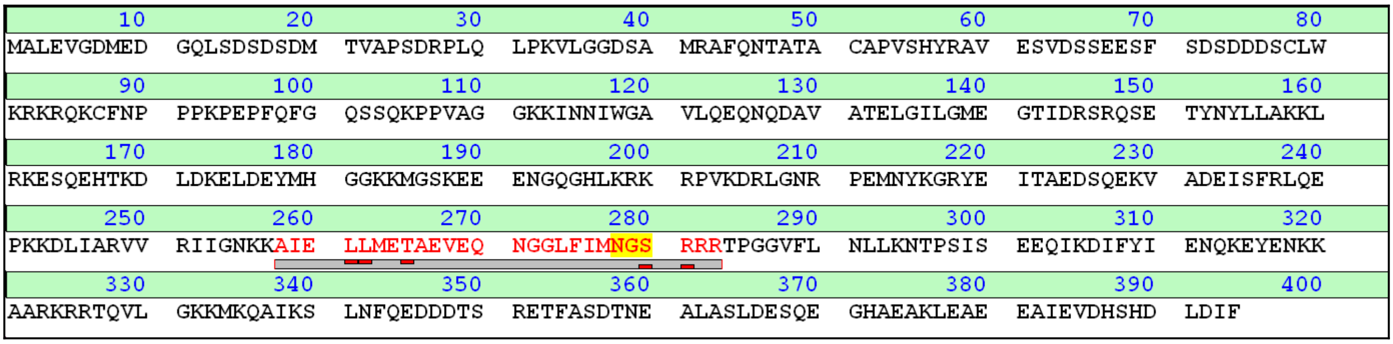
| | | | |
|---|---|---|---|
| **Accession:** | gi\|578815858 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 40.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.6 |
| | | **Sequence Coverage [%]:** | 3.7 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDPNVLRSDV | FVEFLKLAQL | NTFDIATKKA | YLDIFLPNEQ | SIRIEIITSD | TAERVLEVVS | HKIGLCRELL | GYFGLFLIRF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GKEGKLSVVK | KLADFELPYV | SLGSSEVENC | KVGLRKWYMA | PSLDSVLMDC | RVAVDLLYMQ | AIQDIEKGWA | KPTQAQRQKL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EAFQKEDSQT | KFLELAREVR | HYGYLQLDPC | TCDYPESGSG | AVLSVGNNEI | SCCITLPDSQ | TQDIVFQMSR | VKCWQVTFLG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TLLDTDGPQR | TLNQNLELRF | QYSEDSCWQW | FVIYTKQAFL | LSSCLKKMIS | EKMVKLAAEN | TEMQIEVPEQ | SKSKKYHIQQ |
| 330 | 340 | 350 | 360 | | | | |
| SQQKDYSSFL | SRKSKIKIAK | DDCVFGNIKE | EDL | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 84 | 1 | 731.7903 | -172.94 | 2 | 31.0 | 10.3 | 1 | 17-29 | K.LAQLNTFDIATKK.A | |

## Protein 1733: phosphorylated adapter RNA export protein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|66392146 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 44.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.6 |
| | | **No. of unique Peptides:** | 1 |



| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MALEVGDMED | GQLSDSDSDM | TVAPSDRPLQ | LPKVLGGDSA | MRAFQNTATA | CAPVSHYRAV | ESVDSSEESF | SDSDDDSCLW |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | **160** |
| KRKRQKCFNP | PPKPEPFQFG | QSSQKPPVAG | GKKINNIWGA | VLQEQNQDAV | ATELGILGME | GTIDRSRQSE | TYNYLLAKKL |
| **170** | **180** | **190** | **200** | **210** | **220** | **230** | **240** |
| RKESQEHTKD | LDKELDEYMH | GGKKMGSKEE | ENGQGHLKRK | RPVKDRLGNR | PEMNYKGRYE | ITAEDSQEKV | ADEISFRLQE |
| **250** | **260** | **270** | **280** | **290** | **300** | **310** | **320** |
| PKKDLIARVV | RIIGNKKAIE | LLMETAEVEQ | NGGLFIMNGS | RRRTPGGVFL | NLLKNTPSIS | EEQIKDIFYI | ENQKEYENKK |
| **330** | **340** | **350** | **360** | **370** | **380** | **390** | **400** |
| AARKRRTQVL | GKKMKQAIKS | LNFQEDDDTS | RETFASDTNE | ALASLDESQE | GHAEAKLEAE | EAIEVDHSHD | LDIF |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1012 | 1 | 984.1752 | 8.05 | 3 | 41.0 | 10.3 | 2 | 258-283 | K.AIELLMETAEVEQNGGLFIMNGSRRR.T | Oxidation: 6 |

# Detailed Protein Report

## Protein 1734: PREDICTED: potassium channel subfamily T member 2 isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578800878 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 85.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.3 |
| | | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MFSRQDHQTI | LRAWAVKDFA | PNCPLYVQIL | KPENKFHIKF | ADHVVCEEEF | KYAMLALNCI | CPATSTLITL | LVHTSRGQEG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QQSPEQWQKM | YGRCSGNEVY | HIVLEESTFF | AEYEGKSFTY | ASFHAHKKFG | VCLIGVRRED | NKNILLNPGP | RYIMNSTDIC |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FYINITKEEN | SAFKNQDQQR | KSNVSRSFYH | GPSRLPVHSI | IASMGTVAID | LQDTSCRSAS | GPTLSLPTEG | SKEIRRPSIA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PVLEVADTSS | IQTCDLLSDQ | SEDETTPDEE | MSSNLEYAKG | YPPYSPYIGS | SPTFCHLLHE | KVPFCCLRLD | KSCQHNYYED |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AKAYGFKNKL | IIVAAETAGN | GLYNFIVPLR | AYYRPKKELN | PIVLLLDNPP | DMHFLDAICW | FPMVYYMVGS | IDNLDDLLRC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| GVTFAANMVV | VDKESTMSAE | EDYMADAKTI | VNVQTLFRLF | SSLSIITELT | HPANMRFMQF | RAKDCYSLAL | SKLEKKERER |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| GSNLAFMFRL | PFAAGRVFSI | SMLDTLLYQS | FVKDYMISIT | RLLLGLDTTP | GSGFLCSMKI | TADDLWIRTY | ARLYQKLCSS |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TGDVPIGIYR | TESQKLTTSE | SRKIASQSQI | SISVEEWEDT | KDSKEQGHHR | SNHRNSTSSD | QSDHPLLRRK | SMQWARRLSR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KGPKHSGKTA | EKITQQRLNL | YRRSERQELA | ELVKNRMKHL | GLSTVGYDEM | NDHQSTLSYI | LINPSPDTRI | ELNDVVYLIR |
| 730 | 740 | 750 | 760 | | | | |
| PDPLAYLPNS | EPSRRNSICN | VTGQDSREET | QL | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2024 | 1 | 766.2746 | -155.24 | 2 | 55.2 | 10.3 | 1 | 1-12 | -.MFSRQDHQTILR.A | |

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# Detailed Protein Report

## Protein 1735: sodium/hydrogen exchanger 4 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|148727259 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 89.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.4 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530368639 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: sodium/hydrogen exchanger 4 isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MALQMFVTYS | PWNCLLLLVA | LECSEASSDL | NESANSTAQY | ASNAWFAAAS | SEPEEGISVF | ELDYDYVQIP | YEVTLWILLA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SLAKIGFHLY | HRLPGLMPES | CLLILVGALV | GGIIFGTDHK | SPPVMDSSIY | FLYLLPPIVL | EGGYFMPTRP | FFENIGSILW |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WAVLGALINA | LGIGLSLYLI | CQVKAFGLGD | VNLLQNLLFG | SLISAVDPVA | VLAVFEEARV | NEQLYMMIFG | EALLNDGITV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| VLYNMLIAFT | KMHKFEDIET | VDILAGCARF | IVVGLGGVLF | GIVFGFISAF | ITRFTQNISA | IEPLIVFMFS | YLSYLAAETL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YLSGILAITA | CAVTMKKYVE | ENVSQTSYTT | IKYFMKMLSS | VSETLIFIFM | GVSTVGKNHE | WNWAFICFTL | AFCQIWRAIS |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VFALFYISNQ | FRTFPFSIKD | QCIIFYSGVR | GAGSFSLAFL | LPLSLFPRKK | MFVTATLVVI | YFTVFIQGIT | VGPLVRYLDV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KKTNKKESIN | EELHIRLMDH | LKAGIEDVCG | HWSHYQVRDK | FKKFDHRYLR | KILIRKNLPK | SSIVSLYKKL | EMKQAIEMVE |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| TGILSSTAFS | IPHQAQRIQG | IKRLSPEDVE | SIRDILTSNM | YQVRQRTLSY | NKYNLKPQTS | EKQAKEILIR | RQNTLRESMR |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KGHSLPWGKP | AGTKNIRYLS | YPYGNPQSAG | RDTRAAGFSD | DDSSDPGSPS | ITFSACSRIG | SLQKQEAQEI | IPMKSLHRGR |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| KAFSFGYQRN | TSQEEYLGGV | RRVALRPKPL | FHAVDEEGES | GGESEGKASL | VEVRSRWTAD | HGHGRDHHRS | HSPLLQKK |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 534 | 1 | 451.4647 | -195.32 | 3 | 36.3 | 10.3 | 0 | 730-741 | R.NTSQEEYLGGVR.R | |

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# Detailed Protein Report

## Protein 1736: 60S ribosomal protein L23 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4506605 | **Score:** | 10.3 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 14.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 11.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 14.3 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MSKRGRGGSS | GAKFRISLGL | PVGAVINCAD | NTGAKNLYII | SVKGIK**GRLN** | **RLPAAGVGDM** | **VMATVK**KGKP | ELRKKVHPAV |
| **90** | **100** | **110** | **120** | **130** | **140** | **150** | |
| VIRQRKSYRR | KDGVFLYFED | NAGVIVNNKG | EMKGSAITGP | VAKECADLWP | RIASNAGSIA | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2050 | 1 | 1044.4446 | -106.91 | 2 | 55.5 | 10.3 | 2 | 47-66 | K.GRLNRLPAAGVGDMVMATVK.K | Oxidation: 14, 16 |

# Detailed Protein Report

## Protein 1737: PREDICTED: 6-phosphofructokinase type C isoform X3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530392193 | **Score:** | 10.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 81.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.5 |
| | | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MNAAVRAVVR | MGIYVGAKVY | FIYEGYQGMV | DGGSNIAEAD | WESVSSILQV | GGTIIGSARC | QAFRTREGRL | KAACNLLQRG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ITNLCVIGGD | GSLTGANLFR | KEWSGLLEEL | ARNGQIDKEA | VQKYAYLNVV | GMVGSIDNDF | CGTDMTIGTD | SALHRIIEVV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DAIMTTAQSH | QRTFVLEVMG | RHCGYLALVS | ALACGADWVF | LPESPPEEGW | EEQMCVKLSE | NRARKKRLNI | IIVAEGAIDT |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QNKPITSEKI | KELVVTQLGY | DTRVTILGHV | QRGGTPSAFD | RILASRMGVE | AVIALLEATP | DTPACVVSLN | GNHAVRLPLM |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ECVQMTQDVQ | KAMDERRFQD | AVRLRGRSFA | GNLNTYKRLA | IKLPDDQIPK | TNCNVAVINV | GAPAAGMNAA | VRSAVRVGIA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| DGHRMLAIYD | GFDGFAKGQI | KEIGWTDVGG | WTGQGGSILG | TKRVLPGKYL | EEIATQMRTH | SINALLIIGG | FEAYLGLLEL |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SAAREKHEEF | CVPMVMVPAT | VSNNVPGSDF | SIGADTALNT | ITDTCDRIKQ | SASGTKRRVF | IIETMGGYCG | YLANMGGLAA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| GADAAYIFEE | PFDIRDLQSN | VEHLTEKMKT | TIQRGLVLRN | ESCSENYTTD | FIYQLYSEEG | KGVFDCRKNV | LGHMQQGGAP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SPFDRNFGTK | ISARAMEWIT | AKLKEARGRG | KKFTTDDSIC | VLGISKRNVI | FQPVAELKKQ | TDFEHRIPKE | QWWLKLRPLM |
| 730 | 740 | 750 | | | | | |
| KILAKYKASY | DVSDSGQLEH | VQPWSV | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2259 | 1 | 619.2475 | -151.99 | 2 | 56.6 | 10.2 | 1 | 393-404 | R.SAVRVGIADGHR.M | |

# Detailed Protein Report

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## Protein 1738: pre-mRNA 3' end processing protein WDR33 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|56243590 | **Score:** | 10.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 145.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| | | **Sequence Coverage [%]:** | 1.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.72 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.63 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MATEIGSPPR | FFHMPRFQHQ | APRQLFYKRP | DFAQQQAMQQ | LTFDGKRMRK | AVNRKTIDYN | PSVIKYLENR | IWQRDQRDMR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AIQPDAGYYN | DLVPPIGMLN | NPMNAVTTKF | VRTSTNKVKC | PVFVVRWTPE | GRRLVTGASS | GEFTLWNGLT | FNFETILQAH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DSPVRAMTWS | HNDMWMLTAD | HGGYVKYWQS | NMNNVKMFQA | HKEAIREASF | SPTDNKFATC | SDDGTVRIWD | FLRCHEERIL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RGHGADVKCV | DWHPTKGLVV | SGSKDSQQPI | KFWDPKTGQS | LATLHAHKNT | VMEVKLNLNG | NWLLTASRDH | LCKLFDIRNL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KEELQVFRGH | KKEATAVAWH | PVHEGLFASG | GSDGSLLFWH | VGVEKEVGGM | EMAHEGMIWS | LAWHPLGHIL | CSGSNDHTSK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FWTRNRPGDK | MRDRYNLNLL | PGMSEDGVEY | DDLEPNSLAV | IPGMGIPEQL | KLAMEQEQMG | KDESNEIEMT | IPGLDWGMEE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VMQKDQKKVP | QKKVPYAKPI | PAQFQQAWMQ | NKVPIPAPNE | VLNDRKEDIK | LEEKKKTQAE | IEQEMATLQY | TNPQLLEQLK |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| IERLAQKQVE | QIQPPPSSGT | PLLGPQPFPG | QGPMSQIPQG | FQQPHPSQQM | PMNMAQMGPP | GPQGQFRPPG | PQGQMGPQGP |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PLHQGGGGPQ | GFMGPQGPQG | PPQGLPRPQD | MHGPQGMQRH | PGPHGPLGPQ | GPPGPQGSSG | PQGHMGPQGP | PGPQGHIGPQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| GPPGPQGHLG | PQGPPGTQGM | QGPPGPRGMQ | GPPHPHGIQG | GPGSQGIQGP | VSQGPLMGLN | PRGMQGPPGP | RENQGPAPQG |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| MIMGHPPQEM | RGPHPPGGLL | GHGPQEMRGP | QEIRGMQGPP | PQGSMLGPPQ | ELRGPPGSQS | QQGPPQGSLG | PPPQGGMQGP |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| PGPQGQQNPA | RGPHPSQGPI | PFQQQKTPLL | GDGPRAPFNQ | EGQSTGPPPL | IPGLGQQGAQ | GRIPPLNPGQ | GPGPNKGDSR |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GPPNHHMGPM | SERRHEQSGG | PEHGPERGPF | RGGQDCRGPP | DRRGPHPDFP | DDFSRPDDFH | PDKRFGHRLR | EFEGRGGPLP |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| QEEKWRRGGP | GPPFPPDHRE | FSEGDGRGAA | RGPPGAWEGR | RPGDERFPRD | PEDPRFRGRR | EESFRRGAPP | RHEGRAPPRG |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| RDGFPGPEDF | GPEENFDASE | EAARGRDLRG | RGRGTPRGGR | KGLLPTPDEF | PRFEGGRKPD | SWDGNREPGP | GHEHFRDTPR |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PDHPPHDGHS | PASRERSSSL | QGMDMASLPP | RKRPWHDGPG | TSEHREMEAP | GGPSEDRGGK | GRGGPGPAQR | VPKSGRSSSL |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | | |
| DGEHHDGYHR | DEPFGGPPGS | GTPSRGGRSG | SNWGRGSNMN | SGPPRRGASR | GGGRGR | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2371 | 1 | 937.3024 | -144.74 | 2 | 57.9 | 10.2 | 1 | 975-991 | R.HEQSGGPEHGPERGPFR.G | | WUP:QUP 1.63<br>QU:MU 0.72 |

