Detailed Protein Report

Project Info

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

Note:

Sample Info & Protocols

Name: ID-Q **Date:** Dec 8, 2015

Fraction:

Volume: **Concentration:**

Note:

Buffer: **Organism:**

Search Result Info

Search Result	Location	Search Engine	Database
ZT_human_PE_2015-12-08 22:06:22	/teeth-151208/ID-Q/"Combined MS/MS spectra"	Mascot	refseq_human

Protein 1: serum albumin preproprotein [Homo sapiens]

Accession: gi|4502027

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl, Oxidation

Score: 1095.1

MW [kDa]: 69.3

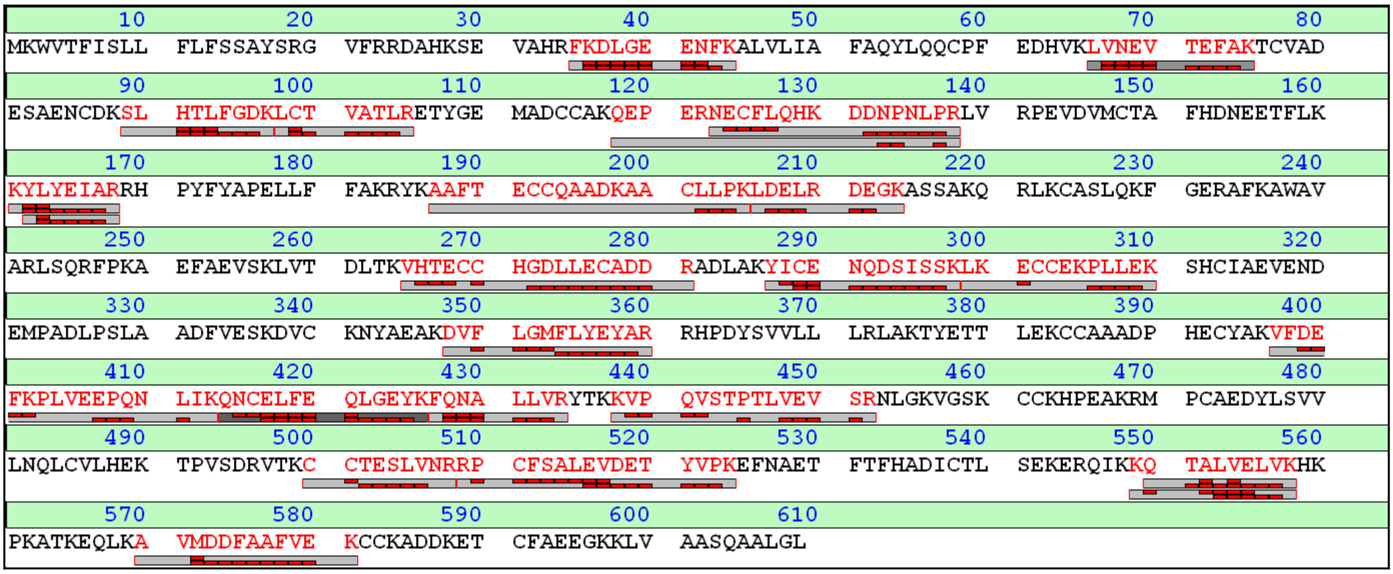
pI: 5.9

Sequence Coverage [%]: 40.7

No. of unique Peptides: 23

Quantitation

QD:QU **Median:** 0.89 **CV:** 66.04 % **No. of Peptides:** 12



```
        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
298	12	613.8004	-9.46	2	32.4	71.1	1	35-44	R.FKDLGEENFK.A		QD:QU 0.75
673	12	575.2020	-189.65	2	37.0	62.9	0	66-75	K.LVNEVTEFAK.T		
529	10	509.2667	-10.16	2	36.6	49.5	0	89-97	K.SLHTLFGDK.L		
299	2	467.2609	-4.27	2	33.7	52.0	0	98-105	K.LCTVATLR.E	Carbamidomethyl: 2	
265	2	879.3978	-18.24	3	33.3	25.7	2	118-138	K.QEPERNECFLQHKDDNPNLPR.L	Carbamidomethyl: 8	QD:QU 1.75
279	1	666.3028	-17.84	3	33.5	40.0	1	123-138	R.NECFLQHKDDNPNLPR.L	Carbamidomethyl: 3	QD:QU 0.64
350	2	528.2959	-3.73	2	34.4	39.6	1	161-168	K.KYLYEIAR.R		QD:QU 2.39
532	5	464.1198	-281.27	2	35.3	30.2	0	162-168	K.YLYEIAR.R		QD:QU 1.13
1590	1	977.4188	-47.42	2	50.1	11.8	1	187-205	K.AAFTECCQAADKAACLLPK.L		
21	2	537.7799	9.21	2	29.9	42.9	1	206-214	K.LDELRDEGK.A		QD:QU 0.46

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
235	3	696.2743	-13.94	3	31.7	57.7	0	265-281	K.VHTECCHGDLLECADDR.A	Carbamidomethyl: 5, 6, 13	QD:QU	0.34
45	2	722.3225	-3.01	2	30.4	77.4	0	287-298	K.YICENQDSISSK.L	Carbamidomethyl: 3	QD:QU	0.70
145	1	516.2727	4.30	3	31.8	19.6	1	299-310	K.LKECCEKPLLEK.S	Carbamidomethyl: 4, 5	QD:QU	1.32
2284	1	820.3190	-92.46	2	59.0	33.1	0	348-360	K.DVFLGMFLYEYAR.R	Oxidation: 6		
2041	21	1022.9463	-102.62	2	55.9	37.1	0	397-413	K.VFDEFKPLVEEPQNLIK.Q			
1582	24	829.3539	-31.44	2	48.3	77.6	0	414-426	K.QNCELFEQLGEYK.F	Carbamidomethyl: 3	QD:QU	0.49
742	9	480.7783	-13.77	2	39.3	53.1	0	427-434	K.FQNALLVR.Y			
890	4	820.4506	-26.72	2	41.2	33.9	1	438-452	K.KVPQVSTPTLVEVSR.N			
77	2	569.7395	-23.11	2	30.9	44.1	0	500-508	K.CCTESLVNR.R	Carbamidomethyl: 1, 2		
1753	4	637.6399	-13.90	3	50.5	67.0	0	509-524	R.RPCFSALEVDETYVPK.E	Carbamidomethyl: 3		
628	1	564.7514	-179.84	2	37.9	25.5	1	549-558	K.KQTALVELVK.H		QD:QU	2.11
1207	5	500.6668	-276.87	2	43.6	45.1	0	550-558	K.QTALVELVK.H		QD:QU	0.77
2104	47	671.7654	-82.73	2	56.7	98.0	0	570-581	K.AVMDDFAAFVEK.C			

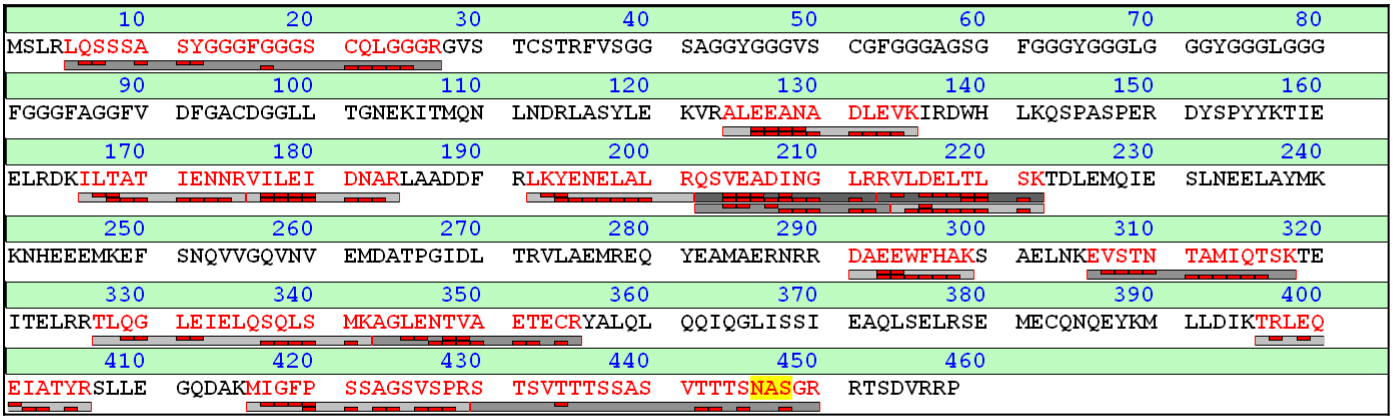
Detailed Protein Report

Protein 2: keratin, type I cytoskeletal 13 isoform a [Homo sapiens]

Accession:	gi|131412225	**Score:**	635.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.5
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	39.7
		No. of unique Peptides:	16

Quantitation

QD:QU **Median:** 0.54 **CV:** 50.97 % **No. of Peptides:** 9



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        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. LQSSSASYGGGFGGGSCQLGGGG	Carbamidomethyl: 17		
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			
667	3	521.7769	-40.77	2	36.9	58.8	0	176-184	R.VILEIDNAR.L		QD:QU	0.46
518	2	624.8405	-16.71	2	36.5	46.5	1	192-201	R.LKYENELALR.Q		QD:QU	0.57
471	2	601.1764	-225.82	2	34.5	42.6	0	202-212	R.QSVEADINGLR.R		QD:QU	0.37
322	1	679.3584	-6.47	2	34.0	14.0	1	202-213	R.QSVEADINGLRR.V		QD:QU	0.24
686	1	587.3207	-42.26	2	37.1	41.5	1	213-222	R.RVLDELTLSK.T			
727	3	509.2783	-32.74	2	39.1	53.0	0	214-222	R.VLDELTLSK.T			
434	3	566.7484	-14.34	2	35.4	31.5	0	291-299	R.DAEEWFHAK.S		QD:QU	0.49
173	1	705.3260	-34.92	2	30.9	13.5	0	306-318	K.EVSTNTAMIQTSK.T		QD:QU	0.73
2903	1	909.4716	-17.49	2	65.4	28.3	0	327-342	R.TLQGLEIELQSQLSMK.A			
178	2	725.3355	-0.10	2	32.2	38.5	0	343-355	K.AGLENTVAETECR.Y	Carbamidomethyl: 12	QD:QU	0.54
370	2	690.3450	-32.66	2	34.6	18.0	1	396-406	K.TRLEQEIATYR.S		QD:QU	0.55
942	3	696.8484	-3.18	2	41.8	28.0	0	416-429	K.MIGFPSSAGSVSPR.S			
28	2	1001.9840	4.13	2	30.1	29.0	0	430-450	R.STSVTTTSSASVTTTSNASGR. R		QD:QU	1.59

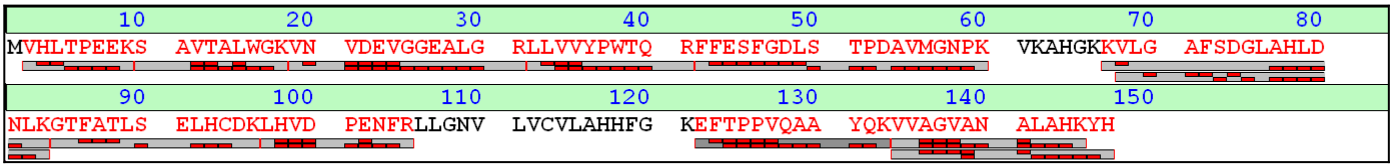
Detailed Protein Report

Protein 3: hemoglobin subunit beta [Homo sapiens]

Accession:	gi|4504349	**Score:**	578.7
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

QD:QU **Median:** 2.34 **CV:** 188.92 % **No. of Peptides:** 4



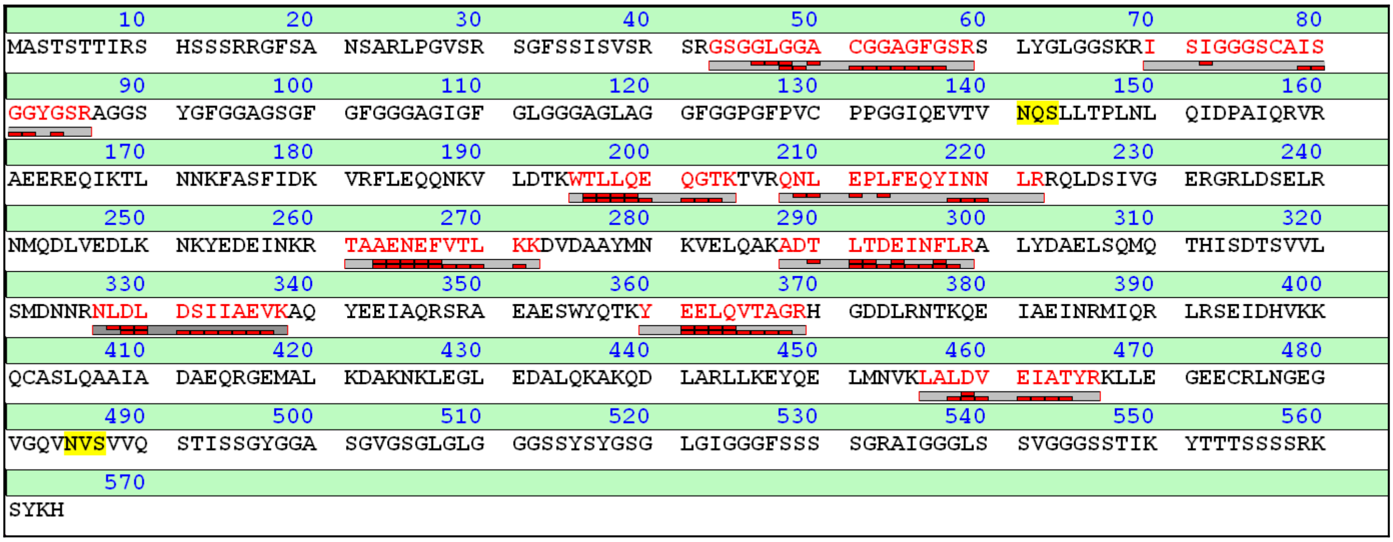
Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
72	1	476.7493	-19.46	2	30.8	23.9	0	2-9	M.VHLTPEEK.S		
849	5	466.6498	-243.95	2	40.7	45.6	0	10-18	K.SAVTALWGK.V		
496	6	657.8496	20.65	2	36.2	81.3	0	19-31	K.VNVDEVGGEALGR.L		QD:QU 0.35
2380	9	637.8625	-6.20	2	58.5	48.9	0	32-41	R.LLVVYPWTQR.F		
2107	11	1029.8517	-122.16	2	56.7	64.9	0	42-60	R.FFESFGDLSTPDAVMGNPK.V		
2794	3	599.9758	-40.56	3	66.1	37.1	1	67-83	K.KVLGAFSDGLAHLDNLK.G		
2791	13	835.4449	-4.99	2	66.1	74.0	0	68-83	K.VLGAFSDGLAHLDNLK.G		
680	1	739.8715	27.96	2	38.5	19.5	0	84-96	K.GTFATLSELHCDK.L	Carbamidomethyl: 11	QD:QU 6.23
340	6	563.7849	-1.35	2	34.3	45.2	0	97-105	K.LHVDPENFR.L		QD:QU 1.81
532	3	689.8492	-6.46	2	36.6	44.0	0	122-133	K.EFTPPVQAAYQK.V		QD:QU 7.65
307	5	575.3418	2.06	2	33.8	76.7	0	134-145	K.VVAGVANALAHK.Y		
430	1	725.3587	-59.21	2	35.4	17.7	1	134-147	K.VVAGVANALAHKYH.-		

Protein 4: keratin, type II cytoskeletal 6C [Homo sapiens]

Accession:	gi|155969697	**Score:**	429.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.0
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	20.6
		No. of unique Peptides:	9

Quantitation

QD:QU **Median:** 1.26 **CV:** 81.26 % **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	2	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	QD:QU 2.01
910	6	602.3097	-20.53	2	39.9	44.2	0	195-204	K.WTLLQEQGTK.T		QD:QU 1.07
2105	4	945.9050	-88.89	2	56.7	16.4	0	208-222	R.QNLEPLFEQYINNLR.R		
328	2	675.8743	11.03	2	34.1	67.2	1	261-272	R.TAAENEFVTLKK.D		QD:QU 1.16
1975	5	704.2826	-108.99	2	55.1	74.7	0	288-299	K.ADTLTDEINFLR.A		
2868	16	665.3564	-15.34	2	65.0	82.6	0	327-338	R.NLDLDSIIAEVK.A		QD:QU 3.28
231	4	583.2587	-63.96	2	31.6	63.1	0	360-369	K.YEELQVTAGR.H		QD:QU 0.39
2191	9	632.2117	-219.91	2	56.0	48.4	0	456-466	K.LALDVEIATYR.K		

Detailed Protein Report

Protein 5: hemoglobin subunit delta [Homo sapiens]

Accession:	gi|4504351	**Score:**	366.3
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

```
         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
467	1	628.8213	-19.13	2	35.8	42.8	0	19-31	K.VNVDAVGGEALGR.L	

Detailed Protein Report

Protein 6: keratin, type I cytoskeletal 15 [Homo sapiens]

Accession:	gi|24430190	**Score:**	329.4
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

QD:QU **Median:** 0.73 **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		
1065	2	515.1664	-260.45	2	41.8	44.4	0	215-223	R.VLDELTLAR.T		QD:QU 0.73

Detailed Protein Report

Protein 7: hemoglobin subunit alpha [Homo sapiens]

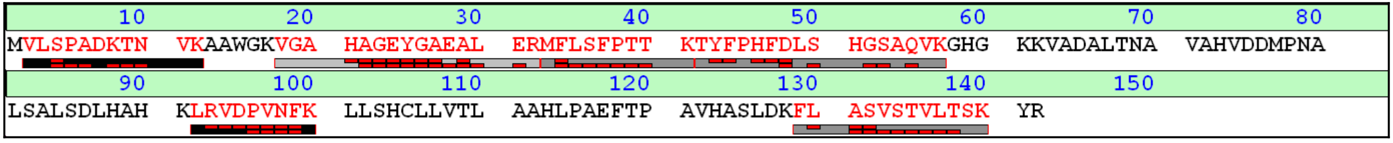
Accession:	gi|4504345	**Score:**	326.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.2
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	50.7
		No. of unique Peptides:	6

Quantitation

QD:QU **Median:** 2.08 **CV:** 25.63 % **No. of Peptides:** 2

Alias proteins:

Accession	Name	Description
gi|4504347	refseq_human (refseq_human_20140103.fasta)	hemoglobin subunit alpha [Homo sapiens]



```
          10         20         30         40         50         60         70         80
MVLSPADKTN VKAAWGKVGA HAGEYGAEAL ERMFLSFPTT KTYFPHFDLS HGSAQVKGHG KKVADALTNA VAHVDDMPNA
          90        100        110        120        130        140        150
LSALSDLHAH KLRVDPVNFK LLSHCLLVTL AAHLPAEFTP AVHASLDKFL ASVSTVLTSK YR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
68	1	586.3403	4.44	2	30.8	24.9	1	2-12	M.VLSPADKTNVK.A		
184	6	765.3829	15.83	2	32.3	76.4	0	18-32	K.VGAHAGEYGAEALER.M		QD:QU 2.68
1886	25	536.2096	-132.70	2	53.9	49.3	0	33-41	R.MFLSFPTTK.T		
1189	11	917.4299	-21.44	2	45.0	51.1	0	42-57	K.TYFPHFDLSHGSAQVK.G		QD:QU 1.62
592	4	544.3095	-13.04	2	37.4	51.7	1	92-100	K.LRVDPVNFK.L		
1619	7	626.8457	-24.38	2	50.5	73.2	0	129-140	K.FLASVSTVLTSK.Y		

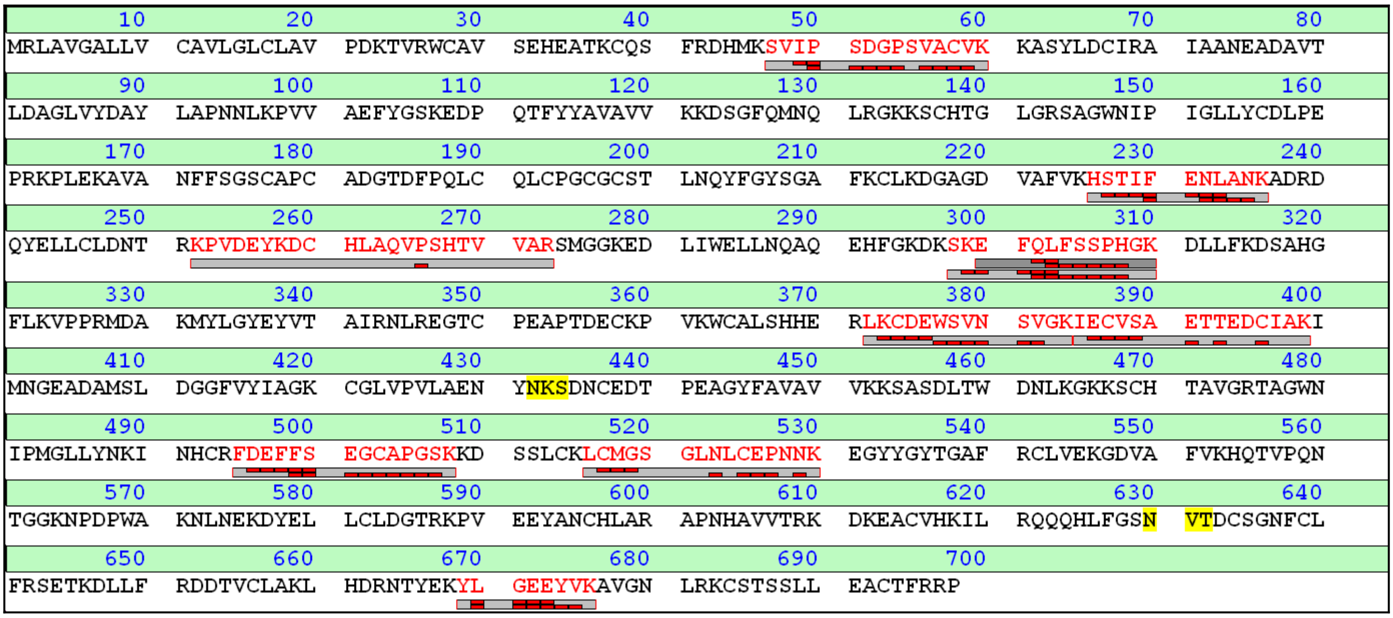
Detailed Protein Report

Protein 8: **serotransferrin precursor [Homo sapiens]**

Accession:	gi|4557871	**Score:**	315.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.0
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	17.9
		No. of unique Peptides:	10

Quantitation

QD:QU **Median:** 0.72 **CV:** 41.99 % **No. of Peptides:** 7



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        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 RQQHLFGSNV TDCSGNFCLF
       650        660        670        680        690        700
RSETKDLLFR DDTVCLAKLH DRNTYEKYLG EEYVKAVGNL RKCSTSSLLE ACTFRRP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
610	3	708.3500	-19.16	2	36.2	66.2	0	47-60	K.SVIPSDGPSVACVK.K	Carbamidomethyl: 12	QD:QU 0.99
583	1	637.3237	-10.51	2	37.3	31.2	0	226-236	K.HSTIFENLANK.A		QD:QU 0.51
302	1	850.4388	3.54	3	33.8	10.5	1	252-273	R. KPVDEYKDCHLAQVPSHTVVAR. S	Carbamidomethyl: 9	
498	1	746.3968	18.25	2	36.2	42.7	1	298-310	K.SKEFQLFSSPHGK.D		
1032	3	638.7248	-148.43	2	41.4	30.2	0	300-310	K.EFQLFSSPHGK.D		
303	1	761.3763	5.77	2	33.8	37.9	1	372-384	R.LKCDEWSVNSVGK.I	Carbamidomethyl: 3	QD:QU 0.82
255	1	863.4074	23.48	2	33.2	14.5	0	385-399	K.IECVSAETTEDCIAK.I	Carbamidomethyl: 3, 12	QD:QU 0.87
954	1	789.3334	1.18	2	40.4	38.9	0	495-508	R.FDEFFSEGCAPGSK.K	Carbamidomethyl: 9	QD:QU 0.80
840	1	853.8816	-5.85	2	40.5	22.5	0	516-530	K.LCMGSGLNLCEPNNK.E	Carbamidomethyl: 2, 10	QD:QU 1.11
330	1	500.6281	-249.21	2	32.8	21.2	0	669-676	K.YLGEEYVK.A		QD:QU 0.32

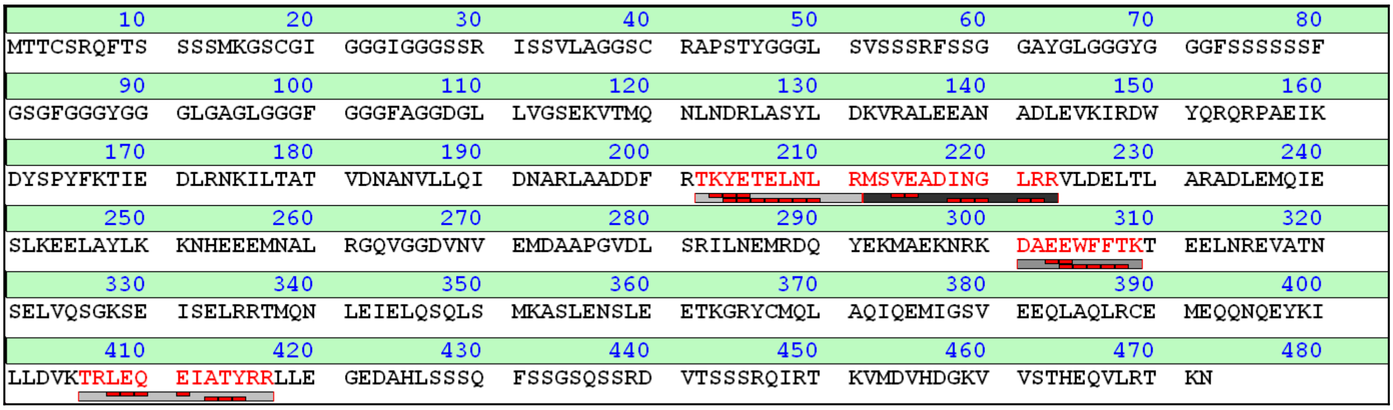
Detailed Protein Report

Protein 9: **keratin, type I cytoskeletal 14 [Homo sapiens]**

Accession:	gi|15431310	**Score:**	291.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.6
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	15.5
		No. of unique Peptides:	4

Quantitation

QD:QU **Median:** 1.31 **CV:** 22.43 % **No. of 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	Ratios
282	1	633.8578	31.13	2	33.5	20.5	1	202-211	R.TKYETELNLR.M		QD:QU 1.09
639	1	680.8203	-49.04	2	36.6	15.5	1	212-223	R.MSVEADINGLRR.V		QD:QU 1.79
1899	3	586.6929	-125.55	2	52.2	33.2	0	301-309	K.DAEEWFFTK.T		QD:QU 1.17
246	1	512.5147	-194.60	3	33.1	22.6	2	406-417	K.TRLEQEIATYRR.L		

Detailed Protein Report

Protein 10: keratin, type II cytoskeletal 5 [Homo sapiens]

Accession:	gi|119395754	**Score:**	260.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	62.3
Database Date:	2015-11-30	**pI:**	8.6
		Sequence Coverage [%]:	12.7
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.60 **CV:** 66.96 % **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
804	1	572.1668	-261.37	2	38.5	48.3	0	432-441	K.LAELEEALQK.A		QD:QU 0.33
477	2	720.3474	-17.32	2	34.6	20.1	0	560-576	R.GLGVGFGSGGGSSSSVK.F		QD:QU 1.10

Detailed Protein Report

Protein 11: apolipoprotein A-I preproprotein [Homo sapiens]

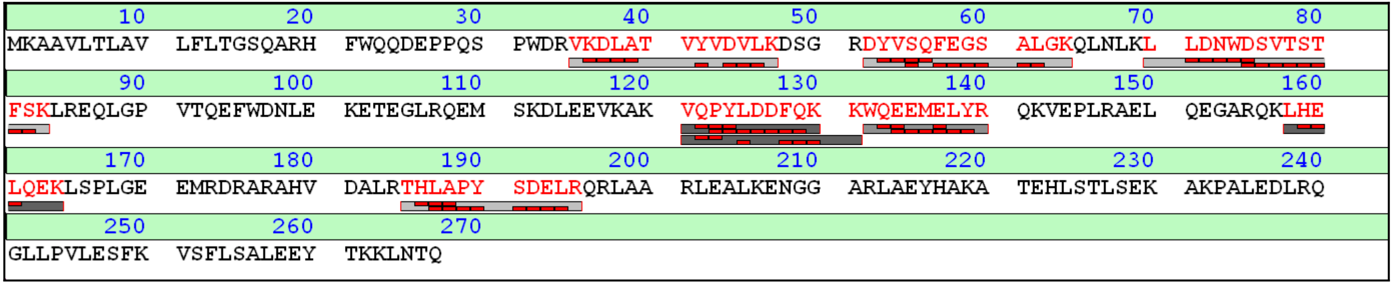
Accession:	gi|4557321	**Score:**	250.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.8
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	29.2
		No. of unique Peptides:	8

Quantitation

QD:QU **Median:** 0.62 **CV:** 31.48 % **No. of Peptides:** 4

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
2106	1	731.8566	-99.42	2	56.7	19.8	1	35-47	R.VKDLATVYVDVLK.D		
916	1	700.9155	110.19	2	41.5	24.5	0	52-64	R.DYVSQFEGSALGK.Q		
1831	7	806.7884	-133.73	2	53.2	64.1	0	70-83	K.LLDNWDSVTSTFSK.L		
681	1	626.6736	-224.11	2	37.1	28.6	0	121-130	K.VQPYLDDFQK.K		QD:QU 0.47
451	2	690.8634	2.76	2	35.6	14.6	1	121-131	K.VQPYLDDFQKK.W		QD:QU 1.04
860	2	642.2972	11.37	2	39.2	28.3	0	132-140	K.WQEEMELYR.Q		QD:QU 0.58
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		QD:QU 0.53

Detailed Protein Report

Protein 12: **keratin, type II cytoskeletal 75 [Homo sapiens]**

Accession:	gi|153791158	**Score:**	247.1
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
566	2	678.9555	96.02	2	35.7	53.0	1	413-424	K.LVDLEEALQKAK.Q	

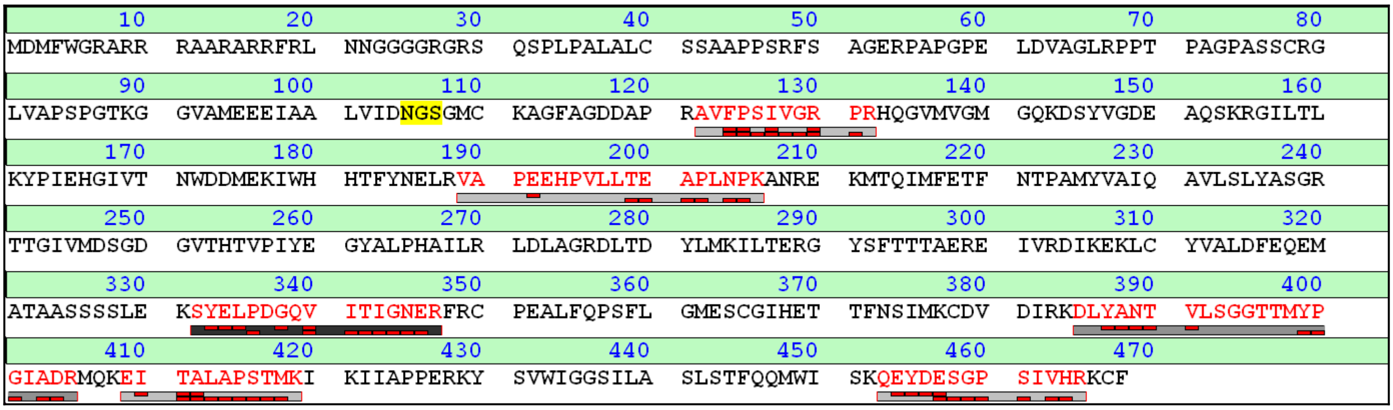
Detailed Protein Report

Protein 13: PREDICTED: actin, cytoplasmic 2 isoform X1 [Homo sapiens]

Accession:	gi|578831328	**Score:**	225.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.2
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	19.2
		No. of unique Peptides:	6

Quantitation

QD:QU **Median:** 0.99 **CV:** 65.74 % **No. of Peptides:** 3



```
        10         20         30         40         50         60         70         80
MDMFWGRARR RAARARRFRL NNGGGGRGRS QSPLPALALC SSAAPPSRFS AGERPAPGPE LDVAGLRPPT PAGPASSCRG
        90        100        110        120        130        140        150        160
LVAPSPGTKG GVAMEEEIAA LVIDNGSGMC KAGFAGDDAP RAVFPSIVGR PRHQGVMVGM GQKDSYVGDE AQSKRGILTL
       170        180        190        200        210        220        230        240
KYPIEHGIVT NWDDMEKIWH HTFYNELRVA PEEHPVLLTE APLNPKANRE KMTQIMFETF NTPAMYVAIQ AVLSLYASGR
       250        260        270        280        290        300        310        320
TTGIVMDSGD GVTHTVPIYE GYALPHAILR LDLAGRDLTD YLMKILTERG YSFTTTAERE IVRDIKEKLC YVALDFEQEM
       330        340        350        360        370        380        390        400
ATAASSSSLE KSYELPDGQV ITIGNERFRC PEALFQPSFL GMESCGIHET TFNSIMKCDV DIRKDLYANT VLSGGTTMYP
       410        420        430        440        450        460        470
GIADRMQKEI TALAPSTMKI KIIAPPERKY SVWIGGSILA SLSTFQQMWI SKQEYDESGP SIVHRKCF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
659	5	599.7070	-249.11	2	36.8	51.4	0	122-132	R.AVFPSIVGRPR.H		
2136	4	651.9448	-125.01	3	55.3	28.9	0	189-206	R.VAPEEHPVLLTEAPLNPK.A		QD:QU 0.93
1678	5	895.8924	-63.80	2	49.5	48.9	0	332-347	K.SYELPDGQVITIGNER.F		
2043	1	1107.8969	-127.87	2	54.1	33.7	0	385-405	K.DLYANTVLSGGTTMYPGIADR.M		
563	1	581.2929	-34.36	2	37.0	51.0	0	409-419	K.EITALAPSTMK.I		QD:QU 2.13
139	1	758.8664	15.04	2	31.7	11.9	0	453-465	K.QEYDESGPSIVHR.K		QD:QU 0.49

Detailed Protein Report

Protein 14:	**titin isoform IC [Homo sapiens]**		
Accession:	gi|388998877	**Score:**	217.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	3992.1
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	14