# Detailed Protein Report

## Protein 1739: regulator of G-protein signaling 4 isoform 4 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|164664490 | **Score:** | 10.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 10.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 18.3 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***QU:MU*** **Median:** 1.17 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MCKGLAGLPA SCLRSAKDMK HRLGFLLQKS DSCEHNSSHN KKDKVVICQR VSQEEVKKWA ESLENLISHE CEPGFLHQGR
         90        100
DKPEHARAYN NLL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 388 | 1 | 588.2883 | -35.27 | 3 | 34.5 | 10.2 | 2 | 1-17 | -.MCKGLAGLPASCLRSAK.D | Carbamidomethyl: 12 | QU:MU 1.17 |

# Detailed Protein Report

## Protein 1740: PREDICTED: serine/arginine-rich splicing factor 12 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578812424 | **Score:** | 10.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 19.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 5.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKSKERHPCS | PSDHRRSRSP | SQRRTRSRSS | SWGRNRRRSD | SLKESRHRRF | SYSQSKSRSK | SLPRRSTSAR | QSRTPRRNFG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SRGRSRSKSL | QKRSKSIGKS | QSSSPQKQTS | SGTKSRSHGR | HSDSIARSPC | KSPKGYTNSE | TKVQTAKHSH | FRSHSRSRSY |
| 170 | | | | | | | |
| RHKNSW | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1684 | 1 | 546.7590 | 42.74 | 2 | 51.3 | 10.2 | 0 | 7-15 | R.HPCSPSDHR.R | Carbamidomethyl: 3 |

# Detailed Protein Report

## Protein 1741: kelch-like protein 4 isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|17017982 | **Score:** | 10.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 80.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.4 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.09 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.83 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSVSGKKEFD | VKQILRLRWR | WFSHPFQGST | NTGSCLQQEG | YEHRGTPVQG | RLKSHSRDRN | GLKKSNSPVH | HNILAPVPGP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| APAHQRAVQN | LQQHNLIVHF | QANEDTPKSV | PEKNLFKEAC | EKRAQDLEMM | ADDNIEDSTA | RLDTQHSEDM | NATRSEEQFH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VINHAEQTLR | KMENYLKEKQ | LCDVLLIAGH | LRIPAHRLVL | SAVSDYFAAM | FTNDVLEAKQ | EEVRMEGVDP | NALNSLVQYA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| YTGVLQLKED | TIESLLAAAC | LLQLTQVIDV | CSNFLIKQLH | PSNCLGIRSF | GDAQGCTELL | NVAHKYTMEH | FIEVIKNQEF |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LLLPANEISK | LLCSDDINVP | DEETIFHALM | QWVGHDVQNR | QGELGMLLSY | IRLPLLPPQL | LADLETSSMF | TGDLECQKLL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MEAMKYHLLP | ERRSMMQSPR | TKPRKSTVGA | LYAVGGMDAM | KGTTTIEKYD | LRTNSWLHIG | TMNGRRLQFG | VAVIDNKLYV |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VGGRDGLKTL | NTVECFNPVG | KIWTVMPPMS | THRHGLGVAT | LEGPMYAVGG | HDGWSYLNTV | ERWDPEGRQW | NYVASMSTPR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| STVGVVALNN | KLYAIGGRDG | SSCLKSMEYF | DPHTNKWSLC | APMSKRRGGV | GVATYNGFLY | VVGGHDAPAS | NHCSRLSDCV |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ERYDPKGDSW | STVAPLSVPR | DAVAVCPLGD | KLYVVGGYDG | HTYLNTVESY | DAQRNEWKEE | VPVNIGRAGA | CVVVVKLP |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1263 | 1 | 857.8774 | -59.82 | 2 | 45.4 | 10.2 | 1 | 425-441 | R.KSTVGALYAVGGMDAMK.G | Oxidation: 16 | QU:MU 2.09<br>WUP:QUP 0.83 |

# Detailed Protein Report

## Protein 1742: cytoskeleton-associated protein 5 isoform b [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|57222563 | **Score:** | 10.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 218.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| | | **Sequence Coverage [%]:** | 0.8 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGDDSEWLKL | PVDQKCEHKL | WKARLSGYEE | ALKIFQKIKD | EKSPEWSKFL | GLIKKFVTDS | NAVVQLKGLE | AALVYVENAH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VAGKTTGEVV | SGVVSKVFNQ | PKAKAKELGI | EICLMYIEIE | KGEAVQEELL | KGLDNKNPKI | IVACIETLRK | ALSEFGSKII |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LLKPIIKVLP | KLFESREKAV | RDEAKLIAVE | IYRWIRDALR | PPLQNINSVQ | LKELEEEWVK | LPTSAPRPTR | FLRSQQELEA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KLEQQQSAGG | DAEGGGDDGD | EVPQIDAYEL | LEAVEILSKL | PKDFYDKIEA | KKWQERKEAL | ESVEVLIKNP | KLEAGDYADL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| VKALKKVVGK | DTNVMLVALA | AKCLTGLAVG | LRKKFGQYAG | HVVPTILEKF | KEKKPQVVQA | LQEAIDAIFL | TTTLQNISED |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VLAVMDNKNP | TIKQQTSLFI | ARSFRHCTAS | TLPKSLLKPF | CAALLKHIND | SAPEVRDAAF | EALGTALKVV | GEKAVNPFLA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DVDKLKLDKI | KECSEKVELI | HGKKAGLAAD | KKEFKPLPGR | TAASGAAGDK | DTKDISAPKP | GPLKKAPAAK | AGGPPKKGKP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AAPGGAGNTG | TKNKKGLETK | EIVEPELSIE | VCEEKASAVL | PPTCIQLLDS | SNWKERLACM | EEFQKAVELM | DRTEMPCQAL |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| VRMLAKKPGW | KETNFQVMQM | KLHIVALIAQ | KGNFSKTSAQ | VVLDGLVDKI | GDVKCGNNAK | EAMTAIAEAC | MLPWTAEQVV |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SMAFSQKNPK | NQSETLNWLS | NAIKEFGFSG | LNVKAFISNV | KTALAATNPA | VRTAAITLLG | VMYLYVGPSL | RMFFEDEKPA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LLSQIDAEFE | KMQGQSPPAP | TRGISKHSTS | GTDEGEDGDE | PDDGSNDVVD | LLPRTEISDK | ITSELVSKIG | DKNWKIRKEG |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| LDEVAGIIND | AKFIQPNIGE | LPTALKGRLN | DSNKILVQQT | LNILQQLAVA | MGPNIKQHVK | NLGIPIITVL | GDSKNNVRAA |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| ALATVNAWAE | QTGMKEWLEG | EDLSEELKKE | NPFLRQELLG | WLAEKLPTLR | STPTDLILCV | PHLYSCLEDR | NGDVRKKAQD |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ALPFFMMHLG | YEKMAKATGK | LKPTSKDQVL | AMLEKAKVNM | PAKPAPPTKA | TSKPMGGSAP | AKFQPASAPA | EDCISSSTEP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KPDPKKAKAP | GLSSKAKSAQ | GKKMPSKTSL | KEDEDKSGPI | FIVVPNGKEQ | RMKDEKGLKV | LKWNFTTPRD | EYIEQLKTQM |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| SSCVAKWLQD | EMFHSDFQHH | NKALAVMVDH | LESEKEGVIG | CLDLILKWLT | LRFFDTNTSV | LMKALEYLKL | LFTLLSEEEY |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| HLTENEASSF | IPYLVVKVGE | PKDVIRKDVR | AILNRMCLVY | PASKMFPFIM | EGTKSKNSKQ | RAECLEELGC | LVESYGMNVC |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| QPTPGKALKE | IAVHIGDRDN | AVRNAALNTI | VTVYNVHGDQ | VFKLIGNLSE | KDMSMLEERI | KRSAKRPSAA | PIKQVEEKPQ |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| RAQNISSNAN | MLRKGPAEDM | SSKLNQARSM | SGHPEAAQMV | RREFQLDLDE | IENDNGTVRC | EMPELVQHKL | DDIFEPVLIP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| EPKIRAVSPH | FDDMHSNTAS | TINFIISQVA | SGDINTSIQA | LTQLFQIESL | AREASTGVLK | DLMHGLITLM | LDSRIEDLEE |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| GQQVIRSVNL | LVVKVLEKSD | QTNILSALLV | LLQDSLLATA | SSPKFSELVM | KCLWRMVRLL | PDTINSINLD | RILLDIHIFM |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| KVFPKEKLKQ | CKSEFPIRTL | KTLLHTLCKL | KGPKILDHLT | MIDNKNESEL | EAHLCRMMKH | SMDQTGSKSD | KETEKGASRI |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| DEKSSKAKVN | DFLAEIFKKI | GSKENTKEGL | AELYEYKKKY | SDADIEPFLK | NSSQFFQSYV | ERGLRVIEME | REGKGRISTS |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| TGISPQMEVT | CVPTPTSTVS | SIGNTNGEEV | GPSVYLERLK | ILRQRCGLDN | TKQDDRPPLT | SLLSKPAVPT | VASSTDMLHS |
| 1930 | 1940 | 1950 | 1960 | 1970 | 1980 | | |
| KLSQLRESRE | QHQHSDLDSN | QTHSSGTVTS | SSSTANIDDL | KKRLERIKSS | RK | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1288 | 1 | 917.4589 | -64.75 | 2 | 46.3 | 10.2 | 1 | 1426-1441 | K.RPSAAPIKQVEEKPQR.A | |

# Detailed Protein Report

## Protein 1743: uncharacterized protein LOC400863 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|572871229 | **Score:** | 10.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 14.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 10.4 |
| | | **No. of unique Peptides:** | 1 |

### Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.78 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.04 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MGTVIPHSPC GESGRAPDGW PKAAQRRSCE EEASGGSESR REPTCGCLSN SRRTWAAGSG VGEKQVDLEV LLQVERKGEF
        90        100        110        120        130        140
CKMLWGPLSS AAEAQLFLWL LLEQPVDQDV AHATPYIRSP FSDALSQLFA CTHL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 930 | 1 | 770.6913 | -164.74 | 2 | 41.2 | 10.2 | 1 | 27-40 | R.RSCEEEASGGSESR.R | Carbamidomethyl: 3 | WUP:QUP 1.04<br>QU:MU 0.78 |

# Detailed Protein Report

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## Protein 1744: zinc finger protein 592 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|108860697 | **Score:** | 10.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 137.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530407316 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: zinc finger protein 592 isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGDMKTPDFD | DLLAAFDIPD | PTSLDAKEAI | QTPSEENESP | LKPPGICMDE | SVSLSHSGSA | PDVPAVSVIV | KNTSRQESFE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AEKDHITPSL | LHNGFRGSDL | PPDPHNCGKF | DSTFMNGDSA | RSFPGKLEPP | KSEPLPTFNQ | FSPISSPEPE | DPIKDNGFGI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KPKHSDSYFP | PPLGCGAVGG | PVLEALAKFP | VPELHMFDHF | CKKEPKPEPL | PLGSQQEHEQ | SGQNTVEPHK | DPDATRFFGE |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ALEFNSHPSN | SIGESKGLAR | ELGTCSSVPP | RQRLKPAHSK | LSSCVAALVA | LQAKRVASVT | KEDQPGHTKD | LSGPTKESSK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GSPKMPKSPK | SPRSPLEATR | KSIKPSDSPR | SICSDSSSKG | SPSVAASSPP | AIPKVRIKTI | KTSSGEIKRT | VTRILPDPDD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| PSKSPVGSPL | GSAIAEAPSE | MPGDEVPVEE | HFPEAGTNSG | SPQGARKGDE | SMTKASDSSS | PSCSSGPRVP | KGAAPGSQTG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KKQQSTALQA | STLAPANLLP | KAVHLANLNL | VPHSVAASVT | AKSSVQRRSQ | PQLTQMSVPL | VHQVKKAAPL | IVEVFNKVLH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SSNPVPLYAP | NLSPPADSRI | HVPASGYCCL | ECGDAFALEK | SLSQHYGRRS | VHIEVLCTLC | SKTLLFFNKC | SLLRHARDHK |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| SKGLVMQCSQ | LLVKPISADQ | MFVSAPVNST | APAAPAPSSS | PKHGLTSGSA | SPPPPALPLY | PDPVRLIRYS | IKCLECHKQM |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RDYMVLAAHF | QRTTEETEGL | TCQVCQMLLP | NQCSFCAHQR | IHAHKSPYCC | PECGVLCRSA | YFQTHVKENC | LHYARKVGYR |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| CIHCGVVHLT | LALLKSHIQE | RHCQVFHKCA | FCPMAFKTAS | STADHSATQH | PTQPHRPSQL | IYKCSCEMVF | NKKRHIQQHF |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| YQNVSKTQVG | VFKCPECPLL | FVQKPELMQH | VKSTHGVPRN | VDELSSLQSS | ADTSSSRPGS | RVPTEPPATS | VAARSSSLPS |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| GRWGRPEAHR | RVEARPRLRN | TGWTCQECQE | WVPDRESYVS | HMKKSHGRTL | KRYPCRQCEQ | SFHTPNSLRK | HIRNNHDTVK |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| KFYTCGYCTE | DSPSFPRPSL | LESHISLMHG | IRNPDLSQTS | KVKPPGGHSP | QVNHLKRPVS | GVGDAPGTSN | GATVSSTKRH |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| KSLFQCAKCS | FATDSGLEFQ | SHIPQHQVDS | STAQCLLCGL | CYTSASSLSR | HLFIVHKVRD | QEEEEEEEAA | AAEMAVEVAE |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | |
| PEEGSGEEVP | METRENGLEE | CAGEPLSADP | EARRLLGPAP | EDDGGHNDHS | QPQASQDQDS | HTLSPQV | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 852 | 1 | 974.4621 | -3.82 | 2 | 39.1 | 10.2 | 1 | 189-203 | K.FPVPELHMFDHFCKK.E | Carbamidomethyl: 13;<br>Oxidation: 8 |