Quantitation

QD:QU	**Median:**	0.44	**CV:**	19.37 %	**No. of Peptides:**	2	

```
        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
1676	1	839.3937	-10.73	2	49.5	10.3	2	1417-1431	R.MSPARMSPARMSPAR.M	Oxidation: 6, 11	
2713	1	698.3756	114.21	2	62.8	14.9	0	8326-8337	K.VDHSDVGEYSCK.A	Carbamidomethyl: 11	
967	1	752.8772	-83.84	2	40.6	12.6	2	10852-10864	K.VPEEPKKPVPEKK.V		
2926	1	713.8984	-28.68	2	65.7	11.1	1	11452-11464	K.VEPPPPPKVPEIK.K		
1106	9	555.2011	-153.95	2	43.9	16.9	0	13889-13899	K.GTAIFACDIAK.D		
1925	1	661.3041	-146.74	2	54.4	13.5	1	15198-15209	R.AAAHLTVIEKLR.I		QD:QU 0.53
707	3	481.1631	-198.64	2	38.8	13.1	0	15703-15710	K.TWVLATDR.A		QD:QU 0.36
1842	1	740.3191	-71.84	2	53.4	15.5	2	16189-16201	K.GYIVERCPRGSDK.W		
2499	1	813.3822	-3.46	2	61.8	12.9	0	19641-19653	R.VPDLLEGCQYEFR.V	Carbamidomethyl: 8	
2869	1	710.3695	-29.92	2	65.0	10.9	0	30145-30156	R.IGHNVHLELPYK.G		
69	1	731.7932	-168.95	2	30.8	10.2	1	31168-31179	K.QLTFTVERLVEK.T		
560	1	607.8375	45.47	2	37.0	10.1	1	32279-32289	R.AQNEKGVSEPR.E		
2686	1	937.4503	-21.14	2	62.5	12.9	0	33057-33072	K.QFTIGGLLEATEYEFR.V		
658	1	677.6643	-16.40	3	38.2	11.8	2	33663-33680	K.DAGFYVVCAKNRFGIDQK.T		

Detailed Protein Report

Protein 15: lactotransferrin isoform 1 precursor [Homo sapiens]

Accession:	gi|54607120	**Score:**	206.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.1
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	12.7
		No. of unique Peptides:	7

Quantitation

QD:QU **Median:** 1.20 **CV:** 40.11 % **No. of Peptides:** 3

```
        10         20         30         40         50         60         70         80
MKLVFLVLLF LGALGLCLAG RRRSVQWCAV SQPEATKCFQ WQRNMRKVRG PPVSCIKRDS PIQCIQAIAE NRADAVTLDG
        90        100        110        120        130        140        150        160
GFIYEAGLAP YKLRPVAAEV YGTERQPRTH YYAVAVVKKG GSFQLNELQG LKSCHTGLRR TAGWNVPIGT LRPFLNWTGP
       170        180        190        200        210        220        230        240
PEPIEAAVAR FFSASCVPGA DKGQFPNLCR LCAGTGENKC AFSSQEPYFS YSGAFKCLRD GAGDVAFIRE STVFEDLSDE
       250        260        270        280        290        300        310        320
AERDEYELLC PDNTRKPVDK FKDCHLARVP SHAVVARSVN GKEDAIWNLL RQAQEKFGKD KSPKFQLFGS PSGQKDLLFK
       330        340        350        360        370        380        390        400
DSAIGFSRVP PRIDSGLYLG SGYFTAIQNL RKSEEEVAAR RARVVWCAVG EQELRKCNQW SGLSEGSVTC SSASTTEDCI
       410        420        430        440        450        460        470        480
ALVLKGEADA MSLDGGYVYT AGKCGLVPVL AENYKSQQSS DPDPNCVDRP VEGYLAVAVV RRSDTSLTWN SVKGKKSCHT
       490        500        510        520        530        540        550        560
AVDRTAGWNI PMGLLFNQTG SCKFDEYFSQ SCAPGSDPRS NLCALCIGDE QGENKCVPNS NERYYGYTGA FRCLAENAGD
       570        580        590        600        610        620        630        640
VAFVKDVTVL QNTDGNNNEA WAKDLKLADF ALLCLDGKRK PVTEARSCHL AMAPNHAVVS RMDKVERLKQ VLLHQQAKFG
       650        660        670        680        690        700        710        720
RNGSDCPDKF CLFQSETKNL LFNDNTECLA RLHGKTTYEK YLGPQYVAGI TNLKKCSTSP LLEACEFLRK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1629	2	695.8567	-18.94	2	48.9	36.9	0	120-132	K.GGSFQLNELQGLK.S		
739	1	787.3768	-43.94	2	39.2	13.3	1	364-376	R.VVWCAVGEQELRK.C	Carbamidomethyl: 4	
1575	3	681.8469	-16.13	2	49.9	23.1	0	424-435	K.CGLVPVLAENYK.S	Carbamidomethyl: 1	
458	1	619.2938	-20.74	2	35.7	45.8	0	463-473	R.SDTSLTWNSVK.G		QD:QU 1.81
593	1	904.3991	-2.21	2	37.4	38.9	0	520-535	R.SNLCALCIGDEQGENK.C	Carbamidomethyl: 4, 7	QD:QU 1.33
2950	4	668.3368	-23.49	2	66.0	27.5	0	587-598	K.LADFALLCLDGK.R	Carbamidomethyl: 8	
1229	1	790.3991	23.83	2	45.5	20.9	0	659-671	K.NLLFNDNTECLAR.L	Carbamidomethyl: 10	QD:QU 0.71

Detailed Protein Report

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

Accession:	gi|47132620	**Score:**	201.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.4
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	5.5
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 1.22 **CV:** 0.00 % **No. of 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	Ratios
412	1	738.3807	-21.14	2	35.1	70.4	0	198-209	R.FLEQQNQVLQTK.W		QD:QU 1.22

Detailed Protein Report

Protein 17: actin, aortic smooth muscle [Homo sapiens]

Accession:	gi|4501883	**Score:**	199.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.0
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	23.3
		No. of unique Peptides:	3

Quantitation

QD:QU **Median:** 0.25 **CV:** 0.00 % **No. of Peptides:** 1

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	Ratios
2365	1	1015.4376	26.15	2	60.0	17.3	0	2-20	M.CEEEDSTALVCDNGSGLCK.A	Carbamidomethyl: 11	
2088	2	652.6205	-100.50	3	54.7	15.4	0	98-115	R.VAPEEHPTLLTEAPLNPK.A		
267	1	750.8467	-14.36	2	32.1	15.2	0	362-374	K.QEYDEAGPSIVHR.K		QD:QU 0.25

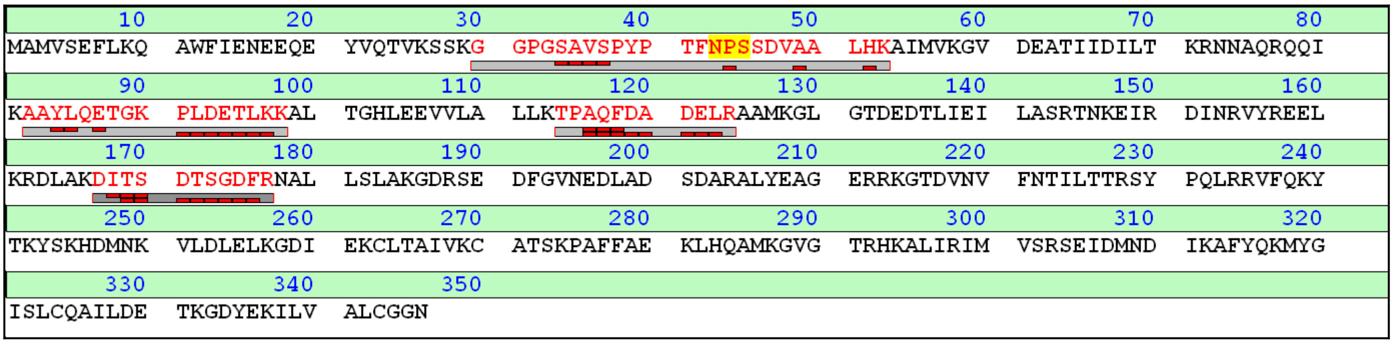
Detailed Protein Report

Protein 18: annexin A1 [Homo sapiens]

Accession:	gi|4502101	**Score:**	185.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.7
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	18.2
		No. of unique Peptides:	4

Quantitation

QD:QU **Median:** 1.18 **CV:** 49.61 % **No. of Peptides:** 3



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
1385	1	786.0874	38.51	3	47.5	12.5	0	30-53	K.GGPGSAVSPYPTFNPSSDVAALHA		
537	1	635.6517	-48.42	3	35.3	22.1	1	82-98	K.AAYLQETGKPLDETLKK.A		QD:QU 1.49
422	1	631.7779	-41.67	2	35.3	82.8	0	114-124	K.TPAQFDADELR.A		QD:QU 0.61
174	1	607.2652	-8.28	2	30.9	68.2	0	167-177	K.DITSDTSGDFR.N		QD:QU 1.80

Detailed Protein Report

Protein 19: **keratin, type II cytoskeletal 79 [Homo sapiens]**

Accession: gi|32567786
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 141.6
MW [kDa]: 57.8
pI: 6.9
Sequence Coverage [%]: 6.7
No. of unique 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
140	1	773.9092	30.36	2	31.7	10.7	2	1-13	-.MRSSVSRQTYSTK.G	Oxidation: 1

Detailed Protein Report

Protein 20: alpha-2-macroglobulin precursor [Homo sapiens]

Accession:	gi|66932947	**Score:**	141.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	163.2
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.4
		No. of unique Peptides:	6

Quantitation

QD:QU	**Median:** 0.93	**CV:** 0.00 %	**No. of Peptides:**	1

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	PGPLNDQDDE
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				
DLKPAIVKVY	DYYETDEFAI	AEYNAPCSKD	LGNA				

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		
2151	2	802.7866	-172.67	2	55.5	12.9	0	175-188	R.IAQWQSFQLEGGLK.Q		
276	1	636.8299	-16.03	2	33.4	30.1	0	587-598	R.VTAAPQSVCALR.A	Carbamidomethyl: 9	
501	1	558.7829	-41.39	2	36.2	34.5	0	854-863	R.QTVSWAVTPK.S		QD:QU 0.93
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-	K.MVSGFIPLKPTVKMLER.S		

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
								1401			

Detailed Protein Report

Protein 21: alpha-1-antitrypsin precursor [Homo sapiens]

Accession:	gi|50363217	**Score:**	136.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.7
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	10.5
		No. of unique Peptides:	3

Quantitation

QD:QU **Median:** 0.69 **CV:** 7.16 % **No. of Peptides:** 2

Alias proteins:

Accession	Name	Description
gi|189163542	refseq_human (refseq_human_20140103.fasta)	alpha-1-antitrypsin precursor [Homo sapiens]
gi|189163540	refseq_human (refseq_human_20140103.fasta)	alpha-1-antitrypsin precursor [Homo sapiens]
gi|189163538	refseq_human (refseq_human_20140103.fasta)	alpha-1-antitrypsin precursor [Homo sapiens]
gi|189163536	refseq_human (refseq_human_20140103.fasta)	alpha-1-antitrypsin precursor [Homo sapiens]
gi|189163534	refseq_human (refseq_human_20140103.fasta)	alpha-1-antitrypsin precursor [Homo sapiens]
gi|189163532	refseq_human (refseq_human_20140103.fasta)	alpha-1-antitrypsin precursor [Homo sapiens]
gi|189163530	refseq_human (refseq_human_20140103.fasta)	alpha-1-antitrypsin precursor [Homo sapiens]
gi|189163528	refseq_human (refseq_human_20140103.fasta)	alpha-1-antitrypsin precursor [Homo sapiens]
gi|50363221	refseq_human (refseq_human_20140103.fasta)	alpha-1-antitrypsin precursor [Homo sapiens]
gi|50363219	refseq_human (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
2910	3	858.7649	-23.64	3	65.6	35.3	0	126-149	R. TLNQPDSQLQLTTGNGLFLSEGLK L		
904	5	555.7989	-12.32	2	39.8	70.1	0	315-324	K.LSITGTYDLK.S		QD:QU 0.64
1288	2	508.1666	-283.94	2	44.6	30.8	0	325-334	K.SVLGQLGITK.V		QD:QU 0.74

Detailed Protein Report

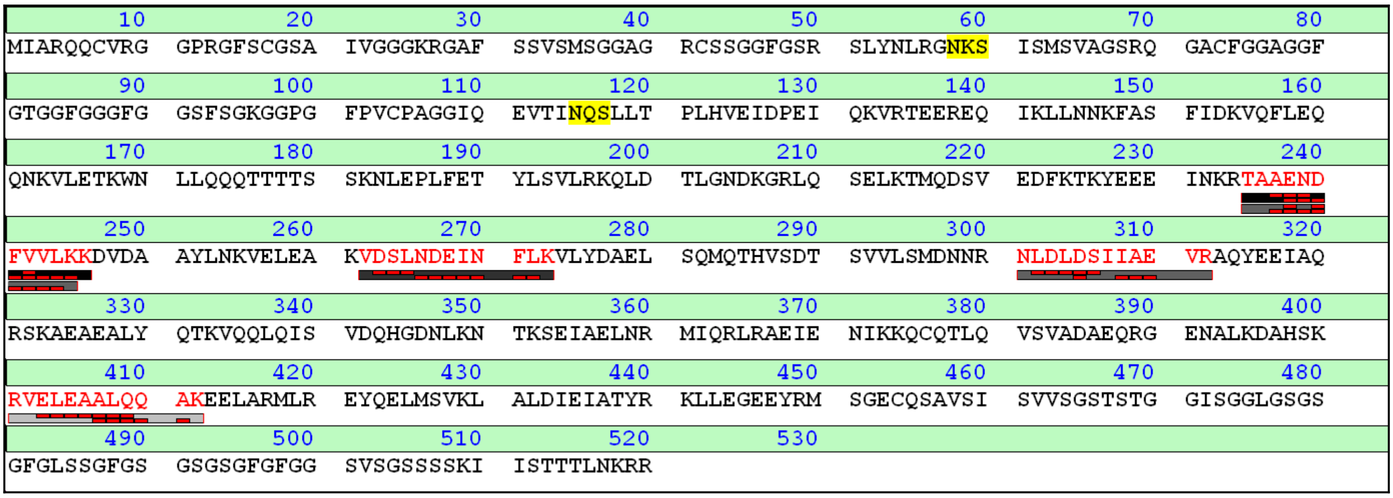
Protein 22: keratin, type II cytoskeletal 4 [Homo sapiens]

Accession: gi|331999954
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 127.3
MW [kDa]: 56.1
pI: 6.2
Sequence Coverage [%]: 9.2
No. of unique Peptides: 5

Quantitation

QD:QU **Median:** 0.40 **CV:** 31.96 % **No. of Peptides:** 4



```
        10         20         30         40         50         60         70         80
MIARQQCVRG GPRGFSCGSA IVGGGKRGAF SSVSMSGGAG RCSSGGFGSR SLYNLRGNKS ISMSVAGSRQ GACFGGAGGF
        90        100        110        120        130        140        150        160
GTGGFGGGFG GSFSGKGGPG FPVCPAGGIQ EVTINQSLLT PLHVEIDPEI QKVRTEEREQ IKLLNNKFAS FIDKVQFLEQ
       170        180        190        200        210        220        230        240
QNKVLETKWN LLQQQTTTTS SKNLEPLFET YLSVLRKQLD TLGNDKGRLQ SELKTMQDSV EDFKTKYEEE INKRTAAEND
       250        260        270        280        290        300        310        320
FVVLKKDVDA AYLNKVELEA KVDSLNDEIN FLKVLYDAEL SQMQTHVSDT SVVLSMDNNR NLDLDSIIAE VRAQYEEIAQ
       330        340        350        360        370        380        390        400
RSKAEAEALY QTKVQQLQIS VDQHGDNLKN TKSEIAELNR MIQRLRAEIE NIKKQCQTLQ VSVADAEQRG ENALKDAHSK
       410        420        430        440        450        460        470        480
RVELEAALQQ AKEELARMLR EYQELMSVKL ALDIEIATYR KLLEGEEYRM SGECQSAVSI SVVSGSTSTG GISGGLGSGS
       490        500        510        520        530
GFGLSSGFGS GSGSGFGFGG SVSGSSSSKI ISTTTLNKRR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
950	1	603.8017	-33.37	2	40.4	11.5	0	235-245	R.TAAENDFVVLK.K		QD:QU	0.46
530	1	667.8552	-21.26	2	35.2	56.2	1	235-246	R.TAAENDFVVLKK.D		QD:QU	0.57
2080	1	703.8136	-68.38	2	54.6	13.6	0	262-273	K.VDSLNDEINFLK.V			
906	1	679.3419	-40.90	2	39.8	17.2	0	301-312	R.NLDLDSIIAEVR.A		QD:QU	0.24
554	1	678.3667	-28.00	2	35.5	28.7	1	401-412	K.RVELEAALQQAK.E		QD:QU	0.41

Detailed Protein Report

Protein 23: keratin, type I cytoskeletal 10 [Homo sapiens]

Accession:	gi|195972866	**Score:**	126.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.8
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	6.0
		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	SFGGGSFGGG	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					
SSSGGHKSSS	SGSVGESSSK	GPRY					

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 24: **POTE ankyrin domain family member E [Homo sapiens]**

Accession:	gi|134133226	**Score:**	123.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	121.3
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 CFPCYRESGK SNVGTSGDHD DSAMKTLRSK MGKWCHHCFP CCRGSGKSNV
        90        100        110        120        130        140        150        160
GASGDHDDSA MKTLRNKMGK WCCHCFPCCR GSGKSKVGAW GDYDDSAFME PRYHVRGEDL DKLHRAAWWG KVPRKDLIVM
       170        180        190        200        210        220        230        240
LRDTDVNKKD 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 ENSNPEQELK LTSEEESQRF KGSENSQPEK
       410        420        430        440        450        460        470        480
MSQELEINKD GDREVEEEMK KHESNNVGLL ENLTNGVTAG NGDNGLIPQR KSRTPENQQF PDNESEEYHR ICELLSDYKE
       490        500        510        520        530        540        550        560
KQMPKYSSEN SNPEQDLKLT SEEESQRLKG SENGQPEKRS QEPEINKDGD RELENFMAIE EMKKHGSTHV 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
EKDVLHENST LREEIAMLRL ELDTMKHQSQ LREKKYLEDI ESVKKKNDNL 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
HPILLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVP SLYTSGRTTG IVMDSGDGVT HTVPIYEGNA LPHATLRLDL
       890        900        910        920        930        940        950        960
AGRELPDYLM KILTERGYRF TTMAEREIVR DIKEKLCYVA LDFEQEMATA 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 HRKCF
```

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 25: beta-actin-like protein 2 [Homo sapiens]

Accession:	gi|63055057	**Score:**	122.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.0
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	14.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTDNELSALV	VDNGSGMCKA	GFGGDDAPRA	VFPSMIGRPR	HQGVMVGMGQ	KDCYVGDEAQ	SKRGVLTLKY	PIEHGVVTNW
90	100	110	120	130	140	150	160
DDMEKIWYHT	FYNELRVAPD	EHPILLTEAP	LNPKINREKM	TQIMFEAFNT	PAMYVAIQAV	LSLYASGRTT	GIVMDSGDGV
170	180	190	200	210	220	230	240
THIVPIYEGY	ALPHAILRLD	LAGRDLTDYL	MKILTERGYN	FTTTAEREIV	RDVKEKLCYV	ALDFEQEMVR	AAASSSPERS
250	260	270	280	290	300	310	320
YELPDGQVIT	IGNERFRCPE	AIFQPSFLGI	ESSGIHETTF	NSIMKCDVDI	RKDLYANTVL	SGGSTMYPGI	ADRMQKEIIT
330	340	350	360	370	380		
LAPSTMKIKI	IAPPERKYSV	WIGGSILASL	STFQQMWISK	QEYDEAGPPI	VHRKCF		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2065	1	1108.9201	-97.52	2	54.4	45.1	0	293-313	K.DLYANTVLSGGSTMYPGIADR.M	Oxidation: 14

Detailed Protein Report

Protein 26: keratin, type II cytoskeletal 1 [Homo sapiens]

Accession:	gi|119395750	**Score:**	122.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	66.0
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	5.6
		No. of unique Peptides:	1

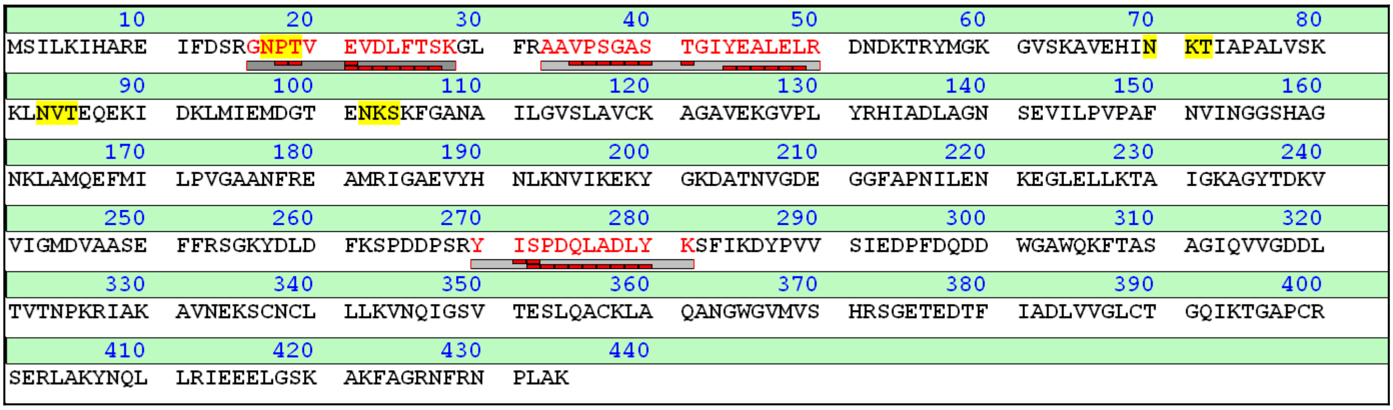
10	20	30	40	50	60	70	80
MSRQFSSRSG	YRSGGGFSSG	SAGIINYQRR	TTSSSTRRSG	GGGGRFSSCG	GGGGSFGAGG	GFGSRSLVNL	GGSKSISISV
90	100	110	120	130	140	150	160
ARGGGRGSGF	GGGYGGGGFG	GGGFGGGGFG	GGGIGGGGFG	GFGSGGGGFG	GGGFGGGGYG	GGYGPVCPPG	GIQEVTINQS
170	180	190	200	210	220	230	240
LLQPLNVEID	PEIQKVKSRE	REQIKSLNNQ	FASFIDKVRF	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 27: alpha-enolase isoform 1 [Homo sapiens]

Accession:	gi|4503571	**Score:**	111.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.1
Database Date:	2015-11-30	**pI:**	7.7
		Sequence Coverage [%]:	9.9
		No. of unique Peptides:	3



```
        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
1541	1	703.8713	13.64	2	47.8	10.1	0	16-28	R.GNPTVEVDLFTSK.G	
2401	1	902.9549	-22.96	2	58.7	34.1	0	33-50	R.AAVPSGASTGIYEALELR.D	
1618	6	713.3563	-14.47	2	50.5	67.0	0	270-281	R.YISPDQLADLYK.S	

Detailed Protein Report

Protein 28: 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

QD:QU	**Median:** 0.95	**CV:** 0.00 %	**No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|124248516	refseq_human(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	2	493.7604	4.77	2	31.8	52.9	0	70-78	R.IPACIAGER.R	Carbamidomethyl: 4	QD:QU	0.95
108	2	559.2630	8.21	2	31.3	55.9	0	80-88	R.YGTCIYQGR.L	Carbamidomethyl: 4		

Detailed Protein Report

Protein 29: haptoglobin isoform 2 preproprotein [Homo sapiens]

Accession:	gi|186910296	**Score:**	99.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.4
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	10.7
		No. of unique Peptides:	3

Quantitation

QD:QU **Median:** 0.85 **CV:** 23.78 % **No. of Peptides:** 2

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
239	1	854.8952	-39.14	2	31.7	13.9	1	58-72	K.LRTEGDGVYTLNNEK.Q		QD:QU 0.67
1734	1	645.7555	-175.50	2	52.0	37.8	0	157-168	K.DIAPTLTLYVGK.K		
741	3	602.2951	-44.79	2	39.2	47.7	0	333-342	K.VTSIQDWVQK.T		QD:QU 1.07

Detailed Protein Report

Protein 30:	**cadherin EGF LAG seven-pass G-type receptor 3 precursor [Homo sapiens]**		
Accession:	gi|145309304	**Score:**	92.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	358.0
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	6

Quantitation

QD:QU	**Median:**	7.67	**CV:**	0.00 %	**No. of Peptides:**	1

```
        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
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1647	5	942.4685	14.29	2	49.1	22.8	1	232-250	R.RNCLPGASGSGPELDSAPR.T		
2719	1	964.4996	-2.09	2	62.9	13.4	2	1519-1534	R.SFPPSSFVMFRGLRQR.F	Oxidation: 9	
2229	1	956.4132	-125.14	2	56.5	12.5	1	2144-2162	K.FGVLATVPCPRGALGAAVR.L	Carbamidomethyl: 9	
1065	3	470.5947	-263.79	2	43.4	12.8	0	2331-2338	R.MEHPSSPR.G		QD:QU 7.67
2129	1	698.8200	-38.23	2	55.2	13.9	2	2331-2342	R.MEHPSSPRGARR.Y	Oxidation: 1	
118	1	1069.1641	-33.12	3	30.2	17.4	1	3083-3111	R.ERLEEAPAPVLRPLSRPGSQECML	Carbamidomethyl: 22; Oxidation: 23	

Detailed Protein Report

Protein 31: fibrinogen beta chain isoform 2 preproprotein [Homo sapiens]

Accession:	gi|296080754	**Score:**	84.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.9
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.3
		No. of unique Peptides:	3

Quantitation

QD:QU	**Median:** 1.17	**CV:** 0.00 %	**No. of Peptides:** 1

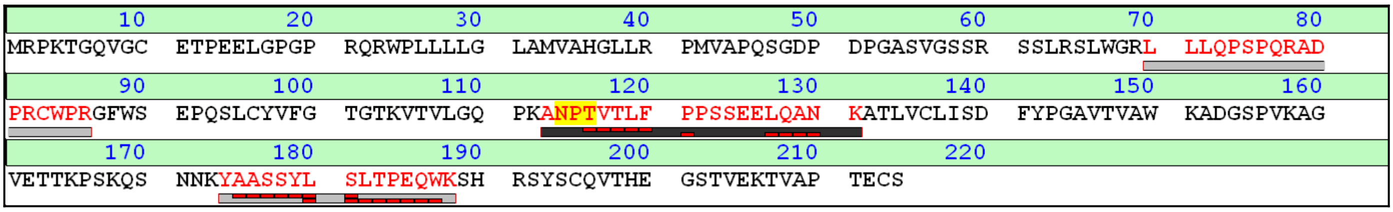
10	20	30	40	50	60	70	80
MKRMVSWSFH	KLKTMKHLLL	LLLCVFLVKS	QGVNDNEEGF	FSARGHRPLD	KKREEALLQQ	ERPIRNSVDE	LNNNVEAVSQ
90	100	110	120	130	140	150	160
TSSSSFQYMY	LLKDLWQKRQ	KQVKDNENVV	NEYSSELEKH	QLYIDETVNS	NIPTNLRVLR	SILENLRSKI	QKLESDVSAQ
170	180	190	200	210	220	230	240
MEYCRTPCTV	SCNIPVVSGK	ECEEIIRKGG	ETSEMYLIQP	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	QD:QU 1.17
1961	3	893.2648	-149.91	2	53.0	20.5	0	255-269	K.NYCGLPGEYWLGNDK.I	Carbamidomethyl: 3	
656	1	620.1188	-231.67	2	36.8	38.6	0	368-377	K.EDGGGWWYNR.C		

Detailed Protein Report

Protein 32: **immunoglobulin lambda-like polypeptide 5 isoform 1 [Homo sapiens]**

Accession:	gi|295986608	**Score:**	83.7
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



```
        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 FYPGAVTVAW 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
2042	1	1045.4503	-102.49	2	55.9	14.4	2	70-86	R.LLLQPSPQRADPRCWPR.G	Carbamidomethyl: 14
1891	3	1021.8855	-134.81	2	52.1	22.0	0	113-131	K.ANPTVTLFPPSSEELQANK.A	
2200	8	872.4511	20.68	2	56.1	47.3	0	174-188	K.YAASSYLSLTPEQWK.S	

Detailed Protein Report

Protein 33: **PREDICTED: plectin isoform X8 [Homo sapiens]**

Accession:	gi|530389157	**Score:**	83.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	513.4
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	3

```
        10          20          30          40          50          60          70          80
MDRYSMEELI  QLGQDERDRV  QKKTFTKWVN  KHLIKAQRHI  SDLYEDLRDG  HNLISLLEVL  SGDSLPREKG  RMRFHKLQNV

        90         100         110         120         130         140         150         160
QIALDYLRHR  QVKLVNIRND  DIADGNPKLT  LGLIWTIILH  FQISDIQVSG  QSEDMTAKEK  LLLWSQRMVE  GYQGLRCDNF

       170         180         190         200         210         220         230         240
TSSWRDGRLF  NAIIHRHKPL  LIDMNKVYRQ  TNLENLDQAF  SVAERDLGVT  RLLDPEDVDV  PQPDEKSIIT  YVSSLYDAMP

       250         260         270         280         290         300         310         320
RVPDVQDGVR  ANELQLRWQE  YRELVLLLLQ  WMRHHTAAFE  ERRFPSSFEE  IEILWSQFLK  FKEMELPAKE  ADKNRSKGIY

       330         340         350         360         370         380         390         400
QSLEGAVQAG  QLKVPPGYHP  LDVEKEWGKL  HVAILEREKQ  LRSEFERLEC  LQRIVTKLQM  EAGLCEEQLN  QADALLQSDV

       410         420         430         440         450         460         470         480
RLLAAGKVPQ  RAGEVERDLD  KADSMIRLLF  NDVQTLKDGR  HPQGEQMYRR  VYRLHERLVA  IRTEYNLRLK  AGVAAPATQV

       490         500         510         520         530         540         550         560
AQVTLQSVQR  RPELEDSTLR  YLQDLLAWVE  ENQHRVDGAE  WGVDLPSVEA  QLGSHRGLHQ  SIEEFRAKIE  RARSDEGQLS

       570         580         590         600         610         620         630         640
PATRGAYRDC  LGRLDLQYAK  LLNSSKARLR  SLESLHSFVA  AATKELMWLN  EKEEEEVGFD  WSDRNTNMTA  KKESYSALMR

       650         660         670         680         690         700         710         720
ELELKEKKIK  ELQNAGDRLL  REDHPARPTV  ESFQAALQTQ  WSWMLQLCCC  IEAHLKENAA  YFQFFSDVRE  AEGQLQKLQE

       730         740         750         760         770         780         790         800
ALRRKYSCDR  SATVTRLEDL  LQDAQDEKEQ  LNEYKGHLSG  LAKRAKAVVQ  LKPRHPAHPM  RGRLPLLAVC  DYKQVEVTVH

       810         820         830         840         850         860         870         880
KGDECQLVGP  AQPSHWKVLS  SSGSEAAVPS  VCFLVPPPNQ  EAQEAVTRLE  AQHQALVTLW  HQLHVDMKSL  LAWQSLRRDV

       890         900         910         920         930         940         950         960
QLIRSWSLAT  FRTLKPEEQR  QALHSLELHY  QAFLRDSQDA  GGFGPEDRLM  AEREYGSCSH  HYQQLLQSLE  QGAQEESRCQ

       970         980         990        1000        1010        1020        1030        1040
RCISELKDIR  LQLEACETRT  VHRLRLPLDK  EPARECAQRI  AEQQKAQAEV  EGLGKGVARL  SAEAEKVLAL  PEPSPAAPTL

      1050        1060        1070        1080        1090        1100        1110        1120
RSELELTLGK  LEQVRSLSAI  YLEKLKTISL  VIRGTQGAEE  VLRAHEEQLK  EAQAVPATLP  ELEATKASLK  KLRAQAEAQQ

      1130        1140        1150        1160        1170        1180        1190        1200
PTFDALRDEL  RGAQEVGERL  QQRHGERDVE  VERWRERVAQ  LLERWQAVLA  QTDVRQRELE  QLGRQLRYYR  ESADPLGAWL

      1210        1220        1230        1240        1250        1260        1270        1280
QDARRRQEQI  QAMPLADSQA  VREQLRQEQA  LLEEIERHGE  KVEECQRFAK  QYINAIKDYE  LQLVTYKAQL  EPVASPAKKP

      1290        1300        1310        1320        1330        1340        1350        1360
KVQSGSESVI  QEYVDLRTHY  SELTTLTSQY  IKFISETLRR  MEEEERLAEQ  QRAEERERLA  EVEAALEKQR  QLAEAHAQAK

      1370        1380        1390        1400        1410        1420        1430        1440
AQAEREAKEL  QQRMQEEVVR  REEAAVDAQQ  QKRSIQEELQ  QLRQSSEAEI  QAKARQAEAA  ERSRLRIEEE  IRVVRLQLEA

      1450        1460        1470        1480        1490        1500        1510        1520
TERQRGGAEG  ELQALRARAE  EAEAQKRQAQ  EEAERLRRQV  QDESQRKRQA  EVELASRVKA  EAEAAREKQR  ALQALEELRL

      1530        1540        1550        1560        1570        1580        1590        1600
QAEEAERRLR  QAEVERARQV  QVALETAQRS  AEAELQSKRA  SFAEKTAQLE  RSLQEEHVAV  AQLREEAERR  AQQQAEAERA

      1610        1620        1630        1640        1650        1660        1670        1680
REEAERELER  WQLKANEALR  LRLQAEEVAQ  QKSLAQAEAE  KQKEEAEREA  RRRGKAEEQA  VRQRELAEQE  LEKQRQLAEG

      1690        1700        1710        1720        1730        1740        1750        1760
TAQQRLAAEQ  ELIRLRAETE  QGEQQRQLLE  EELARLQREA  AAATQKRQEL  EAELAKVRAE  MEVLLASKAR  AEEESRSTSE

      1770        1780        1790        1800        1810        1820        1830        1840
KSKQRLEAEA  GRFRELAEEA  ARLRALAEEA  KRQRQLAEED  AARQRAEAER  VLAEKLAAIG  EATRLKTEAE  IALKEKEAEN

      1850        1860        1870        1880        1890        1900        1910        1920
ERLRRLAEDE  AFQRRRLEEQ  AAQHKADIEE  RLAQLRKASD  SELERQKGLV  EDTLRQRRQV  EEEILALKAS  FEKAAAGKAE

      1930        1940        1950        1960        1970        1980        1990        2000
LELELGRIRS  NAEDTLRSKE  QAELEAARQR  QLAAEEERRR  REAEERVQKS  LAAEEEAARQ  RKAALEEVER  LKAKVEEARR

      2010        2020        2030        2040        2050        2060        2070        2080
LRERAEQESA  RQLQLAQEAA  QKRLQAEEKA  HAFAVQQKEQ  ELQQTLQQEQ  SVLDQLRGEA  EAARRAAEEA  EEARVQAERE

      2090        2100        2110        2120        2130        2140        2150        2160
AAQSRRQVEE  AERLKQSAEE  QAQARAQAQA  AAEKLRKEAE  QEAARRAQAE  QAALRQKQAA  DAEMEKHKKF  AEQTLRQKAQ

      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
2471	1	588.1664	-172.67	2	61.4	13.5	0	1697-1706	R.AETEQGEQQR.Q	
1806	1	582.2479	-40.78	2	52.9	11.0	0	2352-2361	R.QLEMSAEAER.L	
1932	1	1021.8810	-139.60	2	52.6	12.9	2	3841-3858	R.CRRDDGTGQLLLPLSDAR.K	Carbamidomethyl: 1

Detailed Protein Report

Protein 34: coiled-coil domain-containing protein 168 [Homo sapiens]

Accession:	gi|226246554	**Score:**	81.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	801.4
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	4

Quantitation

QD:QU	**Median:**	0.93	**CV:**	117.96 %	**No. of Peptides:**	2

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

Detailed Protein Report

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		QD:QU 0.37
2371	3	974.2361	79.07	3	60.1	12.7	2	5658-5682	R.DEDIYFTGFGTIRSGKRPEWLFTGK		
2107	1	698.3422	-40.67	2	54.9	13.3	1	6680-6691	K.KQSPHENSSLIR.K		QD:QU 2.37

Detailed Protein Report

Protein 35: **PREDICTED: dynein heavy chain 3, axonemal isoform X1 [Homo sapiens]**

Accession:	gi|578828592	**Score:**	81.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	466.0
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	4

Detailed Protein Report

10	20	30	40	50	60	70	80
MGDMDCSSQK	IAKSDSIHHM	SHSQGQPELP	PLPASANEEP	SGLYQTVMSH	SFYPPLMQRT	SWTLAAPFKE	QHHHRGPSDS
90	100	110	120	130	140	150	160
IANNYSLMAQ	DLKLKDLLKV	YQPATISVPR	DRTGQGLPSS	GNRSSSEPMR	KKTKFSSRNK	EDSTRIKLAF	KTSIFSPMKK
170	180	190	200	210	220	230	240
EVKTSLTFPG	SRPMSPEQQL	DVMLQQEMEM	ESKEKKPSES	DLERYYYYLT	NGIRKDMIAP	EEGEVMVRIS	KLISNTLLTS
250	260	270	280	290	300	310	320
PFLEPLMVVL	VQEKENDYYC	SLMKSIVDYI	LMDPMERKRL	FIESIPRLFP	QRVIRAPVPW	HSVYRSAKKW	NEEHLHTVNP
330	340	350	360	370	380	390	400
MMLRLKELWF	AEFRDLRFVR	TAEILAGKLP	LQPQEFWDVI	QKHCLEAHQT	LLNKWIPTCA	QLFTSRKEHW	IHFAPKSNYD
410	420	430	440	450	460	470	480
SSRNIEEYFA	SVASFMSLQL	RELVIKSLED	LVSLFMIHKD	GNDFKEPYQE	MKFFIPQLIM	IKLEVSEPII	VFNPSFDGCW
490	500	510	520	530	540	550	560
ELIRDSFLEI	IKNSNGIPKV	ESVLFPELKG	YNLLLGTVNA	EEKLVSDFLI	QTFKVFQKNQ	VGPCKYLNVY	KKYVDLLDNT
570	580	590	600	610	620	630	640
AEQNIAAFLK	ENHDIDDFVT	KINAIKKRRN	EIASMNITVP	LAMFCLDATA	LNHDLCERAQ	NLKDHLIQFQ	VDVNRDTNTS
650	660	670	680	690	700	710	720
ICNQYSHIAD	KVSEVPANTK	ELVSLIEFLK	KSSAVTVFKL	RRQLRDASER	LEFLMDYADL	PYEDIKLNST	LFLWPDQIED
730	740	750	760	770	780	790	800
IFDNSRNLLL	HKRDQAEMDL	IKRCSEFELR	LEGYHRELES	FRKREVMTTE	EMKHNVEKLN	ELSKNLNRAF	AEFELINKEE
810	820	830	840	850	860	870	880
ELLEKEKSTY	PLLQAMLKNK	VPYEQLWSTA	YEFSIKSEEW	MNGPLFLLNA	EQIAEEIGNM	WRTTYKLIKT	LSDVPAPRRL
890	900	910	920	930	940	950	960
AENVKIKIDK	FKQYIPILSI	SCNPGMKDRH	WQQISEIVGY	EIKPTETTCL	SNMLEFGFGK	FVEKLEPIGA	AASKEYSLEK
970	980	990	1000	1010	1020	1030	1040
NLDRMKLDWV	NVTFSFVKYR	DTDTNILCAI	DDIQMLLDDH	VIKTQTMCGS	PFIKPIEAEC	RKWEEKLIRI	QDNLDAWLKC
1050	1060	1070	1080	1090	1100	1110	1120
QATWLYLEPI	FSSEDIIAQM	PEEGRKFGIV	DSYWKSLMSQ	AVKDNRILVA	ADQPRMAEKL	QEANFLLEDI	QKGLNDYLEK
1130	1140	1150	1160	1170	1180	1190	1200
KRLFFPRFFF	LSNDELLEIL	SETKDPLRVQ	PHLKKCFEGI	AKLEFTDNLE	IVGMISSEKE	TVPFIQKIYP	ANAKGMVEKW
1210	1220	1230	1240	1250	1260	1270	1280
LQQVEQMMLA	SMREVIGLGI	EAYVKVPRNH	WVLQWPGQVV	ICVSSIFWTQ	EVSQALAENT	LLDFLKKSND	QIAQIVQLVR
1290	1300	1310	1320	1330	1340	1350	1360
GKLSSGARLT	LGALTVIDVH	ARDVVAKLSE	DRVSDLNDFQ	WISQLRYYWV	AKDVQVQIIT	TEALYGYEYL	GNSPRLVITP
1370	1380	1390	1400	1410	1420	1430	1440
LTDRCYRTLM	GALKLNLGGA	PEGPAGTGKT	ETTKDLAKAL	AKQCVVFNCS	DGLDYKAMGK	FFKGLAQAGA	WACFDEFNRI
1450	1460	1470	1480	1490	1500	1510	1520
EVEVLSVVAQ	QILSIQQAII	RKLKTFIFEG	TELSLNPTCA	VFITMNPGYA	GRAELPDNLK	ALFRTVAMMV	PDYALIGEIS
1530	1540	1550	1560	1570	1580	1590	1600
LYSMGFLDSR	SLAQKIVATY	RLCSEQLSSQ	HHYDGMRAV	KSVLTAAGNL	KLKYPEENES	VLLLRALLDV	NLAKFLAQDV
1610	1620	1630	1640	1650	1660	1670	1680
PLFQGIISDL	FPGVVLPKPD	YEVFLKVLND	NIKKMKLQPV	PWFIGKIIQI	YEMMLVRHGY	MIVGDPMGGK	TSAYKVLAAA
1690	1700	1710	1720	1730	1740	1750	1760
LGDLHAANQM	EEFAVEYKII	NPKAITMGQL	YGCFDQVSHE	WMDGVLANAF	REQASSLSDD	RKWIIFDGPV	DAIWIENMNT
1770	1780	1790	1800	1810	1820	1830	1840
VLDDNKKLCL	MSGEIIQMNS	KMSLIFEPAD	LEQASPATVS	RCGMIYMEPH	QLGWKPLKDS	YMDTLPSSLT	KEHKELVNDM
1850	1860	1870	1880	1890	1900	1910	1920
FMWLVQPCLE	FGRLHCKFVV	QTSPIHLAFS	MMRLYSSLLD	EIRAVEEEEM	ELGEGLSSQQ	IFLWLQGLFL	FSLVWTVAGT
1930	1940	1950	1960	1970	1980	1990	2000
INADSRKKFD	VFFRNLIMGM	DDNHPRPKSV	KLTKNNIFPE	RGSIYDFYFI	KQASGHWETW	TQYITKEEEK	VPAGAKVSEL
2010	2020	2030	2040	2050	2060	2070	2080
IIPTMETARQ	SFFLKTYLDH	EIPMLFVGPT	GTGKSAITNN	FLLHLPKNTY	LPNCINFSAR	TSANQTQDII	MSKLDRRRKG
2090	2100	2110	2120	2130	2140	2150	2160
LFGPPIGKKA	VVFVDDLNMP	AKEVYGAQPP	IELLRQWIDH	GYWFDKKDTT	RLDIVDMLLV	TAMGPPGGGR	NDITGRFTRH
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
565	1	607.8337	-71.29	2	35.7	10.9	1	1562-1573	K.SVLTAAGNLKLK.Y	
315	1	1201.1883	61.60	2	32.6	16.3	1	2128-2150	K.DTTRLDIVDMLLVTAMGPPGGGR.N	Oxidation: 10
1563	1	949.5033	8.02	2	49.7	12.9	2	2269-2283	R.LIDKEDRQVFFNMVK.E	Oxidation: 13
1965	2	572.7269	-161.97	2	54.9	12.8	1	2924-2934	K.LISGLGGEKDR.W	

Detailed Protein Report

Protein 36: PREDICTED: protein AHNAK2 isoform X1 [Homo sapiens]

Accession:	gi|530403029	**Score:**	80.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	605.3
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	6

Quantitation

QD:QU	**Median:**	1.08	**CV:**	50.25 %	**No. of Peptides:**	2

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

Detailed Protein Report

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		QD:QU 1.73
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		QD:QU 0.67
1307	2	926.0984	-40.13	3	46.5	19.2	1	3391-3417	R. SIEASLDVSAPKVEADVSLSSMQG A		
2190	3	648.2929	-93.26	2	56.0	10.4	1	5599-5610	R.FPKLGFSSSPTK.K		
1329	1	1023.0254	-12.68	2	46.8	11.6	1	5662-5679	R.VMVTSAARTELILPEQDR.K	Oxidation: 2	

Detailed Protein Report

Protein 37: PREDICTED: dynein heavy chain 5, axonemal isoform X1 [Homo sapiens]

Accession:	gi|530378724	**Score:**	75.3
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 [%]:**	1.7
		No. of unique Peptides:	4

Quantitation

QD:QU	**Median:** 0.50	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

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

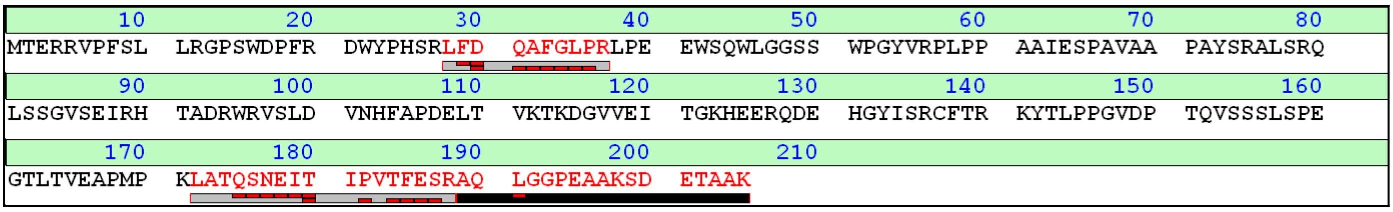
Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1349	1	991.5669	90.75	3	47.0	28.2	1	1947-1976	R.CYITLAQALGMSMGGAPAGPAGTD	Carbamidomethyl: 1; Oxidation: 11, 13	
2802	1	849.0671	-21.12	3	66.2	12.2	2	1999-2021	R.GLGRIFKGLAQSGSWGCFDEFNRI		
2750	1	905.4797	-0.39	2	65.5	16.2	2	3993-4008	R.TIAQARKYIVDSMGEK.Y		
592	1	607.1554	-159.80	2	36.0	18.7	0	4415-4424	R.DALDCMFDAR.I	Carbamidomethyl: 5	QD:QU 0.50

Detailed Protein Report

Protein 38: heat shock protein beta-1 [Homo sapiens]

Accession:	gi|4504517	**Score:**	74.0
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



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
1770	3	582.2260	-151.18	2	52.4	43.9	0	28-37	R.LFDQAFGLPR.L	
2031	2	953.3861	-118.85	2	53.9	17.5	0	172-188	K.LATQSNEITIPVTFESR.A	
2630	2	822.4504	42.56	2	63.7	12.6	1	189-205	R.AQLGGPEAAKSDETAAK.-	

Detailed Protein Report

Protein 39: tenascin-X isoform 1 precursor [Homo sapiens]

Accession:	gi|188528648	**Score:**	68.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	457.9
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	5

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
2799	1	732.8911	134.58	2	64.1	13.0	1	725-737	R.GRGECHDGSCVCK.D	Carbamidomethyl: 10, 12
2882	1	981.9684	-29.71	2	65.2	15.6	1	2349-2366	R.VPGHEDRVTISGLEPDNK.Y	

Detailed Protein Report

Protein 40: zymogen granule protein 16 homolog B precursor [Homo sapiens]

Accession:	gi|94536866	**Score:**	68.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.7
Database Date:	2015-11-30	**pI:**	7.6
		Sequence Coverage [%]:	14.4
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.36 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MGAQGAQESI KAMWRVPGTT RRPVTGESPG MHRPEAMLLL LTLALLGGPT WAGKMYGPGG GKYFSTTEDY DHEITGLRVS
        90        100        110        120        130        140        150        160
VGLLLVKSVQ VKLGDSWDVK LGALGGNTQE VTLQPGEYIT KVFVAFQAFL RGMVMYTSKD RYFYFGKLDG QISSAYPSQE
       170        180        190        200        210
GQVLVGIYGQ YQLLGIKSIG FEWNYPLEEP TTEPPVNLTY SANSPVGR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2510	2	464.1779	-296.31	2	60.1	35.2	0	79-87	R.VSVGLLLVK.S		
1743	6	1095.0646	-10.46	2	50.3	32.9	0	101-121	K.LGALGGNTQEVTLQPGEYITK.V		QD:QU 0.36

Detailed Protein Report

Protein 41: uncharacterized protein C4orf21 [Homo sapiens]

Accession:	gi|254826809	**Score:**	67.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	236.5
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	4

Quantitation

QD:QU	**Median:**	2.59	**CV:**	0.00 %	**No. of Peptides:**	1

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	Ratios
1998	1	902.8620	-77.52	2	55.4	13.3	1	128-144	K.KMVIMESGESAASHEAK.K		
2735	1	973.5207	5.77	2	63.2	10.7	1	167-183	K.KDVNNILADPENIVTYK.N		QD:QU 2.59
2930	6	698.3835	-51.56	2	65.8	21.0	1	282-294	K.QPQGSLKIATKPK.Y		
2757	1	849.0563	-13.52	3	65.6	22.0	2	1166-1187	K.RITDGFFAEAVSGMHFRDTSER.Q	Oxidation: 14	

Detailed Protein Report

Protein 42: fanconi-associated nuclease 1 isoform a [Homo sapiens]

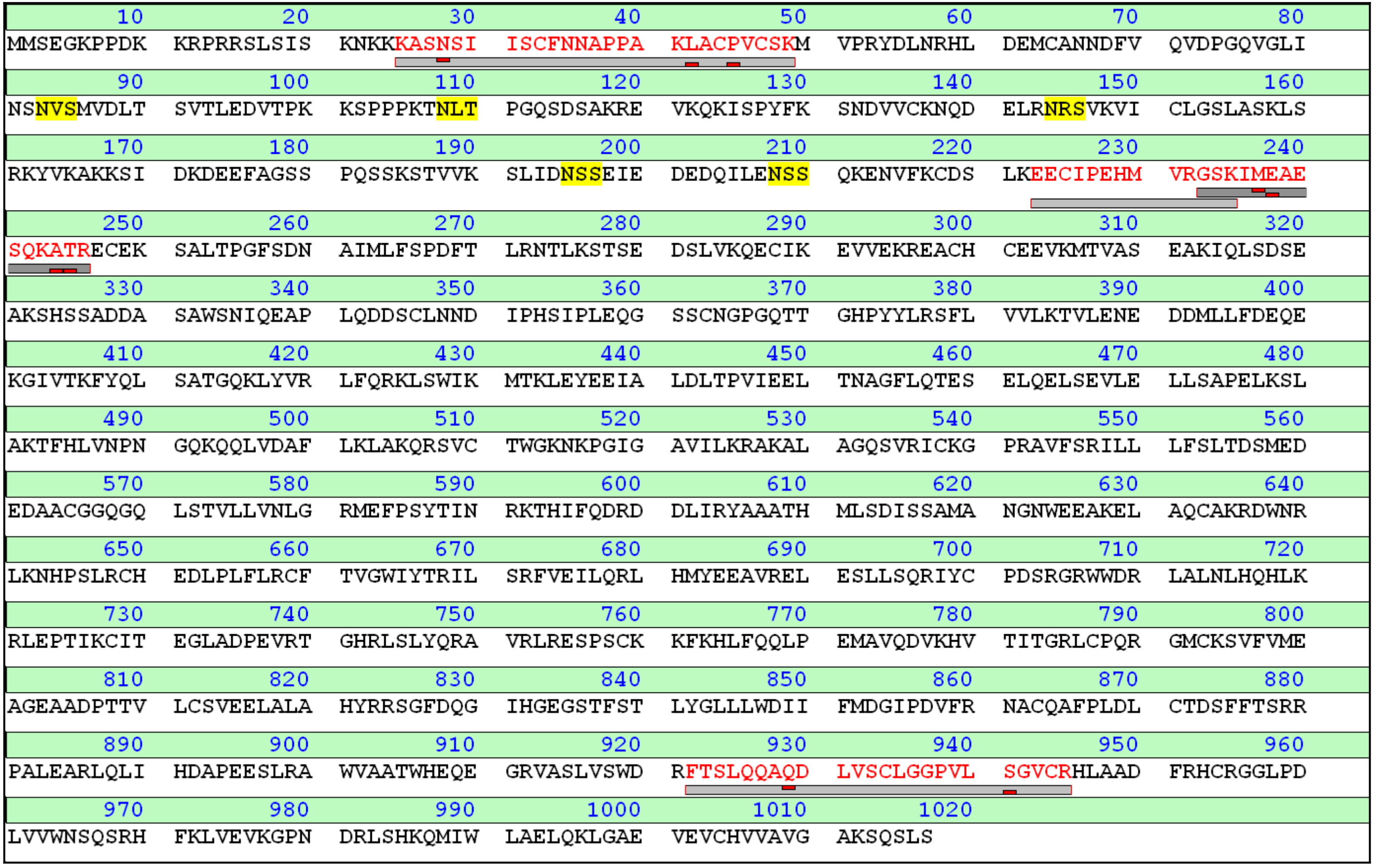
Accession:	gi|226246523	**Score:**	65.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	114.2
Database Date:	2015-11-30	**pI:**	7.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	7.2
		No. of unique Peptides:	4

Quantitation

QD:QU	**Median:**	0.58	**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]



```
        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
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
443	1	874.1657	67.87	3	34.2	13.4	2	25-49	K. KASNSIISCFNNAPPAKLACPVCS M	Carbamidomethyl: 20	
691	1	765.8997	57.54	2	38.6	18.5	1	223-235	K.EECIPEHMVRGSK.I	Oxidation: 8	QD:QU 0.58
56	3	768.3135	-107.30	2	30.6	16.5	2	233-246	R.GSKIMEAESQKATR.E		
97	1	826.6883	-79.67	3	31.1	17.4	0	922-945	R. FTSLQQAQDLVSCLGGPVLSGVC H		

Detailed Protein Report

Protein 43: **PREDICTED: dystonin isoform X7 [Homo sapiens]**

Accession:	gi|530382430	**Score:**	64.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	875.9
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	4

10	20	30	40	50	60	70	80
MGNVCGCVRA	EKEEQYVDPA	KTPLNPEKYS	PGRKYFRRKP	IKKTGGDKES	VGANNENEGK	KKSSSQPSKE	QPAPLSRGLV
90	100	110	120	130	140	150	160
QQESVTLNSA	LGDGIQQKKT	EVVADSVKQK	LLPSAVSSWS	DCVNTSPAKD	SETEVKVSEL	DERISEKDST	PYCAKRKKHL
170	180	190	200	210	220	230	240
DDVNTSEITF	QEKTDVFSFR	KAASLSSIPS	GIERSLEKSG	FPEDPPKSYS	SIQEKQNTER	FCPHATQHFQ	FKKKRCHSLY
250	260	270	280	290	300	310	320
TSMSSVSKDT	DGNEISDIHV	TGESEDMSAK	ERLLLWTQQA	TEGYAGIRCE	NFTTCWRDGK	LFNAIIHKYR	PDLIDMNTVA
330	340	350	360	370	380	390	400
VQSNLANLEH	AFYVAEKIGV	IRLLDPEDVD	VSSPDEKSVI	TYVSSLYDAF	PKVPEGGEGI	GANDVEVKWI	EYQNMVNYLI
410	420	430	440	450	460	470	480
QWIRHHVTTM	SERTFPNNPV	ELKALYNQYL	QFKETEIPPK	ETEKSKIKRL	YKLLEIWIEF	GRIKLLQGYH	PNDIEKEWGK
490	500	510	520	530	540	550	560
LIIAMLEREK	ALRPEVERLE	MLQQIANRVQ	RDSVICEDKL	ILAGNALQSD	SKRLESGVQF	QNEAEIAGYI	LECENLLRQH
570	580	590	600	610	620	630	640
VIDVQILIDG	KYYQADQLVQ	RVAKLRDEIM	ALRNECSSVY	SKGRILTTEQ	TKLMISGITQ	SLNSGFAQTL	HPSLTSGLTQ
650	660	670	680	690	700	710	720
SLTPSLTSSS	MTSGLSSGMT	SRLTPSVTPA	YTPGFPSGLV	PNFSSGVEPN	SLQTLKLMQI	RKPLLKSSLL	DQNLTEEEIN
730	740	750	760	770	780	790	800
MKFVQDLLNW	VDEMQVQLDR	TEWGSDLPSV	ESHLENHKNV	HRAIEEFESS	LKEAKISEIQ	MTAPLKLTYA	EKLHRLESQY
810	820	830	840	850	860	870	880
AKLLNTSRNQ	ERHLDTLHNF	VSRATNELIW	LNEKEEEEVA	YDWSERNTNI	ARKKDYHAEL	MRELDQKEEN	IKSVQEIAEQ
890	900	910	920	930	940	950	960
LLLENHPARL	TIEAYRAAMQ	TQWSWILQLC	QCVEQHIKEN	TAYFEFFNDA	KEATDYLRNL	KDAIQRKYSC	DRSSSIHKLE
970	980	990	1000	1010	1020	1030	1040
DLVQESMEEK	EELLQYKSTI	ANLMGKAKTI	IQLKPRNSDC	PLKTSIPIKA	ICDYRQIEIT	IYKDDECVLA	NNSHRAKWKV
1050	1060	1070	1080	1090	1100	1110	1120
ISPTGNEAMV	PSVCFTVPPP	NKEAVDLANR	IEQQYQNVLT	LWHESHINMK	SVVSWHYLIN	EIDRIRASNV	ASIKTMLPGE
1130	1140	1150	1160	1170	1180	1190	1200
HQQVLSNLQS	RFEDFLEDSQ	ESQVFSGSDI	TQLEKEVNVC	KQYYQELLKS	AEREEQEESV	YNLYISEVRN	IRLRLENCED
1210	1220	1230	1240	1250	1260	1270	1280
RLIRQIRTPL	ERDDLHESVF	RITEQEKLKK	ELERLKDDLG	TITNKCEEFF	SQAAASSSVP	TLRSELNVVL	QNMNQVYSMS
1290	1300	1310	1320	1330	1340	1350	1360
STYIDKLKTV	NLVLKNTQAA	EALVKLYETK	LCEEEAVIAD	KNNIENLIST	LKQWRSEVDE	KRQVFHALED	ELQKAKAISD
1370	1380	1390	1400	1410	1420	1430	1440
EMFKTYKERD	LDFDWHKEKA	DQLVERWQNV	HVQIDNRLRD	LEGIGKSLKY	YRDTYHPLDD	WIQQVETTQR	KIQENQPENS
1450	1460	1470	1480	1490	1500	1510	1520
KTLATQLNQQ	KMLVSEIEMK	QSKMDECQKY	AEQYSATVKD	YELQTMTYRA	MVDSQQKSPV	KRRRMQSSAD	LIIQEFMDLR
1530	1540	1550	1560	1570	1580	1590	1600
TRYTALVTLM	TQYIKFAGDS	LKRLEEEEKS	LEEEKKEHVE	KAKELQKWVS	NISKTLKDAE	KAGKPPFSKQ	KISSEEISTK
1610	1620	1630	1640	1650	1660	1670	1680
KEQLSEALQT	IQLFLAKHGD	KMTDEERNEL	EKQVKTLQES	YNLLFSESLK	QLQESQTSGD	VKVEEKLDKV	IAGTIDQTTG
1690	1700	1710	1720	1730	1740	1750	1760
EVLSVFQAVL	RGLIDYDTGI	RLLETQLMIS	GLISPELRKC	FDLKDAKSHG	LIDEQILCQL	KELSKAKEII	SAASPTTIPV
1770	1780	1790	1800	1810	1820	1830	1840
LDALAQSMIT	ESMAIKVLEI	LLSTGSLVIP	ATGEQLTLQK	AFQQNLVSSA	LFSKVLERQN	MCKDLIDPCT	SEKVSLIDMV
1850	1860	1870	1880	1890	1900	1910	1920
QRSTLQENTG	MWLLPVRPQE	GGRITLKCGR	NISILRAAHE	GLIDRETMFR	LLSAQLLSGG	LINSNSGQRM	TVEEAVREGV
1930	1940	1950	1960	1970	1980	1990	2000
IDRDTASSIL	TYQVQTGGII	QSNPAKRLTV	DEAVQCDLIT	SSSALLVLEA	QRGYVGLIWP	HSGEIFPTSS	SLQQELITNE
2010	2020	2030	2040	2050	2060	2070	2080
LAYKILNGRQ	KIAALYIPES	SQVIGLDAAK	QLGIIDNNTA	SILKNITLPD	KMPDLGDLEA	CKNARRWLSF	CKFQPSTVHD
2090	2100	2110	2120	2130	2140	2150	2160
YRQEEDVFDG	EEPVTTQTSE	ETKKLFLSYL	MINSYMDANT	GQRLLLYDGD	LDEAVGMLLE	GCHAEFDGNT	AIKECLDVLS
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
1902	1	805.7986	-138.23	2	54.1	11.0	1	3613-3626	R.TKQIMLAIDSEMSK.L	Oxidation: 12
779	1	1105.2011	129.15	2	38.2	12.7	2	4246-4264	K.TLDDIVGRYEDLSKSVNER.N	
2575	1	588.6984	-194.01	2	60.9	10.5	0	6269-6278	K.LLDVMELAEK.F	Oxidation: 5
1793	3	781.2979	-163.01	2	52.8	12.6	2	6886-6899	R.SLKEKTSLADDNLK.L	

Detailed Protein Report

Protein 44:	**myosin-6 [Homo sapiens]**		
Accession:	gi|156104908	**Score:**	63.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	223.6
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MTDAQMADFG	AAAQYLRKSE	KERLEAQTRP	FDIRTECFVP	DDKEEFVKAK	ILSREGGKVI	AETENGKTVT	VKEDQVLQQN
90	100	110	120	130	140	150	160
PPKFDKIEDM	AMLTFLHEPA	VLFNLKERYA	AWMIYTYSGL	FCVTVNPYKW	LPVYNAEVVA	AYRGKKRSEA	PPHIFSISDN
170	180	190	200	210	220	230	240
AYQYMLTDRE	NQSILITGES	GAGKTVNTKR	VIQYFASIAA	IGDRGKKDNA	NANKGTLEDQ	IIQANPALEA	FGNAKTVRND
250	260	270	280	290	300	310	320
NSSRFGKFIR	IHFGATGKLA	SADIETYLLE	KSRVIFQLKA	ERNYHIFYQI	LSNKKPELLD	MLLVTNNPYD	YAFVSQGEVS
330	340	350	360	370	380	390	400
VASIDDSEEL	MATDSAFDVL	GFTSEEKAGV	YKLTGAIMHY	GNMKFKQKQR	EEQAEPDGTE	DADKSAYLMG	LNSADLLKGL
410	420	430	440	450	460	470	480
CHPRVKVGNE	YVTKGQSVQQ	VYYSIGALAK	AVYEKMFNWM	VTRINATLET	KQPRQYFIGV	LDIAGFEIFD	FNSFEQLCIN
490	500	510	520	530	540	550	560
FTNEKLQQFF	NHHMFVLEQE	EYKKEGIEWT	FIDFGMDLQA	CIDLIEKPMG	IMSILEEECM	FPKATDMTFK	AKLYDNHLGK
570	580	590	600	610	620	630	640
SNNFQKPRNI	KGKQEAHFSL	IHYAGTVDYN	ILGWLEKNKD	PLNETVVALY	QKSSLKLMAT	LFSSYATADT	GDSGKSKGGK
650	660	670	680	690	700	710	720
KKGSSFQTVS	ALHRENLNKL	MTNLRTTHPH	FVRCIIPNER	KAPGVMDNPL	VMHQLRCNGV	LEGIRICRKG	FPNRILYGDF
730	740	750	760	770	780	790	800
RQRYRILNPV	AIPEGQFIDS	RKGTEKLLSS	LDIDHNQYKF	GHTKVFFKAG	LLGLLEEMRD	ERLSRIITRM	QAQARGQLMR
810	820	830	840	850	860	870	880
IEFKKIVERR	DALLVIQWNI	RAFMGVKNWP	WMKLYFKIKP	LLKSAETEKE	MATMKEEFGR	IKETLEKSEA	RRKELEEKMV
890	900	910	920	930	940	950	960
SLLQEKNDLQ	LQVQAEQDNL	NDAEERCDQL	IKNKIQLEAK	VKEMNERLED	EEEMNAELTA	KKRKLEDECS	ELKKDIDDLE
970	980	990	1000	1010	1020	1030	1040
LTLAKVEKEK	HATENKVKNL	TEEMAGLDEI	IAKLTKEKKA	LQEAHQQALD	DLQVEEDKVN	SLSKSKVKLE	QQVDDLEGSL
1050	1060	1070	1080	1090	1100	1110	1120
EQEKKVRMDL	ERAKRKLEGD	LKLTQESIMD	LENDKLQLEE	KLKKKEFDIN	QQNSKIEDEQ	VLALQLQKKL	KENQARIEEL
1130	1140	1150	1160	1170	1180	1190	1200
EEELEAERTA	RAKVEKLRSD	LSRELEEISE	RLEEAGGATS	VQIEMNKKRE	AEFQKMRRDL	EEATLQHEAT	AAALRKKHAD
1210	1220	1230	1240	1250	1260	1270	1280
SVAELGEQID	NLQRVKQKLE	KEKSEFKLEL	DDVTSNMEQI	IKAKANLEKV	SRTLEDQANE	YRVKLEEAQR	SLNDFTTQRA
1290	1300	1310	1320	1330	1340	1350	1360
KLQTENGELA	RQLEEKEALI	SQLTRGKLSY	TQQMEDLKRQ	LEEEGKAKNA	LAHALQSARH	DCDLLREQYE	EETEAKAELQ
1370	1380	1390	1400	1410	1420	1430	1440
RVLSKANSEV	AQWRTKYETD	AIQRTEELEE	AKKKLAQRLQ	DAEEAVEAVN	AKCSSLEKTK	HRLQNEIEDL	MVDVERSNAA
1450	1460	1470	1480	1490	1500	1510	1520
AAALDKKQRN	FDKILAEWKQ	KYEESQSELE	SSQKEARSLS	TELFKLKNAY	EESLEHLETF	KRENKNLQEE	ISDLTEQLGE
1530	1540	1550	1560	1570	1580	1590	1600
GGKNVHELEK	VRKQLEVEKL	ELQSALEEAE	ASLEHEEGKI	LRAQLEFNQI	KAEIERKLAE	KDEEMEQAKR	NHQRVVDSLQ
1610	1620	1630	1640	1650	1660	1670	1680
TSLDAETRSR	NEVLRVKKKM	EGDLNEMEIQ	LSHANRMAAE	AQKQVKSLQS	LLKDTQIQLD	DAVRANDDLK	ENIAIVERRN
1690	1700	1710	1720	1730	1740	1750	1760
NLLQAELEEL	RAVVEQTERS	RKLAEQELIE	TSERVQLLHS	QNTSLINQKK	KMESDLTQLQ	SEVEEAVQEC	RNAEEKAKKA
1770	1780	1790	1800	1810	1820	1830	1840
ITDAAMMAEE	LKKEQDTSAH	LERMKKNMEQ	TIKDLQHRLD	EAEQIALKGG	KKQLQKLEAR	VRELEGELEA	EQKRNAESVK
1850	1860	1870	1880	1890	1900	1910	1920
GMRKSERRIK	ELTYQTEEDK	KNLLRLQDLV	DKLQLKVKAY	KRQAEEAEEQ	ANTNLSKFRK	VQHELDEAEE	RADIAESQVN
1930	1940						
KLRAKSRDIG	AKQKMHDEE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2955	1	953.4514	-13.99	2	66.1	12.0	2	928-943	R.LEDEEEMNAELTAKKR.K	
202	1	561.6237	-229.75	2	31.3	12.3	0	945-953	K.LEDECSELK.K	Carbamidomethyl: 5
1892	1	628.2831	-7.98	2	54.0	13.1	0	1851-	K.ELTYQTEEDK.K	

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
								1860		

Detailed Protein Report

Protein 45: **14-3-3 protein sigma [Homo sapiens]**

Accession: gi|5454052
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 62.7
MW [kDa]: 27.8
pI: 4.5
Sequence Coverage [%]: 11.3
No. of unique Peptides: 2

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	2	1051.3758	-123.72	2	55.8	15.4	2	10-27	K.AKLAEQAERYEDMAAFMK.G	
2725	2	595.3333	-1.39	2	65.2	47.3	0	215-224	K.DSTLIMQLLR.D	

Detailed Protein Report

Protein 46: **pyruvate kinase PKM isoform a [Homo sapiens]**

Accession:	gi|33286418	**Score:**	61.9
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

QD:QU **Median:** 1.21 **CV:** 15.59 % **No. of Peptides:** 2

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	
859	2	599.3167	-17.70	2	39.2	51.2	0	33-43	R.LDIDSPPITAR.N		QD:QU	1.41
183	1	628.6439	7.16	3	32.3	10.8	0	74-89	R.LNFSHGTHEYHAETIK.N		QD:QU	1.04

Detailed Protein Report

Protein 47: glyceraldehyde-3-phosphate dehydrogenase isoform 2 [Homo sapiens]

Accession:	gi|378404908	**Score:**	60.9
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

QD:QU **Median:** 3.46 **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
772	2	917.4517	-12.88	2	39.6	40.3	0	104-120	K.IISNASCTTNCLAPLAK.V	Carbamidomethyl: 7, 11	QD:QU 3.46
1648	3	882.4064	1.76	2	50.9	20.6	0	268-281	K.LISWYDNEFGYSNR.V		

Detailed Protein Report

Protein 48: PREDICTED: dedicator of cytokinesis protein 11 isoform X2 [Homo sapiens]

Accession:	gi|530422336	**Score:**	60.8
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:	4

Detailed Protein Report

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	2	682.9130	127.21	2	57.2	18.0	1	279-289	R.SMHPELMKYGR.E	Oxidation: 7
1995	1	682.7325	-137.16	2	53.4	18.8	1	279-289	R.SMHPELMKYGR.E	Oxidation: 2
2045	1	731.3221	-60.47	2	56.0	10.6	1	1650-1662	K.KITPNIDEEGAMK.E	Oxidation: 12

Detailed Protein Report

Protein 49: **hemoglobin subunit epsilon [Homo sapiens]**

Accession: gi|4885393
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 60.7
MW [kDa]: 16.2
pI: 9.4
Sequence Coverage [%]: 15.0
No. of unique Peptides: 1

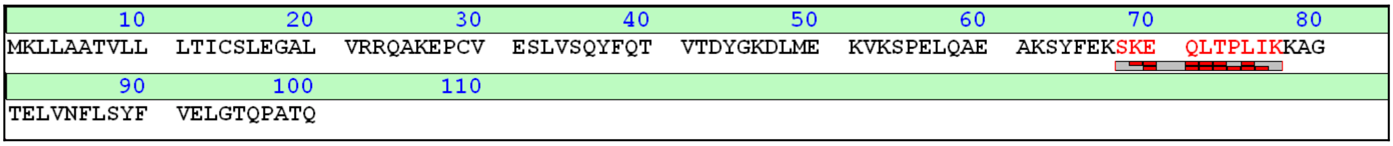
```
        10         20         30         40         50         60         70         80
MVHFTAEEKA AVTSLWSKMN VEEAGGEALG RLLVVYPWTQ RFFDSFGNLS SPSAILGNPK VKAHGKKVLT SFGDAIKNMD
        90        100        110        120        130        140        150
NLKPAFAKLS ELHCDKLHVD PENFKLLGNV MVIILATHFG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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2153	1	596.7262	-248.11	2	57.3	11.8	0	134-145	K.LVSAVAIALAHK.Y	