# Detailed Protein Report

**Protein 1745:** **spermatogenesis- and oogenesis-specific basic helix-loop-helix-containing protein 1 isoform b [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|156119601 | **Score:** | 10.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 34.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 7.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MASRCSEPYP | EVSRIPTVRG | CNGSLSGALS | CCEDSAQGSG | PPKAPTVAEG | PSSCLRRNVI | SERERRKRMS | LSCERLRALL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PQFDGRREDM | ASVLEMSVQF | LRLASALGPS | QEQHAILASS | KEMWHSLQED | VLQLTLSSQI | QAGVPDPGTG | ASSGTRTPDV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KAFLESPWSL | DPASASPEPV | PHILASSRQW | DPASCTSLGT | DKCEALLGLC | QVRGGLPPFS | EPSSLVPWPP | GRSLPKAVRP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PLSWPPFSQQ | QTLPVMSGEA | LGWLGQAGPL | AMGAAPLGEP | AKEDPMLAQE | AGSALGSDVD | DGTSFLLTAG | PSSWPGEWGP |
| 330 | | | | | | | |
| GFRAGPPA | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1133 | 1 | 955.7571 | -26.57 | 3 | 44.3 | 10.2 | 1 | 189-213 | R.QWDPASCTSLGTDKCEALLGLCQVR.G | Carbamidomethyl: 7, 15, 22 |

# Detailed Protein Report

## Protein 1746: succinate dehydrogenase assembly factor 1, mitochondrial [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|111038124 | **Score:** | 10.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 12.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 12.0 |
| | | **Sequence Coverage [%]:** | 17.4 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSRHSRLQRQ VLSLYRDLLR AGRGKPGAEA RVRAEFRQHA GLPRSDVLRI EYLYRRGRRQ LQLLRSGHAT AMGAFVRPRA
        90        100        110        120
PTGEPGGVGS QPDDGDSPRN PHDSTGAPET RPDGR
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1571 | 1 | 948.4992 | 81.45 | 2 | 48.0 | 10.2 | 0 | 80-99 | R.APTGEPGGVGSQPDDGDSPR.N | |

# Detailed Protein Report

## Protein 1747: kinase D-interacting substrate of 220 kDa [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|55741641 | **Score:** | 10.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 196.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 0.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 1.66 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.78 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

# Detailed Protein Report

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MSVLISQSVI | NYVEEENIPA | LKALLEKCKD | VDERNECGQT | PLMIAAEQGN | LEIVKELIKN | GANCNLEDLD | NWTALISASK |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| EGHVHIVEEL | LKCGVNLEHR | DMGGWTALMW | ACYKGRTDVV | ELLLSHGANP | SVTGLYSVYP | IIWAAGRGHA | DIVHLLLQNG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| AKVNCSDKYG | TTPLVWAARK | GHLECVKHLL | AMGADVDQEG | ANSMTALIVA | VKGGYTQSVK | EILKRNPNVN | LTDKDGNTAL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MIASKEGHTE | IVQDLLDAGT | YVNIPDRSGD | TVLIGAVRGG | HVEIVRALLQ | KYADIDIRGQ | DNKTALYWAV | EKGNATMVRD |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ILQCNPDTEI | CTKDGETPLI | KATKMRNIEV | VELLLDKGAK | VSAVDKKGDT | PLHIAIRGRS | RKLAELLLRN | PKDGRLLYRP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| NKAGETPYNI | DCSHQKSILT | QIFGARHLSP | TETDGDMLGY | DLYSSALADI | LSEPTMQPPI | CVGLYAQWGS | GKSFLLKKLE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| DEMKTFAGQQ | IEPLFQFSWL | IVFLTLLLCG | GLGLLFAFTV | HPNLGIAVSL | SFLALLYIFF | IVIYFGGRRE | GESWNWAWVL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| STRLARHIGY | LELLLKLMFV | NPPELPEQTT | KALPVRFLFT | DYNRLSSVGG | ETSLAEMIAT | LSDACEREFG | FLATRLFRVF |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| KTEDTQGKKK | WKKTCCLPSF | VIFLFIIGCI | ISGITLLAIF | RVDPKHLTVN | AVLISIASVV | GLAFVLNCRT | WWQVLDSLLN |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SQRKRLHNAA | SKLHKLKSEG | FMKVLKCEVE | LMARMAKTID | SFTQNQTRLV | VIIDGLDACE | QDKVLQMLDT | VRVLFSKGPF |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| IAIFASDPHI | IIKAINQNLN | SVLRDSNING | HDYMRNIVHL | PVFLNSRGLS | NARKFLVTSA | TNGDVPCSDT | TGIQEDADRR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| VSQNSLGEMT | KLGSKTALNR | RDTYRRRQMQ | RTITRQMSFD | LTKLLVTEDW | FSDISPQTMR | RLLNIVSVTG | RLLRANQISF |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| NWDRLASWIN | LTEQWPYRTS | WLILYLEETE | GIPDQMTLKT | IYERISKNIP | TTKDVEPLLE | IDGDIRNFEV | FLSSRTPVLV |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| ARDVKVFLPC | TVNLDPKLRE | IIADVRAARE | QISIGGLAYP | PLPLHEGPPR | APSGYSQPPS | VCSSTSFNGP | FAGGVVSPQP |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| HSSYYSGMTG | PQHPFYNRPF | FAPYLYTPRY | YPGGSQHLIS | RPSVKTSLPR | DQNNGLEVIK | EDAAEGLSSP | TDSSRGSGPA |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| PGPVVLLNSL | NVDAVCEKLK | QIEGLDQSML | PQYCTTIKKA | NINGRVLAQC | NIDELKKEMN | MNFGDWHLFR | STVLEMRNAE |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| SHVVPEDPRF | LSESSSGPAP | HGEPARRASH | NELPHTELSS | QTPYTLNFSF | EELNTLGLDE | GAPRHSNLSW | QSQTRRTPSL |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| SSLNSQDSSI | EISKLTDKVQ | AEYRDAYREY | IAQMSQLEGG | PGSTTISGRS | SPHSTYYMGQ | SSSGGSIHSN | LEQEKGKDSE |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| PKPDDGRKSF | LMKRGDVIDY | SSSGVSTNDA | SPLDPITEED | EKSDQSGSKL | LPGKKSSERS | SLFQTDLKLK | GSGLRYQKLP |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| SDEDESGTEE | SDNTPLLKDD | KDRKAEGKVE | RVPKSPEHSA | EPIRTFIKAK | EYLSDALLDK | KDSSDSGVRS | SESSPNHSLH |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| NEVADDSQLE | KANLIELEDD | SHSGKRGIPH | SLSGLQDPII | ARMSICSEDK | KSPSECSLIA | SSPEENWPAC | QKAYNLNRTP |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| STVTLNNNSA | PANRANQNFD | EMEGIRETSQ | VILRPSSSPN | PTTIQNENLK | SMTHKRSQRS | SYTRLSKDPP | ELHAAASSES |
| 1770 | 1780 | | | | | | |
| TGFGEERESI | L | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2608 | 1 | 913.4638 | -3.43 | 2 | 63.3 | 10.2 | 1 | 304-319 | K.TALYWAVEKGNATMVR.D | Oxidation: 14 | WUP:QUP 0.78<br>QU:MU 1.66 |

# Detailed Protein Report

## Protein 1748: apoptosis-inducing factor 3 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|65787454 | **Score:** | 10.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 65.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| | | **Sequence Coverage [%]:** | 4.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 2.31 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 0.73 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGGCFSKPKP | VELKIEVVLP | EKERGKEELS | ASGKGSPRAY | QGNGTARHFH | TEERLSTPHP | YPSPQDCVEA | AVCHVKDLEN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| GQMREVELGW | GKVLLVKDNG | EFHALGHKCP | HYGAPLVKGV | LSRGRVRCPW | HGACFNISTG | DLEDFPGLDS | LHKFQVKIEK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EKVYVRASKQ | ALQLQRRTKV | MAKCISPSAG | YSSSTNVLIV | GAGAAGLVCA | ETLRQEGFSD | RIVLCTLDRH | LPYDRPKLSK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SLDTQPEQLA | LRPKEFFRAY | GIEVLTEAQV | VTVDVRTKKV | VFKDGFKLEY | SKLLLAPGSS | PKTLSCKGKE | VENVFTIRTP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| EDANRVVRLA | RGRNVVVVGA | GFLGMEVAAY | LTEKAHSVSV | VELEETPFRR | FLGERVGRAL | MKMFENNRVK | FYMQTEVSEL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RGQEGKLKEV | VLKSSKVVRA | DVCVVGIGAV | PATGFLRQSG | IGLDSRGFIP | VNKMMQTNVP | GVFAAGDAVT | FPLAWRNNRK |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| VNIPHWQMAH | AQGRVAAQNM | LAQEAEMSTV | PYLWTAMFGK | SLRYAGYGEG | FDDVIIQGDL | EELKFVAFYT | KGDEVIAVAS |
| 570 | 580 | 590 | 600 | | | | |
| MNYDPIVSKV | AEVLASGRAI | RKREVETGDM | SWLTGKGS | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 185 | 1 | 896.4274 | -19.41 | 3 | 32.3 | 10.2 | 1 | 521-544 | K.SLRYAGYGEGFDDVIIQGDLEELKF | | QU:MU 2.31<br>WUP:QUP 0.73 |

# Detailed Protein Report

## Protein 1749: EPM2A-interacting protein 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|7662294 | **Score:** | 10.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 70.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.7 |
| | | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWMTPKRSKM | EVDEALVFRP | EWTQRYLVVE | PPEGDGALCL | VCRRLIVATR | ERDVRRHYEA | EHEYYERYVA | DGERAALVER |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LRQGDLPVAS | FTPEERAARA | GLGLCRLLAL | KGRGWGEGDF | VYQCMEVLLR | EVLPEHVSVL | QGVDLSPDIT | RQRILSIDRN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LRNQLFNRAR | DFKAYSLALD | DQAFVAYENY | LLVFIRGVGP | ELEVQEDLLT | IINLTHHFSV | GALMSAILES | LQTAGLSLQR |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| MVGLTTTHTL | RMIGENSGLV | SYMREKAVSP | NCWNVIHYSG | FLHLELLSSY | DVDVNQIINT | ISEWIVLIKT | RGVRRPEFQT |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LLTESESEHG | ERVNGRCLNN | WLRRGKTLKL | IFSLRKEMEA | FLVSVGATTV | HFSDKQWLCD | FGFLVDIMEH | LRELSEELRV |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SKVFAAAAFD | HICTFEVKLN | LFQRHIEEKN | LTDFPALREV | VDELKQQNKE | DEKIFDPDRY | QMVICRLQKE | FERHFKDLRF |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| IKKDLELFSN | PFNFKPEYAP | ISVRVELTKL | QANTNLWNEY | RIKDLGQFYA | GLSAESYPII | KGVACKVASL | FDSNQICEKA |
| 570 | 580 | 590 | 600 | 610 | | | |
| FSYLTRNQHT | LSQPLTDEHL | QALFRVATTE | MEPGWDDLVR | ERNESNP | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 829 | 1 | 859.6189 | 172.24 | 2 | 39.9 | 10.2 | 2 | 68-82 | R.YVADGERAALVERLR.Q | |

# Detailed Protein Report

## Protein 1750: cis-aconitate decarboxylase [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|385719224 | **Score:** | 10.2 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 52.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.2 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMLKSITESF | ATAIHGLKVG | HLTDRVIQRS | KRMILDTLGA | GFLGTTTEVF | HIASQYSKIY | SSNISSTVWG | QPDIRLPPTY |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AAFVNGVAIH | SMDFDDTWHP | ATHPSGAVLP | VLTALAEALP | RSPKFSGLDL | LLAFNVGIEV | QGRLLHFAKE | ANDMPKRFHP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| PSVVGTLGSA | AAASKFLGLS | STKCREALAI | AVSHAGAPMA | NAATQTKPLH | IGNAAKHGIE | AAFLAMLGLQ | GNKQVLDLEA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GFGAFYANYS | PKVLPSIASY | SWLLDQQDVA | FKRFPAHLST | HWVADAAASV | RKHLVAERAL | LPTDYIKRIV | LRIPNVQYVN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| RPFPVSEHEA | RHSFQYVACA | MLLDGGITVP | SFHECQINRP | QVRELLSKVE | LEYPPDNLPS | FNILYCEISV | TLKDGATFTD |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| RSDTFYGHWR | KPLSQEDLEE | KFRANASKML | SWDTVESLIK | IVKNLEDLED | CSVLTTLLKG | PSPPEVASNS | PACNNSITNL |
| 490 | | | | | | | |
| S | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 779 | 1 | 737.7855 | -153.30 | 2 | 39.7 | 10.2 | 0 | 5-18 | K.SITESFATAIHGLK.V | |

# Detailed Protein Report

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## Protein 1751: PREDICTED: IQ motif and SEC7 domain-containing protein 3-like [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578797721 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 20.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 5.9 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

***WUP:QUP*** **Median:** 0.88 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MESLLENPVR | AVLCLKELTA | IVQKQQSLIH | TQRERIDELE | RRLDELSTEN | RSLWEHQQLL | QAQPPPGLVP | PSSAPLPAAP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ATAPAAAARA | QEPLQDQGQR | SAAAPHPAPD | RPPRQHHGQL | LEQPQRGPGS | RAHTPQSPQK | HLGTQGAVTD | KEKERPPSCC |
| 170 | 180 | 190 | | | | | |
| AAAGALLQHK | SPSALGKGVL | SRRPE | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2227 | 1 | 698.3590 | -24.64 | 2 | 56.2 | 10.1 | 1 | 25-35 | K.QQSLIHTQRER.I | | WUP:QUP 0.88 |

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# Detailed Protein Report

## Protein 1752: uncharacterized protein LOC101928436 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|558757363 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 11.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 7.7 |
| | | **Sequence Coverage [%]:** | 18.6 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|578798182 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: uncharacterized protein LOC101928436 isoform X1 [Homo sapiens] |

```
         10         20         30         40         50         60         70         80
MRCVKSMAMD ANSLCVSGFK QLYTLMLSYT QQQFVTSLGN SSYSFELQPN FLSITALGLT LPEEKGKTQP ECPLKVKKCP
         90        100        110
HFYVQIVDLW NLHSTFDTAC DS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2094 | 1 | 1023.8994 | -81.91 | 2 | 56.1 | 10.1 | 2 | 2-20 | M.RCVKSMAMDANSLCVSGFK.Q | |

# Detailed Protein Report

## Protein 1753: lymphocyte antigen 86 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4758708 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 17.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| **Modification(s):** | Carbamidomethyl, Oxidation | **Sequence Coverage [%]:** | 8.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | |
|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.86 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.98 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKGFTATLFL | WTLIFPSCSG | GGGGKAWPTH | VVCSDSGLEV | LYQSCDPLQD | FGFSVEKCSK | QLKSNINIRF | GIILREDIKE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LFLDLALMSQ | GSSVLNFSYP | ICEAALPKFS | FCGRRKGEQI | YYAGPVNNPE | FTIPQGEYQV | LLELYTEKRS | TVACANATIM |
| 170 | | | | | | | |
| CS | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1187 | 1 | 672.8242 | 60.78 | 2 | 45.0 | 10.1 | 0 | 150-162 | R.STVACANATIMCS.- | Carbamidomethyl: 5;<br>Oxidation: 11 | QU:MU 0.86<br>WUP:QUP 1.98 |

# Detailed Protein Report

## Protein 1754: dual specificity protein kinase CLK2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|47717134 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 59.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 1.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPHPRRYHSS | ERGSRGSYRE | HYRSRKHKRR | RSRSWSSSSD | RTRRRRREDS | YHVRSRSSYD | DRSSDRRVYD | RRYCGSYRRN |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DYSRDRGDAY | YDTDYRHSYE | YQRENSSYRS | QRSSRRKHRR | RRRRSRTFSR | SSSHSSRRAK | SVEDDAEGHL | IYHVGDWLQE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RYEIVSTLGE | GTFGRVVQCV | DHRRGGARVA | LKIIKNVEKY | KEAARLEINV | LEKINEKDPD | NKNLCVQMFD | WFDYHGHMCI |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SFELLGLSTF | DFLKDNNYLP | YPIHQVRHMA | FQLCQAVKFL | HDNKLTHTDL | KPENILFVNS | DYELTYNLEK | KRDERSVKST |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AVRVVDFGSA | TFDHEHHSTI | VSTRHYRAPE | VILELGWSQP | CDVWSIGCII | FEYYVGFTLF | QTHDNREHLA | MMERILGPIP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SRMIRKTRKQ | KYFYRGRLDW | DENTSAGRYV | RENCKPLRRY | LTSEAEEHHQ | LFDLIESMLE | YEPAKRLTLG | EALQHPFFAR |
| 490 | 500 | | | | | | |
| LRAEPPNKLW | DSSRDISR | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1198 | 1 | 985.2519 | -184.18 | 1 | 44.6 | 10.1 | 1 | 55-62 | R.SRSSYDDR.S | |

# Detailed Protein Report

## Protein 1755: F-box only protein 8 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|48928044 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 37.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.7 |
| | | **Sequence Coverage [%]:** | 4.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MGQGLWRVVR | NQQLQQEGYS | EQGYLTREQS | RRMAASNISN | TNHRKQVQGG | IDIYHLLKAR | KSKEQEGFIN | LEMLPPELSF |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TILSYLNATD | LCLASCVWQD | LANDELLWQG | LCKSTWGHCS | IYNKNPPLGF | SFRKLYMQLD | EGSLTFNANP | DEGVNYFMSK |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GILDDSPKEI | AKFIFCTRTL | NWKKLRIYLD | ERRDVLDDLV | TLHNFRNQFL | PNALREFFRH | IHAPEERGEY | LETLITKFSH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RFCACNPDLM | RELGLSPDAV | YVLCYSLILL | SIDLTSPHVK | NKMSKREFIR | NTRRAAQNIS | EDFVGHLYDN | IYLIGHVAA |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 750 | 1 | 848.7476 | -154.71 | 2 | 38.9 | 10.1 | 1 | 238-251 | K.FSHRFCACNPDLMR.E | |

# Detailed Protein Report

## Protein 1756: alpha/beta hydrolase domain-containing protein 14B isoform 1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|14249382 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 22.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.9 |
| | | **Sequence Coverage [%]:** | 6.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|226443152 | refseq_huma (refseq_human_20140103.fasta) | alpha/beta hydrolase domain-containing protein 14B isoform 1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAASVEQREG | TIQVQGQALF | FREALPGSGQ | ARFSVLLLHG | IRFSSETWQN | LGTLHRLAQA | GYRAVAIDLP | GLGHSKEAAA |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| PAPIGELAPG | SFLAAVVDAL | ELGPPVVISP | SLSGMYSLPF | LTAPGSQLPG | FVPVAPICTD | KINAANYASV | KTPALIVYGD |
| 170 | 180 | 190 | 200 | 210 | 220 | | |
| QDPMGQTSFE | HLKQLPNHRV | LIMKGAGHPC | YLDKPEEWHT | GLLDFLQGLQ | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2744 | 1 | 639.3386 | -40.09 | 2 | 62.8 | 10.1 | 0 | 64-76 | R.AVAIDLPGLGHSK.E | |

# Detailed Protein Report

**Protein 1757:** **centrosomal protein of 112 kDa isoform b [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|82880654 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 24.5 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| | | **Sequence Coverage [%]:** | 5.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MWASLSLDHP | SAKENQALRL | IEMREENGNV | PKTEQAGSLK | PLRDTGKSNL | KEKKANSKLK | QIEKEYTQKL | AKSSQIIAEL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QTTISSLKEE | NSQQQLAAER | RLQDVRQKFE | DEKKQLIRDN | DQAIKVLQDE | LENRSNQVRC | AEKKLQHKEL | ESQEQITYIR |
| 170 | 180 | 190 | 200 | 210 | 220 | | |
| QEYETKLKGL | MPASLRQELE | DTISSLKSQV | NFLQKRASIL | QEELTTYQGR | R | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2475 | 1 | 701.6910 | -200.17 | 2 | 60.9 | 10.1 | 0 | 89-100 | K.EENSQQQLAAER.R | |

# Detailed Protein Report

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## Protein 1758: collagen alpha-1(XXV) chain isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|366392941 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 63.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.0 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.5 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MLLKKHAGKG GGREPRSEDP TPAEQHCART MPPCAVLAAL LSVVAVVSCL YLGVKTNDLQ ARIAALESAK GAPSIHLLPD
        90        100        110        120        130        140        150        160
TLDHLKTMVQ EKVERLLAQK SYEHMAKIRI AREAPSECNC PAGPPGKRGK RGRRGESGPP GQPGPQGPPG PKGDKGEQGD
       170        180        190        200        210        220        230        240
QGPRGLPGFP TVAALHSNQI LTVKGDQGQA GPPGPPGPPG PRGPPGDTGK DGPRGMPGVP GEPGKPGEQG LMGPLGPPGQ
       250        260        270        280        290        300        310        320
KGSIGAPGIP GMNGQKGEPG LPGAVGQNGI PGPKGEPGEQ GEKGDAGENG PKGDTGEKGD PGSSAAGIKG EPGESGRPGQ
       330        340        350        360        370        380        390        400
KGEPGLPGLP GLPGIKGEPG FIGPQGEPGL PGLPGTKGER GEAGPPGRGE RGEPGAPGPK GDRGEKGDSG AQGPRGPPGQ
       410        420        430        440        450        460        470        480
KGDQGATEII DYNGNLHEAL QGPPGPPGPQ GLQGPKGEQG SPGIPGMDGE QGLKGSKGDM GDPGMTGEKG GIGLPGLPGA
       490        500        510        520        530        540        550        560
NGMKGEKGDS GMPGPQGPSI IGPPGPPGPH GPPGPMGPHG LPGPKGEPGL NGVKGLKGEP GQKGDRGPLG LPGASGLDGK
       570        580        590        600        610        620        630        640
PGSRGTDGPM GPHGPAGPKG ERGEKGAMGE PGPRGPYGLP GFPGPRGEKG DLGEKGEKVT SPSQHVPCLI LLLLSALLFS
       650
LCDSI
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1307 | 1 | 835.3650 | -11.55 | 2 | 45.9 | 10.1 | 1 | 113-128 | R.EAPSECNCPAGPPGKR.G | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 1759: transmembrane protein 68 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|557786131 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 15.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 12.6 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MIDKNQTCGV GQDSVPYMIC LIHILEEWFG VEQLEDYLNF ANYLLWVFTP LILLILPYFT IFLLYLTIIF LHIYKRKNVL
        90        100        110        120        130        140
KEAYSHNLWD GARKTVATLW DGHAAVWHGK QGYFHLCVAI HVCCIGTVLP FHFID
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1673 | 1 | 938.9125 | -87.28 | 2 | 49.2 | 10.1 | 1 | 94-110 | R.KTVATLWDGHAAVWHGK.Q | |

# Detailed Protein Report

**Protein 1760:** **PREDICTED: kynurenine/alpha-aminoadipate aminotransferase, mitochondrial isoform X1 [Homo sapiens]**

**Accession:** gi|578809158
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 10.1
**MW [kDa]:** 51.7
**pI:** 9.0
**Sequence Coverage [%]:** 2.4
**No. of unique Peptides:** 1

## Quantitation

***WUP:QUP*** **Median:** 2.35 **CV:** 0.00 % **No. of Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLKFVLVAGM | LPRRVPRVSL | TKDGPQPLKK | KLDAWLSEDM | NYARFITAAS | AARNPSPIRT | MTDILSRGPK | SMISLAGGLP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NPNMFPFKTA | VITVENGKTI | QFGEEMMKRA | LQYSPSAGIP | ELLSWLKQLQ | IKLHNPPTIH | YPPSQGQMDL | CVTSGSQQGL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| CKVFEMIINP | GDNVLLDEPA | YSGTLQSLHP | LGCNIINVAS | DESGIVPDSL | RDILSRWKPE | DAKNPQKNTP | KFLYTVPNGN |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| NPTGNSLTSE | RKKEIYELAR | KYDFLIIEDD | PYYFLQFNKF | RVPTFLSMDV | DGRVIRADSF | SKIISSGLRI | GFLTGPKPLI |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| ERVILHIQVS | TLHPSTFNQL | MISQLLHEWG | EEGFMAHVDR | VIDFYSNQKD | AILAAADKWL | TGLAEWHVPA | AGMFLWIKVK |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | |
| GINDVKELIE | EKAVKMGVLM | LPGNAFYVDS | SAPSPYLRAS | FSSASPEQMD | VAFQVLAQLI | KESL | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2581 | 1 | 637.8494 | -38.12 | 2 | 60.5 | 10.1 | 1 | 4-14 | K.FVLVAGMLPRR.V | Oxidation: 7 | WUP:QUP 2.35 |

# Detailed Protein Report

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## Protein 1761: pleckstrin homology domain-containing family G member 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|55749621 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 128.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.3 |
| | | **Sequence Coverage [%]:** | 1.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MPVSTSLHQD | GSQERPVSLT | STTSSSGSSC | DSRSAMEEPS | SSEAPAKNGA | GSLRSRHLPN | SNNNSSSWLN | VKGPLSPFNS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RAAAGPAHHK | LSYLGRVVRE | IVETERMYVQ | DLRSIVESQE | FDIYTQYCNN | YPNSVAALTE | CMRDKQQAKF | FRDRQELLQH |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SLPLGSYLLK | PVQRILKYHL | LLQEIAKHFD | EEEDGFEVVE | DAIDTMTCVA | WYINDMKRRH | EHAVRLQEIQ | SLLINWKGPD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LTTYGELVLE | GTFRVHRVRN | ERTFFLFDKT | LLITKKRGDH | FVYKGNIPCS | SLMLIESTRD | SLCFTVTHYK | HSKQQYSIQA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KTVEEKRNWT | HHIKRLILEN | HHATIPQKAK | EAILEMDSYY | PNRYRCSPER | LKKAWSSQDE | VSTNVRQGRR | QSEPTKHLLR |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| QLNEKARAAG | MKGKGRRESE | SSRSSRRPSG | RSPTSTEKRM | SFESISSLPE | VEPDPEAGSE | QEVFSAVEGP | SAEETPSDTE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| SPEVLETQLD | AHQGLLGMDP | PGDMVDFVAA | ESTEDLKALS | SEEEEEMGGA | AQEPESLLPP | SVLDQASVIA | ERFVSSFSRR |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SSVAQEDSKS | SGFGSPRLVS | RSSSVLSLEG | SEKGLARHGS | ATDSLSCQLS | PEVDISVGVA | TEDSPSVNGM | EPPSPGCPVE |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PDRSSCKKKE | SALSTRDRLL | LDKIKSYYEN | AEHHDAGFSV | RRRESLSYIP | KGLVRNSISR | FNSLPRPDPE | PVPPVGSKRQ |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| VGSRPTSWAL | FELPGPSQAV | KGDPPPISDA | EFRPSSEIVK | IWEGMESSGG | SPGKGPGQGQ | ANGFDLHEPL | FILEEHELGA |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| ITEESATASP | ESSSPTEGRS | PAHLARELKE | LVKELSSSTQ | GELVAPLHPR | IVQLSHVMDS | HVSERVKNKV | YQLARQYSLR |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| IKSNKPVMAR | PPLQWEKVAP | ERDGKSPTVP | CLQEEAGEPL | GGKGKRKPVL | SLFDYEQLMA | QEHSPPKPSS | AGEMSPQRFF |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| FNPSAVSQRT | TSPGGRPSAR | SPLSPTETFS | WPDVRELCSK | YASRDEARRA | GGGRPRGPPV | NRSHSVPENM | VEPPLSGRVG |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| RCRSLSTKRG | RGGGEAAQSP | GPLPQSKPDG | GETLYVTADL | TLEDNRRVIV | MEKGPLPSPT | AGLEESSGQG | PSSPVALLGQ |
| 1130 | 1140 | 1150 | 1160 | 1170 | | | |
| VQDFQQSAEC | QPKEEGSRDP | ADPSQQGRVR | NLREKFQALN | SVG | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2130 | 1 | 789.2959 | -119.98 | 2 | 57.0 | 10.1 | 2 | 418-431 | R.ESESSRSSRRPSGR.S | |

# Detailed Protein Report

## Protein 1762: PREDICTED: disintegrin and metalloproteinase domain-containing protein 32 isoform X2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578839796 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 76.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.2 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 2.8 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MFRLWLLLAG LCGLLASRPG FQNSLLQIVI PEKIQTNTND SSEIEYEQIS YIIPIDEKLY TVHLKQRYFL ADNFMIYLYN

        90        100        110        120        130        140        150        160
QGSMNTYSSD IQTQCYYQGN IEGYPDSMVT LSTCSGLRGI LQFENVSYGI EPLESAVEFQ HVLYKLKNED NDIAIFIDRS

       170        180        190        200        210        220        230        240
LKEQPMDDNI FISEKSEPAV PDLFPLYLEM HIVVDKTLYD YWGSDSMIVT NKVIEIVGLA NSMFTQFKVT IVLSSLELWS

       250        260        270        280        290        300        310        320
DENKISTVGE ADELLQKFLE WKQSYLNLRP HDIAYLLIYM DYPRYLGAVF PGTMCITRYS AGVALQCGPA SCCDFRTCVL

       330        340        350        360        370        380        390        400
KDGAKCYKGL CCKDCQILQS GVECRPKAHP ECDIAENCNG SSPECGPDIT LINGLSCKNN KFICYDGDCH DLDARCESVF

       410        420        430        440        450        460        470        480
GKGSRNAPFA CYEEIQSQSD RFGNCGRDRN NKYVFCGWRN LICGRLVCTY PTRKPFHQEN GDVIYAFVRD SVCITVDYKL

       490        500        510        520        530        540        550        560
PRTVPDPLAV KNGSQCDIGR VCVNRECVES RIIKASAHVC SQQCSGHGVC DSRNKCHCSP GYKPPNCQIR SKGFSIFPEE

       570        580        590        600        610        620        630        640
DMGSIMERAS GKTENTWLLG FLIALPILIV TTAIVLARKQ LKKWFAKEEE FPSSESKSEG STQTYASQSS SEGSTQTYAS

       650        660        670        680        690
QTRSESSSQA DTSKSKSEDS AEAYTSRSKS QDSTQTQSSS N
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2111 | 1 | 682.6273 | 16.60 | 3 | 56.8 | 10.1 | 0 | 515-533 | K.ASAHVCSQQCSGHGVCDSR.N | Carbamidomethyl: 6, 16 |

# Detailed Protein Report

## Protein 1763: CUB domain-containing protein 2 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|72384339 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 48.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.8 |
| | | **Sequence Coverage [%]:** | 2.9 |
| | | **No. of unique Peptides:** | 1 |

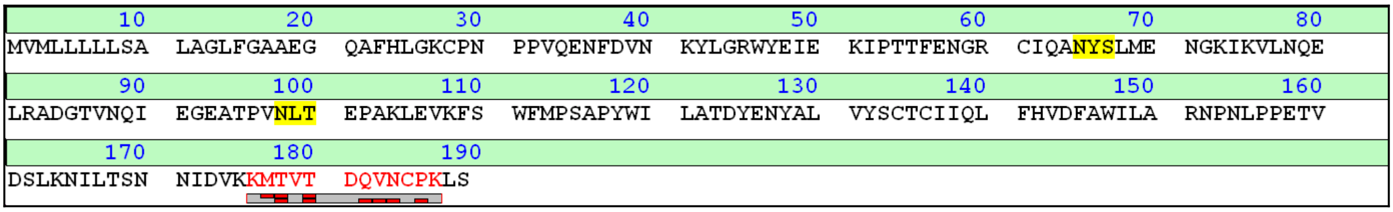
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MLAEWGACLL | LAVALLGPGL | QAQAMEGVKC | GGVLSAPSGN | FSSPNFPRLY | PYNTECSWLI | VVAEGSSVLL | TFHAFDLEYH |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DTCSFDFLEI | YNGASPDKGN | LLGRFCGKVP | PPPFTSSWHV | MSVIFHSDKH | VASHGFSAGY | QKDVCGGVLT | GLSGVLTSPE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YPNNYPNSME | CHWVIRAAGP | AHVKLVFVDF | QVEGNEECTY | DYVAVLGGPG | PTRGHHYCGS | TRPPTLVSLG | HELQVVFKSD |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| FNIGGRGFKA | YYFSGECQEV | YMAMRGNFSS | PQYPSSYPNN | IRCHWTIRLP | PGYQVKVFFL | DLDLEEPNSL | TKTCDFDHLA |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| AFDGASEEAP | LLGNWCGHHL | PPPVTSSHNQ | LLLLLHTDRS | TTRRGFSVAY | IGGQLGCGSG | STEGEGEALQ | PQSLQSPSSI |
| 410 | 420 | 430 | 440 | 450 | | | |
| PPVCPAPPMN | GLLQLLLHWL | HPCPLSGPLR | LDGTAPACFH | YCRASFPSF | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1336 | 1 | 727.1974 | -170.25 | 2 | 46.3 | 10.1 | 0 | 431-443 | R.LDGTAPACFHYCR.A | |

# Detailed Protein Report

## Protein 1764: apolipoprotein D precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4502163 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 21.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.9 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 6.3 |
| | | **No. of unique Peptides:** | 1 |