Detailed Protein Report

Protein 50: apolipoprotein A-II preproprotein [Homo sapiens]

Accession:	gi|4502149	**Score:**	60.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.2
Database Date:	2015-11-30	**pI:**	7.1
		Sequence Coverage [%]:	10.0
		No. of unique Peptides:	1



```
        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	

Detailed Protein Report

Protein 51: DNA-dependent protein kinase catalytic subunit isoform 1 [Homo sapiens]

Accession:	gi|13654237	**Score:**	59.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	468.8
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	4

Quantitation

QD:QU	**Median:**	9.31	**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	2	473.1745	-251.80	2	44.3	15.1	0	1643-1651	K.MAVLALLAK.I	Oxidation: 1	
935	1	512.1405	-273.82	2	41.8	10.3	0	2434-2441	K.VCLDIIYK.M	Carbamidomethyl: 2	QD:QU 9.31
272	1	898.1750	46.75	3	33.4	12.1	2	3030-3050	K.IWSEPFYQETYLPYMIRSKLK.L		
2232	1	937.4206	-14.54	2	56.5	22.1	1	3682-3696	K.ECSPWMSDFKVEFLR.N		

Detailed Protein Report

Protein 52: 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 53: 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 54: **dynein heavy chain 1, axonemal [Homo sapiens]**

Accession:	gi|197927452	**Score:**	58.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	487.2
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	4

Alias proteins:

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

Detailed Protein Report

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
1951	1	918.3840	-119.21	2	54.8	12.2	2	559-574	K.DSWISSLKVAMRSSLR.D	
2181	1	990.9291	-65.49	2	55.9	12.3	2	1828-1844	R.EACRNSNLKDVEGFLTK.C	Carbamidomethyl: 3
318	1	715.6717	-189.89	2	32.7	11.8	0	2496-2506	R.CMEQWEVTFNK.V	Oxidation: 2
972	1	730.6935	389.04	1	40.6	12.0	0	3422-3428	K.AAEIQAK.V	

Detailed Protein Report

Protein 55: nesprin-2 isoform 1 [Homo sapiens]

Accession:	gi|118918403	**Score:**	58.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	795.9
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	2

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
289	1	715.8764	45.86	2	32.3	10.0	0	1817-1828	K.QYESVSDLFNTK.K	
2908	1	922.9773	-1.53	2	65.5	11.3	1	3576-3590	K.ELVQTEIQERHSFTK.E	

Detailed Protein Report

Protein 56: **PREDICTED: nesprin-1 isoform X19 [Homo sapiens]**

Accession:	gi|578812604	**Score:**	57.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	1002.8
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	4

Detailed Protein Report

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1807	1	945.8341	-138.33	2	51.1	10.6	2	1681-1698	R.GEAKASSPEMDISADRVK.V	
742	1	524.3579	134.01	2	37.8	10.5	1	2443-2452	R.TGDSKVLEAK.L	
280	1	607.8593	-49.80	2	33.5	10.5	1	3327-3337	R.TLKLEALLSVK.Q	
2878	1	913.4666	-41.53	2	65.2	14.8	1	7089-7104	K.EVEKIEQNGLALIQNK.K	

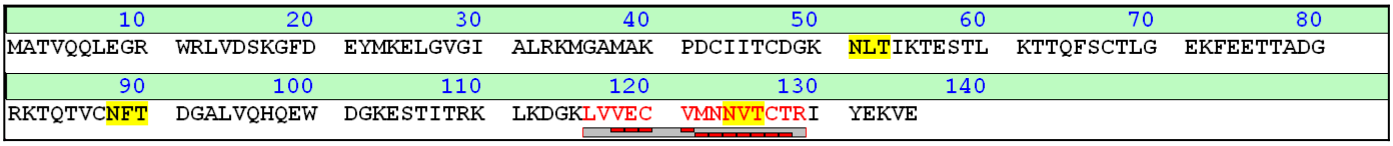
Detailed Protein Report

Protein 57: 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

Quantitation

QD:QU **Median:** 2.02 **CV:** 0.00 % **No. of 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	Ratios
1139	2	847.8676	-43.89	2	44.4	57.2	0	116-129	K.LVVECVMNNVTCTR.I	Carbamidomethyl: 5, 12	QD:QU 2.02

Protein 58: PREDICTED: intersectin-1 isoform X1 [Homo sapiens]

Accession: gi|530419020
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 57.2
MW [kDa]: 194.7
pI: 8.5
Sequence Coverage [%]: 3.1
No. of unique Peptides: 3

10	20	30	40	50	60	70	80
MAQFPTPFGG	SLDIWAITVE	ERAKHDQQFH	SLKPISGFIT	GDQARNFFFQ	SGLPQPVLAQ	IWALADMNND	GRMDQVEFSI
90	100	110	120	130	140	150	160
AMKLIKLKLQ	GYQLPSALPP	VMKQQPVAIS	SAPAFGMGGI	ASMPPLTAVA	PVPMGSIPVV	GMSPTLVSSV	PTAAVPPLAN
170	180	190	200	210	220	230	240
GAPPVIQPLP	AFAHPAATLP	KSSSFSRSGP	GSQLNTKLQK	AQSFDVASVP	PVAEWAVPQS	SRLKYRQLFN	SHDKTMSGHL
250	260	270	280	290	300	310	320
TGPQARTILM	QSSLPQAQLA	SIWNLSDIDQ	DGKLTAEEFI	LAMHLIDVAM	SGQPLPPVLP	PEYIPPSFRR	VRSGSGISVI
330	340	350	360	370	380	390	400
SSTSVDQRLP	EEPVLEDEQQ	QLEKKLPVTF	EDKKRENFER	GNLELEKRRQ	ALLEQQRKEQ	ERLAQLERAE	QERKERERQE
410	420	430	440	450	460	470	480
QERKRQLELE	KQLEKQRELE	RQREEERRKE	IERREAAKRE	LERQRQLEWE	RNRRQELLNQ	RNKEQEDIVV	LKAKKKTLEF
490	500	510	520	530	540	550	560
ELEALNDKKH	QLEGKLQDIR	CRLTTQRQEI	ESTNKSRELR	IAEITHLQQQ	LQESQQMLGR	LIPEKQILND	QLKQVQQNSL
570	580	590	600	610	620	630	640
HRDSLVTLKR	ALEAKELARQ	HLRDQLDEVE	KETRSKLQEI	DIFNNQLKEL	REIHNKQQLQ	KQKSMEAERL	KQKEQERKII
650	660	670	680	690	700	710	720
ELEKQKEEAQ	RRAQERDKQW	LEHVQQEDEH	QRPRKLHEEE	KLKREESVKK	KDGEEKGKQE	AQDKLGRLFH	QHQEPAKPAV
730	740	750	760	770	780	790	800
QAPWSTAEKG	PLTISAQENV	KVVYYRALYP	FESRSHDEIT	IQPGDIVMVD	ESQTGEPGWL	GGELKGKTGW	FPANYAEKIP
810	820	830	840	850	860	870	880
ENEVPAPVKP	VTDSTSAPAP	KLALRETPAP	LAVTSSEPST	TPNNWADFSS	TWPTSTNEKP	ETDNWDAWAA	QPSLTVPSAG
890	900	910	920	930	940	950	960
QLRQRSAFTP	ATATGSSPSP	VLGQGEKVEG	LQAQALYPWR	AKKDNHLNFN	KNDVITVLEQ	QDMWWFGEVQ	GQKGWFPKSY
970	980	990	1000	1010	1020	1030	1040
VKLISGPIRK	STSMDSGSSE	SPASLKRVAS	PAAKPVVSGE	EFIAMYTYES	SEQGDLTFQQ	GDVILVTKKD	GDWWTGTVGD
1050	1060	1070	1080	1090	1100	1110	1120
KAGVFPSNYV	RLKDSEGSGT	AGKTGSLGKK	PEIAQVIASY	TATGPEQLTL	APGQLILIRK	KNPGGWWEGE	LQARGKKRQI
1130	1140	1150	1160	1170	1180	1190	1200
GWFPANYVKL	LSPGTSKITP	TEPPKSTALA	AVCQVIGMYD	YTAQNDDELA	FNKGQIINVL	NKEDPDWWKG	EVNGQVGLFP
1210	1220	1230	1240	1250	1260	1270	1280
SNYVKLTTDM	DPSQQWCSDL	HLLDMLTPTE	RKRQGYIHEL	IVTEENYVND	LQLVTEIFQK	PLMESELLTE	KEVAMIFVNW
1290	1300	1310	1320	1330	1340	1350	1360
KELIMCNIKL	LKALRVRKKM	SGEKMPVKMI	GDILSAQLPH	MQPYIRFCSR	QLNGAALIQQ	KTDEAPDFKE	FVKRLAMDPR
1370	1380	1390	1400	1410	1420	1430	1440
CKGMPLSSFI	LKPMQRVTRY	PLIIKNILEN	TPENHPDHSH	LKHALEKAEE	LCSQVNEGVR	EKENSDRLEW	IQAHVQCEGL
1450	1460	1470	1480	1490	1500	1510	1520
SEQLVFNSVT	NCLGPRKFLH	SGKLYKAKSN	KELYGFLFND	FLLLTQITKP	LGSSGTDKVF	SPKSNLQYKM	YKTPIFLNEV
1530	1540	1550	1560	1570	1580	1590	1600
LVKLPTDPSG	DEPIFHISHI	DRVYTLRAES	INERTAWVQK	IKAASELYIE	TEKKKREKAY	LVRSQRATGI	GRLMVNVVEG
1610	1620	1630	1640	1650	1660	1670	1680
IELKPCRSHG	KSNPYCEVTM	GSQCHITKTI	QDTLNPKWNS	NCQFFIRDLE	QEVLCITVFE	RDQFSPDDFL	GRTEIRVADI
1690	1700	1710	1720				
KKDQGSKGPV	TKCLLLHEVP	TGEIVVRLDL	QLFDEP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
85	1	827.0046	76.69	2	31.0	15.0	1	73-86	R.MDQVEFSIAMKLIK.L	
2747	1	1045.5347	10.58	2	65.5	12.9	0	886-907	R.SAFTPATATGSSPSPVLGQGEK.V	

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2785	1	874.5334	88.10	1	63.9	14.2	1	1354-1360	K.RLAMDPR.C	Oxidation: 4

Detailed Protein Report

Protein 59: treslin [Homo sapiens]

Accession: gi|118421085
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 57.0
MW [kDa]: 210.7
pI: 9.8
Sequence Coverage [%]: 2.1
No. of unique Peptides: 4

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
1123	3	473.1123	-310.61	2	44.2	19.5	1	1005-1012	K.GDEISLRR.S	
2455	1	669.2124	-220.96	2	61.2	12.2	1	1311-1322	K.LFTSPLCDVSKK.S	
2584	1	658.2319	-124.03	2	61.0	10.7	0	1330-1341	K.IECPSPGELDQK.E	
1623	2	516.2455	-91.18	2	50.5	14.5	2	1786-1794	R.GAKRICDLR.E	

Detailed Protein Report

Protein 60: PREDICTED: keratin, type I cytoskeletal 24 isoform X1 [Homo sapiens]

Accession:	gi|578830527	**Score:**	55.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.1
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSCSSRASSS	RAGGSSSARV	SAGGSSFSSG	SRCGLGGSSA	QGFRGGASSC	SLSGGSSDKV	RALEEANTDL	ENKIKEWYDK
90	100	110	120	130	140	150	160
YGPGSGDGGS	GRDYSKYYSI	IEDLRNQIIA	ATVENAGIIL	HIDNARLAAD	DFRLKYENEL	CLRQSVEADI	NGLRKVLDDL
170	180	190	200	210	220	230	240
TMTRSDLEMQ	IESFTEELAY	LRKNHEEEMK	NMQGSSGGEV	TVEMNAAPGT	DLTKLLNDMR	AQYEELAEQN	RREAEERFNK
250	260	270	280	290	300	310	320
QSASLQAQIS	TDAGAATSAK	NEITELKRTL	QALEIELQSQ	LAMKSSLEGT	LADTEAGYVA	QLSEIQTQIS	ALEEEICQIW
330	340	350	360	370	380	390	400
GETKCQNAEY	KQLLDIKTRL	EVEIETYRRL	LDGEGGGSSF	AEFGGRNSGS	VNMGSRDLVS	GDSRSGSCSG	QGRDSSKTRV
410	420	430					
TKTIVEELVD	GKVVSSQVSS	ISEVKVK					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
587	1	512.7149	-24.47	2	35.9	12.9	0	367-376	R.NSGSVNMGSR.D	Oxidation: 7

Detailed Protein Report

Protein 61: DNA-directed RNA polymerase I subunit RPA2 isoform 4 [Homo sapiens]

Accession:	gi|544346215	**Score:**	55.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	107.8
Database Date:	2015-11-30	**pI:**	8.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MDPGSRWRNL	PSGPSLKHLT	DPSYGIPREQ	QKAALQELTR	AHVESFNYAV	HEGLGLAVQA	IPPFEFAFKD	ERISFTILDA
90	100	110	120	130	140	150	160
VISPPTVPKG	TICKEANVYP	AECRGRRSTY	RGKLTADINW	AVNGISKGII	KQFLGYVPIM	VKSKLCNLRN	LPPQALIEHH
170	180	190	200	210	220	230	240
EEAEEMGGYF	IINGIEKVIR	MLIMPRRNFP	IAMIRPKWKT	RGPGYTQYGV	SMHCVREEHS	AVNMNLHYLE	NGTVMLNFIY
250	260	270	280	290	300	310	320
RKELFFLPLG	FALKALVSFS	DYQIFQELIK	GKEDDSFLRN	SVSQMLRIVM	EEGCSTQKQV	LNYLGECFRV	KLNVPDWYPN
330	340	350	360	370	380	390	400
EQAAEFLFNQ	CICIHLKSNT	EKFYMLCLMT	RKLFALAKGE	CMEDNPDSLV	NQEVLTPGQL	FLMFLKGSLP	LMELPTDHTV
410	420	430	440	450	460	470	480
LREKRIPPWM	EVVLIPMTGK	PSLYPGLFLF	TTPCRLVRPV	QNLALGKEEL	IGTMEQIFMN	VAIFEDEVFA	GVTTHQELFP
490	500	510	520	530	540	550	560
HSLLSVIANF	IPFSDHNQSP	RNMYQCQMGK	QTMGFPLLTY	QDRSDNKLYR	LQTPQSPLVR	PSMYDYYDMD	NYPIGTNAIV
570	580	590	600	610	620	630	640
AVISYTGYDM	EDAMIVNKAS	WERGFAHGSV	YKSEFIDLSE	KIKQGDSSLV	FGIKPGDPRV	LQKLDDDGLP	FIGAKLQYGD
650	660	670	680	690	700	710	720
PYYSYLNLNT	GESFVMYYKS	KENCVVDNIK	VCSNDTGSGK	FKCVCITMRV	PRNPTIGDKF	ASRHGQKGIL	SRLWPAEDMP
730	740	750	760	770	780	790	800
FTESGMVPDI	LFNPHGFPSR	MTIGMLIESM	AGKSAALHGL	CHDATPFIFS	EENSALEYFG	EMLKAAGYNF	YGTERLYSGI
810	820	830	840	850	860	870	880
SGLELEADIF	IGVVYYQRLR	HMVSDKFQVR	TTGARDRVTN	QPIGGRNVQG	GIRFGEMERD	ALLAHGTSFL	LHDRLFNCSD
890	900	910	920	930	940	950	960
RSVAHVCVKC	GSLLSPLLEK	PPPSWSAMRN	RKYNCTLCSR	SDTIDTVSVP	YVFRYFVAEL	AAMNIKVKLD	VV

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
354	1	1026.5219	-20.89	2	34.4	35.4	1	387-404	K.GSLPLMELPTDHTVLREK.R	Oxidation: 6
2962	1	1019.9724	-91.71	2	66.2	19.9	2	935-952	R.YFVAELAAMNIKVKLDVV.-	Oxidation: 9

Detailed Protein Report

Protein 62:	**PREDICTED: striated muscle preferentially expressed protein kinase isoform X14 [Homo sapiens]**		
Accession:	gi|578803490	**Score:**	55.2
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:	2

Quantitation

QD:QU	**Median:** 3.82	**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	ALLKCMHFD	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
146	1	531.9457	-37.14	3	31.8	25.5	2	2089-2103	R.GPLLESLGGRARDPR.M		QD:QU 3.82
257	2	765.3459	-79.23	2	33.2	16.1	0	2578-2592	R.SESVPSLGLEAAIEK.L		

Detailed Protein Report

Protein 63: 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 64: **PREDICTED: ryanodine receptor 1 isoform X3 [Homo sapiens]**

Accession:	gi|578834746	**Score:**	54.2
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 [%]:**	1.1
		No. of unique Peptides:	3

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	PPATPTPLRL	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

Protein 65: **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

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
1649	2	942.4739	-4.87	2	50.9	53.5	0	56-71	K.FQDGDLTLYQSNTILR.H	

Detailed Protein Report

Protein 66: **coagulation factor VIII isoform a precursor [Homo sapiens]**

Accession:	gi|4503647	**Score:**	52.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	266.8
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	3

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2170	1	937.3499	-130.54	2	55.7	11.5	0	1-15	-.MQIELSTCFFLCLLR.F	Carbamidomethyl: 12
2966	1	953.4397	1.72	2	66.3	11.8	0	1101-1117	K.EGPIPPDAQNPDMSFFK.M	Oxidation: 13
843	1	653.3686	-17.24	2	40.6	10.7	2	1167-1178	K.NKVVVGKGEFTK.D	

Detailed Protein Report

Protein 67: **PREDICTED: centriolin isoform X3 [Homo sapiens]**

Accession:	gi|578817016	**Score:**	52.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	258.5
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	4

Detailed Protein Report

10	20	30	40	50	60	70	80
MKKGSQQKIF	SKAKIPSSSH	SPIPSSMSNM	RSRSLSPLIG	SETLPFHSGG	QWCEQVEIAD	ENNMLLDYQD	HKGADSHAGV
90	100	110	120	130	140	150	160
RYITEALIKK	LTKQDNLALI	KSLNLSLSKD	GGKKFKYIEN	LEKCVKLEVL	NLSYNLIGKI	EKLDKLLKLR	ELNLSYNKIS
170	180	190	200	210	220	230	240
KIEGIENMCN	LQKLNLAGNE	IEHIPVWLGK	KLKSLRVLNL	KGNKISSLQD	ISKLKPLQDL	ISLILVENPV	VTLPHYLQFT
250	260	270	280	290	300	310	320
IFHLRSLESL	EGQPVTTQDR	QEAFERFSLE	EVERLERDLE	KKMIETEELK	SKQTRFLEEI	KNQDKLNKSL	KEEAMLQKQS
330	340	350	360	370	380	390	400
CEELKSDLNT	KNELLKQKTI	ELTRACQKQY	ELEQELAFYK	IDAKFEPLNY	YPSEYAEIDK	APDESPYIGK	SRYKRNMFAT
410	420	430	440	450	460	470	480
ESYIIDSAQA	VQIKKMEPDE	QLRNDHMNLR	GHTPLDTQLE	DKEKKISAAQ	TRLSELHDEI	EKAEQQILRA	TEEFKQLEEA
490	500	510	520	530	540	550	560
IQLKKISEAG	KDLLYKQLSG	RLQLVNKLRQ	EALDLELQME	KQKQEIAGKQ	KEIKDLQIAI	DSLDSKDPKH	SHMKAQKSGK
570	580	590	600	610	620	630	640
EQQLDIMNKQ	YQQLESRLDE	ILSRIAKETE	EIKDLEEQLT	EGQIAANEAL	KKDLEGVISG	LQEYLGTIKG	QATQAQNECR
650	660	670	680	690	700	710	720
KLRDEKETLL	QRLTEVEQER	DQLEIVAMDA	ENMRKELAEL	ESALQEQHEV	NASLQQTQGD	LSAYEAELEA	RLNLRDAEAN
730	740	750	760	770	780	790	800
QLKEELEKVT	RLTQLEQSAL	QAELEKERQA	LKNALGKAQF	SEEKEQENSE	LHAKLKHLQD	DNNLLKQQLK	DFQNHLNHVV
810	820	830	840	850	860	870	880
DGLVRPEEVA	ARVDELRRKL	KLGTGEMNIH	SPSDVLGKSL	ADLQKQFSEI	LARSKWERDE	AQVRERKLQE	EMALQQEKLA
890	900	910	920	930	940	950	960
TGQEEFRQAC	ERALEARMNF	DKRQHEARIQ	QMENEIHYLQ	ENLKSMEEIQ	GLTDLQLQEA	DEEKERILAQ	LRELEKKKKL
970	980	990	1000	1010	1020	1030	1040
EDAKSQEQVF	GLDKELKKLK	KAVATSDKLA	TAELTIAKDQ	LKSLHGTVMK	INQERAEELQ	EAERFSRKAA	QAARDLTRAE
1050	1060	1070	1080	1090	1100	1110	1120
AEIELLQNLL	RQKGEQFRLE	MEKTGVGTGA	NSQVLEIEKL	NETMERQRTE	IARLQNVLDL	TGSDNKGGFE	NVLEEIAELR
1130	1140	1150	1160	1170	1180	1190	1200
REVSYQNDYI	SSMADPFKRR	GYWYFMPPPP	SSKVSSHSSQ	ATKDSGVGLK	YSASTPVRKP	RPGQQDGKEG	SQPPPASGYW
1210	1220	1230	1240	1250	1260	1270	1280
VYSPIRSGLH	KLFPSRDADS	GGDSQEESEL	DDQEEPPFVP	PPGYMMYTVL	PDGSPVPQGM	ALYAPPPPLP	NNSRPLTPGT
1290	1300	1310	1320	1330	1340	1350	1360
VVYGPPPAGA	PMVYGPPPPN	FSIPFIPMGV	LHCNVPEHHN	LENEVSRLED	IMQHLKSKKR	EERWMRASKR	QSEKEMEELH
1370	1380	1390	1400	1410	1420	1430	1440
HNIDDLLQEK	KSLECEVEEL	HRTVQKRQQQ	KDFIDGNVES	LMTELEIEKS	LKHHEDIVDE	IECIEKTLLK	RRSELREADR
1450	1460	1470	1480	1490	1500	1510	1520
LLAEAESELS	CTKEKTKNAV	EKFTDAKRSL	LQTESDAEEL	ERRAQETAVN	LVKADQQLRS	LQADAKDLEQ	HKIKQEEILK
1530	1540	1550	1560	1570	1580	1590	1600
EINKIVAAKD	SDFQCLSKKK	EKLTEELQKL	QKDIEMAERN	EDHHLQVLKE	SEVLLQAKRA	ELEKLKSQVT	SQQQEMAVLD
1610	1620	1630	1640	1650	1660	1670	1680
RQLGHKKEEL	HLLQGSMVQA	KADLQEALRL	GETEVTEKCN	HIREVKSLLE	ELSFQKGELN	VQISERKTQL	TLIKQEIEKE
1690	1700	1710	1720	1730	1740	1750	1760
EENLQVVLRQ	MSKHKTELKN	ILDMLQLENH	ELQGLKLQHD	QRVSELEKTQ	VAVLEEKLEL	ENLQQISQQQ	KGEIEWQKQL
1770	1780	1790	1800	1810	1820	1830	1840
LERDKREIER	MTAESRALQS	CVECLSKEKE	DLQEKCDIWE	KKLAQTKRVL	AAAEENSKME	QSNLEKLELN	VRKLQQELDQ
1850	1860	1870	1880	1890	1900	1910	1920
LNRDKLSLHN	DISAMQQQLQ	EKREAVNSLQ	EELANVQDHL	NLAKQDLLHT	TKHQDVLLSE	QTRLQKDISE	WANRFEDCQK
1930	1940	1950	1960	1970	1980	1990	2000
EEETKQQQLQ	VLQNEIEENK	LKLVQQEMMF	QRLQKERESE	ESKLETSKVT	LKEQQHQLEK	ELTDQKSKLD	QVLSKVLAAE
2010	2020	2030	2040	2050	2060	2070	2080
ERVRTLQEEE	RWCESLEKTL	SQTKRQLSER	EQQLVEKSGE	LLALQKEADS	MRADFSLLRN	QFLTERKKAE	KQVASLKEAL
2090	2100	2110	2120	2130	2140	2150	2160
KIQRSQLEKN	LLFLPELPAD	LEAILERNEN	LEGELESLKE	NLPFTMNEGP	FEEKLNFSQV	HIMDEHWRGE	ALREKLRHRE
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
951	1	677.3400	12.76	3	40.4	10.0	1	13-31	K.AKIPSSSHSPIPSSMSNMR.S	Oxidation: 18
1818	1	582.2582	-133.26	1	53.1	16.6	0	1602-1606	R.QLGHK.K	
1797	1	638.2204	-128.45	3	51.0	10.7	1	1771-1787	R.MTAESRALQSCVECLSK.E	Carbamidomethyl: 14
36	1	721.8221	18.43	2	30.3	15.4	1	1915-1925	R.FEDCQKEEETK.Q	Carbamidomethyl: 4

Detailed Protein Report

Protein 68: PREDICTED: rho GTPase-activating protein 26 isoform X6 [Homo sapiens]

Accession:	gi|530380462	**Score:**	51.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.9
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	9.0
		No. of unique 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
2004	1	710.2849	-115.96	2	55.4	11.7	1	35-48	R.ARHAGVPAVGPECR.A	
47	2	768.2750	-160.02	2	30.4	15.4	1	340-353	K.QITMVPFDQKSGGK.G	

Detailed Protein Report

Protein 69: PREDICTED: protein KIAA1199 isoform X3 [Homo sapiens]

Accession:	gi|578827243	**Score:**	51.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.7
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	4.2
		No. of unique Peptides:	1

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
737	1	936.9549	11.85	2	39.2	10.8	0	570-584	R.SHYYWDEDSGLLFLK.L	

Detailed Protein Report

Protein 70: myosin-7B [Homo sapiens]

Accession:	gi|114842389	**Score:**	51.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	225.7
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	3

Quantitation

QD:QU	**Median:**	1.05	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MSGNKRGSRA	SCPHRGAECL	LPWAALNLQG	FQLLLLHPSA	TAMMDVSELG	ESARYLRQGY	QEMTKVHTIP	WDGKKRVWVP
90	100	110	120	130	140	150	160
DEQDAYVEAE	VKSEATGGRV	TVETKDQKVL	MVREAELQPM	NPPRFDLLED	MAMMTHLNEA	SVLHNLRQRY	ARWMIYTYSG
170	180	190	200	210	220	230	240
LFCVTINPYK	WLPVYTASVV	AAYKGKRRSD	SPPHIYAVAD	NAYNDMLRNR	DNQSMLITGE	SGAGKTVNTK	RVIQYFAIVA
250	260	270	280	290	300	310	320
ALGDGPGKKA	QFLATKTGGT	LEDQIIEANP	AMEAFGNAKT	LRNDNSSRFG	KFIRIHFGPS	GKLASADIDS	YLLEKSRVIF
330	340	350	360	370	380	390	400
QLPGERSYHV	YYQILSGRKP	ELQDMLLLSM	NPYDYHFCSQ	GVITVDNMND	GEELIATDHA	MDILGFSVDE	KCACYKIVGA
410	420	430	440	450	460	470	480
LLHFGNMKFK	QKQREEQAEA	DGTESADKAA	YLMGVSSGDL	LKGLLHPRVR	VGNEYVTKGQ	SVEQVVFAVG	ALAKATYDRL
490	500	510	520	530	540	550	560
FRWLVSRINQ	TLDTKLPRQF	FIGVLDIAGF	EIFEFNSFEQ	LCINFTNEKL	QQFFNQHMFV	LEQEEYKREG	IDWVFIDFGL
570	580	590	600	610	620	630	640
DLQPCIDLIE	KPLGILSILE	EECMFPKASD	ASFRAKLYDN	HAGKSPNFQQ	PRPDKKRKYQ	AHFEVVHYAG	VVPYSIVGWL
650	660	670	680	690	700	710	720
EKNKDPLNET	VVPIFQKSQN	RLLATLYENY	AGSCSTEPPK	SGVKEKRKKA	ASFQTVSQLH	KENLNKLMTN	LRATQPHFVR
730	740	750	760	770	780	790	800
CIVPNENKTP	GVMDAFLVLH	QLRCNGVLEG	IRICRQGFPN	RLLYTDFRQR	YRILNPSAIP	DDTFMDSRKA	TEKLLGSLDL
810	820	830	840	850	860	870	880
DHTQYQFGHT	KVFFKAGLLG	VLEELRDQRL	AKVLTLLQAR	SRGRLMRLEY	QRLLGGRDAL	FTIQWNIRAF	NAVKNWSWMK
890	900	910	920	930	940	950	960
LFFKMKPLLR	SAQAEEELAA	LRAELRGLRG	ALAAAEAKRQ	ELEETHVSIT	QEKNDLALQL	QAEQDNLADA	EERCHLLIKS
970	980	990	1000	1010	1020	1030	1040
KVQLEGKVKE	LSERLEDEEE	VNADLAARRR	KLEDECTELK	KDIDDLKLTL	AKAEKEKQAT	ENKVKNLTEE	MAALDESVAR
1050	1060	1070	1080	1090	1100	1110	1120
LTKEKKALQE	AHQQALGDLQ	AEEDRVSALT	KAKLRLEQQV	EDLECSLEQE	KKLRMDTERA	KRKLEGDLKL	TQESVADAAQ
1130	1140	1150	1160	1170	1180	1190	1200
DKQQLEEKLK	KKDSELSQLS	LRVEDEQLLG	AQMQKKIKEL	QARAEELEEE	LEAERAARAR	VEKQRAEAAR	ELEELSERLE
1210	1220	1230	1240	1250	1260	1270	1280
EAGGASAGQR	EGCRKREAEL	GRLRRELEEA	ALRHEATVAA	LRRKQAEGAA	ELGEQVDSLQ	RVRQKLEKEK	SELRMEVDDL
1290	1300	1310	1320	1330	1340	1350	1360
AANVETLTRA	KASAEKLCRT	YEDQLSEAKI	KVEELQRQLA	DASTQRGRLQ	TESGELSRLL	EEKECLISQL	SRGKALAAQS
1370	1380	1390	1400	1410	1420	1430	1440
LEELRRQLEE	ESKAKSALAH	AVQALRHDCD	LLREQHEEEA	EAQAELQRLL	SKANAEVAQW	RSKYEADAIQ	RTEELEEAKK
1450	1460	1470	1480	1490	1500	1510	1520
KLALRLQEAE	EGVEAANAKC	SSLEKAKLRL	QTESEDVTLE	LERATSAAAA	LDKKQRHLER	ALEERRRQEE	EMQRELEAAQ
1530	1540	1550	1560	1570	1580	1590	1600
RESRGLGTEL	FRLRHGHEEA	LEALETLKRE	NKNLQEEISD	LTDQVSLSGK	SIQELEKTKK	ALEGEKSEIQ	AALEEAEGAL
1610	1620	1630	1640	1650	1660	1670	1680
ELEETKTLRI	QLELSQVKAE	VDRKLAEKDE	ECANLRRNHQ	RAVESLQASL	DAETRARNEA	LRLKKKMEGD	LNDLELQLGH
1690	1700	1710	1720	1730	1740	1750	1760
ATRQATEAQA	ATRLMQAQLK	EEQAGRDEEQ	RLAAELHEQA	QALERRASLL	AAELEELRAA	LEQGERSRRL	AEQELLEATE
1770	1780	1790	1800	1810	1820	1830	1840
RLNLLHSQNT	GLLNQKKKLE	ADLAQLSGEV	EEAAQERREA	EEKAKKAITD	AAMMAEELKK	EQDTSAHLER	MKKTLEQTVR
1850	1860	1870	1880	1890	1900	1910	1920
ELQARLEEAE	QAALRGGKKQ	VQKLEAKVRE	LEAELDAEQK	KHAEALKGVR	KHERRVKELA	YQAEEDRKNL	ARMQDLVDKL
1930	1940	1950	1960	1970	1980	1990	
QSKVKSYKRQ	FEEAEQQANT	NLAKYRKAQH	ELDDAEERAD	MAETQANKLR	ARTRDALGPK	HKE	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
987	1	574.1653	-236.77	2	40.8	12.3	0	1133-1142	K.DSELSQLSLR.V		QD:QU 1.05
2175	1	1031.4134	-120.21	2	55.8	11.8	2	1515-	R.ELEAAQRESRGLGTELFR.L		

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
								1532			
2480	3	625.3103	-63.96	2	61.5	13.4	2	1831-1840	R.MKKTLEQTVR.E	Oxidation: 1	

Detailed Protein Report

Protein 71: lysine-specific demethylase 3A [Homo sapiens]

Accession:	gi|20357522	**Score:**	51.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	147.2
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|226442779	refseq_human (refseq_human_20140103.fasta)	lysine-specific demethylase 3A [Homo sapiens]

10	20	30	40	50	60	70	80
MVLTLGESWP	VLVGRRFLSL	SAADGSDGSH	DSWDVERVAE	WPWLSGTIRA	VSHTDVTKKD	LKVCVEFDGE	SWRKRRWIEV
90	100	110	120	130	140	150	160
YSLLRRAFLV	EHNLVLAERK	SPEISERIVQ	WPAITYKPLL	DKAGLGSITS	VRFLGDQQRV	FLSKDLLKPI	QDVNSLRLSL
170	180	190	200	210	220	230	240
TDNQIVSKEF	QALIVKHLDE	SHLLKGDKNL	VGSEVKIYSL	DPSTQWFSAT	VINGNPASKT	LQVNCEEIPA	LKIVDPSLIH
250	260	270	280	290	300	310	320
VEVVHDNLVT	CGNSARIGAV	KRKSSENNGT	LVSKQAKSCS	EASPSMCPVQ	SVPTTVFKEI	LLGCTAATPP	SKDPRQQSTP
330	340	350	360	370	380	390	400
QAANSPPNLG	AKIPQGCHKQ	SLPEEISSCL	NTKSEALRTK	PDVCKAGLLS	KSSQIGTGDL	KILTEPKGSC	TQPKTNTDQE
410	420	430	440	450	460	470	480
NRLESVPQAL	TGLPKECLPT	KASSKAELEI	ANPPELQKHL	EHAPSPSDVS	NAPEVKAGVN	SDSPNNCSGK	KVEPSALACR
490	500	510	520	530	540	550	560
SQNLKESSVK	VDNESCCSRS	NNKIQNAPSR	KSVLTDPAKL	KKLQQSGEAF	VQDDSCVNIV	AQLPKCRECR	LDSLRKDKEQ
570	580	590	600	610	620	630	640
QKDSPVFCRF	FHFRRLQFNK	HGVLRVEGFL	TPNKYDNEAI	GLWLPLTKNV	VGIDLDTAKY	ILANIGDHFC	QMVISEKEAM
650	660	670	680	690	700	710	720
STIEPHRQVA	WKRAVKGVRE	MCDVCDTTIF	NLHWVCPRCG	FGVCVDCYRM	KRKNCQQGAA	YKTFSWLKCV	KSQIHEPENL
730	740	750	760	770	780	790	800
MPTQIIPGKA	LYDVGDIVHS	VRAKWGIKAN	CPCSNRQFKL	FSKPASKEDL	KQTSLAGEKP	TLGAVLQQNP	SVLEPAAVGG
810	820	830	840	850	860	870	880
EAASKPAGSM	KPACPASTSP	LNWLADLTSG	NVNKENKEKQ	PTMPILKNEI	KCLPPLPPLS	KSSTVLHTFN	STILTPVSNN
890	900	910	920	930	940	950	960
NSGFLRNLLN	SSTGKTENGL	KNTPKILDDI	FASLVQNKTT	SDLSKRPQGL	TIKPSILGFD	TPHYWLCDNR	LLCLQDPNNK
970	980	990	1000	1010	1020	1030	1040
SNWNVFRECW	KQGQPVMVSG	VHHKLNSELW	KPESFRKEFG	EQEVDLVNCR	TNEIITGATV	GDFWDGFEDV	PNRLKNEKEP
1050	1060	1070	1080	1090	1100	1110	1120
MVLKLKDWPP	GEDFRDMMPS	RFDDLMANIP	LPEYTRRDGK	LNLASRLPNY	FVRPDLGPKM	YNAYGLITPE	DRKYGTTNLH
1130	1140	1150	1160	1170	1180	1190	1200
LDVSDAANVM	VYVGIPKGQC	EQEEEVLKTI	QDGDSDELTI	KRFIEGKEKP	GALWHIYAAK	DTEKIREFLK	KVSEEQGQEN
1210	1220	1230	1240	1250	1260	1270	1280
PADHDPIHDQ	SWYLDRSLRK	RLHQEYGVQG	WAIVQFLGDV	VFIPAGAPHQ	VHNLYSCIKV	AEDFVSPEHV	KHCFWLTQEF
1290	1300	1310	1320	1330			
RYLSQTHTNH	EDKLQVKNVI	YHAVKDAVAM	LKASESSFGK	P			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
62	1	675.3854	139.53	2	29.5	11.1	0	457-470	K.AGVNSDSPNNCSGK.K	
755	1	472.1298	-292.09	2	39.4	27.4	0	840-847	K.QPTMPILK.N	Oxidation: 4

Detailed Protein Report

Protein 72: **biorientation of chromosomes in cell division protein 1-like 1 [Homo sapiens]**

Accession:	gi|87299628	**Score:**	51.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	330.3
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	1

Detailed Protein Report

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
TIKCAESLQP	VAAAVEERAT	GPVLISTADF	EGPMPSAPPE	AESPLASTSK	EEKDECALIS	TSIAEECEAS	VSGVVVESEN
2250	2260	2270	2280	2290	2300	2310	2320
ERAGTVMEEK	DGSGIISTSS	VEDCEGPVSS	AVPQEEGDPS	VTPAEEMGDT	AMISTSTSEG	CEAVMIGAVL	QDEDRLTITR
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
1228	1	954.9820	37.30	2	45.5	23.8	0	658-674	R.TSTPVIMEGVQEETDTR.D	Oxidation: 7

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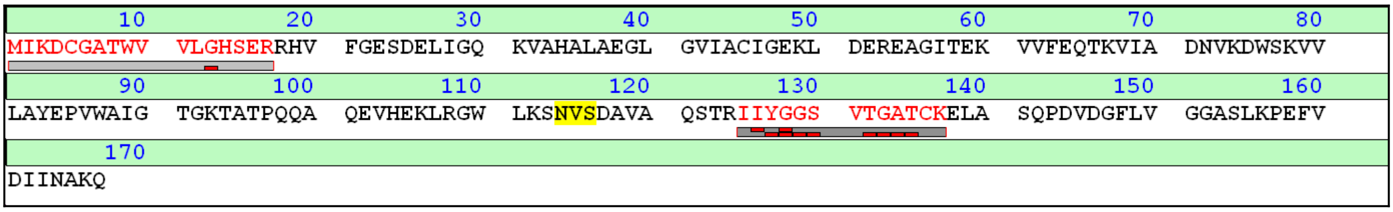
Detailed Protein Report

Protein 73: triosephosphate isomerase isoform 3 [Homo sapiens]

Accession:	gi|384475517	**Score:**	50.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.9
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	18.0
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 1.54 **CV:** 0.00 % **No. of 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	Ratios
2923	1	951.4595	-12.75	2	65.7	13.3	1	1-17	-.MIKDCGATWVVLGHSER.R		QD:QU 1.54
219	1	663.8152	-36.93	2	32.7	37.4	0	125-137	R.IIYGGSVTGATCK.E	Carbamidomethyl: 12	

Detailed Protein Report

Protein 74: dynein heavy chain 9, axonemal isoform 2 [Homo sapiens]

Accession:	gi|114155133	**Score:**	49.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	511.6
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	3

```
        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
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
106	1	1068.1367	75.32	2	30.1	13.8	2	182-201	K.GKTLLPLPAGSEKMEFADSK.S	Oxidation: 14
1912	2	634.8166	-103.44	2	54.3	17.9	0	2134-2144	K.VVQLEELLAVR.H	
1679	5	648.2912	-180.05	2	51.3	17.9	0	4475-4486	K.WVLAGVALLLQI.-	

Detailed Protein Report

Protein 75: **pogo transposable element with ZNF domain isoform 3 [Homo sapiens]**

Accession:	gi|302699211	**Score:**	49.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	145.2
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	4

Quantitation

QD:QU **Median:** 0.31 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MADTDLFMEC EEEELEPWQK ISDVIEDSVV EDYNSVDKTT TVSVSQQPVS APVPIAAHAS VAGHLSTSTT VSSSGAQNSD
        90        100        110        120        130        140        150        160
STKKTLVTLI ANNNAPGTQF VKPTVGVPQV FSQMTPVRPG STMPVRPTTN TFTTVIPATL TIRSTVPQSQ SQQTKSTPST
       170        180        190        200        210        220        230        240
STTPTATQPT SLGQLAVQSP GQSNQTTNPK LAPSFPSPPA VSIASFVTVK RPGVTGENSN EVAKLVNTLN TIPSLGQSPG
       250        260        270        280        290        300        310        320
PVVVSNNSSA HGSQRTSGPE SSMKVTSSIP VFDLQDGGRK ICPRCNAQFR VTEALRGHMC YCCPEMVEYQ KKGKSLDSEP
       330        340        350        360        370        380        390        400
SVPSAAKPPS PEKTAPVAST PSSTPIPALS PPTKVPEPNE NVGDAVQTKL IMLVDDFYYG RDGGKVAQLT NFPKVATSFR
       410        420        430        440        450        460        470        480
CPHCTKRLKN NIRFMNHMKH HVELDQQNGE VDGHTICQHC YRQFSTPFQL QCHLENVHSP YESTTKCKIC EWAFESEPLF
       490        500        510        520        530        540        550        560
LQHMKDTHKP GEMPYVCQVC QYRSSLYSEV DVHFRMIHED TRHLLCPYCL KVFKNGNAFQ QHYMRHQKRN VYHCNKCRLQ
       570        580        590        600        610        620        630        640
FLFAKDKIEH KLQHHKTFRK PKQLEGLKPG TKVTIRASRG QPRTVPVSSN DTPPSALQEA APLTSSMDPL PVFLYPPVQR
       650        660        670        680        690        700        710        720
SIQKRAVRKM SVMGRQTCLE CSFEIPDFPN HFPTYVHCSL CRYSTCCSRA YANHMINNHV PRKSPKYLAL FKNSVSGIKL
       730        740        750        760        770        780        790        800
ACTSCTFVTS VGDAMAKHLV FNPSHRSSSI LPRGLTWIAH SRHGQTRDRV HDRNVKNMYP PPSFPTNKAA TVKSAGATPA
       810        820        830        840        850        860        870        880
EPEELLTPLA PALPSPASTA TPPPTPTHPQ ALALPPLATE GAECLNVDDQ DEGSPVTQEP ELASGGGGSG GVGKKEQLSV
       890        900        910        920        930        940        950        960
KKLRVVLFAL CCNTEQAAEH FRNPQRRIRR WLRRFQASQG ENLEGKYLSF EAEEKLAEWV LTQREQQLPV NEETLFQKAT
       970        980        990       1000       1010       1020       1030       1040
KIGRSLEGGF KISYEWAVRF MLRHHLTPHA RRAVAHTLPK DVAENAGLFI DFVQRQIHNQ DLPLSMIVAI DEISLFLDTE
      1050       1060       1070       1080       1090       1100       1110       1120
VLSSDDRKEN ALQTVGTGEP WCDVVLAILA DGTVLPTLVF YRGQMDQPAN MPDSILLEAK ESGYSDDEIM ELWSTRVWQK
      1130       1140       1150       1160       1170       1180       1190       1200
HTACQRSKGM LVMDCHRTHL SEEVLAMLSA SSTLPAVVPA GCSSKIQPLD VCIKRTVKNF LHKKWKEQAR EMADTACDSD
      1210       1220       1230       1240       1250       1260       1270       1280
VLLQLVLVWL GEVLGVIGDC PELVQRSFLV ASVLPGPDGN INSPTRNADM QEELIASLEE QLKLSGEHSE SSTPRPRSSP
      1290       1300       1310       1320
EETIEPESLH QLFEGESETE SFYGFEEADL DLMEI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
343	1	939.2438	-175.61	1	34.3	13.8	0	256-264	R.TSGPESSMK.V	Oxidation: 8	
240	1	732.8262	-63.03	2	31.7	14.2	1	285-296	R.CNAQFRVTEALR.G	Carbamidomethyl: 1	QD:QU 0.31
2117	1	990.8950	2.39	2	55.0	10.3	1	297-312	R.GHMCYCCPEMVEYQKK.G	Oxidation: 3, 10	
2186	1	1031.8206	-95.59	2	55.9	11.0	1	297-312	R.GHMCYCCPEMVEYQKK.G	Carbamidomethyl: 4, 6	

Detailed Protein Report

Protein 76: **SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 [Homo sapiens]**