```
        10         20         30         40         50         60         70         80
MVMLLLLLSA LAGLFGAAEG QAFHLGKCPN PPVQENFDVN KYLGRWYEIE KIPTTFENGR CIQANYSLME NGKIKVLNQE
        90        100        110        120        130        140        150        160
LRADGTVNQI EGEATPVNLT EPAKLEVKFS WFMPSAPYWI LATDYENYAL VYSCTCIIQL FHVDFAWILA RNPNLPPETV
       170        180        190
DSLKNILTSN NIDVKKMTVT DQVNCPKLS
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 368 | 1 | 690.4400 | 149.87 | 2 | 33.2 | 10.1 | 1 | 176-187 | K.KMTVTDQVNCPK.L | Oxidation: 2 |

# Detailed Protein Report

**Protein 1765:** **interleukin-26 precursor [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|8923756 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 19.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.8 |
| | | **Sequence Coverage [%]:** | 12.3 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLVNFILRCG | LLLVTLSLAI | AKHKQSSFTK | SCYPRGTLSQ | AVDALYIKAA | WLKATIPEDR | IKNIRLLKKK | TKKQFMKNCQ |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FQEQLLSFFM | EDVFGQLQLQ | GCKKIRFVED | FHSLRQKLSH | CISCASSARE | MKSITRMKRI | FYRIGNKGIY | KAISELDILL |
| 170 | 180 | | | | | | |
| SWIKKLLESS | Q | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1712 | 1 | 1135.8238 | 104.36 | 2 | 51.7 | 10.1 | 1 | 2-22 | M.LVNFILRCGLLLVTLSLAIAK.H | |

# Detailed Protein Report

## Protein 1766: ATP-dependent RNA helicase DDX18 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|38327634 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 75.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 1.8 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MSHLPMKLLR KKIEKRNLKL RQRNLKFQGA SNLTLSETQN GDVSEETMGS RKVKKSKQKP MNVGLSETQN GGMSQEAVGN

        90        100        110        120        130        140        150        160
IKVTKSPQKS TVLTNGEAAM QSSNSESKKK KKKKRKMVND AEPDTKKAKT ENKGKSEEES AETTKETENN VEKPDNDEDE

       170        180        190        200        210        220        230        240
SEVPSLPLGL TGAFEDTSFA SLCNLVNENT LKAIKEMGFT NMTEIQHKSI RPLLEGRDLL AAAKTGSGKT LAFLIPAVEL

       250        260        270        280        290        300        310        320
IVKLRFMPRN GTGVLILSPT RELAMQTFGV LKELMTHHVH TYGLIMGGSN RSAEAQKLGN GINIIVATPG RLLDHMQNTP

       330        340        350        360        370        380        390        400
GFMYKNLQCL VIDEADRILD VGFEEELKQI IKLLPTRRQT MLFSATQTRK VEDLARISLK KEPLYVGVDD DKANATVDGL

       410        420        430        440        450        460        470        480
EQGYVVCPSE KRFLLLFTFL KKNRKKKLMV FFSSCMSVKY HYELLNYIDL PVLAIHGKQK QNKRTTTFFQ FCNADSGTLL

       490        500        510        520        530        540        550        560
CTDVAARGLD IPEVDWIVQY DPPDDPKEYI HRVGRTARGL NGRGHALLIL RPEELGFLRY LKQSKVPLSE FDFSWSKISD

       570        580        590        600        610        620        630        640
IQSQLEKLIE KNYFLHKSAQ EAYKSYIRAY DSHSLKQIFN VNNLNLPQVA LSFGFKVPPF VDLNVNSNEG KQKKRGGGGG

       650        660        670        680
FGYQKTKKVE KSKIFKHISK KSSDSRQFSH
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1269 | 1 | 697.8175 | -17.16 | 2 | 44.2 | 10.1 | 0 | 428-439 | K.LMVFFSSCMSVK.Y | Oxidation: 9 |

# Detailed Protein Report

## Protein 1767: zinc finger with UFM1-specific peptidase domain protein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|292494919 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 65.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.0 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLSCNICGET | VTSEPDMKAH | LIVHMESEII | CPFCKLSGVN | YDEMCFHIET | AHFEQNTLER | NFERINTVQY | GTSDNKKDNT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LQCGMEVNSS | ILSGCASNHP | KNSAQNLTKD | STLKHEGFYS | ENLTESRKFL | KSREKQSSLT | EIKGSVYETT | YSPPECPFCG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KIEEHSEDME | THVKTKHANL | LDIPLEDCDQ | PLYDCPMCGL | ICTNYHILQE | HVDLHLEENS | FQQGMDRVQC | SGDLQLAHQL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QQEEDRKRRS | EESRQEIEEF | QKLQRQYGLD | NSGGYKQQQL | RNMEIEVNRG | RMPPSEFHRR | KADMMESLAL | GFDDGKTKTS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GIIEALHRYY | QNAATDVRRV | WLSSVVDHFH | SSLGDKGWGC | GYRNFQMLLS | SLLQNDAYND | CLKGMLIPCI | PKIQSMIEDA |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| WKEGFDPQGA | SQLNNRLQGT | KAWIGACEVY | ILLTSLRVKC | HIVDFHKSTG | PLGTHPRLFE | WILNYYSSEG | EGSPKVVCTS |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KPPIYLQHQG | HSRTVIGIEE | KKNRTLCLLI | LDPGCPSREM | QKLLKQDIEA | SSLKQLRKSM | GNLKHKQYQI | LAVEGALSLE |
| 570 | 580 | | | | | | |
| EKLARRQASQ | VFTAEKIP | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1352 | 1 | 500.6107 | -252.46 | 2 | 47.1 | 10.1 | 0 | 292-299 | R.MPPSEFHR.R | |

# Detailed Protein Report

**Protein 1768:** **aftiphilin isoform c [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|50409856 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 99.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 4.3 |
| | | **Sequence Coverage [%]:** | 1.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEPDIIRMYS | SSPPPLDNGA | EDDDDDEFGE | FGGFSEVSPS | GVGFVDFDTP | DYTRPKEEFV | PSNHFMPIHE | FSENVDSLTS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| FKSIKNGNDK | DITAELSAPV | KGQSDVLLST | TSKEIISSEM | LATSIDGMER | PGNLNKVVEQ | RQNVGTLESF | SPGDFRTNMN |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VVHQNKQLES | CNGEKPPCLE | ILTNGFAVLE | TVNPQGTDDL | DNVADSKGRK | PLSTHSTEYN | LDSVPSPAEE | FADFATFSKK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ERIQLEEIEC | AVLNDREALT | IRENNKINRV | NELNSVKEVA | LGRSLDNKGD | TDGEDQVCVS | EISIVTNRGF | SVEKQGLPTL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QQDEFLQSGV | QSKAWSLVDS | ADNSEAIRRE | QCKTEEKLDL | LTSKCAHLCM | DSVKTSDDEV | GSPKEESRKF | TNFQSPNIDP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| TEENDLDDSL | SVKNGDSSND | FVTCNDINED | DFGDFGDFGS | ASGSTPPFVT | GTQDSMSDAT | FEESSEHFPH | FSEPGDDFGE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FGDINAVSCQ | EETILTKSDL | KQTSDNLSEE | CQLARKSSGT | GTEPVAKLKN | GQEGEIGHFD | SVPNIQDDCN | GFQDSDDFAD |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FSSAGPSQVV | DWNAFEDEQK | DSCSWAAFGD | QQATESHHRK | EAWQSHRTDE | NIDTPGTPKT | HSVPSATSKG | AVASGHLQES |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| ATSVQTALLN | RLERIFEACF | PSILVPDAEE | EVTSLKHLLE | TSTLPIKTRE | ALPESGELLD | VWTELQDIHD | AHGLRYQWGG |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| SHSNKKLLSS | LGIDTRNILF | TGNKKQPVIV | PMYAAGLGML | EPTKEPLKPL | SAAEKIASIG | QTATMSPDMN | TCTSDQFQES |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LPPVQFDWSS | SGLTNPLDGV | DPELYELTTS | KLEISTSSLK | VTDAFARLMS | TVEKTSTSTR | KPKREEHLSE | EAIKVIAGLP |
| 890 | 900 | 910 | | | | | |
| DLTFMHAKVL | MFPATLTPST | SSQEKADG | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1684 | 1 | 938.8574 | -120.08 | 2 | 49.4 | 10.1 | 1 | 358-374 | K.LDLLTSKCAHLCMDSVK.T | |