Accession:	gi|325651836	**Score:**	49.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	121.8
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	2

```
        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
2920	2	710.3768	22.23	2	65.7	14.6	1	431-443	K.DIDILNSAGKMDK.M	
971	1	706.9594	14.52	2	42.2	20.7	2	485-496	K.MVVLDKLLPKLK.E	Oxidation: 1

Detailed Protein Report

Protein 77: keratin, type II cuticular Hb4 [Homo sapiens]

Accession:	gi|15431316	**Score:**	48.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.8
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	5.8
		No. of unique Peptides:	2

Quantitation

QD:QU	**Median:** 1.02	**CV:** 61.49 %	**No. of Peptides:** 2

10	20	30	40	50	60	70	80
MSCRSYRVSS	GHRVGNFSSC	SAMTPQNLNR	FRANSVSCWS	GPGFRGLGSF	GSRSVITFGS	YSPRIAAVGS	RPIHCGVRFG
90	100	110	120	130	140	150	160
AGCGMGFGDG	RGVGLGPRAD	SCVGLGFGAG	SGIGYGFGGP	GFGYRVGGVG	VPAAPSITAV	TVNKSLLTPL	NLEIDPNAQR
170	180	190	200	210	220	230	240
VKKDEKEQIK	TLNNKFASFI	DKVRFLEQQN	KLLETKWSFL	QEQKCIRSNL	EPLFESYITN	LRRQLEVLVS	DQARLQAERN
250	260	270	280	290	300	310	320
HLQDVLEGFK	KKYEEEVVCR	ANAENEFVAL	KKDVDAAFMN	KSDLEANVDT	LTQEIDFLKT	LYMEEIQLLQ	SHISETSVIV
330	340	350	360	370	380	390	400
KMDNSRDLNL	DGIIAEVKAQ	YEEVARRSRA	DAEAWYQTKY	EEMQVTAGQH	CDNLRNIRNE	INELTRLIQR	LKAEIEHAKA
410	420	430	440	450	460	470	480
QRAKLEAAVA	EAEQQGEATL	SDAKCKLADL	ECALQQAKQD	MARQLCEYQE	LMNAKLGLDI	EIATYRRLLE	GEESRLCEGV
490	500	510	520	530	540	550	560
GPVNISVSSS	RGGLVCGPEP	LVAGSTLSRG	GVTFSGSSSV	CATSGVLASC	GPSLGGARVA	PATGDLLSTG	TRSGSMLISE
570	580	590	600	610			
ACVPSVPCPL	PTQGGFSSCS	GGRSSSVRFV	STTTSCRTKY				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
535	2	607.3148	1.02	2	36.7	15.6	0	54-64	R.SVITFGSYSPR.I		QD:QU	1.80
816	1	652.6427	-181.17	2	38.7	11.9	0	79-91	R.FGAGCGMGFGDGR.G	Carbamidomethyl: 5; Oxidation: 7	QD:QU	0.58

Detailed Protein Report

Protein 78: PREDICTED: sp110 nuclear body protein isoform X3 [Homo sapiens]

Accession: gi|530370295
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 48.3
MW [kDa]: 58.5
pI: 10.2
Sequence Coverage [%]: 13.5
No. of unique Peptides: 3

10	20	30	40	50	60	70	80
MNAEEDSEEM	PSLLTSTVQV	ASDNLIPQIR	DKEDPQEMPH	SPLGSMPEIR	DNSPEPNDPE	EPQEVSSTPS	DKKGKKRKRC
90	100	110	120	130	140	150	160
IWSTPKRRHK	KKSLPGGTAS	SRHGIQKKLK	RVDQVPQKKD	DSTCNSTVET	RAQKARTECA	RKSRSEEIID	GTSEMNEGKR
170	180	190	200	210	220	230	240
SQKTPSTPRR	VTQGAASPGH	GIQEKLQVVD	KVTQRKDDST	WNSEVMMRVQ	KARTKCARKS	RLKEKKKEKD	ICSSSKRRFQ
250	260	270	280	290	300	310	320
KNIHRRGKPK	SDTVDFHCSK	LPVTCGEAKG	ILYKKKMKHG	SSVKCIRNED	GTWLTPNEFE	VEGKGRNAKN	WKRNIRCEGM
330	340	350	360	370	380	390	400
TLGELLKRKN	SDECEVCCQG	GQLLCCGTCP	RVFHEDCHIP	PVEAKRMLWS	CTFCRMKRSS	GSQQCHHVSK	TLERQMQPQD
410	420	430	440	450	460	470	480
QLKCEFLLLK	AYCHPQSSFF	TGIPFNIRDY	GEPFQEAMWL	DLVKERLITE	MYTVAWFVRD	MRLMFRNHKT	FYKASDFGQV
490	500	510	520				
GLDLEAEFEK	DLKDVLGFHE	ANDGGFWTLP					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
220	1	978.1311	-3.65	3	32.7	10.8	2	279-304	K.HGSSVKCIRNEDGTWLTPNEFEVEGK.G	
1829	1	781.3008	-84.17	2	53.2	11.5	2	366-377	K.RMLWSCTFCRMK.R	
2818	1	989.4652	-45.70	2	64.4	15.5	1	395-410	R.QMQPQDQLKCEFLLLK.A	Oxidation: 2

Detailed Protein Report

Protein 79: PREDICTED: ubiquitin carboxyl-terminal hydrolase 24 isoform X2 [Homo sapiens]

Accession:	gi|530362260	**Score:**	48.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	228.6
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	2

Quantitation

QD:QU	**Median:**	0.45	**CV:**	0.00 %		**No. of Peptides:**	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MDSRQQGGLT	GDYVSLPGYT	ETKQRSSQLN	NPQFVWVVPA	LRQLHEITRS	FIKQTYQKQD	KSIIQDLKKN	FEIVKLVTGS
90	100	110	120	130	140	150	160
LIACHRLAAA	VAGPGGLSGS	TLVDGRYTYR	EYLEAHLKFL	AFFLQEATLY	LGWNRAKEIW	ECLVTGQDVC	ELDREMCFEW
170	180	190	200	210	220	230	240
FTKGQHDLES	DVQQQLFKEK	ILKLESYEIT	MNGFNLFKTF	FENVNLCDHR	LKRQGAQLYV	EKLELIGMDF	IWKIAMESPD
250	260	270	280	290	300	310	320
EEIANEAIQL	IINYSYINLN	PRLKKDSVSL	HKKFIADCYT	RLEAASSALG	GPTLTHAVTR	ATKMLTATAM	PTVATSVQSP
330	340	350	360	370	380	390	400
YRSTKLVIIE	RLLLLAERYV	ITIEDFYSVP	RTILPHGASF	HGHLLTLNVT	YESTKDTFTV	EAHSNETIGS	VRWKIAKQLC
410	420	430	440	450	460	470	480
SPVDNIQIFT	NDSLLTVNKD	QKLLHQLGFS	DEQILTVKTS	GSGTPSGSSA	DSSTSSSSSS	SGVFSSSYAM	EQEKSLPGVV
490	500	510	520	530	540	550	560
MALVCNVFDM	LYQLANLEEP	RITLRVRKLL	LLIPTDPAIQ	EALDQLDSLG	RKKTLLSESS	SQSSKSPSLS	SKQQHQPSAS
570	580	590	600	610	620	630	640
SILESLFRSF	APGMSTFRVL	YNLEVLSSKL	MPTADDDMAR	SCAKSFCENF	LKAGGLSLVV	NVMQRDSIPS	EVDYETRQGV
650	660	670	680	690	700	710	720
YSICLQLARF	LLVGQTMPTL	LDEDLTKDGI	EALSSRPFRN	VSRQTSRQMS	LCGTPEKSSY	RQLSVSDRSS	IRVEEIIPAA
730	740	750	760	770	780	790	800
RVAIQTMEVS	DFTSTVACFM	RLSWAAAAGR	LDLVGSSQPI	KESNSLCPAG	IRNRLSSSGS	NCSSGSEGEP	VALHAGICVR
810	820	830	840	850	860	870	880
QQSVSTKDSL	IAGEALSLLV	TCLQLRSQQL	ASFYNLPCVA	DFIIDILLGS	PSAEIRRVAC	DQLYTLSQTD	TSAHPDVQKP
890	900	910	920	930	940	950	960
NQFLLGVILT	AQLPLWSPTS	IMRGVNQRLL	SQCMEYFDLR	CQLLDDLTTS	EMEQLRISPA	TMLEDEITWL	DNFEPNRTAE
970	980	990	1000	1010	1020	1030	1040
CETSEADNIL	LAGHLRLIKT	LLSLCGAEKE	MLGSSLIKPL	LDDFLFRASR	IILNSHSPAG	SAAISQQDFH	PKCSTANSRL
1050	1060	1070	1080	1090	1100	1110	1120
AAYEVLVMLA	DSSPSNLQII	IKELLSMHHQ	PDPALTKEFD	YLPPVDSRSS	SGFVGLRNGG	ATCYMNAVFQ	QLYMQPGLPE
1130	1140	1150	1160	1170	1180	1190	1200
SLLSVDDDTD	NPDDSVFYQV	QSLFGHLMES	KLQYYVPENF	WKIFKMWNKE	LYVREQQDAY	EFFTSLIDQM	DEYLKKMGRD
1210	1220	1230	1240	1250	1260	1270	1280
QIFKNTFQGI	YSDQKICKDC	PHRYEREEAF	MALNLGVTSC	QSLEISLDQF	VRGEVLEGSN	AYYCEKCKEK	RITVKRTCIK
1290	1300	1310	1320	1330	1340	1350	1360
SLPSVLVIHL	MRFGFDWESG	RSIKYDEQIR	FPWMLNMEPY	TVSGMARQDS	SSEVGENGRS	VDQGGGGSPR	KKVALTENYE
1370	1380	1390	1400	1410	1420	1430	1440
LVGVIVHSGQ	AHAGHYYSFI	KDRRGCGKGK	WYKFNDTVIE	EFDLNDETLE	YECFGGEYRP	KVYDQTNPYT	DVRRRYWNAY
1450	1460	1470	1480	1490	1500	1510	1520
MLFYQRVSDQ	NSPVLPKKSR	VSVVRQEAED	LSLSAPSSPE	ISPQSSPRPH	RPNNDRLSIL	TKLVKKGEKK	GLFVEKMPAR
1530	1540	1550	1560	1570	1580	1590	1600
IYQMVRDENL	KFMKNRDVYS	SDYFSFVLSL	ASLNATKLKH	PYYPCMAKVS	LQLAIQFLFQ	TYLRTKKKLR	VDTEEWIATI
1610	1620	1630	1640	1650	1660	1670	1680
EALLSKSFDA	CQWLVEYFIS	SEGRELIKIF	LLECNVREVR	VAVATILEKT	LDSALFYQDK	LKSLHQLLEV	LLALLDKDVP
1690	1700	1710	1720	1730	1740	1750	1760
ENCKNCAQYF	FLFNTFVQKQ	GIRAGDLLLR	HSALRHMISF	LLGASRQNNQ	IRRWSSAQAR	EFGNLHNTVA	LLVLHSDVSS
1770	1780	1790	1800	1810	1820	1830	1840
QRNVAPGIFK	QRPPISIAPS	SPLLPLHEEV	EALLFMSEGK	PYLLEVMFAL	RELTGSLLAL	IEMVVYCCFC	NEHFSFTMLH
1850	1860	1870	1880	1890	1900	1910	1920
FIKNQLETAP	PHELKNTFQL	LHEILVIEDP	IQVERVKFVF	ETENGLLALM	HHSNHVDSSR	CYQCVKFLVT	LAQKCPAAKE
1930	1940	1950	1960	1970	1980	1990	2000
YFKENSHHWS	WAVQWLQKKM	SEHYWTPQSN	VSNETSTGKT	FQRTISAQDT	LAYATALLNE	KEQSGSSNGS	ESSPANENGD
2010	2020	2030					
RHLQQGSESP	MMIGELRSDL	DDVDP					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
226	1	849.2201	-174.43	2	31.6	10.1	1	590-604	K.LMPTADDDMARSCAK.S	Carbamidomethyl: 13; Oxidation: 2	QD:QU 0.45
2168	1	841.4140	51.38	2	57.5	11.5	1	590-604	K.LMPTADDDMARSCAK.S	Carbamidomethyl: 13	

Detailed Protein Report

Protein 80: PREDICTED: obscurin isoform X19 [Homo sapiens]

Accession:	gi|530366567	**Score:**	48.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	945.1
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.5
		No. of unique Peptides:	3

Quantitation

QD:QU	**Median:** 1.75	**CV:** 0.00 %	**No. of Peptides:** 1

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
LRVSEPKAVF	AKEQPACREV	QAEVGASATL	SCEVAQDQME	VTWYKDGKKL	SSSSKVHVEA	VGCMRRLVVQ	QVGQADSGEY
970	980	990	1000	1010	1020	1030	1040
SCEARGQRVS	FRLDVAEPKV	VFAKEQLARR	KLQAEAGASA	TLSCEVAQAQ	TEVTWYKDGK	KLSSSSKVCM	EATGCTRRLV
1050	1060	1070	1080	1090	1100	1110	1120
VQQAGQADAG	EYSCEAGGQR	LSFHLDVKEP	KVVFAKDQVA	HSEVQAEAGA	SATLSCEVAQ	AQTEVMWYKD	GKKLSSSLKV
1130	1140	1150	1160	1170	1180	1190	1200
HVEAKGCRRR	LVVQQAGKTD	AGDYSCEARG	QRVSFRLHIT	EPKMMFAKEQ	SVHNEVQAEA	GASAMLSCEV	AQAQTEVTWY
1210	1220	1230	1240	1250	1260	1270	1280
KDGKKLSSSS	KVGMEVKGCT	RRLVLPQAGK	ADAGEYSCEA	GGQRVSFHLH	ITEPKGVFAK	EQSVHNEVQA	EAGTTAMLSC
1290	1300	1310	1320	1330	1340	1350	1360
EVAQPQTEVT	WYKDGKKLSS	SSKVRMEVKG	CTRRLVVQQV	GKADAGEYSC	EAGGQRVSFQ	LHITEPKAVF	AKEQLVHNEV
1370	1380	1390	1400	1410	1420	1430	1440
RTEAGASATL	SCEVAQAQTE	VTWYKDGKKL	SSSSKVRIEA	AGCMRQLVVQ	QAGQADAGEY	TCEAGGQRLS	FHLDVSEPKA
1450	1460	1470	1480	1490	1500	1510	1520
VFAKEQLAHR	KVQAEAGAIA	TLSCEVAQAQ	TEVTWYKDGK	KLSSSSKVRM	EAVGCTRRLV	VQQACQADTG	EYSCEAGGQR
1530	1540	1550	1560	1570	1580	1590	1600
LSFSLDVAEP	KVVFAKEQPV	HREVQAQAGA	STTLSCEVAQ	AQTEVMWYKD	GKKLSFSSKV	RMEAVGCTRR	LVVQQAGQAV
1610	1620	1630	1640	1650	1660	1670	1680
AGEYSCEAGS	QRLSFHLHVA	EPKAVFAKEQ	PASREVQAEA	GTSATLSCEV	AQAQTEVTWY	KDGKKLSSSS	KVRMEAVGCT
1690	1700	1710	1720	1730	1740	1750	1760
RRLVVQEAGQ	ADAGEYSCKA	GDQRLSFHLH	VAEPKVVFAK	EQPAHREVQA	EAGASATLSC	EVAQAQTEVT	WYKDGKKLSS
1770	1780	1790	1800	1810	1820	1830	1840
SSKVRVEAVG	CTRRLVVQQA	GQAEAGEYSC	EAGGQQLSFR	LQVAEPKAVF	AKEQVVFAKD	QPVHREVQAE	AGTSTMLSCE
1850	1860	1870	1880	1890	1900	1910	1920
VAQAQTEVMW	YKDGKKLSSS	SKMRVEAVGC	TRRLVVQEAG	QADAGEYSCE	AGGQRLSFHL	HVAEPKVVFA	KEQPACREVQ
1930	1940	1950	1960	1970	1980	1990	2000
AEAGASATLS	CEVAQGQMEV	TWYKDGKKLS	SSSKVHMEAS	GYTRRLVVQQ	AGQADAGEYS	CEAGGQRLSF	RLHVAELEPQ
2010	2020	2030	2040	2050	2060	2070	2080
ISERPCRREP	LVVKEHEDII	LTATLATPSA	ATVTWLKDGV	EIRRSKRHET	ASQGDTHTLT	VHGAQVLDSA	IYSCRVGAEG
2090	2100	2110	2120	2130	2140	2150	2160
QDFPVQVEEV	AAKFCRLLEP	VCGELGGTVT	LACELSPACA	EVVWRCGNTQ	LRVGKRFQMV	AEGPVRSLTV	LGLRAEDAGE
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
961	1	512.1292	-217.77	2	42.1	10.5	0	872-880	R.VGEDSVDFR.L		QD:QU 1.75
2890	1	922.9785	45.19	2	65.3	10.6	2	1021-1037	K.KLSSSSKVCMEATGCTR.R	Carbamidomethyl: 15	
2727	1	846.9286	-83.14	2	65.2	13.0	2	8400-8415	K.ASGRALAAKIIPYHPK.D		

Detailed Protein Report

Protein 81:	**PREDICTED: dmX-like protein 2 isoform X3 [Homo sapiens]**		
Accession:	gi|530405585	**Score:**	47.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	291.5
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MHLHQVLTGA	VNPGDNCYSV	GSVGDVPFTA	YGSGCDIVIL	ANDFECVQII	PGAKHGNIQV	SCVECSNQQG	RIAASYGNAV
90	100	110	120	130	140	150	160
CIFEPLGINS	HKRNCQLKCQ	WLKTGQFFLS	SVTYNLAWDP	QDNRLLTATD	SIQLWAPPGD	DILEEEEEID	NTVPPVLNDW
170	180	190	200	210	220	230	240
KCVWQCKTSV	SVHLMEWSPD	GEYFATAGKD	DCLLKVWYPM	TGWKSSIIPQ	DHHEVKRRQS	STQFSFVYLA	HPRAVTGFSW
250	260	270	280	290	300	310	320
RKTSKYMPRG	SVCNVLLTSC	HDGVCRLWAE	TLLPEDCLLG	EQICETTTSS	IASSLSHAGR	HKDRIQHALE	TIHHLKNLRK
330	340	350	360	370	380	390	400
GQRRSSVLVT	HAELMPDQTA	MHEVQRHISH	HANALCHFHI	AASINPATDI	PNVLVGTAFN	VDDGNGGFVV	HWLNNKEFHF
410	420	430	440	450	460	470	480
TSSTEVFMHQ	LRKLSDKQVD	HENDDADRED	EEHSQEDRER	GLHMKLDHDL	SLDRESEAGT	GSSEHEDGER	EGSPRTYSRL
490	500	510	520	530	540	550	560
SVPMPLPTVL	LDRKIETLLT	EWNKNPDMLF	TIHPVDGTFL	VWHVKYLDEY	NPGIFRQVQV	SFSSRIPVAF	PSGDASSLSK
570	580	590	600	610	620	630	640
NIMMYACINA	TKDSHHTLLH	QEGMSVGSPH	GSQPHSRSHS	THMNILAPTV	MMISKHIDGS	LNQWAVTFAD	KSAFTTVLTV
650	660	670	680	690	700	710	720
SHKFRYCGHR	FHLNDLACHS	VLPLLLTSSH	HNALLTPELD	CQWDSDNKLS	RLMDPVKHIK	GSSKQPLRNA	ATRTFHDPNA
730	740	750	760	770	780	790	800
IYSELILWRV	DPIGPLSYTG	GVSELARINS	LHTSAFSNVA	WLPTLIPSYC	LGTYCNSASA	CFVASDGKNL	RLYQAVVDAR
810	820	830	840	850	860	870	880
KLLDELSDPE	SSKLIGEVFN	IVSQQSTARP	GCIIELDAIT	NQCGSNTQLL	HVFQEDFIIG	YKPHKEDMEK	KETEIFFQPS
890	900	910	920	930	940	950	960
QGYRPPPFSE	KFFLVVIEKD	SNNNSILHMW	HLHLKSVQAC	LAKASEGASS	ESLLSVPGQK	NVDSSPETSP	SVSPMPHSSS
970	980	990	1000	1010	1020	1030	1040
IANLQTASKL	ILSSRLVYSQ	PLDLPESVEV	IRATPSAGHL	SSSSIYPVCL	APYLVVTTCS	DNKVRFWKCC	MEANPECNKS
1050	1060	1070	1080	1090	1100	1110	1120
DEKEIYHWKR	WPLMNDEGED	NSSTVSIVGR	PVAVSCSYTG	RLAVAYKQPI	HHNGFVSKEF	SMHVCIFECE	STGGSEWVLE
1130	1140	1150	1160	1170	1180	1190	1200
QTIHLDDLVK	VGSVLDSRVS	VDSNLFVYSK	SDALLSKDRY	LIPNIKHLVH	LDWVSKEDGS	HILTVGVGAN	IFMYGRLSGI
1210	1220	1230	1240	1250	1260	1270	1280
VTEQTNSKDG	VAVITLPLGG	SIKQGVKSRW	VLLRSIDLVS	SVDGTPSLPV	SLSWVRDGIL	VVGMDCEMHV	YAQWKHAVKF
1290	1300	1310	1320	1330	1340	1350	1360
GDTEADSSNA	EEAAMQDHST	FKSNMLARKS	VVEGTAISDD	VFCSPTVIQD	GGLFEAAHVL	SPTLPQYHPT	QLLELMDLGK
1370	1380	1390	1400	1410	1420	1430	1440
VRRAKAILSH	LVKCIAGEVA	IVRDPDAGEG	TKRHLSRTIS	VSGSTAKETV	TVGKDGTRDY	TEIDSIPPLP	LYALLAADQD
1450	1460	1470	1480	1490	1500	1510	1520
TSYRISEEST	KIPQSYEDQT	VSQPEDQYSE	LFQIQDIPTD	DIDLEPEKRE	NKSKVINLSQ	YGPAYFGQEH	ARVLSSHLMH
1530	1540	1550	1560	1570	1580	1590	1600
SSLPGLTRLE	QMFLVALADT	VATTSTELDE	SRDKSCSGRD	TLDECGLRYL	LAMRLHTCLL	TSLPPLYRVQ	LLHQGVSTCH
1610	1620	1630	1640	1650	1660	1670	1680
FAWAFHSEAE	EELINMIPAI	QRGDPQWSEL	RAMGIGWWVR	NINTLRRCIE	KVAKASFQRN	NDALDAALFY	LSMKKKAVVW
1690	1700	1710	1720	1730	1740	1750	1760
GLFRSQHDEK	MTTFFSHNFN	EDRWRKAALK	NAFSLLGKQR	FEQSAAFFLL	AGSLKDAIEV	CLEKMEDIQL	AMVIARLYES
1770	1780	1790	1800	1810	1820	1830	1840
EFETSSTYIS	ILNQKILGCQ	KDGSGFSCKR	LHPDPFLRSL	AYWVMKDYTR	ALDTLLEQTP	KEDDEHQVII	KSCNPVAFSF
1850	1860	1870	1880	1890	1900	1910	1920
YNYLRTHPLL	IRRNLASPEG	TLATLGLKTE	KNFVDKINLI	ERKLFFTTAN	AHFKVGCPVL	ALEVLSKIPK	VTKTSALSAK
1930	1940	1950	1960	1970	1980	1990	2000
KDQPDFISHR	MDDVPSHSKA	LSDGNGSSGI	EWSNVTSSQY	DWSQPIVKVD	EEPLNLDWGE	DHDSALDEEE	DDAVGLVMKS
2010	2020	2030	2040	2050	2060	2070	2080
TDAREKDKQS	DQKASDPNML	LTPQEEDDPE	GDTEVDVIAE	QLKFRACLKI	LMTELRTLAT	GYEVDGGKLR	FQLYNWLEKE
2090	2100	2110	2120	2130	2140	2150	2160
IAALHEICNH	ESVIKEYSSK	TYSKVESDLL	DQEEMVDKPD	IGSYERHQIE	RRRLQAKREH	AERRKSWLQK	NQDLLRVFLS
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
1518	1	816.3814	-111.76	2	49.2	16.9	2	2557-2569	R.SFKRHLLDIFSLR.K	
1839	1	780.2904	-91.58	2	51.5	14.1	1	2574-2588	R.VSCSSHRGVPGGMGR.K	Carbamidomethyl: 3; Oxidation: 13

Detailed Protein Report

Protein 82: **A-kinase anchor protein 9 isoform 3 [Homo sapiens]**

Accession:	gi|22538393	**Score:**	47.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	451.8
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MEDEERQKKL	EAGKAKLAQF	RQRKAQSDGQ	SPSKKQKKKR	KTSSSKHDVS	AHHDLNIDQS	QCNEMYINSS	QRVESTVIPE
90	100	110	120	130	140	150	160
STIMRTLHSG	EITSHEQGFS	VELESEISTT	ADDCSSEVNG	CSFVMRTGKP	TNLLREEEFG	VDDSYSEQGA	QDSPTHLEMM
170	180	190	200	210	220	230	240
ESELAGKQHE	IEELNRELEE	MRVTYGTEGL	QQLQEFEAAI	KQRDGIITQL	TANLQQARRE	KDETMREFLE	LTEQSQKLQI
250	260	270	280	290	300	310	320
QFQQLQASET	LRNSTHSSTA	ADLLQAKQQI	LTHQQQLEEQ	DHLLEDYQKK	KEDFTMQISF	LQEKIKVYEM	EQDKKVENSN
330	340	350	360	370	380	390	400
KEEIQEKETI	IEELNTKIIE	EEKKTLELKD	KLTTADKLLG	ELQEQIVQKN	QEIKNMKLEL	TNSKQKERQS	SEEIKQLMGT
410	420	430	440	450	460	470	480
VEELQKRNHK	DSQFETDIVQ	RMEQETQRKL	EQLRAELDEM	YGQQIVQMKQ	ELIRQHMAQM	EEMKTRHKGE	MENALRSYSN
490	500	510	520	530	540	550	560
ITVNEDQIKL	MNVAINELNI	KLQDTNSQKE	KLKEELGLIL	EEKCALQRQL	EDLVEELSFS	REQIQRARQT	IAEQESKLNE
570	580	590	600	610	620	630	640
AHKSLSTVED	LKAEIVSASE	SRKELELKHE	AEVTNYKIKL	EMLEKEKNAV	LDRMAESQEA	ELERLRTQLL	FSHEEELSKL
650	660	670	680	690	700	710	720
KEDLEIEHRI	NIEKLKDNLG	IHYKQQIDGL	QNEMSQKIET	MQFEKDNLIT	KQNQLILEIS	KLKDLQQSLV	NSKSEEMTLQ
730	740	750	760	770	780	790	800
INELQKEIEI	LRQEEKEKGT	LEQEVQELQL	KTELLEKQMK	EKENDLQEKF	AQLEAENSIL	KDEKKTLEDM	LKIHTPVSQE
810	820	830	840	850	860	870	880
ERLIFLDSIK	SKSKDSVWEK	EIEILIEENE	DLKQQCIQLN	EEIEKQRNTF	SFAEKNFEVN	YQELQEEYAC	LLKVKDDLED
890	900	910	920	930	940	950	960
SKNKQELEYK	SKLKALNEEL	HLQRINPTTV	KMKSSVFDED	KTFVAETLEM	GEVVEKDTTE	LMEKLEVTKR	EKLELSQRLS
970	980	990	1000	1010	1020	1030	1040
DLSEQLKQKH	GEISFLNEEV	KSLKQEKEQV	SLRCRELEII	INHNRAENVQ	SCDTQVSSLL	DGVVTMTSRG	AEGSVSKVNK
1050	1060	1070	1080	1090	1100	1110	1120
SFGEESKIMV	EDKVSFENMT	VGEESKQEQL	ILDHLPSVTK	ESSLRATQPS	ENDKLQKELN	VLKSEQNDLR	LQMEAQRICL
1130	1140	1150	1160	1170	1180	1190	1200
SLVYSTHVDQ	VREYMENEKD	KALCSLKEEL	IFAQEEKIKE	LQKIHQLELQ	TMKTQETGDE	GKPLHLLIGK	LQKAVSEECS
1210	1220	1230	1240	1250	1260	1270	1280
YFLQTLCSVL	GEYYTPALKC	EVNAEDKENS	GDYISENEDP	ELQDYRYEVQ	DFQENMHTLL	NKVTEEYNKL	LVLQTRLSKI
1290	1300	1310	1320	1330	1340	1350	1360
WGQQTDGMKL	EFGEENLPKE	ETEFLSIHSQ	MTNLEDIDVN	HKSKLSSLQD	LEKTKLEEQV	QELESLISSL	QQQLKETEQN
1370	1380	1390	1400	1410	1420	1430	1440
YEAEIHCLQK	RLQAVSESTV	PPSLPVDSVV	ITESDAQRTM	YPGSCVKKNI	DGTIEFSGEF	GVKEETNIVK	LLEKQYQEQL
1450	1460	1470	1480	1490	1500	1510	1520
EEEVAKVIVS	MSIAFAQQTE	LSRISGGKEN	TASSKQAHAV	CQQEQHYFNE	MKLSQDQIGF	QTFETVDVKF	KEEFKPLSKE
1530	1540	1550	1560	1570	1580	1590	1600
LGEHGKEILL	SNSDPHDIPE	SKDCVLTISE	EMFSKDKTFI	VRQSIHDEIS	VSSMDASRQL	MLNEEQLEDM	RQELVRQYQE
1610	1620	1630	1640	1650	1660	1670	1680
HQQATELLRQ	AHMRQMERQR	EDQEQLQEEI	KRLNRQLAQR	SSIDNENLVS	ERERVLLEEL	EALKQLSLAG	REKLCCELRN
1690	1700	1710	1720	1730	1740	1750	1760
SSTQTQNGNE	NQGEVEEQTF	KEKELDRKPE	DVPPEILSNE	RYALQKANNR	LLKILLEVVK	TTAAVEETIG	RHVLGILDRS
1770	1780	1790	1800	1810	1820	1830	1840
SKSQSSASLI	WRSEAEASVK	SCVHEEHTRV	TDESIPSYSG	SDMPRNDINM	WSKVTEEGTE	LSQRLVRSGF	AGTEIDPENE
1850	1860	1870	1880	1890	1900	1910	1920
ELMLNISSRL	QAAVEKLLEA	ISETSSQLEH	AKVTQTELMR	ESFRQKQEAT	ESLKCQEELR	ERLHEESRAR	EQLAVELSKA
1930	1940	1950	1960	1970	1980	1990	2000
EGVIDGYADE	KTLFERQIQE	KTDIIDRLEQ	ELLCASNRLQ	ELEAEQQQIQ	EERELLSRQK	EAMKAEAGPV	EQQLLQETEK
2010	2020	2030	2040	2050	2060	2070	2080
LMKEKLEVQC	QAEKVRDDLQ	KQVKALEIDV	EEQVSRFIEL	EQEKNTELMD	LRQQNQALEK	QLEKMRKFLD	EQAIDREHER
2090	2100	2110	2120	2130	2140	2150	2160
DVFQQEIQKL	EQQLKVVPRF	QPISEHQTRE	VEQLANHLKE	KTDKCSELLL	SKEQLQRDIQ	ERNEEIEKLE	FRVRELEQAL
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
562	1	884.4457	-18.56	2	37.0	21.3	0	3081-3096	R.SLLSEIQALHAQMNGR.K	
49	1	819.8727	-87.95	2	29.3	12.5	1	3777-3790	R.WHRVTGSVSININR.D	

Detailed Protein Report

Protein 83: PREDICTED: kinesin-like protein KIF23 isoform X8 [Homo sapiens]

Accession:	gi|578827640	**Score:**	47.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.1
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	14.0
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MSFPPLPSCE	ILDINDEQTL	PRLIEALEKR	HNLRQMMIDE	FNKQSNAFKA	LLQEFDNAVL	SKENHMQGKL	NEKEKMISGQ
90	100	110	120	130	140	150	160
KLEIERLEKK	NKTLEYKIEI	LEKTTTIYEE	DKRNLQQELE	TQNQKLQRQF	SDKRRLEARL	QGMVTETTMK	WEKECERRVA
170	180	190	200	210	220	230	240
AKQLEMQNKL	WVKDEKLKQL	KAIVTEPKTE	KPERPSRERD	REKVTQRSVS	PSPVPLSSNY	IAQISNGQQL	MSQPQLHRRS
250	260	270	280	290	300	310	320
NSCSSISVAS	CISEWEQKIP	TYNTPLKVTS	IARRRQQEPG	QSKTCIVSDR	RRGMYWTEGR	EVVPTFRNEI	EIEEDHCGRL
330	340	350	360	370	380	390	400
LFQPDQNAPP	IRLRHRRSRS	AGDRWVDHKP	ASNMQTETVM	QPHVPHAITV	SVANEKALAK	CEKYMLTHQE	LASDGEIETK
410	420	430	440	450	460	470	480
LIKGDIYKTR	GGGQSVQFTD	IETLKQESPN	GSRKRRSSTV	APAQPDGAES	EWTDVETRCS	VAVEMRAGSQ	LGPGYQHHAQ
490							
PKRKKP							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1489	2	1023.0105	58.00	2	48.8	13.4	0	240-258	R.SNSCSSISVASCISEWEQK.I	
1786	1	916.3119	-158.99	2	52.7	11.0	2	275-290	R.RQQEPGQSKTCIVSDR.R	
243	1	838.3874	-37.26	2	31.8	11.3	0	467-482	R.AGSQLGPGYQHHAQPK.R	

Detailed Protein Report

Protein 84: semaphorin-5B isoform 3 precursor [Homo sapiens]

Accession:	gi|373432662	**Score:**	47.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	116.0
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.0
		No. of unique Peptides:	1

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	2	682.6902	75.49	3	58.4	22.5	2	113-129	R.SCQSKGKTEEECQNYVR.V	Carbamidomethyl: 2

Detailed Protein Report

Protein 85: probable helicase senataxin [Homo sapiens]

Accession:	gi|113722133	**Score:**	47.0
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 [%]:**	1.8
		No. of unique Peptides:	3

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
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	
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 86: PREDICTED: protein PRR14L isoform X4 [Homo sapiens]

Accession:	gi|578837142	**Score:**	46.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	219.9
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	2

Quantitation

QD:QU	**Median:**	0.99	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MQSSKELSHV DLPEDFLRSK EGNVQITAET LLKSAEVQGM KVNGTKTDNN EGHKNGNVSK DLSAGCGEFQ EVDKIMTSDE

        90        100        110        120        130        140        150        160
VSETSTLVTP EPLTFVDPVL TEATPKEKEC EELKSCPWLS LPGNSAISNV DNGKEELCKP NLVCEADDNH QQLHGHHNEQ

       170        180        190        200        210        220        230        240
PSSTHDSPTA TSPLKENSEV SCFTSDLSGP ESRTISLENC GFEGGGLLKR SAEKTDSSYF YRGDDQGKNL ASREENEERL

       250        260        270        280        290        300        310        320
LIPRSERGGP FLFNAREPEK EISGRCSGEK EPVVSPKENI HNNCIQDSLH TGNSSSLMPN SFTEATEVML NKNDLKITVH

       330        340        350        360        370        380        390        400
VQGNLTNPED HKETFTNMSH PGGHSEESSF SSLMQIEEAG QTTPVEPNIL SKSFYTKDCN SLVSIQRNLE GNTQLNEASC

       410        420        430        440        450        460        470        480
NDFLFERKSI VSLMPEDQIS PVSEVLKPKQ GTALLLPSPE FDYRPESEKV IQTSHDDIPL LDEQSIACEM NELSCTNELV

       490        500        510        520        530        540        550        560
VNKVESECVL NQQVSLNSQE HANLPTDSLL HLNKEMPLAT GRDAHQSHHP PLEGRADVIA DIQTIPIQTK IKDISPPGNQ

       570        580        590        600        610        620        630        640
TCGASSNCPT LNIKPVSLER KKEMADSGTK ALHSRLRSNK REAAGFPQVV SVIECHSVQS QDISSCHRVR KNVSQENMCS

       650        660        670        680        690        700        710        720
ASAAFKSSKI SLQVDNSLIT KYENAFQHRD HCCQGTGHSV EKSSCKVSYT SQERELDGKE TNGSLPGDKI RNKMVAGLLN

       730        740        750        760        770        780        790        800
SGISNKTIHT SSSIKLSEEG LEGKEQDVSK ETVFCKYNIS DHAIQELNQT VNIPGPEKVL DQSPTVMFSS FKNVKSVETL

       810        820        830        840        850        860        870        880
DQKADEVLDC QSNQNRPDEC KSEGQSAKEM LSSDQRETVT EPHGEVNHNQ KDLLVSSGSN NSLPCGSPKK CNLKGAFVKM

       890        900        910        920        930        940        950        960
SGCDESTEGM VDIVYTDCSN KLAEGVLDVK ASNLLDCGAR QEKLAFQEDS RSTLSRRELD AAHTGTTGQD SDFPVTAAST

       970        980        990       1000       1010       1020       1030       1040
VDFLKIKKSC EENVCRSLKD CEMEKCPDSC AHEMESVADH EPNKRILGRV NLSLNDSHYG QQDKGTSLRE TQEMTEGSRL

      1050       1060       1070       1080       1090       1100       1110       1120
EPNSEFGKES TFGISSKESM SCHDESSVSL RSLKSIEIMP SQENSETNVN SEETDLKNLC KPKDGEMLCE NVKDCTVLPE

      1130       1140       1150       1160       1170       1180       1190       1200
MKEIVSRDWS NSSDRDSVCT CVEKNACKAC HPHENSSDRH LPLTVKTDIK VKGEETEEHQ RGRLGYLTVG EQSEELVTRE

      1210       1220       1230       1240       1250       1260       1270       1280
TGDGDPVSNI SQTHFKCRGI LNHAEKQQSP EVLDYMLQKE EKYIRQQKAH TISQQCISSS LLLDDAQNQN QPKADKDEST

      1290       1300       1310       1320       1330       1340       1350       1360
MINEITLAKL AKDSIVAQTQ KLEDQKEERL HHPLRKDTES CTSPCLLGAP RKAQDPSSAG CDQIHGAFAK KGVLPLKKQP

      1370       1380       1390       1400       1410       1420       1430       1440
HRTCKKVSYQ EQIIVGRKIG KIRSSAFLKS SSNPIPTKAH RLLSLCTLSA PTRLEPETAP TKSLVSHIPK QMSTPCHPLR

      1450       1460       1470       1480       1490       1500       1510       1520
SLNFRKTTKE SALLNKLSIL ASKLAPAMKT QKLRYRRCSS ELLPMAKSYK RLRYKRLLDG FSSSTEQLNP YLAASGWDKR

      1530       1540       1550       1560       1570       1580       1590       1600
PNSKPMALYS LESIKMTFID LSNKMPSLLF GSEIFPVSFH VKSSSSDCTT ESSRTFPEHC APARLALGEA LQCPSQPPKW

      1610       1620       1630       1640       1650       1660       1670       1680
TFSFFLSHGC PGMATFREDT GVHSQTHTQA PPQPPAPLQD YGGTAIVQTR ADCSVLGLHT LLALCSPGCY RIWTKKRSFS

      1690       1700       1710       1720       1730       1740       1750       1760
SHMPTMQRLF MTQFTQGLKG LRSPASIADK VFCSLPYSVG RVLSIWSQHG PSVCSFEISS LHSPHCKRQP SLGTTSSHTM

      1770       1780       1790       1800       1810       1820       1830       1840
LPYVPLPGME ATYNTSGSQT RLEPPFPALV PKSCLVAESA VSKLLLSASE FQVRGLDELD GVKAACPCPQ SSPPEQKEAE

      1850       1860       1870       1880       1890       1900       1910       1920
PEKRPKKVSQ IRIRKTIPRP DPNLTPMGLP RPKRLKKKEF SLEEIYTNKN YKSPPANRCL ETIFEEPKER NGTLISISQQ

      1930       1940       1950       1960       1970       1980       1990
KRKRVLEFQD FTVPRKRRAR GKVKVAGSFT RAQKAAVQSR ELDALLIQKL MELETFFAKE EEQEQSSGC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1682	1	917.4150	-55.34	2	49.6	13.4	2	245-260	R.SERGGPFLFNAREPEK.E		
1702	2	867.8891	-25.32	2	49.8	17.0	1	1316-1331	R.KDTESCTSPCLLGAPR.K	Carbamidomethyl: 10	QD:QU 0.99

Detailed Protein Report

Protein 87: putative RNA polymerase II subunit B1 CTD phosphatase RPAP2 [Homo sapiens]

Accession:	gi|226246608	**Score:**	46.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.5
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	6.4
		No. of unique Peptides:	2

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        10         20         30         40         50         60         70         80
MADFAGPSSA GRKAGAPRCS RKAAGTKQTS TLKQEDASKR KAELEAAVRK KIEFERKALH IVEQLLEENI TEEFLMECGR
        90        100        110        120        130        140        150        160
FITPAHYSDV VDERSIVKLC GYPLCQKKLG IVPKQKYKIS TKTNKVYDIT ERKSFCSNFC YQASKFFEAQ IPKTPVWVRE
       170        180        190        200        210        220        230        240
EERHPDFQLL KEEQSGHSGE EVQLCSKAIK TSDIDNPSHF EKQYESSSSS THSDSSSDNE QDFVSSILPG NRPNSTNIRP
       250        260        270        280        290        300        310        320
QLHQKSIMKK KAGHKANSKH KDKEQTVVDV TEQLGDCKLD SQEKDATCEL PLQKVNTQSS SNSTLPERLK ASENSESEYS
       330        340        350        360        370        380        390        400
RSEITLVGIS KKSAEHFKRK FAKSNQVSRS VSSSVQVCPE VGKRNLLKVL KETLIEWKTE ETLRFLYGQN YASVCLKPEA
       410        420        430        440        450        460        470        480
SLVKEELDED DIISDPDSHF PAWRESQNSL DESLPFRGSG TAIKPLPSYE NLKKETEKLN LRIREFYRGR YVLGEETTKS
       490        500        510        520        530        540        550        560
QDSEEHDSTF PLIDSSSQNQ IRKRIVLEKL SKVLPGLLVP LQITLGDIYT QLKNLVRTFR LTNRNIIHKP AEWTLIAMVL
       570        580        590        600        610        620
LSLLTPILGI QKHSQEGMVF TRFLDTLLEE LHLKNEDLES LTIIFRTSCL PE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1581	1	583.8284	105.83	2	48.3	11.8	0	1-12	-.MADFAGPSSAGR.K	
1728	1	725.3276	-76.17	2	50.1	11.1	0	595-606	K.NEDLESLTIIFR.T	

Detailed Protein Report

Protein 88: TATA element modulatory factor [Homo sapiens]

Accession: gi|110347443
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 46.1
MW [kDa]: 122.8
pI: 4.7
Sequence Coverage [%]: 4.8
No. of unique Peptides: 3

10	20	30	40	50	60	70	80
MSWFNASQLS	SFAKQALSQA	QKSIDRVLDI	QEEEPSIWAE	TIPYGEPGIS	SPVSGGWDTS	TWGLKSNTEP	QSPPIASPKA
90	100	110	120	130	140	150	160
ITKPVRRTVV	DESENFFSAF	LSPTDVQTIQ	KSPVVSKPPA	KSQRPEEEVK	SSLHESLHIG	QSRTPETTES	QVKDSSLCVS
170	180	190	200	210	220	230	240
GETLAAGTSS	PKTEGKHEET	VNKESDMKVP	TVSLKVSESV	IDVKTTMESI	SNTSTQSLTA	ETKDIALEPK	EQKHEDRQSN
250	260	270	280	290	300	310	320
TPSPPVSTFS	SGTSTTSDIE	VLDHESVISE	SSASSRQETT	DSKSSLHLMQ	TSFQLLSASA	CPEYNRLDDF	QKLTESCCSS
330	340	350	360	370	380	390	400
DAFERIDSFS	VQSLDSRSVS	EINSDDELSG	KGYALVPIIV	NSSTPKSKTV	ESAEGKSEEV	NETLVIPTEE	AEMEESGRSA
410	420	430	440	450	460	470	480
TPVNCEQPDI	LVSSTPINEG	QTVLDKVAEQ	CEPAESQPEA	LSEKEDVCKT	VEFLNEKLEK	REAQLLSLSK	EKALLEEAFD
490	500	510	520	530	540	550	560
NLKDEMFRVK	EESSSISSLK	DEFTQRIAEA	EKKVQLACKE	RDAAKKEIKN	IKEELATRLN	SSETADLLKE	KDEQIRGLME
570	580	590	600	610	620	630	640
EGEKLSKQQL	HNSNIIKKLR	AKDKENENMV	AKLNKKVKEL	EEELQHLKQV	LDGKEEVEKQ	HRENIKKLNS	MVERQEKDLG
650	660	670	680	690	700	710	720
RLQVDMDELE	EKNRSIQAAL	DSAYKELTDL	HKANAAKDSE	AQEAALSREM	KAKEELSAAL	EKAQEEARQQ	QETLAIQVGD
730	740	750	760	770	780	790	800
LRLALQRTEQ	AAARKEDYLR	HEIGELQQRL	QEAENRNQEL	SQSVSSTTRP	LLRQIENLQA	TLGSQTSSWE	KLEKNLSDRL
810	820	830	840	850	860	870	880
GESQTLLAAA	VERERAATEE	LLANKIQMSS	MESQNSLLRQ	ENSRFQAQLE	SEKNRLCKLE	DENNRYQVEL	ENLKDEYVRT
890	900	910	920	930	940	950	960
LEETRKEKTL	LNSQLEMERM	KVEQERKKAI	FTQETIKEKE	RKPFSVSSTP	TMSRSSSISG	VDMAGLQTSF	LSQDESHDHS
970	980	990	1000	1010	1020	1030	1040
FGPMPISANG	SNLYDAVRMG	AGSSIIENLQ	SQLKLREGEI	THLQLEIGNL	EKTRSIMAEE	LVKLTNQNDE	LEEKVKEIPK
1050	1060	1070	1080	1090	1100		
LRTQLRDLDQ	RYNTILQMYG	EKAEEAEELR	LDLEDVKNMY	KTQIDELLRQ	SLS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1573	1	1023.5251	43.32	2	49.9	12.3	0	205-223	K.TTMESISNTSTQSLTAETK.D	Oxidation: 3
2457	1	647.2076	-217.62	2	61.2	10.6	1	489-500	R.VKEESSSISSLK.D	
1116	1	555.1899	-177.69	2	42.4	11.2	0	741-749	R.HEIGELQQR.L	

Detailed Protein Report

Protein 89: voltage-dependent R-type calcium channel subunit alpha-1E isoform 2 [Homo sapiens]

Accession:	gi|329663531	**Score:**	45.8
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 [%]:**	2.5
		No. of unique Peptides:	4

Quantitation

QD:QU	**Median:** 0.88	**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
2939	1	649.3454	56.93	3	65.9	11.0	1	734-750	K.EVSPMSAPNMPSIERER.R	Oxidation: 10	
27	1	814.2746	-93.66	2	30.0	10.4	1	1296-1308	K.FFYCTDSSKDTEK.E	Carbamidomethyl: 4	
118	1	753.3697	-54.70	2	31.4	13.4	0	1426-1439	R.ACIDFAISAKPLTR.Y		QD:QU 0.88
1976	1	698.7954	-42.34	2	53.2	11.0	1	1728-1739	R.VWAEYDRAACGR.I		

Detailed Protein Report

Protein 90: C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8 [Homo sapiens]

Accession:	gi|118600977	**Score:**	45.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	211.2
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	2

Detailed Protein Report

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        10         20         30         40         50         60         70         80
MAPGALRGGC EQRAPGGGAR TAALGPWPWP SPGPAPSPGA APPRSRKMSG ALLWPLLPLL LLLLSARDGV RAAQPQAPGY
        90        100        110        120        130        140        150        160
LIAAPSVFRA GVEEVISVTI FNSPREVTVQ AQLVAQGEPV VQSQGAILDK GTIKLKVPTG LRGQALLKVW GRGWQAEEGP
       170        180        190        200        210        220        230        240
LFHNQTSVTV DGRGASVFIQ TDKPVYRPQH RVLISIFTVS PNLRPVNEKL EAYILDPRGS RMIEWRHLKP FCCGITNMSF
       250        260        270        280        290        300        310        320
PLSDQPVLGE WFIFVEMQGH AYNKSFEVQK YVLPKFELLI DPPRYIQDLD ACETGTVRAR YTFGKPVAGA LMINMTVNGV
       330        340        350        360        370        380        390        400
GYYSHEVGRP VLRTTKILGS RDFDICVRDM IPADVPEHFR GRVSIWAMVT SVDGSQQVAF DDSTPVQRQL VDIRYSKDTR
       410        420        430        440        450        460        470        480
KQFKPGLAYV GKVELSYPDG SPAEGVTVQI KAELTPKDNI YTSEVVSQRG LVGFEIPSIP TSAQHVWLET KVMALNGKPV
       490        500        510        520        530        540        550        560
GAQYLPSYLS LGSWYSPSQC YLQLQPPSHP LQVGEEAYFS VKSTCPCNFT LYYEVAARGN IVLSGQQPAH TTQQRSKRAA
       570        580        590        600        610        620        630        640
PALEKPIRLT HLSETEPPPA PEAEVDVCVT SLHLAVTPSM VPLGRLLVFY VRENGEGVAD SLQFAVETFF ENQVSVTYSA
       650        660        670        680        690        700        710        720
NETQPGEVVD LRIRAARGSC VCVAAVDKSV YLLRSGFRLT PAQVFQELED YDVSDSFGVS REDGPFWWAG LTAQRRRRSS
       730        740        750        760        770        780        790        800
VFPWPWGITK DSGFAFTETG LVVMTDRVSL NHRQDGGLYT DEAVPAFQPH TGSLVAVAPS RHPPRTEKRK RTFFPETWIW
       810        820        830        840        850        860        870        880
HCLNISDPSG EGTLSVKVPD SITSWVGEAV ALSTSQGLGI AEPSLLKTFK PFFVDFMLPA LIIRGEQVKI PLSVYNYMGT
       890        900        910        920        930        940        950        960
CAEVYMKLSV PKGIQFVGHP GKRHVTKKMC VAPGEAEPIW VVLSFSDLGL NNITAKALAY GDTNCCRDGR SSKHPEENHA
       970        980        990       1000       1010       1020       1030       1040
DRRVPIGVDH VRRSVMVEAE GVPRAYTYSA FFCPSERVHI STPNKYEFQY VQRPLRLTRF DVAVRAHNDA RVALSSGPQD
      1050       1060       1070       1080       1090       1100       1110       1120
TAGMIEIVLG GHQNTRSWIS TSKMGEPVAS AHTAKILSWD EFRTFWISWR GGLIQVGHGP EPSNESVIVA WTLPRPPEVQ
      1130       1140       1150       1160       1170       1180       1190       1200
FIGFSTGWGS MGEFRIWRKM EVDESYSEAF TLGVPHGAIP GSERATASII GDVMGPTLNH LNNLLRLPFG CGEQNMIHFA
      1210       1220       1230       1240       1250       1260       1270       1280
PNVFVLKYLQ KTQQLSPEVE RETTDYLVQG YQRQLTYKRQ DGSYSAFGER DASGSMWLTA FVLKSFAQAR SFIFVDPREL
      1290       1300       1310       1320       1330       1340       1350       1360
AAAKSWIIQQ QQADGSFLAV GRVLNKDIQG GIHGTVPLTA YVVVALLETG TASEEERGST DKARHFLESA APLAMDPYSC
      1370       1380       1390       1400       1410       1420       1430       1440
ALTTYALTLL RSPAAPEALR KLRSLAIMRD GVTHWSLSNS WDVDKGTFLS FSDRVSQSVV SAEVEMTAYA LLTYTLLGDV
      1450       1460       1470       1480       1490       1500       1510       1520
AAALPVVKWL SQQRNALGGF SSTQDTCVAL QALAEYAILS YAGGINLTVS LASTNLDYQE TFELHRTNQK VLQTAAIPSL
      1530       1540       1550       1560       1570       1580       1590       1600
PTGLFVSAKG DGCCLMQIDV TYNVPDPVAK PAFQLLVSLQ EPEAQGRPPP MPASAAEGSR GDWPPADDDD PAADQHHQEY
      1610       1620       1630       1640       1650       1660       1670       1680
KVMLEVCTRW LHAGSSNMAV LEVPLLSGFR ADIESLEQLL LDKHMGMKRY EVAGRRVLFY FDEIPSRCLT CVRFRALREC
      1690       1700       1710       1720       1730       1740       1750       1760
VVGRTSALPV SVYDYYEPAF EATRFYNVST HSPLARELCA GPACNEVERA PARGPGWFPG ESGPAVAPEE GAAIARCGCD
      1770       1780       1790       1800       1810       1820       1830       1840
HDCGAQGNPV CGSDGVVYAS ACRLREAACR QAAPLEPAPP SCCALEQRLP ASSSSTYGDD LASVAPGPLQ QDVKLNGAGL
      1850       1860       1870       1880       1890       1900       1910       1920
EVEDSDPEPE GEAEDRVTAG PRPPVSSGNL ESSTQSASPF HRWGQTPAPQ RHSGRVVGAH RPGLLSPVFV YSPAFQSGGE
      1930       1940
EGLWMSNTCT LR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2723	1	973.5045	12.24	2	65.2	13.4	2	702-717	R.EDGPFWWAGLTAQRRR.R	
968	1	820.0912	-24.82	3	40.6	16.4	1	1285-1306	K.SWIIQQQQADGSFLAVGRVLNK.D	

Detailed Protein Report

Protein 91: leucine-, glutamate- and lysine-rich protein 1 isoform 1 [Homo sapiens]

Accession:	gi|262263420	**Score:**	45.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.2
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.8
		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 92: PREDICTED: ceruloplasmin isoform X4 [Homo sapiens]

Accession: gi|578807068
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 45.6
MW [kDa]: 103.1
pI: 5.4
Sequence Coverage [%]: 1.6
No. of unique Peptides: 1

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					
STVDQVKDLY	CKEGEKKWSR	L					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2714	3	735.4243	1.19	2	65.0	45.6	0	188-201	K.DIASGLIGPLIICK.K	Carbamidomethyl: 13

Detailed Protein Report

Protein 93: death-inducer obliterator 1 isoform c [Homo sapiens]

Accession:	gi|301129165	**Score:**	45.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	243.7
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	2

Quantitation

QD:QU	**Median:** 1.22	**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]

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		QD:QU 1.22
116	5	768.2858	-124.81	2	30.2	17.6	1	1408-1421	R.HEVERAPEAAAAER.E		

Detailed Protein Report

Protein 94: 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

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        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 95: nuclear receptor coactivator 4 isoform 3 [Homo sapiens]

Accession:	gi|14149617	**Score:**	44.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.7
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.0
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|223890287	refseq_huma (refseq_human_20140103.fasta)	nuclear receptor coactivator 4 isoform 3 [Homo sapiens]
gi|223890284	refseq_huma (refseq_human_20140103.fasta)	nuclear receptor coactivator 4 isoform 3 [Homo sapiens]

10	20	30	40	50	60	70	80
MNTFQDQSGS	SSNREPLLRC	SDARRDLELA	IGGVLRAEQQ	IKDNLREVKA	QIHSCISRHL	ECLRSREVWL	YEQVDLIYQL
90	100	110	120	130	140	150	160
KEETLQQQAQ	QLYSLLGQFN	CLTHQLECTQ	NKDLANQVSV	CLERLGSLTL	KPEDSTVLLF	EADTITLRQT	ITTFGSLKTI
170	180	190	200	210	220	230	240
QIPEHLMAHA	SSANIGPFLE	KRGCISMPEQ	KSASGIVAVP	FSEWLLGSKP	ASGYQAPYIP	STDPQDWLTQ	KQTLENSQTS
250	260	270	280	290	300	310	320
SRACNFFNNV	GGNLKGLENW	LLKSEKSSYQ	KCNSHSTTSS	FSIEMEKVGD	QELPDQDEMD	LSDWLVTPQE	SHKLRKPENG
330	340	350	360	370	380	390	400
SRETSEKFKL	LFQSYNVNDW	LVKTDSCTNC	QGNQPKGVEI	ENLGNLKCLN	DHLEAKKPLS	TPSMVTEDWL	VQNHQDPCKV
410	420	430	440	450	460	470	480
EEVCRANEPC	TSFAECVCDE	NCEKEALYKW	LLKKEGKDKN	GMPVEPKPEP	EKHKDSLNMW	LCPRKEVIEQ	TKAPKAMTPS
490	500	510	520	530	540	550	560
RIADSFQVIK	NSPLSEWLIR	PPYKEGSPKE	VPGTEDRAGK	QKFKSPMNTS	WCSFNTADWV	LPGKKMGNLS	QLSSGEDKWL
570	580	590	600	610	620		
LRKKAQEVLL	NSPLQEEHNF	PPDHYGLPAV	CDLFACMQLK	VDKEKWLYRT	PLQM		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2959	2	698.3575	103.79	2	66.2	17.3	0	344-356	K.TDSCTNCQGNQPK.G	
14	2	1103.5194	96.25	2	29.8	16.4	0	406-424	R.ANEPCTSFAECVCDENCEK.E	Carbamidomethyl: 5, 17

Detailed Protein Report

Protein 96: PREDICTED: beta-enolase isoform X1 [Homo sapiens]

Accession:	gi|530410063	**Score:**	44.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.0
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.2
		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 97: **constitutive coactivator of peroxisome proliferator-activated receptor gamma isoform a [Homo sapiens]**

Accession:	gi|556503397	**Score:**	44.6
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 [%]:**	6.8
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.38 **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
1639	3	839.3743	-22.36	2	49.0	11.4	1	258-271	K.CLSSYTSVKENFDK.K	Carbamidomethyl: 1	
1242	1	666.6715	-165.15	2	45.6	11.1	0	412-422	R.EVPMCSDPEPR.Q	Carbamidomethyl: 5; Oxidation: 4	QD:QU 0.38

Detailed Protein Report

Protein 98: 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

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
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
1581	1	698.7063	-184.90	2	50.0	12.1	1	1707-1717	K.EFLMENSSRQR.A	

Detailed Protein Report

Protein 99: transthyretin precursor [Homo sapiens]

Accession:	gi|4507725	**Score:**	44.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.9
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	9.5
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.59 **CV:** 12.51 % **No. of Peptides:** 2

```
        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
594	1	761.8596	-3.46	2	37.4	15.4	1	55-68	R.KAADDTWEPFASGK.T		QD:QU 0.66
810	2	697.8221	10.50	2	40.1	29.0	0	56-68	K.AADDTWEPFASGK.T		QD:QU 0.52

Detailed Protein Report

Protein 100: protein inscuteable homolog isoform d [Homo sapiens]