# Detailed Protein Report

**Protein 1769:** **PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X1 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530417278 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 69.6 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 2.2 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MHKEGGWVPE | CGCLCKVEGL | HVQGKCLLGR | MCIQRNCVEP | ARGKNKKGGW | QDIRAEERRQ | VCKGDFARKC | REQKGLSRTR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HFEAMWLKVG | GLLRGTGGQL | GQTVGWPCGA | LGPGPHRWGP | CGGSWAQKFY | QDGPGRGLGE | EDIRRAREAR | PRKTPRPQLS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DRSRERKVPA | SRISRLANFG | GLAVGLGLGV | LAEMAKKSMP | GGRLQSEGGS | GLDSSPFLSE | ANAERIVQTL | CTVRGAALKV |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| GQMLSIQDNS | FISPQLQHIF | ERVRQSADFM | PRWQMLRVLE | EELGRDWQAK | VASLEEVPFA | AASIGQVHQG | LLRDGTEVAV |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KIQYPGIAQS | IQSDVQNLLA | VLKMSAALPA | GLFAEQSLQA | LQQELAWECD | YRREAACAQN | FRQLLANDPF | FRVPAVVKEL |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| CTTRVLGMEL | AGGVPLDQCQ | GLSQDLRNQI | CFQLLTLCLR | ELFEFRFMQT | DPNWANFLYD | ASSHQVTLLD | FGASREFGTE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| FTDHYIEVVK | AAADGDRDCV | LQKSRDLKFL | TGFETKAFSD | AHVEAVMILG | EPFATQGPYD | FGSGETARRI | QDLIPVLLRH |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| RLCPPPEETY | ALHRKLAGAF | LACAHLRAHI | ACRDLFQDTY | HRYWASRQPD | AATAGSLPTK | GDSWVDPS | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1716 | 1 | 802.7734 | -150.85 | 2 | 51.7 | 10.1 | 2 | 31-44 | R.MCIQRNCVEPARGK.N | |

# Detailed Protein Report

## Protein 1770: synaptotagmin-13 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|351542146 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 31.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 8.9 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.9 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578820656 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: synaptotagmin-13 isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| METWNPEKAA | SWNQAPKLHY | CLDYDCQKAE | LFVTRLEAVT | SNHDGGCDCY | VQGSVANRTG | SVEAQTALKK | RQLHTTWEEG |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| LVLPLAEEEL | PTATLTLTLR | TCDRFSRHSV | AGELRLGLDG | TSVPLGAAQW | GELKTSAKEP | SAGAGEVLLS | ISYLPAANRL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LVVLIKAKNL | HSNQSKELLG | KDVSVKVTLK | HQARKLKKKQ | TKRAKHKINP | VWNEMIMFEL | PDDLLQASSV | ELEVLGQDDS |
| 250 | 260 | 270 | 280 | 290 | | | |
| GQSCALGHCS | LGLHTSGSER | SHWEEMLKNP | RRQIAMWHQL | HL | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2945 | 1 | 729.3727 | 81.79 | 2 | 65.6 | 10.1 | 0 | 18-28 | K.LHYCLDYDCQK.A | Carbamidomethyl: 9 |

# Detailed Protein Report

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**Protein 1771:** **type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase isoform 2 [Homo sapiens]**

| | | | |
|---|---|---|---|
| **Accession:** | gi\|154816184 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 29.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.8 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAADGERSPL | LSEPIDGGAG | GNGLVGPGGS | GAGPGGGLTP | SAPPYGAAFP | PFPEGHPAVL | PGEDPPPYSP | LTSPDSGSAP |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| MITCRVCQSL | INVEGKMHQH | VVKCGVCNEA | TPIKNAPPGK | KYVRCPCNCL | LICKVTSQRI | ACPRPYCKRI | INLGPVHPGP |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LSPEPQPMGV | RVICGHCKNT | FLWTEFTDRT | LARCPHCRKV | SSIGRRYPRK | RCICCFLLGL | LLAVTATGLA | FGTWKHARRY |
| 250 | 260 | 270 | 280 | | | | |
| GGIYAAWAFV | ILLAVLCLGR | ALYWACMKVS | HPVQNFS | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2003 | 1 | 621.2942 | -43.69 | 2 | 53.4 | 10.1 | 2 | 190-199 | R.TLARCPHCRK.V | Carbamidomethyl: 8 |

# Detailed Protein Report

## Protein 1772: glutamate receptor 3 isoform 3 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|376319256 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 16.1 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.8 |
| | | **Sequence Coverage [%]:** | 9.7 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MARQKKMGQS VLRAVFFLVL GLLGHSHGGF PNTISIGGLF MRNTVQEHSA FRFAVQLYNT NQNTTEKPFH LNYHVDHLDS
        90        100        110        120        130        140        150
SNSFSVTNAC PAERDYLPWP GSIRENNWTA LPCCKDHGLL HLKCSPGGAR QNWAYCIWGV TGEL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 939 | 1 | 820.2508 | -160.33 | 2 | 41.8 | 10.1 | 0 | 131-144 | R.QNWAYCIWGVTGEL.- | |

# Detailed Protein Report

## Protein 1773: PREDICTED: glutaminase kidney isoform, mitochondrial isoform X5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|578804102 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 72.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.7 |
| | | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MMRLRGSGML | RDLLLRSPAG | VSATLRRAQP | LVTLCRRPRG | GGRPAAGPAA | AARLHPWWGG | GGWPAEPLAR | GLSSSPSEIL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| QELGKGSTHP | QPGVSPPAAP | AAPGPKDGPG | ETDAFGNSEG | KELVASGENK | IKQGLLPSLE | DLLFYTIAEG | QEKIPVHKFI |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| TALKSTGLRT | SDPRLKECMD | MLRLTLQTTS | DGVMLDKDLF | KKCVQSNIVL | LTQAFRRKFV | IPDFMSFTSH | IDELYESAKK |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| QSGGKVADYI | PQLAKFSPDL | WGVSVCTVDG | QRHSTGDTKV | PFCLQSCVKP | LKYAIAVNDL | GTEYVHRYVG | KEPSGLRFNK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LFLNEDDKPH | NPMVNAGAIV | VTSLIKQGVN | NAEKFDYVMQ | FLNKMAGNEY | VGFSNATFQS | ERESGDRNFA | IGYYLKEKKC |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| FPEGTDMVGI | LDFYFQLCSI | EVTCESASVM | AATLANGGFC | PITGERVLSP | EAVRNTLSLM | HSCGMYDFSG | QFAFHVGLPA |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| KSGVAGGILL | VVPNVMGMMC | WSPPLDKMGN | SVKGIHFCHD | LVSLCNFHNY | DNLRHFAKKL | DPRREGGDQR | VKSVINLLFA |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| AYTGDVSALR | RFALSAMDME | QRDYDSRTAL | HVAAAEGGIT | LPWMKHCTLD | TMMYLKFSKN | TKSSTHLKEI | LTTGRKIKPS |
| 650 | 660 | 670 | | | | | |
| IRILMDCCNG | LKSQDLNHLP | I | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1071 | 1 | 555.1310 | -234.61 | 2 | 43.5 | 10.1 | 0 | 643-652 | R.ILMDCCNGLK.S | |

# Detailed Protein Report

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## Protein 1774: beta-defensin 125 preproprotein [Homo sapiens]

**Accession:** gi|76563936
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 10.1
**MW [kDa]:** 17.5
**pI:** 5.2
**Sequence Coverage [%]:** 6.4
**No. of unique Peptides:** 1

## Quantitation

***WUP:QUP*** **Median:** 0.85 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MNILMLTFII CGLLTRVTKG SFEPQKCWKN NVGHCRRRCL DTERYILLCR NKLSCCISII SHEYTRRPAF PVIHLEDITL
        90        100        110        120        130        140        150        160
DYSDVDSFTG SPVSMLNDLI TFDTTKFGET MTPETNTPET TMPPSEATTP ETTMPPSETA TSETMPPPSQ TALTHN
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 973 | 1 | 637.3502 | 98.48 | 2 | 42.2 | 10.1 | 1 | 27-36 | K.CWKNNVGHCR.R | Carbamidomethyl: 1 | WUP:QUP 0.85 |

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# Detailed Protein Report

## Protein 1775: PREDICTED: solute carrier family 35 member F3 isoform X1 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|530366073 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| | | **Sequence Coverage [%]:** | 2.6 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MKKHSARVAP | LSACNSPVLT | LTKVEGEERP | RDSPGPAEAQ | APAGVEAGGR | ASRRCWTCSR | AQLKKIFWGV | AVVLCVCSSW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| AGSTQLAKLT | FRKFDAPFTL | TWFATNWNFL | FFPLYYVGHV | CKSTEKQSVK | QRYRECCRFF | GDNGLTLKVF | FTKAAPFGVL |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| WTLTNYLYLH | AIKKINTTDV | SVLFCCNKAF | VFLLSWIVLR | DRFMGVRIVA | AILAIAGIVM | MTYADGFHSH | SVIGIALVVA |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| SASMSALYKV | LFKLLLGSAK | FGEAALFLSI | LGVFNILFIT | CIPIILYFTK | VEYWSSFDDI | PWGNLCGFSV | LLLTFNIVLN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| FGIAVTYPTL | MSLGIVLSIP | VNAVIDHYTS | QIVFNGVRVI | AIIIIGLGFL | LLLLPEEWDV | WLIKLLTRLK | VRKKEEPAEG |
| 410 | 420 | 430 | | | | | |
| AADLSSGPQS | KNRRARPSFA | R | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1522 | 1 | 676.3418 | 3.04 | 2 | 49.2 | 10.1 | 2 | 54-64 | R.RCWTCSRAQLK.K | |

# Detailed Protein Report

**Protein 1776:** **transmembrane and immunoglobulin domain-containing protein 2 isoform 2 precursor [Homo sapiens]**

**Accession:** gi|281306840
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 10.1
**MW [kDa]:** 30.3
**pI:** 10.3
**Sequence Coverage [%]:** 6.8
**No. of unique Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MGSPGMVLGL | LVQIWALQEA | SSLSVQQGPN | LLQVRQGSQA | TLVCQVDQAT | AWERLRVKWT | KDGAILCQPY | ITNGSLSLGV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| CGPQGRLSWQ | APSHLTLQLD | PVSLNHSGAY | VCWAAVEIPE | LEEAEGNITR | LFVDPDDPTQ | NRNRIASFPG | FLFVLLGVGS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| MGVAAIVWGA | WFWGRRSCQQ | RDSGNAFYSN | VLYRPRGAPK | KSEDCSGEGK | DQRGQSIYST | SFPQPAPRQP | HLASRPCPSP |
| 250 | 260 | 270 | 280 | | | | |
| RPCPSPRPGH | PVSMVRVSPR | PSPTQQPRPK | GFPKVGEE | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1886 | 1 | 1045.8876 | -107.32 | 2 | 51.9 | 10.1 | 0 | 36-54 | R.QGSQATLVCQVDQATAWER.L | |

# Detailed Protein Report

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## Protein 1777: ethylmalonyl-CoA decarboxylase isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|50593027 | **Score:** | 10.1 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 15.9 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.0 |
| | | **Sequence Coverage [%]:** | 17.2 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|530383866 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: ethylmalonyl-CoA decarboxylase isoform X4 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAKSLLKTAS | LSGRTKLLHQ | TGLSLYSTSH | GFYEEEVKKT | LQQFPGGSID | LQKEDNGIGI | LTLNNPSRMN | AFSGVMMLQL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | |
| LEKVIELENW | TEGKGLIVRG | AKNTFSSGSD | LNAVKSLGTP | ETSFNKCCAG | SRLGIGWRSR | IYYSM | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1572 | 1 | 724.6476 | 27.56 | 4 | 49.9 | 10.1 | 2 | 15-39 | R.TKLLHQTGLSLYSTSHGFYEEEVKK.T | |

# Detailed Protein Report

## Protein 1778: carboxypeptidase B preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|54607080 | **Score:** | 10.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 47.3 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 2.4 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530373933 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: carboxypeptidase B isoform X1 [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLALLVLVTV | ALASAHHGGE | HFEGEKVFRV | NVEDENHINI | IRELASTTQI | DFWKPDSVTQ | IKPHSTVDFR | VKAEDTVTVE |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NVLKQNELQY | KVLISNLRNV | VEAQFDSRVR | ATGHSYEKYN | KWETIEAWTQ | QVATENPALI | SRSVIGTTFE | GRAIYLLKVG |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| KAGQNKPAIF | MDCGFHAREW | ISPAFCQWFV | REAVRTYGRE | IQVTELLDKL | DFYVLPVLNI | DGYIYTWTKS | RFWRKTRSTH |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TGSSCIGTDP | NRNFDAGWCE | IGASRNPCDE | TYCGPAAESE | KETKALADFI | RNKLSSIKAY | LTIHSYSQMM | IYPYSYAYKL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| GENNAELNAL | AKATVKELAS | LHGTKYTYGP | GATTIYPAAG | GSDDWAYDQG | IRYSFTFELR | DTGRYGFLLP | ESQIRATCEE |
| 410 | 420 | | | | | | |
| TFLAIKYVAS | YVLEHLY | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1781 | 1 | 582.7206 | -111.97 | 2 | 52.6 | 10.0 | 0 | 99-108 | R.NVVEAQFDSR.V | |

# Detailed Protein Report

## Protein 1779: A disintegrin and metalloproteinase with thrombospondin motifs 2 isoform 2 preproprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|11038659 | **Score:** | 10.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 61.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 6.2 |
| | | **Sequence Coverage [%]:** | 3.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDPPAGAARR | LLCPALLLLL | LLLPPPLLPP | PPPPANARLA | AAADPPGGPL | GHGAERILAV | PVRTDAQGRL | VSHVVSAATS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| RAGVRARRAA | PVRTPSFPGG | NEEEPGSHLF | YNVTVFGRDL | HLRLRPNARL | VAPGATMEWQ | GEKGTTRVEP | LLGSCLYVGD |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| VAGLAEASSV | ALSNCDGLAG | LIRMEEEEFF | IEPLEKGLAA | QEAEQGRVHV | VYRRPPTSPP | LGGPQALDTG | ASLDSLDSLS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| RALGVLEEHA | NSSRRRARRH | AADDDYNIEV | LLGVDDSVVQ | FHGKEHVQKY | LLTLMNIVNE | IYHDESLGAH | INVVLVRIIL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| LSYGKSMSLI | EIGNPSQSLE | NVCRWAYLQQ | KPDTGHDEYH | DHAIFLTRQD | FGPSGMQGYA | PVTGMCHPVR | SCTLNHEDGF |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| SSAFVVAHET | GHVLGMEHDG | QGNRCGDEVR | LGSIMAPLVQ | AAFHRFHWSR | CSQQELSRYL | HSYDCLLDDP | FAHDWPALPQ |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LPGLHYSMNE | QCRFDFGLGY | MMCTAFRTFD | PCKQLWCSHP | DNPYFCKTKK | GPPLDGTMCA | PGKFRPGAVA | HACYPSTLGG |
| 570 | | | | | | | |
| QGRWIA | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1523 | 1 | 682.3537 | 16.13 | 3 | 49.2 | 10.0 | 0 | 544-563 | K.FRPGAVAHACYPSTLGGQGR.W | |

## Protein 1780: sodium channel protein type 3 subunit alpha isoform 3 [Homo sapiens]

**Accession:** gi|126362955
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 10.0
**MW [kDa]:** 221.3
**pI:** 5.5
**Sequence Coverage [%]:** 1.0
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAQALLVPPG | PESFRLFTRE | SLAAIEKRAA | EEKAKKPKKE | QDNDDENKPK | PNSDLEAGKN | LPFIYGDIPP | EMVSEPLEDL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DPYYINKKTF | IVMNKGKAIF | RFSATSALYI | LTPLNPVRKI | AIKILVHSLF | SMLIMCTILT | NCVFMTLSNP | PDWTKNVEYT |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| FTGIYTFESL | IKILARGFCL | EDFTFLRDPW | NWLDFSVIVM | AYVTEFVSLG | NVSALRTFRV | LRALKTISVI | PGLKTIVGAL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| IQSVKKLSDV | MILTVFCLSV | FALIGLQLFM | GNLRNKCLQW | PPSDSAFETN | TTSYFNGTMD | SNGTFVNVTM | STFNWKDYIG |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| DDSHFYVLDG | QKDPLLCGNG | SDAGQCPEGY | ICVKAGRNPN | YGYTSFDTFS | WAFLSLFRLM | TQDYWENLYQ | LTLRAAGKTY |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MIFFVLVIFL | GSFYLVNLIL | AVVAMAYEEQ | NQATLEEAEQ | KEAEFQQMLE | QLKKQQEEAQ | AVAAASAASR | DFSGIGGLGE |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| LLESSSEASK | LSSKSAKEWR | NRRKKRRQRE | HLEGNNKGER | DSFPKSESED | SVKRSSFLFS | MDGNRLTSDK | KFCSPHQSLL |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| SIRGSLFSPR | RNSKTSIFSF | RGRAKDVGSE | NDFADDEHST | FEDSESRRDS | LFVPHRHGER | RNSNGTTTET | EVRKRRLSSY |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| QISMEMLEDS | SGRQRAVSIA | SILTNTMEEL | EESRQKCPPC | WYRFANVFLI | WDCCDAWLKV | KHLVNLIVMD | PFVDLAITIC |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| IVLNTLFMAM | EHYPMTEQFS | SVLTVGNLVF | TGIFTAEMVL | KIIAMDPYYY | FQEGWNIFDG | IIVSLSLMEL | GLSNVEGLSV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LRSFRLLRVF | KLAKSWPTLN | MLIKIIGNSV | GALGNLTLVL | AIIVFIFAVV | GMQLFGKSYK | ECVCKINDDC | TLPRWHMNDF |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| FHSFLIVFRV | LCGEWIETMW | DCMEVAGQTM | CLIVFMLVMV | IGNLVVLNLF | LALLLSSFSS | DNLAATDDDN | EMNNLQIAVG |
| 970 | 980 | 990 | 1000 | 1010 | 1020 | 1030 | 1040 |
| RMQKGIDYVK | NKMRECFQKA | FFRKPKVIEI | HEGNKIDSCM | SNNTGIEISK | ELNYLRDGNG | TTSGVGTGSS | VEKYVIDEND |
| 1050 | 1060 | 1070 | 1080 | 1090 | 1100 | 1110 | 1120 |
| YMSFINNPSL | TVTVPIAVGE | SDFENLNTEE | FSSESELEES | KEKLNATSSS | EGSTVDVVLP | REGEQAETEP | EEDLKPEACF |
| 1130 | 1140 | 1150 | 1160 | 1170 | 1180 | 1190 | 1200 |
| TEGCIKKFPF | CQVSTEEGKG | KIWWNLRKTC | YSIVEHNWFE | TFIVFMILLS | SGALAFEDIY | IEQRKTIKTM | LEYADKVFTY |
| 1210 | 1220 | 1230 | 1240 | 1250 | 1260 | 1270 | 1280 |
| IFILEMLLKW | VAYGFQTYFT | NAWCWLDFLI | VDVSLVSLVA | NALGYSELGA | IKSLRTLRAL | RPLRALSRFE | GMRVVVNALV |
| 1290 | 1300 | 1310 | 1320 | 1330 | 1340 | 1350 | 1360 |
| GAIPSIMNVL | LVCLIFWLIF | SIMGVNLFAG | KFYHCVNMTT | GNMFDISDVN | NLSDCQALGK | QARWKNVKVN | FDNVGAGYLA |
| 1370 | 1380 | 1390 | 1400 | 1410 | 1420 | 1430 | 1440 |
| LLQVATFKGW | MDIMYAAVDS | RDVKLQPVYE | ENLYMYLYFV | IFIIFGSFFT | LNLFIGVIID | NFNQQKKKFG | GQDIFMTEEQ |
| 1450 | 1460 | 1470 | 1480 | 1490 | 1500 | 1510 | 1520 |
| KKYYNAMKKL | GSKKPQKPIP | RPANKFQGMV | FDFVTRQVFD | ISIMILICLN | MVTMMVETDD | QGKYMTLVLS | RINLVFIVLF |
| 1530 | 1540 | 1550 | 1560 | 1570 | 1580 | 1590 | 1600 |
| TGEFVLKLVS | LRHYYFTIGW | NIFDFVVVIL | SIVGMFLAEM | IEKYFVSPTL | FRVIRLARIG | RILRLIKGAK | GIRTLLFALM |
| 1610 | 1620 | 1630 | 1640 | 1650 | 1660 | 1670 | 1680 |
| MSLPALFNIG | LLLFLVMFIY | AIFGMSNFAY | VKKEAGIDDM | FNFETFGNSM | ICLFQITTSA | GWDGLLAPIL | NSAPPDCDPD |
| 1690 | 1700 | 1710 | 1720 | 1730 | 1740 | 1750 | 1760 |
| TIHPGSSVKG | DCGNPSVGIF | FFVSYIIISF | LVVVNMYIAV | ILENFSVATE | ESAEPLSEDD | FEMFYEVWEK | FDPDATQFIE |
| 1770 | 1780 | 1790 | 1800 | 1810 | 1820 | 1830 | 1840 |
| FSKLSDFAAA | LDPPLLIAKP | NKVQLIAMDL | PMVSGDRIHC | LDILFAFTKR | VLGESGEMDA | LRIQMEDRFM | ASNPSKVSYE |
| 1850 | 1860 | 1870 | 1880 | 1890 | 1900 | 1910 | 1920 |
| PITTTLKRKQ | EEVSAAIIQR | NFRCYLLKQR | LKNISSNYNK | EAIKGRIDLP | IKQDMIIDKL | NGNSTPEKTD | GSSSTTSPPS |
| 1930 | 1940 | 1950 | 1960 | | | | |
| YDSVTKPDKE | KFEKDKPEKE | SKGKEVRENQ | K | | | | |

# Detailed Protein Report

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2533 | 1 | 1045.0400 | -2.11 | 2 | 61.6 | 10.0 | 1 | 1082-1101 | K.EKLNATSSSEGSTVDVVLPR.E | |

# Detailed Protein Report

## Protein 1781: retinoic acid receptor responder protein 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|149588791 | **Score:** | 10.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 18.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 7.9 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MASPHQEPKP GDLIEIFRLG YEHWALYIGD GYVIHLAPPS EYPGAGSSSV FSVLSNSAEV KRERLEDVVG GCCYRVNNSL
        90        100        110        120        130        140        150        160
DHEYQPRPVE VIISSAKEMV GQKMKYSIVS RNCEHFVTQL RYGKSRCKQV EKAKVEVGVA TALGILVVAG CSFAIRRYQK
       170
KATA
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2835 | 1 | 826.4327 | 34.55 | 2 | 65.9 | 10.0 | 1 | 112-124 | R.NCEHFVTQLRYGK.S | Carbamidomethyl: 2 |

# Detailed Protein Report

## Protein 1782: PREDICTED: binder of sperm protein homolog 1 isoform X2 [Homo sapiens]

**Accession:** gi|578833811
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Carbamidomethyl

**Score:** 10.0
**MW [kDa]:** 15.3
**pI:** 8.9
**Sequence Coverage [%]:** 13.1
**No. of unique Peptides:** 1

```
        10         20         30         40         50         60         70         80
MARHMGLLLV WVCLIRGVVG GVVGAVFNVL EEDELSSTVD GECVFPFHYK NGTYYDCIKS KARHKWCSLN KTYEGYWKFC
        90        100        110        120        130        140
SAEDFANCVF PFWYRRLIYW ECTDDGEAFG KKWCSLTKNF NKDRIWKYCE
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2210 | 1 | 1044.3865 | -105.22 | 2 | 57.5 | 10.0 | 2 | 96-112 | R.RLIYWECTDDGEAFGKK.W | Carbamidomethyl: 7 |

# Detailed Protein Report

## Protein 1783: kell blood group glycoprotein [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4557691 | **Score:** | 10.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 82.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.1 |
| | | **Sequence Coverage [%]:** | 1.4 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MEGGDQSEEE | PRERSQAGGM | GTLWSQESTP | EERLPVEGSR | PWAVARRVLT | AILILGLLLC | FSVLLFYNFQ | NCGPRPCETS |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VCLDLRDHYL | ASGNTSVAPC | TDFFSFACGR | AKETNNSFQE | LATKNKNRLR | RILEVQNSWH | PGSGEEKAFQ | FYNSCMDTLA |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| IEAAGTGPLR | QVIEELGGWR | ISGKWTSLNF | NRTLRLLMSQ | YGHFPFFRAY | LGPHPASPHT | PVIQIDQPEF | DVPLKQDQEQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| KIYAQIFREY | LTYLNQLGTL | LGGDPSKVQE | HSSLSISITS | RLFQFLRPLE | QRRAQGKLFQ | MVTIDQLKEM | APAIDWLSCL |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| QATFTPMSLS | PSQSLVVHDV | EYLKNMSQLV | EEMLLKQRDF | LQSHMILGLV | VTLSPALDSQ | FQEARRKLSQ | KLRELTEQPP |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| MPARPRWMKC | VEETGTFFEP | TLAALFVREA | FGPSTRSAAM | KLFTAIRDAL | ITRLRNLPWM | NEETQNMAQD | KVAQLQVEMG |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| ASEWALKPEL | ARQEYNDIQL | GSSFLQSVLS | CVRSLRARIV | QSFLQPHPQH | RWKVSPWDVN | AYYSVSDHVV | VFPAGLLQPP |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| FFHPGYPRAV | NFGAAGSIMA | HELLHIFYQL | LLPGGCLACD | NHALQEAHLC | LKRHYAAFPL | PSRTSFNDSL | TFLENAADVG |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| GLAIALQAYS | KRLLRHHGET | VLPSLDLSPQ | QIFFRSYAQV | MCRKPSPQDS | HDTHSPPHLR | VHGPLSSTPA | FARYFRCARG |
| 730 | 740 | | | | | | |
| ALLNPSSRCQ | LW | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 941 | 1 | 593.7466 | -114.09 | 2 | 41.3 | 10.0 | 0 | 171-180 | R.QVIEELGGWR.I | |

# Detailed Protein Report

## Protein 1784: properdin precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|4505737 | **Score:** | 10.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 51.2 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.1 |
| | | **Sequence Coverage [%]:** | 3.0 |
| | | **No. of unique Peptides:** | 1 |

## Quantitation

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ***QU:MU*** | **Median:** | 0.76 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |
| ***WUP:QUP*** | **Median:** | 1.52 | **CV:** | 0.00 % | **No. of Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|223671861 | refseq_human (refseq_human_20140103.fasta) | properdin precursor [Homo sapiens] |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MITEGAQAPR | LLLPPLLLLL | TLPATGSDPV | LCFTQYEESS | GKCKGLLGGG | VSVEDCCLNT | AFAYQKRSGG | LCQPCRSPRW |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| SLWSTWAPCS | VTCSEGSQLR | YRRCVGWNGQ | CSGKVAPGTL | EWQLQACEDQ | QCCPEMGGWS | GWGPWEPCSV | TCSKGTRTRR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| RACNHPAPKC | GGHCPGQAQE | SEACDTQQVC | PTHGAWATWG | PWTPCSASCH | GGPHEPKETR | SRKCSAPEPS | QKPPGKPCPG |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| LAYEQRRCTG | LPPCPVAGGW | GPWGPVSPCP | VTCGLGQTME | QRTCNHPVPQ | HGGPFCAGDA | TRTHICNTAV | PCPVDGEWDS |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| WGEWSPCIRR | NMKSISCQEI | PGQQSRGRTC | RGRKFDGHRC | AGQQQDIRHC | YSIQHCPLKG | SWSEWSTWGL | CMPPCGPNPT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | |
| RARQRLCTPL | LPKYPPTVSM | VEGQGEKNVT | FWGRPLPRCE | ELQGQKLVVE | EKRPCLHVPA | CKDPEEEEL | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification | Ratios |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1362 | 1 | 816.4149 | -5.18 | 2 | 45.4 | 10.0 | 1 | 439-452 | R.CEELQGQKLVVEEK.R | | QU:MU 0.76<br>WUP:QUP 1.52 |

# Detailed Protein Report

## Protein 1785: zona pellucida sperm-binding protein 3 isoform 2 [Homo sapiens]

**Accession:** gi|38327649
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30
**Modification(s):** Oxidation

**Score:** 10.0
**MW [kDa]:** 41.2
**pI:** 5.7
**Sequence Coverage [%]:** 7.2
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MVMVSKDLFG | TGKLIRAADL | TLGPEACEPL | VSMDTEDVVR | FEVGLHECGN | SMQVTDDALV | YSTFLLHDPR | PVGNLSIVRT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| NRAEIPIECR | YPRQGNVSSQ | AILPTWLPFR | TTVFSEEKLT | FSLRLMEENW | NAEKRSPTFH | LGDAAHLQAE | IHTGSHVPLR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| LFVDHCVATP | TPDQNASPYH | TIVDFHGCLV | DGLTDASSAF | KVPRPGPDTL | QFTVDVFHFA | NDSRNMIYIT | CHLKVTLAEQ |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| DPDELNKACS | FSKPSNSWFP | VEGSADICQC | CNKGDCGTPS | HSRRQPHVMS | QWSRSASRNR | RHVTEEADVT | VGPLIFLDRR |
| 330 | 340 | 350 | 360 | 370 | 380 | | |
| GDHEVEQWAL | PSDTSVVLLG | VGLAVVVSLT | LTAVILVLTR | RCRTASHPVS | ASE | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1418 | 1 | 977.1197 | -40.88 | 3 | 47.9 | 10.0 | 1 | 14-40 | K.LIRAADLTLGPEACEPLVSMDTEDVVR.F | Oxidation: 20 |

# Detailed Protein Report

## Protein 1786: prohibitin-2 isoform 3 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|390608669 | **Score:** | 10.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 29.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.4 |
| | | **Sequence Coverage [%]:** | 6.9 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MAQNLKDLAG | RLPAGPRGMG | TALKLLLGAG | AVAYGVRESV | FTVEGGHRAI | FFNRIGGVQQ | DTILAEGLHF | RIPWFQYPII |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| YDIRARPRKI | SSPTGSKDLQ | MVNISLRVLS | RPNAQELPSM | YQRLGLDYEE | RVLPSIVNEV | LKSVVAKFNA | SQLITQRAQV |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| SLLIRRELTE | RAKDFSLILD | DVAITELSFS | REYTAAVEAK | QVALSKNPGY | IKLRKIRAAQ | NISKTIATSQ | NRIYLTADNL |
| 250 | 260 | 270 | | | | | |
| VLNLQDESFT | RGSDSLIKGK | K | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2763 | 1 | 973.5204 | -2.06 | 2 | 63.1 | 10.0 | 1 | 90-107 | K.ISSPTGSKDLQMVNISLR.V | |

# Detailed Protein Report

## Protein 1787: calsyntenin-3 precursor [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|42475534 | **Score:** | 10.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 106.0 |
| **Database Date:** | 2015-11-30 | **pI:** | 5.1 |
| **Modification(s):** | Carbamidomethyl | **Sequence Coverage [%]:** | 1.5 |
| | | **No. of unique Peptides:** | 1 |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MTLLLLPLLL | ASLLASCSCN | KANKHKPWIE | AEYQGIVMEN | DNTVLLNPPL | FALDKDAPLR | YAGEICGFRL | HGSGVPFEAV |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| ILDKATGEGL | IRAKEPVDCE | AQKEHTFTIQ | AYDCGEGPDG | ANTKKSHKAT | VHVRVNDVNE | FAPVFVERLY | RAAVTEGKLY |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| DRILRVEAID | GDCSPQYSQI | CYYEILTPNT | PFLIDNDGNI | ENTEKLQYSG | ERLYKFTVTA | YDCGKKRAAD | DAEVEIQVKP |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TCKPSWQGWN | KRIEYAPGAG | SLALFPGIRL | ETCDEPLWNI | QATIELQTSH | VAKGCDRDNY | SERALRKLCG | AATGEVDLLP |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| MPGPNANWTA | GLSVHYSQDS | SLIYWFNGTQ | AVQVPLGGPS | GLGSGPQDSL | SDHFTLSFWM | KHGVTPNKGK | KEEETIVCNT |
| 410 | 420 | 430 | 440 | 450 | 460 | 470 | 480 |
| VQNEDGFSHY | SLTVHGCRIA | FLYWPLLESA | RPVKFLWKLE | QVCDDEWHHY | ALNLEFPTVT | LYTDGISFDP | ALIHDNGLIH |
| 490 | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| PPRREPALMI | GACWTEEKNK | EKEKGDNSTD | TTQGDPLSIH | HYFHGYLAGF | SVRSGRLESR | EVIECLYACR | EGLDYRDFES |
| 570 | 580 | 590 | 600 | 610 | 620 | 630 | 640 |
| LGKGMKVHVN | PSQSLLTLEG | DDVETFNHAL | QHVAYMNTLR | FATPGVRPLR | LTTAVKCFSE | ESCVSIPEVE | GYVVVLQPDA |
| 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| PQILLSGTAH | FARPAVDFEG | TNGVPLFPDL | QITCSISHQV | EAKKDESWQG | TVTDTRMSDE | IVHNLDGCEI | SLVGDDLDPE |
| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |
| RESLLLDTTS | LQQRGLELTN | TSAYLTIAGV | ESITVYEEIL | RQARYRLRHG | AALYTRKFRL | SCSEMNGRYS | SNEFIVEVNV |
| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 880 |
| LHSMNRVAHP | SHVLSSQQFL | HRGHQPPPEM | AGHSLASSHR | NSMIPSAATL | IIVVCVGFLV | LMVVLGLVRI | HSLHRRVSGA |
| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 960 |
| GGPPGASSDP | KDPDLFWDDS | ALTIIVNPME | SYQNRQSCVT | GAVGGQQEDE | DSSDSEVADS | PSSDERRIIE | TPPHRY |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2025 | 1 | 899.3750 | -66.39 | 2 | 53.7 | 10.0 | 1 | 537-550 | R.LESREVIECLYACR.E | Carbamidomethyl: 9, 13 |

# Detailed Protein Report

## Protein 1788: NADH dehydrogenase [ubiquinone] 1 subunit C2, isoform 2 isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|323276586 | **Score:** | 10.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 13.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.3 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 22.8 |
| | | **No. of unique Peptides:** | 1 |