Accession:	gi|507417931	**Score:**	44.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.2
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	9.6
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MMALPGGRHL	DSVTLPGQRL	HLMQVDSVQR	WMEDLKLMTE	CECMCVLQAK	PISLEEDAQG	DLILAGGPGP	GDPLQLLLKR
90	100	110	120	130	140	150	160
GWVISTELRR	IGQKLAQDRW	ARVHSMSVRL	TCHARSMVSE	YSAVSRNSLK	EMGEIEKLLM	EKCSELSAVT	ERCLQVENEH
170	180	190	200	210	220	230	240
VLKSMKACVS	ETLSMLGQHF	GQLLELALTR	EVQALVRKID	ASDNIYTTES	TTGNLFSLTQ	EGAPLCRIIA	KEGGVVALFK
250	260	270	280	290	300	310	320
VCRQDSFRCL	YPQALRTLAS	ICCVEEGVHQ	LEKVDGVLCL	ADILTDNSHS	EATRAEAAAV	VAQVTSPHLP	VTQHLSSFLE
330	340	350	360	370	380	390	400
SMEEIVTALV	KLCQEASSGE	VFLLASAALA	NITFFDTMAC	EMLLQLNAIR	VLLEACSDKQ	RVDTPYTRDQ	IVTILANMSV
410	420	430	440	450	460	470	480
LEQCASDIIQ	ENGVQLIMGM	LSEKPRSGTP	AEVAACERVQ	QKAAVTLARL	SRDPDVAREA	VRLSCMSRLI	ELCRSPSERN
490	500	510	520	530			
SSDAVLVACL	AMGIQLQVKK	TNISALLLWF	LFWHIQGCSA				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2221	1	953.0764	69.85	2	58.2	17.7	1	2-19	M.MALPGGRHLDSVTLPGQR.L	
561	1	592.8217	-63.15	2	35.6	12.3	1	439-449	R.VQQKAAVTLAR.L	
2976	1	754.4009	-4.94	3	66.4	14.1	1	480-500	R.NSSDAVLVACLAMGIQLQVKK.T	Carbamidomethyl: 10; Oxidation: 13

Detailed Protein Report

Protein 101: neuralized-like protein 4 isoform 2 [Homo sapiens]

Accession:	gi|53829368	**Score:**	43.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	166.6
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MAAGSGGSGG	SGGGPGPGPG	GGGGPSGSGS	GPGSNGGLGS	GGELHPRTGR	LVSLSACGRT	ARRQQPGQEF	NHGLVLSREP
90	100	110	120	130	140	150	160
LRDGRVFTVR	IDRKVNSWSG	SIEIGVTALD	PSVLDFPSSA	TGLKGGSWVV	SGCSVLRDGR	SVLEEYGQDL	DQLGEGDRVG
170	180	190	200	210	220	230	240
VERTVAGELR	LWVNGRDCGV	AATGLPPRVW	AVVDLYGKCT	QITVLPPEPG	FSPPTPIPTP	PLEPLAPTED	SALAEQGTSA
250	260	270	280	290	300	310	320
DEAFMVSPAQ	ARPETFPNSL	ESHNDFANME	LSEVVSNTIL	SAYNGGLLNV	NLSSPPAGEG	LGSSGAATSP	ILTSNDALLF
330	340	350	360	370	380	390	400
HEKCGTLIKL	SNNNKTAERR	RPLDEFNNGV	VMTNRPLRDN	EMFEIRIDKL	VDKWSGSIEI	GVTTHNPNSL	EYPATMTNLQ
410	420	430	440	450	460	470	480
SGTIMMSGCG	ILTNGKGTRR	EYCEFSLDEL	QEGDHIGLTR	KSNSALHFFI	NGIDQGVATP	LTPPVVYGVV	DLYGMAVKVT
490	500	510	520	530	540	550	560
IVHNNNHSDR	LRRNNAILRA	LSPEGALRRA	APAAQAEPER	LLFHPNCGQK	AAITHEGRTA	LRPHATDDFN	HGVVLSSRAL
570	580	590	600	610	620	630	640
RDGEVFQVRI	DKMVDKWAGS	IEIGVTTHNP	AYLQLPSTMT	NLRSGTWMMT	GNGVMHNGTT	ILDEYGHNLD	RLKAGDTVGV
650	660	670	680	690	700	710	720
VRREDGTLHF	FVNGMTQGPA	AWNVPPGVYA	VVDLYGQAAQ	ATIVDDVEVA	PVPEPLPEGN	NQVSPSSPSS	GAGGSDLRFH
730	740	750	760	770	780	790	800
QLHGSNAVIT	NGGRTALRHN	CRSEFNDAIV	ISNRALRDGE	LFEIVIQKMV	DRWSGSIEAG	VTAIRPEDLE	FPNTMTDIDY
810	820	830	840	850	860	870	880
DTWMLSGTAI	MQDGNTMRNN	YGCDLDALGT	GARIGMMRTA	KGDLHYFING	QDQGAACSGL	PPEVYAVVDL	YGQCVQVSIT
890	900	910	920	930	940	950	960
NATGPMDNSL	ATSNTATEKS	FPLHSPVAGV	AHRFHSTCGK	NVTLEEDGTR	AVRAAGYAHG	LVFSTKELRA	EEVFEVKVEE
970	980	990	1000	1010	1020	1030	1040
LDEKWAGSLR	LGLTTLAPGE	MGPGAGGGGP	GLPPSLPELR	TKTTWMVSSC	EVRRDGQLQR	MNYGRNLERL	GVGSRVGVRR
1050	1060	1070	1080	1090	1100	1110	1120
GADDTMHILV	DGEDMGPAAT	GIAKNVWAVL	DLYGPVRGVS	IVSSTRLEES	EGTQPPSPSS	DTGSEGEEDD	EGEEHGLGGQ
1130	1140	1150	1160	1170	1180	1190	1200
NEVGIIPTTL	EFLENHGKNI	LLSNGNRTAT	RVASYNQGIV	VINQPLVPQL	LVQVRIDFLN	RQWTSSLVLG	VITCAPERLN
1210	1220	1230	1240	1250	1260	1270	1280
FPASACALKR	AAWLLRGRGV	FHNGLKICEK	FGPNLDTCPE	GTILGLRLDS	SGGLHLHVNG	VDQGVAVPDV	PQPCHALVDL
1290	1300	1310	1320	1330	1340	1350	1360
YGQCEQVTIV	NPEPGAASGK	SAGTQGDMEK	ADMVDGIKES	VCWGPPPAAS	PLKSCEYHAL	CSRFQELLLL	PEDYFMPPPK
1370	1380	1390	1400	1410	1420	1430	1440
RSLCYCESCR	KLRGDEAHRR	RGEPPREYAL	PFGWCRFNLR	VNPRLEAGTL	TKKWHMAYHG	SNVAAVRRVL	DRGELGAGTA
1450	1460	1470	1480	1490	1500	1510	1520
SILSCRPLKG	EPGVGFEEPG	ENCAPPREEQ	PPPVLLSPSL	QYAGAETLAS	KVQFRDPKSQ	RTHQAQVAFQ	VCVRPGSYTP
1530	1540	1550	1560	1570			
GPPSAALGEP	PDPHFSPAEL	EWVTKEKGAT	LLCALLVRVE				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
512	1	457.1269	-288.36	2	35.0	10.5	0	500-508	R.ALSPEGALR.R	
1492	1	555.2127	-156.80	2	47.2	20.0	2	1372-1380	K.LRGDEAHRR.R	
2678	1	693.8667	-63.13	2	64.6	13.3	1	1546-1558	K.EKGATLLCALLVR.V	

Detailed Protein Report

Protein 102: protein furry homolog-like [Homo sapiens]

Accession:	gi|119874201	**Score:**	43.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	339.4
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MSNITIDPDV	KPGEYVIKSL	FAEFAVQAEK	KIEVVMAEPL	EKLLSRSLQR	GEDLQFDQLI	SSMSSVAEHC	LPSLLRTLFD
90	100	110	120	130	140	150	160
WYRRQNGTED	ESYEYRPRSS	TKSKGDEQQR	ERDYLLERRD	LAVDFIFCLV	LVEVLKQIPV	HPVPDPLVHE	VLNLAFKHFK
170	180	190	200	210	220	230	240
HKEGYSGTNT	GNVHIIADLY	AEVIGVLAQS	KFQAVRKKFV	TELKELRQKE	QSPHVVQSVI	SLIMGMKFFR	VKMYPVEDFE
250	260	270	280	290	300	310	320
ASFQFMQECA	QYFLEVKDKD	IKHALAGLFV	EILIPVAAAV	KNEVNVPCLK	NFVEMLYQTT	FELSSRKKHS	LALYPLITCL
330	340	350	360	370	380	390	400
LCVSQKQFFL	NNWHIFLQNC	LSHLKNKDPK	MSRVALESLY	RLLWVYVIRI	KCESNTVTQS	RLMSIVSALF	PKGSRSVVPR
410	420	430	440	450	460	470	480
DTPLNIFVKI	IQFIAQERLD	FAMKEIIFDL	LSVGKSTKTF	TINPERMNIG	LRVFLVIADS	LQQKDGEPPM	PTTGVILPSG
490	500	510	520	530	540	550	560
NTLRVKKIFL	NKTLTDEEAK	VIGMSVYYPQ	VRKALDSILR	HLDKEVGRPM	CMTSVQMSNK	EPEDMITGER	KPKIDLFRTC
570	580	590	600	610	620	630	640
IAAIPRLIPD	GMSRTDLIEL	LARLTIHMDE	ELRALAFNTL	QALMLDFPDW	REDVLSGFVY	FIVREVTDVH	PTLLDNAVKM
650	660	670	680	690	700	710	720
LVQLINQWKQ	AAQMHNKNQD	TQHGVANGAS	HPPPLERSPY	SNVFHVVEGF	ALVILCSSRP	ATRRLAVSVL	REIRALFALL
730	740	750	760	770	780	790	800
EIPKGDDELA	IDVMDRLSPS	ILESFIHLTG	ADQTTLLYCP	SSIDLQTLAE	WNSSPISHQF	DVISPSHIWI	FAHVTQGQDP
810	820	830	840	850	860	870	880
WIISLSSFLK	QENLPKHCST	AVSYAWMFAY	TRLQLLSPQV	DINSPINAKK	VNTTTSSDSY	IGLWRNYLIL	CCSAATSSSS
890	900	910	920	930	940	950	960
TSAGSVRCSP	PETLASTPDS	GYSIDSKIIG	IPSPSSLFKH	IVPMMRSESM	EITESLVLGL	GRTNPGAFRE	LIEELHPIIK
970	980	990	1000	1010	1020	1030	1040
EALERRPENM	KRRRRRDILR	VQLVRIFELL	ADAGVISHSA	SGGLDNETHF	LNNTLLEYVD	LTRQLLEAEN	EKDSDTLKDI
1050	1060	1070	1080	1090	1100	1110	1120
RCHFSALVAN	IIQNVPVHQR	RSIFPQQSLR	HSLFMLFSHW	AGPFSIMFTP	LDRYSDRNMQ	INRHQYCALK	AMSAVLCCGP
1130	1140	1150	1160	1170	1180	1190	1200
VADNVGLSSD	GYLYKWLDNI	LDSLDKKVHQ	LGCEAVTLLL	ELNPDQSNLM	YWAVDRCYTG	SGRVAAGCFK	AIANVFQNRD
1210	1220	1230	1240	1250	1260	1270	1280
YQCDTVMLLN	LILFKAADSS	RSIYEVAMQL	LQILEPKMFR	YAHKLEVQRT	DGVLSQLSPL	PHLYSVSYYQ	LSEELARAYP
1290	1300	1310	1320	1330	1340	1350	1360
ELTLAIFSEI	SQRIQTAHPA	GRQVMLHYLL	PWMNNIELVD	LKPLPTARRH	DEDEDDSLKD	RELMVTSRRW	LRGEGWGSPQ
1370	1380	1390	1400	1410	1420	1430	1440
ATAMVLNNLM	YMTAKYGDEL	AWSEVENVWT	TLADGWPKNL	KIILHFLISI	CGVNSEPSLL	PYVKKVIVYL	GRDKTMQLLE
1450	1460	1470	1480	1490	1500	1510	1520
ELVSELQLTD	PVSSGVTHMD	NPPYYRITSS	YKIPSVTSGT	TSSSNTMVAP	TDGNPDNKPI	KENIEESYVH	LDIYSGLNSH
1530	1540	1550	1560	1570	1580	1590	1600
LNRQHHRLES	RYSSSSGGSY	EEEKSDSMPL	YSNWRLKVME	HNQGEPLPFP	PAGGCWSPLV	DYVPETSSPG	LPLHRCNIAV
1610	1620	1630	1640	1650	1660	1670	1680
ILLTDLIIDH	SVKVEWGSYL	HLLLHAIFIG	FDHCHPEVYE	HCKRLLLHLL	IVMGPNSNIR	TVASVLLRNK	EFNEPRVLTV
1690	1700	1710	1720	1730	1740	1750	1760
KQVAHLDYNF	TAGINDFIPD	YQPSPMTDSG	LSSSSTSSSI	SLGNNSAAIS	HLHTTILNEV	DISVEQDGKV	KTLMEFITSR
1770	1780	1790	1800	1810	1820	1830	1840
KRGPLWNHED	VSAKNPSIKS	AEQLTTFLKH	VVSVFKQSSS	EGIHLEHHLS	EVALQTALSC	SSRHYAGRSF	QIFRALKQPL
1850	1860	1870	1880	1890	1900	1910	1920
TATTLSDVLS	RLVETVGDPG	EDAQGFVIEL	LLTLESAIDT	LAETMKHYDL	LSALSQTSYH	DPIMGNKYAA	NRKSTGQLNL
1930	1940	1950	1960	1970	1980	1990	2000
STSPINSSSY	LGYNSNARSN	SLRLSLIGDR	RGDRRRSNTL	DIMDGRINHS	SSLARTRSLS	SLREKGMYDV	QSTTEPTNLM
2010	2020	2030	2040	2050	2060	2070	2080
ATIFWIAASL	LESDYEYEYL	LALRLLNKLL	IHLPLDKSES	REKIENVQSK	LKWTNFPGLQ	QLFLKGFTSA	STQEMTVHLL
2090	2100	2110	2120	2130	2140	2150	2160
SKLISVSKHT	LVDPSQLSGF	PLNILCLLPH	LIQHFDSPTQ	FCKETASRIA	KVCAEEKCPT	LVNLAHMMSL	YSTHTYSRDC
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
2945	2	753.3939	-46.69	2	66.0	18.1	1	382-395	R.LMSIVSALFPKGSR.S	
2730	1	725.3873	9.20	3	65.2	13.7	2	541-558	K.EPEDMITGERKPKIDLFR.T	

Detailed Protein Report

Protein 103: rho GTPase-activating protein 11A isoform 3 [Homo sapiens]

Accession:	gi|557128992	**Score:**	43.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.6
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	7.4
		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	
2613	2	822.4595	113.47	2	63.4	14.2	0	684-700	K.SVSCDGALSSCIESASK.D	
2804	1	698.3677	40.53	4	64.2	18.2	2	716-741	K.SMSCEESNIGAISKSSMELPSKSFLK.M	

Detailed Protein Report

Protein 104: ATP-dependent RNA helicase DDX42 [Homo sapiens]

Accession:	gi|45446743	**Score:**	43.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	102.9
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	3

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
1875	1	990.8378	-137.62	2	51.9	12.0	0	31-50	K.LPQQSHSAFGATSSSSGFGK.S	
2705	1	558.6699	147.14	3	64.9	15.6	1	819-833	R.HSHGETGNRHSDSPR.H	
2100	1	753.3769	8.39	2	56.6	15.7	2	896-908	K.MEPKMEPKVDSSK.M	

Detailed Protein Report

Protein 105: Golgi apparatus protein 1 isoform 3 precursor [Homo sapiens]

Accession:	gi|224586817	**Score:**	43.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.5
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAACGRVRRM	FRLSAALHLL	LLFAAGAEKL	PGQGVHSQGQ	GPGANFVSFV	GQAGGGGPAG	QQLPQLPQSS	QLQQQQQQQQ
90	100	110	120	130	140	150	160
QQQQPQPPQP	PFPAGGPPAR	RGGAGAGGGW	KLAEEESCRE	DVTRVCPKHT	WSNNLAVLEC	LQDVREPENE	ISSDCNHLLW
170	180	190	200	210	220	230	240
NYKLNLTTDP	KFESVAREVC	KSTITEIKEC	ADEPVGKGYM	VSCLVDHRGN	ITEYQCHQYI	TKMTAIIFSD	YRLICGFMDD
250	260	270	280	290	300	310	320
CKNDINILKC	GSIRLGEKDA	HSQGEVVSCL	EKGLVKEAEE	REPKIQVSEL	CKKAILRVAE	LSSDDFHLDR	HLYFACRDDR
330	340	350	360	370	380	390	400
ERFCENTQAG	EGRVYKCLFN	HKFEESMSEK	CREALTTRQK	LIAQDYKVSY	SLAKSCKSDL	KKYRCNVENL	PRSREARLSY
410	420	430	440	450	460	470	480
LLMCLESAVH	RGRQVSSECQ	GEMLDYRRML	MEDFSLSPEI	ILSCRGEIEH	HCSGLHRKGR	TLHCLMKVVR	GEKGNLGMNC
490	500	510	520	530	540	550	560
QQALQTLIQE	TDPGADYRID	RALNEACESV	IQTACKHIRS	GDPMILSCLM	EHLYTEKMVE	DCEHRLLELQ	YFISRDWKLD
570	580	590	600	610	620	630	640
PVLYRKCQGD	ASRLCHTHGW	NETSEFMPQG	AVFSCLYRHA	YRTEEQGRRL	SRECRAEVQR	ILHQRAMDVK	LDPALQDKCL
650	660	670	680	690	700	710	720
IDLGKWCSEK	TETGQELECL	QDHLDDLVVE	CRDIVGNLTE	LESEDIQIEA	LLMRACEPII	QNFCHDVADN	QIDSGDLMEC
730	740	750	760	770	780	790	800
LIQNKHQKDM	NEKCAIGVTH	FQLVQMKDFR	FSYKFKMACK	EDVLKLCPNI	KKKVDVVICL	STTVRNDTLQ	EAKEHRVSLK
810	820	830	840	850	860	870	880
CRRQLRVEEL	EMTEDIRLEP	DLYEACKSDI	KNFCSAVQYG	NAQIIECLKE	NKKQLSTRCH	QKVFKLQETE	MMDPELDYTL
890	900	910	920	930	940	950	960
MRVCKQMIKR	FCPEADSKTM	LQCLKQNKNS	ELMDPKCKQM	ITKRQITQNT	DYRLNPMLRK	ACKADIPKFC	HGILTKAKDD
970	980	990	1000	1010	1020	1030	1040
SELEGQVISC	LKLRYADQRL	SSDCEDQIRI	IIQESALDYR	LDPQLQLHCS	DEISSLCAEE	AAAQEQTGQV	EECLKVNLLK
1050	1060	1070	1080	1090	1100	1110	1120
IKTELCKKEV	LNMLKESKAD	IFVDPVLHTA	CALDIKHHCA	AITPGRGRQM	SCLMEALEDK	RVRLQPECKK	RLNDRIEMWS
1130	1140	1150	1160	1170	1180		
YAAKVAPADG	FSDLAMQVMT	SPSKNYILSV	ISGSICILFL	IGLMCGRITK	RVTRELKDR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
484	1	546.2461	55.39	2	34.7	15.7	0	538-545	K.MVEDCEHR.L	Carbamidomethyl: 5; Oxidation: 1

Detailed Protein Report

Protein 106: 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

QD:QU **Median:** 1.39 **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	QD:QU 1.39
6	2	1205.0350	-25.71	2	29.5	22.9	1	218-238	K.LSVYLTDHTGDIPCICKECGK.V	Carbamidomethyl: 14, 19	

Detailed Protein Report

Protein 107: PREDICTED: histone-lysine N-methyltransferase 2A isoform X1 [Homo sapiens]

Accession:	gi|578822195	**Score:**	42.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	323.9
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
908	1	541.3264	90.29	3	41.4	12.3	2	242-256	R.EDPAPKKSSSEPPPR.K	

Detailed Protein Report

Protein 108: dynein heavy chain 7, axonemal [Homo sapiens]

Accession:	gi|151301127	**Score:**	42.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	460.9
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
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

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 109: testis-expressed sequence 10 protein isoform 2 [Homo sapiens]

Accession:	gi|239787844	**Score:**	42.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	103.8
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSRMTKKRKR	QHDFQKVKLK	VGKKKPKLQN	ATPTNFKTKT	IHLPEQLKED	GTLPTNNRKL	NIKDLLSQMH	HYNAGVKQSA
90	100	110	120	130	140	150	160
LLGLKDLLSQ	YPFIIDAHLS	NILSEVTAVF	TDKDANVRLA	AVQLLQFLAP	KIRAEQISPF	FPLVSAHLSS	AMTHITEGIQ
170	180	190	200	210	220	230	240
EDSLKVLDIL	LEQYPALITG	RSSILLKNFV	ELISHQQLSK	GLINRDRSQS	WILSVNPNRR	LTSQQWRLKV	LVRLSKFLQA
250	260	270	280	290	300	310	320
LADGSSRLRE	SEGLQEQKEN	PHATSNSIFI	NWKEHANDQQ	HIQVYENGGS	QPNVSSQFRL	RYLVGGLSGV	DEGLSSTENL
330	340	350	360	370	380	390	400
KGFIEIIIPL	LIECWVEAVP	PQLATPVGNG	IEREPLQVMQ	QVLNIISLLW	KLSKQQDETH	KLESWLRKNY	LIDFKHHFMS
410	420	430	440	450	460	470	480
RFPYVLKEIT	KHKRKEPNKS	IKHCTVLSNN	IDHLLLNLTL	SDIMVSLANA	STLQKDCSWI	EMIRKFVTET	LEDGSRLNSK
490	500	510	520	530	540	550	560
QLNRLLGVSW	RLMQIQPNRE	DTETLIKAVY	TLYQQRGLIL	PVRTLLLKFF	SKIYQTEELR	SCRFRYRSKV	LSRWLAGLPL
570	580	590	600	610	620	630	640
QLAHLGSRNP	ELSTQLIDII	HTAAARANKE	LLKSLQATAL	RIYDPQEGAV	VVLPADSQQR	LVQLVYFLPS	LPADLLSRLS
650	660	670	680	690	700	710	720
RCCIMGRLSS	SLAAMLIGIL	HMRSSFSGWK	YSAKDWLMSD	VDYFSFLFST	LTGFSKEELT	WLQSLRGVPH	VIQTQLSPVL
730	740	750	760	770	780	790	800
LYLTDLDQFL	HHWDVTEAVF	HSLLVIPARS	QNFDILQSAI	SKHLVGLTVI	PDSTAGCVFG	VICKLLDHTC	VVSETLLPFL
810	820	830	840	850	860	870	880
ASCCYSLLYF	LLTIEKGEAE	HLRKRLMLQS	LRVNRVGPEE	LPVVGQLLRL	LLQHAPLRTH	MLTNAILVQQ	IIKNITTLKS
890	900	910	920				
GSVQEQWLTD	LHYCFNVYIT	GHPQGPSALA	TVY				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2188	2	945.6234	75.93	2	57.8	12.1	1	508-523	K.AVYTLYQQRGLILPVR.T	

Detailed Protein Report

Protein 110: PREDICTED: uncharacterized protein KIAA1551 isoform X1 [Homo sapiens]

Accession:	gi|530399223	**Score:**	42.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	194.7
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	2.1
		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
2776	1	710.3755	7.84	2	63.8	11.0	0	816-830	K.VDVSGPVASTATSTK.I	
258	1	585.2801	-84.98	2	32.0	19.7	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		

Detailed Protein Report

Protein 111: dynein heavy chain 17, axonemal [Homo sapiens]

Accession:	gi|256542310	**Score:**	42.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	509.0
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTMAPDVRLE	YLEEVASIVL	KFKPDKWSKL	IGAEENVALF	TEFFEKPDVQ	VLVLTLNAAG	MIIPCLGFPQ	SLKSKGVYFI
90	100	110	120	130	140	150	160
KTKSENINKD	NYRARLLYGD	ISPTPVDQLI	AVVEEVLSSL	LNQSENMAGW	PQVVSEDIVK	QVHRLKNEMF	VMSGKIKGKT
170	180	190	200	210	220	230	240
LLPIPEHLGS	LDGTLESMER	IPSSLDNLLL	HAIETTIIDW	SHQIRDVLSK	DSAQALLDGL	HPLPQVEFEF	WDTRLLNLKC
250	260	270	280	290	300	310	320
IHEQLNRPKV	NKIVEILEKA	KSCYWPALQN	VYTNVTEGLK	EANDIVLYLK	PLRILLEEME	QADFTMLPTF	IAKVLDTICF
330	340	350	360	370	380	390	400
IWATSEYYNT	PARIIVILQE	FCNQIIEMTR	TFLSPEEVLK	GLQGEIEEVL	SGISLAVNVL	KELYQTYDFC	CVNMKLFFKD
410	420	430	440	450	460	470	480
KEPVPWEFPS	SLAFSRINSF	FQRIQTIEEL	YKTAIEFLKL	EKIELGGVRG	NLLGSLVTRI	YDEVFELVKV	FADCKYDPLD
490	500	510	520	530	540	550	560
PGDSNFDRDY	ADFEIKIQDL	DRRLATIFCQ	GFDDCSCIKS	SAKLLYMCGG	LMERPLILAE	VAPRYSVMLE	LFDAELDNAK
570	580	590	600	610	620	630	640
ILYDAQMAAS	EEGNIPLIHK	NMPPVAGQLK	WSLELQERLE	VSMKHLKHVE	HPVMSGAEAK	LTYQKYDEMM	ELLRCHREKI
650	660	670	680	690	700	710	720
YQQWVAGVDQ	DCHFNLGQPL	ILRDAASNLI	HVNFSKALVA	VLREVKYLNF	QQQKEIPDSA	ESLFSENETF	RKFVGNLELI
730	740	750	760	770	780	790	800
VGWYNEIKTI	VKAVEFLLIK	SELEAIDVKL	LSAETTLFWN	GEGVFQYIQE	VREILHNLQN	RMQKAKQNIE	GISQAMKDWS
810	820	830	840	850	860	870	880
ANPLFERKDN	KKEALLDLDG	RIANLNKRYA	AVRDAGVKIQ	AMVAENAELF	RADTLSLPWK	DYVIYIDDMV	LDEFDQFIRK
890	900	910	920	930	940	950	960
SLSFLMDNMV	IDESIAPLFE	IRMELDEDGL	TFNPTLEVGS	DRGFLALIEG	LVNDIYNVAR	LIPRLAKDRM	NYKMDLEDNT
970	980	990	1000	1010	1020	1030	1040
DLIEMREEVS	SLVINAMKEA	EEYQDSFERY	SYLWTDNLQE	FMKNFLIYGC	AVTAEDLDTW	TDDTIPKTPP	TLAQFQEQID
1050	1060	1070	1080	1090	1100	1110	1120
SYEKLYEEVS	KCENTKVFHG	WLQCDCRPFK	QALLSTIRRW	GFMFKRHLSN	HVTNSLADLE	AFMKVARMGL	TKPLKEGDYD
1130	1140	1150	1160	1170	1180	1190	1200
GLVEVMGHLM	KVKERQAATD	NMFEPLKQTI	ELLKTYGEEM	PEEIHLKLQE	LPEHWANTKK	LAIQVKLTVA	PLQANEVSIL
1210	1220	1230	1240	1250	1260	1270	1280
RRKCQQFELK	QHEFRERFRR	EAPFSFSDPN	PYKSLNKQQK	SISAMEGIME	ALSKSGGLFE	VPVPDYKQLK	ACHREVRLLK
1290	1300	1310	1320	1330	1340	1350	1360
ELWDMVVVVN	TSIEDWKTTK	WKDINVEQMD	IDCKKFAKDM	RSLDKEMKTW	DAFVGLDNTV	KNVITSLRAV	SELQNPAIRE
1370	1380	1390	1400	1410	1420	1430	1440
RHWQQLMQAT	QVKFKMSEET	TLADLLQLNL	HSYEDEVRNI	VDKAVKESGM	EKVLKALDST	WSMMEFQHEP	HPRTGTMMLK
1450	1460	1470	1480	1490	1500	1510	1520
SSEVLVETLE	DNQVQLQNLM	MSKYLAHFLK	EVTSWQQKLS	TADSVISIWF	EVQRTWSHLE	SIFIGSEDIR	TQLPGDSQRF
1530	1540	1550	1560	1570	1580	1590	1600
DDINQEFKAL	MEDAVKTPNV	VEATSKPGLY	NKLEALKKSL	AICEKALAEY	LETKRLAFPR	FYFVSSADLL	DILSNGNDPV
1610	1620	1630	1640	1650	1660	1670	1680
EVSRHLSKLF	DSLCKLKFRL	DASDKPLKVG	LGMYSKEDEY	MVFDQECDLS	GQVEVWLNRV	LDRMCSTLRH	EIPEAVVTYE
1690	1700	1710	1720	1730	1740	1750	1760
EKPREQWILD	YPAQVALTCT	QIWWTTEVGL	AFARLEEGYE	NAIRDYNKKQ	ISQLNVLITL	LMGNLNAGDR	MKIMTICTID
1770	1780	1790	1800	1810	1820	1830	1840
VHARDVVAKM	IVAKVESSQA	FTWQAQLRHR	WDEEKRHCFA	NICDAQIQYS	YEYLGNTPRL	VITPLTDRCY	ITLTQSLHLI
1850	1860	1870	1880	1890	1900	1910	1920
MGGAPAGPAG	TGKTETTKDL	GRALGTMVYV	FNCSEQMDYK	SCGNIYKGLA	QTGAWGCFDE	FNRISVEVLS	VIAVQVKCVQ
1930	1940	1950	1960	1970	1980	1990	2000
DAIRAKKKAF	NFLGEIIGLI	PTVGIFITMN	PGYAGRAELP	ENLKALFRPC	AMVVPDFELI	CEIMLMAEGF	LEARLLARKF
2010	2020	2030	2040	2050	2060	2070	2080
ITLYTLCKEL	LSKQDHYDWG	LRAIKSVLVV	AGSLKRGDPS	RAEDQVLMRA	LRDFNIPKIV	TDDLPVFMGL	IGDLFPALDV
2090	2100	2110	2120	2130	2140	2150	2160
PRKRDLNFEK	IIKQSIVELK	LQAEDSFVLK	VVQLEELLQV	RHSVFIVGNA	GSGKSQVLKS	LNKTYQNLKR	KPVAVDLDPK
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
637	1	635.8011	-148.78	2	36.5	10.8	2	4247-4257	R.RSLKELNLGLK.G	

Detailed Protein Report

Protein 112: **PREDICTED: LOW QUALITY PROTEIN: UPF0627 protein ENSP00000364708 [Homo sapiens]**

Accession:	gi|410171120	**Score:**	42.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.2
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.9
		No. of unique Peptides:	3

```
        10         20         30         40         50         60         70         80
MGCSKGLWKE RPSAHTSECF STTACPVAFI LLVWNSQSPA GLQSFCTGRH PSLSVRAQRA GPGASREEGT XWTECVGQER
        90        100        110        120        130        140        150        160
RLIHSGSSEN ESQEDEGADL IPYTGLKADN RRKSSTWANE VEDRRPQSTP ALNLTPSHPH PPRPLITFLR SVIGIQILPG
       170
LVAAGGTVA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2122	1	937.3818	-36.45	2	55.1	13.6	1	0-0	.EEGTHWTECVGQERR.	Carbamidomethyl: 9
1988	1	918.3938	-29.29	2	55.2	12.1	1	67-81	R.EEGTVWTECVGQERR.L	Carbamidomethyl: 9
1963	2	918.3504	-82.67	2	54.9	16.4	2	67-81	R.EEGTRWTECVGQERR.L	

Detailed Protein Report

Protein 113: dynein heavy chain 11, axonemal [Homo sapiens]

Accession:	gi|459642365	**Score:**	42.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	520.0
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	1

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 114: PREDICTED: zinc finger protein 665 isoform X5 [Homo sapiens]

Accession:	gi|578834915	**Score:**	41.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.3
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 1.17 **CV:** 0.00 % **No. of 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	Ratios	
2877	5	937.4629	1.55	2	65.1	10.5	0	1-18	-.MVCPCSGLLLAVGGMPPR.C	Carbamidomethyl: 5; Oxidation: 15	QD:QU	1.17
2957	4	937.4644	3.23	2	66.1	16.2	0	1-18	-.MVCPCSGLLLAVGGMPPR.C	Carbamidomethyl: 3; Oxidation: 15		

Detailed Protein Report

Protein 115: PREDICTED: peroxidasin-like protein isoform X2 [Homo sapiens]

Accession:	gi|530388290	**Score:**	41.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	95.0
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	2

```
        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
1881	1	628.2724	57.53	2	53.9	12.9	0	679-688	R.VWQDCCADCR.S	Carbamidomethyl: 5
1949	1	656.8239	117.11	2	54.8	14.5	0	679-688	R.VWQDCCADCR.S	Carbamidomethyl: 5, 9

Detailed Protein Report

Protein 116: **PREDICTED: polyamine-modulated factor 1-binding protein 1 isoform X3 [Homo sapiens]**

Accession:	gi|578829261	**Score:**	41.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	118.6
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.42 **CV:** 0.00 % **No. of 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	Ratios
293	1	477.5768	-43.77	3	32.4	14.6	1	261-273	R.NKLACSNALVLER.E		QD:QU 0.42
1491	1	472.2634	90.28	2	48.8	14.3	1	1011-1017	K.NKCDFFL.-	Carbamidomethyl: 3	

Detailed Protein Report

Protein 117: 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; 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 118: **PREDICTED: chromodomain-helicase-DNA-binding protein 9 isoform X9 [Homo sapiens]**

Accession:	gi|530424378	**Score:**	41.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	269.5
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	3