```
        10         20         30         40         50         60         70         80
MIARRNPEPL RFLPDEARSL PPPKLTDPRL LYIGFLGYCS GLIDNLIRRR PIATAGLHRQ LLYITAFFFA GYYLVKREDY
        90        100        110        120
LYAVRDREMF GYMKLHPEDF PEEDVYCCGA ERRG
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 1844 | 1 | 1056.3547 | -90.54 | 3 | 53.4 | 10.0 | 2 | 88-113 | R.EMFGYMKLHPEDFPEEDVYCCGAERR.G | Oxidation: 2 |

# Detailed Protein Report

## Protein 1789: putative polypeptide N-acetylgalactosaminyltransferase-like protein 5 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|281485547 | **Score:** | 10.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 51.4 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.6 |
| **Modification(s):** | Oxidation | **Sequence Coverage [%]:** | 3.6 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| **Accession** | **Name** | **Description** |
|---|---|---|
| gi\|578813950 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: putative polypeptide N-acetylgalactosaminyltransferase-like protein 5 isoform X2 [Homo sapiens] |
| gi\|578813948 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: putative polypeptide N-acetylgalactosaminyltransferase-like protein 5 isoform X1 [Homo sapiens] |

```
        10         20         30         40         50         60         70         80
MRNAIIQGLF YGSLTFGIWT ALLFIYLHHN HVSSWQKKSQ EPLSAWSPGK KVHQQIIYGS EQIPKPHVIV KRTDEDKAKS
        90        100        110        120        130        140        150        160
MLGTDFNHTN PELHKELLKY GFNVIISRSL GIEREVPDTR SKMCLQKHYP ARLPTASIVI CFYNEECNAL FQTMSSVTNL
       170        180        190        200        210        220        230        240
TPHYFLEEII LVDDMSKVDD LKEKLDYHLE TFRGKVKIIR NKKREGLIRA RLIGASHASG DVLVFLDSHC EVNRVWLEPL
       250        260        270        280        290        300        310        320
LHAIAKDPKM VVCPLIDVID DRTLEYKPSP LVRGTFDWNL QFKWDNVFSY EMDGPEGSTK PIRSPAMSGG IFAIRRHYFN
       330        340        350        360        370        380        390        400
EIGQYDKDMD FWGRENLELS LRIWMCGGQL FIIPCSRVGH ISKKQTGKPS TIISAMTHNY LRLVHVWLDE YKEQFFLRKP
       410        420        430        440        450
GLKYVTYGNI RERVELRKRL GCKSFQWYLD NVFPELEASV NSL
```

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2735 | 1 | 928.9724 | 42.01 | 2 | 62.7 | 10.0 | 0 | 80-95 | K.SMLGTDFNHTNPELHK.E | Oxidation: 2 |

# Detailed Protein Report

## Protein 1790: protein salvador homolog 1 [Homo sapiens]

**Accession:** gi|11141889
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 10.0
**MW [kDa]:** 44.6
**pI:** 9.5
**Sequence Coverage [%]:** 2.1
**No. of unique Peptides:** 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MLSRKKTKNE | VSKPAEVQGK | YVKKETSPLL | RNLMPSFIRH | GPTIPRRTDI | CLPDSSPNAF | STSGDVVSRN | QSFLRTPIQR |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| TPHEIMRRES | NRLSAPSYLA | RSLADVPREY | GSSQSFVTEV | SFAVENGDSG | SRYYYSDNFF | DGQRKRPLGD | RAHEDYRYYE |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| YNHDLFQRMP | QNQGRHASGI | GRVAATSLGN | LTNHGSEDLP | LPPGWSVDWT | MRGRKYYIDH | NTNTTHWSHP | LEREGLPPGW |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| ERVESSEFGT | YYVDHTNKKA | QYRHPCAPSV | PRYDQPPPVT | YQPQQTERNQ | SLLVPANPYH | TAEIPDWLQV | YARAPVKYDH |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | |
| ILKWELFQLA | DLDTYQGMLK | LLFMKELEQI | VKMYEAYRQA | LLTELENRKQ | RQQWYAQQHG | KNF | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 504 | 1 | 472.1588 | -261.22 | 2 | 34.7 | 10.0 | 1 | 24-31 | K.KETSPLLR.N | |

# Detailed Protein Report

## Protein 1791: uncharacterized protein C7orf72 [Homo sapiens]

**Accession:** gi|332634960
**Database:** refseq_human(refseq_human_20140103.fasta)
**Database Date:** 2015-11-30

**Score:** 10.0
**MW [kDa]:** 49.6
**pI:** 9.3
**Sequence Coverage [%]:** 3.0
**No. of unique Peptides:** 1

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MDVEIQDTPG | KISISKRSIL | SGTVENIDYP | HYCDLLRKMN | MPFVKGLENR | HNYGRFEKKC | NPAFLKFHPY | PPSVLPDYHL |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| HDPYPPPYGP | HYPLFPLRDD | VTLGDSCSGF | MSPGGDADLN | PGIGRTIPTL | VDFSDVKPQH | RVPRPDTGFQ | TTIKRQKILS |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| EELQQNRRWN | SREVPDISIR | ARLGGWTSPL | KVTPLQPHHE | GRSLSHIFTF | DEEATCTDEG | EPLVQTNKKC | NAKDSFYKSS |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| TQKAYEDVPW | DKMLPPKLVP | EETTLEKAAD | PISQCFTLKR | YKGVPAITQM | VGELWDRFQT | RSFLAPVKPI | NFVSSSSRSK |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| YIPLYTGHVQ | STNADDVDNP | LGDIASLAKQ | RYSKPLYTNT | SRAANIPGYT | GKVHFTATHP | ANSNIPSTTP | SPDSELHRVF |
| 410 | 420 | 430 | 440 | | | | |
| QKEMAVDLFR | HQAPLSRLVT | TVRPYNPFNK | KDKETIDY | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 19 | 1 | 814.3556 | -99.68 | 2 | 29.9 | 10.0 | 2 | 168-180 | R.RWNSREVPDISIR.A | |

# Detailed Protein Report

## Protein 1792: casein kinase I isoform delta isoform 2 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|20544145 | **Score:** | 10.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.8 |
| **Database Date:** | 2015-11-30 | **pI:** | 10.2 |
| | | **Sequence Coverage [%]:** | 2.7 |
| | | **No. of unique Peptides:** | 1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| MELRVGNRYR | LGRKIGSGSF | GDIYLGTDIA | AGEEVAIKLE | CVKTKHPQLH | IESKIYKMMQ | GGVGIPTIRW | CGAEGDYNVM |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| VMELLGPSLE | DLFNFCSRKF | SLKTVLLLAD | QMISRIEYIH | SKNFIHRDVK | PDNFLMGLGK | KGNLVYIIDF | GLAKKYRDAR |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| THQHIPYREN | KNLTGTARYA | SINTHLGIEQ | SRRDDLESLG | YVLMYFNLGS | LPWQGLKAAT | KRQKYERISE | KKMSTPIEVL |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| CKGYPSEFAT | YLNFCRSLRF | DDKPDYSYLR | QLFRNLFHRQ | GFSYDYVFDW | NMLKFGASRA | ADDAERERRD | REERLRHSRN |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| PATRGLPSTA | SGRLRGTQEV | APPTPLTPTS | HTANTSPRPV | SGMERERKVS | MRLHRGAPVN | ISSSDLTGRQ | DTSRMSTSQN |
| 410 | | | | | | | |
| SIPFEHHGK | | | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 2016 | 1 | 709.7814 | -72.59 | 2 | 55.6 | 10.0 | 0 | 260-270 | R.FDDKPDYSYLR.Q | |

# Detailed Protein Report

## Protein 1793: BTB/POZ domain-containing protein KCTD18 [Homo sapiens]

| | | | |
|---|---|---|---|
| **Accession:** | gi\|45387953 | **Score:** | 10.0 |
| **Database:** | refseq_human(refseq_human_20140103.fasta) | **MW [kDa]:** | 46.7 |
| **Database Date:** | 2015-11-30 | **pI:** | 9.9 |
| | | **Sequence Coverage [%]:** | 2.1 |
| | | **No. of unique Peptides:** | 1 |

**Alias proteins:**

| Accession | Name | Description |
|---|---|---|
| gi\|530369815 | refseq_human (refseq_human_20140103.fasta) | PREDICTED: BTB/POZ domain-containing protein KCTD18 isoform X1 [Homo sapiens] |

| 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|---|---|---|---|---|---|---|---|
| MEGHKAEEEV | LDVLRLNVGG | CIYTARRESL | CRFKDSMLAS | MFSGRFPLKT | DESGACVIDR | DGRLFKYLLD | YLHGEVQIPT |
| 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| DEQTRIALQE | EADYFGIPYP | YSLSDHLANE | METYSLRSNI | ELKKALTDFC | DSYGLVCNKP | TVWVLHYLNT | SGASCESRII |
| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 240 |
| GVYATKTDGT | DAIEKQLGGR | IHSKGIFKRE | AGNNVQYIWS | YYSVAELKKM | MDAFDAWEGK | GVSYWRVPHE | LIECWTLEER |
| 250 | 260 | 270 | 280 | 290 | 300 | 310 | 320 |
| PLLGSLRHMA | PIRKRRLITF | NEADESVNYK | TGPKPVRFLG | PSTSTQIKVK | NSASVTVSPA | SAIQTSAGAT | ANRFQSGSRR |
| 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| KAAQRSAPSR | ATALVGTGAP | GHPQASPGAA | SAENGGTHLP | PAKVLLSDKK | PTPQRVIKLK | RTPLCATAPC | LPSPTATRQA |
| 410 | 420 | 430 | | | | | |
| NSLKPLPGEA | ARALGVRTEN | GKNKGN | | | | | |

| Cmpd. | No. of Cmpds. | m/z meas. | Δ m/z [ppm] | z | Rt [min] | Score | P | Range | Sequence | Modification |
|---|---|---|---|---|---|---|---|---|---|---|
| 588 | 1 | 472.1621 | -200.95 | 2 | 36.9 | 10.0 | 1 | 322-330 | K.AAQRSAPSR.A | |