Quantitation

QD:QU	**Median:** 0.76	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

```
        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
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
2753	2	937.4586	-76.18	2	63.4	14.1	2	813-830	R.ASLKLGLDKAVLQSMSGR.E			
2019	1	719.3122	-83.44	2	55.6	13.7	0	1342-1354	R.VVSTFGVVFDPDR.G			
2569	1	449.6413	-314.31	2	60.8	13.6	1	2055-2061	R.VQLINRR.N		QD:QU	0.76

Detailed Protein Report

Protein 119: ATPase family AAA domain-containing protein 2 [Homo sapiens]

Accession:	gi|24497618	**Score:**	41.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	158.5
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 10.05 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVVLRSSLEL	HNHSAASATG	SLDLSSDFLS	LEHIGRRRLR	SAGAAQKKPA	ATTAKAGDGS	SVKEVETYHR	TRALRSLRKD
90	100	110	120	130	140	150	160
AQNSSDSSFE	KNVEITEQLA	NGRHFTRQLA	RQQADKKKEE	HREDKVIPVT	RSLRARNIVQ	STEHLHEDNG	DVEVRRSCRI
170	180	190	200	210	220	230	240
RSRYSGVNQS	MLFDKLITNT	AEAVLQKMDD	MKKMRRQRMR	ELEDLGVFNE	TEESNLNMYT	RGKQKDIQRT	DEETTDNQEG
250	260	270	280	290	300	310	320
SVESSEEGED	QEHEDDGEDE	DDEDDDDDDD	DDDDDDDEDD	EDEEDGEEEN	QKRYYLRQRK	ATVYYQAPLE	KPRHQRKPNI
330	340	350	360	370	380	390	400
FYSGPASPAR	PRYRLSSAGP	RSPYCKRMNR	RRHAIHSSDS	TSSSSSEDEQ	HFERRRKRSR	NRAINRCLPL	NFRKDELKGI
410	420	430	440	450	460	470	480
YKDRMKIGAS	LADVDPMQLD	SSVRFDSVGG	LSNHIAALKE	MVVFPLLYPE	VFEKFKIQPP	RGCLFYGPPG	TGKTLVARAL
490	500	510	520	530	540	550	560
ANECSQGDKR	VAFFMRKGAD	CLSKWVGESE	RQLRLLFDQA	YQMRPSIIFF	DEIDGLAPVR	SSRQDQIHSS	IVSTLLALMD
570	580	590	600	610	620	630	640
GLDSRGEIVV	IGATNRLDSI	DPALRRPGRF	DREFLFSLPD	KEARKEILKI	HTRDWNPKPL	DTFLEELAEN	CVGYCGADIK
650	660	670	680	690	700	710	720
SICAEAALCA	LRRRYPQIYT	TSEKLQLDLS	SINISAKDFE	VAMQKMIPAS	QRAVTSPGQA	LSTVVKPLLQ	NTVDKILEAL
730	740	750	760	770	780	790	800
QRVFPHAEFR	TNKTLDSDIS	CPLLESDLAY	SDDDVPSVYE	NGLSQKSSHK	AKDNFNFLHL	NRNACYQPMS	FRPRILIVGE
810	820	830	840	850	860	870	880
PGFGQGSHLA	PAVIHALEKF	TVYTLDIPVL	FGVSTTSPEE	TCAQVIREAK	RTAPSIVYVP	HIHVWWEIVG	PTLKATFTTL
890	900	910	920	930	940	950	960
LQNIPSFAPV	LLLATSDKPH	SALPEEVQEL	FIRDYGEIFN	VQLPDKEERT	KFFEDLILKQ	AAKPPISKKK	AVLQALEVLP
970	980	990	1000	1010	1020	1030	1040
VAPPPEPRSL	TAEEVKRLEE	QEEDTFRELR	IFLRNVTHRL	AIDKRFRVFT	KPVDPDEVPD	YVTVIKQPMD	LSSVISKIDL
1050	1060	1070	1080	1090	1100	1110	1120
HKYLTVKDYL	RDIDLICSNA	LEYNPDRDPG	DRLIRHRACA	LRDTAYAIIK	EELDEDFEQL	CEEIQESRKK	RGCSSSKYAP
1130	1140	1150	1160	1170	1180	1190	1200
SYYHVMPKQN	STLVGDKRSD	PEQNEKLKTP	STPVACSTPA	QLKRKIRKKS	NWYLGTIKKR	RKISQAKDDS	QNAIDHKIES
1210	1220	1230	1240	1250	1260	1270	1280
DTEETQDTSV	DHNETGNTGE	SSVEENEKQQ	NASESKLELR	NNSNTCNIEN	ELEDSRKTTA	CTELRDKIAC	NGDASSSQII
1290	1300	1310	1320	1330	1340	1350	1360
HISDENEGKE	MCVLRMTRAR	RSQVEQQQLI	TVEKALAILS	QPTPSLVVDH	ERLKNLLKTV	VKKSQNYNIF	QLENLYAVIS
1370	1380	1390	1400				
QCIYRHRKDH	DKTSLIQKME	QEVENFSCSR					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2101	1	1057.6924	66.12	1	54.8	10.3	2	38-47	R.RLRSAGAAQK.K		
2087	7	937.3467	-131.35	2	54.7	19.5	0	407-424	K.IGASLADVDPMQLDSSVR.F		QD:QU 10.05

Detailed Protein Report

Protein 120: **PREDICTED: keratin, type I cytoskeletal 26 isoform X2 [Homo sapiens]**

Accession:	gi|578830847	**Score:**	41.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.6
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	8.4
		No. of unique Peptides:	3

Quantitation

QD:QU **Median:** 0.81 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSFRLSGGSR	RICSRTGSGR	LSGGGTGFVA	GNVCVGSGAR	SSFSCTLEGI	SSGGSFCNSG	GGLGSGACAG	FLGNEHSLLS
90	100	110	120	130	140	150	160
GNEKVTMQNL	NDRLASYLDH	VHALEEANAD	LEQKIKGWYE	KCEPGSSREH	DHDYSRYFSV	IEDLKRQIIS	ATICNASIVL
170	180	190	200	210	220	230	240
QNDNARLTAD	DFRLKYENEL	ALHHSVEADT	SGLRRVLDEL	TLCTTDLEIQ	CETLSEELTY	LKKSHEEEME	VLQYTAGGNV
250	260	270	280	290	300	310	320
NVEMNATPGV	DLTVLLNNMR	AEYEDLAEQN	RKDAEAWFNE	RSATLQQQIS	DHEGAATAAR	NELTELKRNL	QTLEIELQSL
330	340	350	360	370	380	390	400
MAVKHSYECS	LAETEGNYCN	QLQQIQDQIG	VMEEQLQQIR	TETEGQKLEY	EQLLDVKIFL	EKEIDIYCNL	LDGEERKSKS
410	420	430	440	450	460	470	
TCYKSKGYRP	VNSGNQAKEE	TIVKTVVEEL	DQIGNLLSLR	VHSVEEKSSK	ISNITVEQRV	PSKAP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
559	2	625.3768	63.05	2	35.6	11.4	0	368-377	K.LEYEQLLDVK.I		QD:QU 0.81
1697	1	905.3389	-109.42	2	49.8	10.8	1	383-397	K.EIDIYCNLLDGEERK.S		
2812	1	753.3845	-13.35	2	64.3	19.2	1	405-418	K.SKGYRPVNSGNQAK.E		

Detailed Protein Report

Protein 121: hexokinase-1 isoform HKI-R [Homo sapiens]

Accession:	gi|15991827	**Score:**	41.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	102.1
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.3
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MDCEHSLSLP	CRGAEAWEIG	IDKYLYAMRL	SDETLIDIMT	RFRKEMKNGL	SRDFNPTATV	KMLPTFVRSI	PDGSEKGDFI
90	100	110	120	130	140	150	160
ALDLGGSSFR	ILRVQVNHEK	NQNVHMESEV	YDTPENIVHG	SGSQLFDHVA	ECLGDFMEKR	KIKDKKLPVG	FTFSFPCQQS
170	180	190	200	210	220	230	240
KIDEAILITW	TKRFKASGVE	GADVVKLLNK	AIKKRGDYDA	NIVAVVNDTV	GTMMTCGYDD	QHCEVGLIIG	TGTNACYMEE
250	260	270	280	290	300	310	320
LRHIDLVEGD	EGRMCINTEW	GAFGDDGSLE	DIRTEFDREI	DRGSLNPGKQ	LFEKMVSGMY	LGELVRLILV	KMAKEGLLFE
330	340	350	360	370	380	390	400
GRITPELLTR	GKFNTSDVSA	IEKNKEGLHN	AKEILTRLGV	EPSDDDCVSV	QHVCTIVSFR	SANLVAATLG	AILNRLRDNK
410	420	430	440	450	460	470	480
GTPRLRTTVG	VDGSLYKTHP	QYSRRFHKTL	RRLVPDSDVR	FLLSESGSGK	GAAMVTAVAY	RLAEQHRQIE	ETLAHFHLTK
490	500	510	520	530	540	550	560
DMLLEVKKRM	RAEMELGLRK	QTHNNAVVKM	LPSFVRRTPD	GTENGDFLAL	DLGGTNFRVL	LVKIRSGKKR	TVEMHNKIYA
570	580	590	600	610	620	630	640
IPIEIMQGTG	EELFDHIVSC	ISDFLDYMGI	KGPRMPLGFT	FSFPCQQTSL	DAGILITWTK	GFKATDCVGH	DVVTLLRDAI
650	660	670	680	690	700	710	720
KRREEFDLDV	VAVVNDTVGT	MMTCAYEEPT	CEVGLIVGTG	SNACYMEEMK	NVEMVEGDQG	QMCINMEWGA	FGDNGCLDDI
730	740	750	760	770	780	790	800
RTHYDRLVDE	YSLNAGKQRY	EKMISGMYLG	EIVRNILIDF	TKKGFLFRGQ	ISETLKTRGI	FETKFLSQIE	SDRLALLQVR
810	820	830	840	850	860	870	880
AILQQLGLNS	TCDDSILVKT	VCGVVSRRAA	QLCGAGMAAV	VDKIRENRGL	DRLNVTVGVD	GTLYKLHPHF	SRIMHQTVKE
890	900	910	920				
LSPKCNVSFL	LSEDGSGKGA	ALITAVGVRL	RTEASS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2596	1	658.6717	-179.19	2	61.1	11.3	0	2-12	M.DCEHSLSLPCR.G	Carbamidomethyl: 10
2975	1	953.4552	-46.39	2	66.4	14.7	1	433-450	R.LVPDSDVRFLLSESGSGK.G	

Detailed Protein Report

Protein 122: cystatin-S precursor [Homo sapiens]

Accession:	gi|4503109	**Score:**	41.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.2
Database Date:	2015-11-30	**pI:**	4.8
		Sequence Coverage [%]:	7.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MARPLCTLLL LMATLAGALA SSSKEENRII PGGIYDADLN DEWVQRALHF AISEYNKATE DEYYRRPLQV LRAREQTFGG
        90        100        110        120        130        140        150
VNYFFDVEVG RTICTKSQPN LDTCAFHEQP ELQKKQLCSF EIYEVPWEDR MSLVNSRCQE A
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
887	1	646.8226	-19.68	2	39.6	41.3	0	47-57	R.ALHFAISEYNK.A	

Detailed Protein Report

Protein 123: **PREDICTED: polyribonucleotide nucleotidyltransferase 1, mitochondrial isoform X1 [Homo sapiens]**

Accession:	gi|530368250	**Score:**	41.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.3
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.59 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MVTAVSKTKP SPSQFMPLVV DYRQKAAAAG RIPTNYLRRE IGTSDKEILT SRIIDRSIRP LFPAGYFYDT QVLCNLLAVD
        90        100        110        120        130        140        150        160
GVNEPDVLAI NGASVALSLS DIPWNGPVGA VRIGIIDGEY VVNPTRKEMS SSTLNLVVAG APKSQIVMLE ASAENILQQD
       170        180        190        200        210        220        230        240
FCHAIKVGVK YTQQIIQGIQ QLVKETGVTK RTPQKLFTPS PEIVKYTHKL AMERLYAVFT DYEHDKVSRD EAVNKIRLDT
       250        260        270        280        290        300        310        320
EEQLKEKFPE ADPYEIIESF NVVAKEVFRS IVLNEYKRCD GRDLTSLRNV SCEVDMFKTL HGSALFQRGQ TQVLCTVTFD
       330        340        350        360        370        380        390        400
SLESGIKSDQ VITAINGIKD KNFMLHYEFP PYATNEIGKV TGLNRRELGH GALAEKALYP VIPRDFPFTI RVTSEVLESN
       410        420        430        440        450        460        470        480
GSSSMASACG GSLALMDSGV PISSAVAGVA IGLVTKTDPE KGEIEDYRLL TDILGIEDYN GDMDFKIAGT NKGITALQAD
       490        500        510        520        530        540        550        560
IKLPGIPIKI VMEAIQQASV AKKEILQIMN KTISKPRASR KENGPVVETV QVPLSKRAKF VGPGGYNLKK LQAETGVTIS
       570        580        590        600        610        620        630        640
QVDEETFSVF APTPSAMHEA RDFITEICKD DQEQQLEFGA VYTATITEIR DTGVMVKLYP NMTAVLLHNT QLDQRKIKHP
       650        660        670        680        690        700        710
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
2395	4	973.4016	-133.24	2	60.4	12.8	2	40-56	R.EIGTSDKEILTSRIIDR.S		QD:QU 0.59
80	1	586.3280	116.43	2	30.9	28.4	0	289-298	R.NVSCEVDMFK.T		

Detailed Protein Report

Protein 124: PREDICTED: ankyrin repeat domain-containing protein 11 isoform X4 [Homo sapiens]

Accession:	gi|578828959	**Score:**	41.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	286.8
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	2

Quantitation

QD:QU	**Median:**	0.61	**CV:**	0.00 %	**No. of Peptides:**	1	

Detailed Protein Report

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			
1383	2	637.4051	150.05	3	45.8	14.2	0	454-471	K.TISSPAWSEVSSLSDSTR.T		QD:QU	0.61

Detailed Protein Report

Protein 125: filaggrin [Homo sapiens]

Accession:	gi|60097902	**Score:**	40.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	434.9
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

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
SGHSGSHHSH	TTSQGRSDAS	RGQSGSRSAS	RKTYDKEQSG	DGSRHSGSHH	HEASSWADSS	RHSLVGQGQS	SGPRTSRPRG
2250	2260	2270	2280	2290	2300	2310	2320
SSVSQDSDSE	GHSEDSERRS	GSASRNHHGS	AQEQSRDGSR	HPRSHHEDRA	GHGHSAESSR	QSGTHHAENS	SGGQAASSHE
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
371	1	938.4376	1.41	2	34.6	15.1	2	3797-3814	R.SDASHGQSGSRSASRETR.N	

Detailed Protein Report

Protein 126: **zinc finger protein 638 isoform 2 [Homo sapiens]**

Accession:	gi|357933604	**Score:**	40.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	218.1
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

Detailed Protein Report

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        10         20         30         40         50         60         70         80
MSRPRFNPRG DFPLQRPRAP NPSGMRPPGP FMRPGSMGLP RFYPAGRARG IPHRFAGHES YQNMGPQRMN VQVTQHRTDP
        90        100        110        120        130        140        150        160
RLTKEKLDFH EAQQKKGKPH GSRWDDEPHI SASVAVKQSS VTQVTEQSPK VQSRYTKESA SSILASFGLS NEDLEELSRY
       170        180        190        200        210        220        230        240
PDEQLTPENM PLILRDIRMR KMGRRLPNLP SQSRNKETLG SEAVSSNVID YGHASKYGYT EDPLEVRIYD PEIPTDEVEN
       250        260        270        280        290        300        310        320
EFQSQQNISA SVPNPNVICN SMFPVEDVFR QMDFPGESSN NRSFFSVESG TKMSGLHISG GQSVLEPIKS VNQSINQTVS
       330        340        350        360        370        380        390        400
QTMSQSLIPP SMNQQPFSSE LISSVSQQER IPHEPVINSS NVHVGSRGSK KNYQSQADIP IRSPFGIVKA SWLPKFSHAD
       410        420        430        440        450        460        470        480
AQKMKRLPTP SMMNDYYAAS PRIFPHLCSL CNVECSHLKD WIQHQNTSTH IESCRQLRQQ YPDWNPEILP SRRNEGNRKE
       490        500        510        520        530        540        550        560
NETPRRRSHS PSPRRSRRSS SSHRFRRSRS PMHYMYRPRS RSPRICHRFI SRYRSRSRSR SPYRIRNPFR GSPKCFRSVS
       570        580        590        600        610        620        630        640
PERMSRRSVR SSDRKKALED VVQRSGHGTE FNKQKHLEAA DKGHSPAQKP KTSSGTKPSV KPTSATKSDS NLGGHSIRCK
       650        660        670        680        690        700        710        720
SKNLEDDTLS ECKQVSDKAV SLQRKLRKEQ SLHYGSVLLI TELPEDGCTE EDVRKLFQPF GKVNDVLIVP YRKEAYLEME
       730        740        750        760        770        780        790        800
FKEAITAIMK YIETTPLTIK GKSVKICVPG KKKAQNKEVK KKTLESKKVS ASTLKRDADA SKAVEIVTST SAAKTGQAKA
       810        820        830        840        850        860        870        880
SVAKVNKSTG KSASSVKSVV TVAVKGNKAS IKTAKSGGKK SLEAKKTGNV KNKDSNKPVT IPENSEIKTS IEVKATENCA
       890        900        910        920        930        940        950        960
KEAISDAALE ATENEPLNKE TEEMCVMLVS NLPNKGYSVE EVYDLAKPFG GLKDILILSS HKKAYIEINR KAAESMVKFY
       970        980        990       1000       1010       1020       1030       1040
TCFPVLMDGN QLSISMAPEN MNIKDEEAIF ITLVKENDPE ANIDTIYDRF VHLDNLPEDG LQCVLCVGLQ FGKVDHHVFI
      1050       1060       1070       1080       1090       1100       1110       1120
SNRNKAILQL DSPESAQSMY SFLKQNPQNI GDHMLTCSLS PKIDLPEVQI EHDPELEKES PGLKNSPIDE SEVQTATDSP
      1130       1140       1150       1160       1170       1180       1190       1200
SVKPNELEEE STPSIQTETL VQQEEPCEEE AEKATCDSDF AVETLELETQ GEEVKEEIPL VASASVSIEQ FTENAEECAL
      1210       1220       1230       1240       1250       1260       1270       1280
NQQMFNSDLE KKGAEIINPK TALLPSDSVF AEERNLKGIL EESPSEAEDF ISGITQTMVE AVAEVEKNET VSEILPSTCI
      1290       1300       1310       1320       1330       1340       1350       1360
VTLVPGIPTG DEKTVDKKNI SEKKGNMDEK EEKEFNTKET RMDLQIGTEK AEKNEGRMDA EKVEKMAAMK EKPAENTLFK
      1370       1380       1390       1400       1410       1420       1430       1440
AYPNKGVGQA NKPDETSKTS ILAVSDVSSS KPSIKAVIVS SPKAKATVSK TENQKSFPKS VPRDQINAEK KLSAKEFGLL
      1450       1460       1470       1480       1490       1500       1510       1520
KPTSARSGLA ESSSKFKPTQ SSLTRGGSGR ISALQGKLSK LDYRDITKQS QETEARPSIM KRDDSNNKTL AEQNTKNPKS
      1530       1540       1550       1560       1570       1580       1590       1600
TTGRSSKSKE EPLFPFNLDE FVTVDEVIEE VNPSQAKQNP LKGKRKETLK NVPFSELNLK KKKGKTSTPR GVEGELSFVT
      1610       1620       1630       1640       1650       1660       1670       1680
LDEIGEEEDA AAHLAQALVT VDEVIDEEEL NMEEMVKNSN SLFTLDELID QDDCISHSEP KDVTVLSVAE EQDLLKQERL
      1690       1700       1710       1720       1730       1740       1750       1760
VTVDEIGEVE ELPLNESADI TFATLNTKGN EGDTVRDSIG FISSQVPEDP STLVTVDEIQ DDSSDLHLVT LDEVTEEDED
      1770       1780       1790       1800       1810       1820       1830       1840
SLADFNNLKE ELNFVTVDEV GEEEDGDNDL KVELAQSKND HPTDKKGNRK KRAVDTKKTK LESLSQVGPV NENVMEEDLK
      1850       1860       1870       1880       1890       1900       1910       1920
TMIERHLTAK TPTKRVRIGK TLPSEKAVVT EPAKGEEAFQ MSEVDEESGL KDSEPERKRK KTEDSSSGKS VASDVPEGEK
      1930       1940       1950       1960
AMTNHCKSTR HKQNTEKFMA KQRKEKEQNE AEERSSR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
503	1	658.4149	37.36	2	34.9	13.0	1	703-713	K.VNDVLIVPYRK.E	

Detailed Protein Report

Protein 127: zinc finger protein DZIP1 isoform 1 [Homo sapiens]

Accession:	gi|7662436	**Score:**	40.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.6
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.9
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MQAEAADWFS	SMPFQKHVYY	PLASGPEGPD	VAVAAAAAGA	ASMACAPPSA	ASGPLPFFQF	RPRLESVDWR	RLSAIDVDKV
90	100	110	120	130	140	150	160
AGAVDVLTLQ	ENIMNITFCK	LEDEKCPHCQ	SGVDPVLLKL	IRLAQFTIEY	LLHSQEFLTS	QLHTLEERLR	LSHCDGEQSK
170	180	190	200	210	220	230	240
KLLTKQAGEI	KTLKEECKRR	KKMISTQQLM	IEAKANYYQC	HFCDKAFMNQ	AFLQSHIQRR	HTEENSHFEY	QKNAQIEKLR
250	260	270	280	290	300	310	320
SEIVVLKEEL	QLTRSELEAA	HHASAVRFSK	EYEMQKTKEE	DFLKLFDRWK	EEEKEKLVDE	MEKVKEMFMK	EFKELTSKNS
330	340	350	360	370	380	390	400
ALEYQLSEIQ	KSNMQIKSNI	GTLKDAHEFK	EDRSPYPQDF	HNVMQLLDSQ	ESKWTARVQA	IHQEHKKEKG	RLLSHIEKLR
410	420	430	440	450	460	470	480
TSMIDDLNAS	NVFYKKRIEE	LGQRLQEQNE	LIITQRQQIK	DFTCNPLNSI	SEPKVNAPAL	HTLETKSSLP	MVHEQAFSSH
490	500	510	520	530	540	550	560
ILEPIEELSE	EEKGRENEQK	LNNNKMHLRK	ALKSNSSLTK	GLRTMVEQNL	MEKLETLGIN	ADIRGISSDQ	LHRVLKSVES
570	580	590	600	610	620	630	640
ERHKQEREIP	NFHQIREFLE	HQVSCKIEEK	ALLSSDQCSV	SQMDTLSTGE	VPKMIQLPSK	NRQLIRQKAV	STDRTSVPKI
650	660	670	680	690	700	710	720
KKNVMEDPFP	RKSSTITTPP	FSSEEEQEDD	DLIRAYASPG	PLPVPPPQNK	GSFGKNTVKS	DADGTEGSEI	EDTDDSPKPA
730	740	750	760	770	780	790	800
GVAVKTPTEK	VEKMFPHRKN	VNKPVGGTNV	PEMFIKKEEL	QELKCADVED	EDWDISSLEE	EISLGKKSGK	EQKEPPPAKN
810	820	830	840	850			
EPHFAHVLNA	WGAFNPKGPK	GEGLQENESS	TLKSSLVTVT	DWSDTSDV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1895	3	704.7670	-135.29	2	52.2	17.1	0	183-194	K.MISTQQLMIEAK.A	Oxidation: 8
2012	1	616.7504	-93.75	2	55.5	10.3	1	643-652	K.NVMEDPFPRK.S	

Detailed Protein Report

Protein 128: centromere protein F [Homo sapiens]

Accession:	gi|55770834	**Score:**	40.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	357.3
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	1.4
		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	KLKERERERND	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
1209	1	573.1437	-261.24	2	43.6	14.6	0	981-990	K.EINASLNQEK.M	
1276	1	917.4679	30.80	2	46.1	11.7	0	2267-2283	K.ELNEAVAALCGDQEIMK.A	
2721	2	974.5198	32.44	2	63.0	14.2	1	2466-2482	K.AKEQNLSSQVECLELEK.A	

Detailed Protein Report

Protein 129:	**PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X10 [Homo sapiens]**		
Accession:	gi|578799003	**Score:**	40.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	433.5
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	2

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
RAAGVPSATI	TWRKEGGSLP	PQARSERTDI	ATLLIPAITT	ADAGFYLCVA	TSPAGTAQAR	IQVVVLSASD	ASPPPVKIES
2250	2260	2270	2280	2290	2300	2310	2320
SSPSVTEGQT	LDLNCVVAGS	AHAQVTWYRR	GGSLPPHTQV	HGSRLRLPQV	SPADSGEYVC	RVENGSGPKE	ASITVSVLHG
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
2083	1	1052.3950	-135.43	2	56.4	13.6	0	643-661	R.GMLEPVQRPDVVLMGAGYR.L	Oxidation: 2
1714	1	1011.6020	66.80	3	51.7	12.9	1	3926-3953	R.FDAGSGMATIRHPTPLALGHFHTVTLLR.S	Oxidation: 7

Detailed Protein Report

Protein 130: PREDICTED: zinc finger protein 737 isoform X3 [Homo sapiens]

Accession:	gi|530414417	**Score:**	40.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.4
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGPLQFRDVA IEFSLEEWHC LDTAQRNLYR NVMLENYRNL VFLGIVVSKP DLITCLEQGK KPLTMKKHEM VANPSVTCSH
        90        100        110        120        130        140        150        160
FARDLWPEQS IKDSFQKVTL RRYENYGHDN LQFKKGCESV DECKVHKRGY NGLNQYLTTT QSKIFQCDKY VKVIHKFSNS
       170        180        190        200        210        220        230        240
NRHKIRHTGK KPFKCIECGK AFNQSSTLTT HKKIHTGEKP FKCEECGKAF NWSSHLTTHK RIHTGEKRYK CEDCGKAFSR
       250        260        270        280        290        300        310        320
FSYLTAHKII HSGEKPYKCE ECGKAFKRSS ILTAHKIIHS GEKPYKCEEC GKAFKHPSVL TTHKRIHTGE KPYKCEECGR
       330        340        350        360        370        380        390        400
AFKYFSSLTT HKIIHSGEKP YKCEECGKAF NWSSHLTTHK RIHTGEKPYK CEECGEAFKY SSSLTTHKII HTGQQPFKCE
       410        420        430        440        450        460        470        480
ECGKAFKCFS ILTTHKRIHT GEKPYKCEEC GKAFNSSSHL TAHKRIHTGE KPYKCERCGK AFKRSFILTR HKRIHTGEKP
       490        500        510        520        530
YKCEECGKGF KCPSTLTTHK RSGCPTRKLL LSSVSTLNNS EWK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2919	1	981.9597	-7.66	2	65.7	10.8	2	305-320	K.RIHTGEKPYKCEECGR.A	Carbamidomethyl: 11

Detailed Protein Report

Protein 131: **rapamycin-insensitive companion of mTOR isoform 3 [Homo sapiens]**

Accession: gi|550544215
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 40.3
MW [kDa]: 155.8
pI: 6.8
Sequence Coverage [%]: 1.9
No. of unique 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 GESTEDTGLQ EHTDDNCLYC
      1210       1220       1230       1240       1250       1260       1270       1280
VCIEILGFQP SNQLSAICSH SDFQDIPYSD WCEQTIHNPL EVVPSKFSGI SGCSDGVSQE GSASSTKSTE LLLGVKTIPD
      1290       1300       1310       1320       1330       1340       1350       1360
DTPMCRILLR KEVLRLVINL SSSVSTKCHE TGLLTIKEKY PQTFDDICLY SEVSHLLSHC TFRLPCRRFI QELFQDVQFL
      1370       1380       1390
QMHEEAEAVL ATPPKQPIVD TSAES
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2622	1	658.3808	-6.32	2	61.5	16.9	2	182-193	R.LRASAALNCLKR.F	
2751	1	805.9143	-22.12	2	65.5	23.4	1	435-449	K.ILTAATDACRLYATK.H	

Detailed Protein Report

Protein 132: myosin-2 [Homo sapiens]

Accession:	gi|153791586	**Score:**	40.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	222.9
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|153792663	refseq_human (refseq_human_20140103.fasta)	myosin-2 [Homo sapiens]

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
1958	1	745.7963	-141.38	2	54.9	15.0	1	1312-	K.QAFTQQIEELKR.Q	

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
								1323		

Detailed Protein Report

Protein 133: **myosin-4 [Homo sapiens]**

Accession:	gi|110611903	**Score:**	39.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	222.9
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MSSDSEMAIF	GEAAPFLRKS	EKERIEAQNK	PFDAKTSVFV	VDPKESYVKA	IVQSREGGKV	TAKTEAGATV	TVKEDQVFSM
90	100	110	120	130	140	150	160
NPPKYDKIED	MAMMTHLHEP	AVLYNLKERY	AAWMIYTYSG	LFCVTVNPYK	WLPVYNPEVV	TAYRGKKRQE	APPHIFSISD
170	180	190	200	210	220	230	240
NAYQFMLTDR	ENQSILITGE	SGAGKTVNTK	RVIQYFATIA	VTGEKKKEEP	ASGKMQGTLE	DQIISANPLL	EAFGNAKTVR
250	260	270	280	290	300	310	320
NDNSSRFGKF	IRIHFGATGK	LASADIETYL	LEKSRVTFQL	KAERSYHIFY	QILSNKKPEL	IEMLLITTNP	YDFAFVSQGE
330	340	350	360	370	380	390	400
ITVPSIDDQE	ELMATDSAVD	ILGFTADEKV	AIYKLTGAVM	HYGNMKFKQK	QREEQAEPDG	TEVADKAAYL	TSLNSADLLK
410	420	430	440	450	460	470	480
SLCYPRVKVG	NEFVTKGQTV	QQVYNAVGAL	AKAIYEKMFL	WMVTRINQQL	DTKQPRQYFI	GVLDIAGFEI	FDFNSLEQLC
490	500	510	520	530	540	550	560
INFTNEKLQQ	FFNHHMFVLE	QEEYKKEGIE	WEFIDFGMDL	AACIELIEKP	MGIFSILEEE	CMFPKATDTS	FKNKLYEQHL
570	580	590	600	610	620	630	640
GKSNNFQKPK	PAKGKPEAHF	SLVHYAGTVD	YNIAGWLDKN	KDPLNETVVG	LYQKSAMKTL	AFLFSGAQTA	EAEGGGGKKG
650	660	670	680	690	700	710	720
GKKKGSSFQT	VSALFRENLN	KLMTNLRSTH	PHFVRCIIPN	ETKTPGAMEH	ELVLHQLRCN	GVLEGIRICR	KGFPSRILYA
730	740	750	760	770	780	790	800
DFKQRYKVLN	ASAIPEGQFI	DSKKASEKLL	GSIEIDHTQY	KFGHTKVFFK	AGLLGTLEEM	RDEKLAQLIT	RTQAICRGFL
810	820	830	840	850	860	870	880
MRVEFRKMME	RRESIFCIQY	NIRAFMNVKH	WPWMKLYFKI	KPLLKSAETE	KEMANMKEEF	EKTKEELAKT	EAKRKELEEK
890	900	910	920	930	940	950	960
MVTLMQEKND	LQLQVQAEAD	ALADAEERCD	QLIKTKIQLE	AKIKEVTERA	EDEEEINAEL	TAKKRKLEDE	CSELKKDIDD
970	980	990	1000	1010	1020	1030	1040
LELTLAKVEK	EKHATENKVK	NLTEEMAGLD	ETIAKLTKEK	KALQEAHQQT	LDDLQMEEDK	VNTLTKAKTK	LEQQVDDLEG
1050	1060	1070	1080	1090	1100	1110	1120
SLEQEKKLCM	DLERAKRKLE	GDLKLAQEST	MDTENDKQQL	NEKLKKKEFE	MSNLQGKIED	EQALAIQLQK	KIKELQARIE
1130	1140	1150	1160	1170	1180	1190	1200
ELEEEIEAER	ASRAKAEKQR	SDLSRELEEI	SERLEEAGGA	TSAQIEMNKK	REAEFQKMRR	DLEESTLQHE	ATAAALRKKH
1210	1220	1230	1240	1250	1260	1270	1280
ADSVAELGEQ	IDSLQRVKQK	LEKEKSELKM	EINDLASNME	TVSKAKANFE	KMCRTLEDQL	SEIKTKEEEQ	QRLINELSAQ
1290	1300	1310	1320	1330	1340	1350	1360
KARLHTESGE	FSRQLDEKDA	MVSQLSRGKQ	AFTQQIEELK	RQLEEETKAK	STLAHALQSA	RHDCDLLREQ	YEEEQEAKAE
1370	1380	1390	1400	1410	1420	1430	1440
LQRGMSKANS	EVAQWRTKYE	TDAIQRTEEL	EEAKKKLAQR	LQDAEEHVEA	VNSKCASLEK	TKQRLQNEVE	DLMIDVERSN
1450	1460	1470	1480	1490	1500	1510	1520
AACIALDKKQ	RNFDKVLAEW	KQKYEETQAE	LEASQKESRS	LSTELFKVKN	AYEESLDHLE	TLKRENKNLQ	QEISDLTEQI
1530	1540	1550	1560	1570	1580	1590	1600
AEGGKHIHEL	EKVKKQLDHE	KSELQTSLEE	AEASLEHEEG	KILRIQLELN	QVKSEIDRKI	AEKDEELDQL	KRNHLRVVES
1610	1620	1630	1640	1650	1660	1670	1680
MQSTLDAEIR	SRNDALRIKK	KMEGDLNEME	IQLNHANRQA	AEALRNLRNT	QGILKDTQLH	LDDAIRGQDD	LKEQLAMVER
1690	1700	1710	1720	1730	1740	1750	1760
RANLMQAEVE	ELRASLERTE	RGRKMAEQEL	LDASERVQLL	HTQNTSLINT	KKKLETDISQ	IQGEMEDIVQ	EARNAEEKAK
1770	1780	1790	1800	1810	1820	1830	1840
KAITDAAMMA	EELKKEQDTS	AHLERMKKNM	EQTVKDLQLR	LDEAEQLALK	GGKKQIQKLE	ARVRELESEV	ESEQKHNVEA
1850	1860	1870	1880	1890	1900	1910	1920
VKGLRKHERR	VKELTYQTEE	DRKNILRLQD	LVDKLQTKVK	AYKRQAEEAE	EQSNVNLAKF	RKLQHELEEA	KERADIAESQ
1930	1940						
VNKLRVKSRE	VHTKVISEE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1578	1	873.9352	-55.16	2	48.2	12.5	2	56-73	R.EGGKVTAKTEAGATVTVK.E	

Detailed Protein Report

Protein 134: vacuolar protein sorting-associated protein 13A isoform D [Homo sapiens]

Accession:	gi|66346676	**Score:**	39.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	347.5
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	2

Quantitation

QD:QU	**Median:** 0.62	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVFESVVVDV	LNRFLGDYVV	DLDTSQLSLG	IWKGAVALKN	LQIKENALSQ	LDVPFKVKVG	HIGNLKLIIP	WKNLYTQPVE
90	100	110	120	130	140	150	160
AVLEEIYLLI	VPSSRIKYDP	LKEEKQLMEA	KQQELKRIEE	AKQKVVDQEQ	HLPEKQDTFA	EKLVTQIIKN	LQVKISSIHI
170	180	190	200	210	220	230	240
RYEDDITNRD	KPLSFGISLQ	NLSMQTTDQY	WVPCLHDETE	KLVRKLIRLD	NLFAYWNVKS	QMFYLSDYDN	SLDDLKNGIV
250	260	270	280	290	300	310	320
NENIVPEGYD	FVFRPISANA	KLVMNRRSDF	DFSAPKINLE	IELHNIAIEF	NKPQYFSIME	LLESVDMMAQ	NLPYRKFKPD
330	340	350	360	370	380	390	400
VPLHHHAREW	WAYAIHGVLE	VNVCPRLWMW	SWKHIRKHRQ	KVKQYKELYK	KKLTSKKPPG	ELLVSLEELE	KTLDVFNITI
410	420	430	440	450	460	470	480
ARQTAEVEVK	KAGYKIYKEG	VKDPEDNKGW	FSWLWSWSEQ	NTNEQQPDVQ	PETLEEMLTP	EEKALLYEAI	GYSETAVDPT
490	500	510	520	530	540	550	560
LLKTFEALKF	FVHLKSMSIV	LRENHQKPEL	VDIVIEEFST	LIVQRPGAQA	IKFETKIDSF	HITGLPDNSE	KPRLLSSLDD
570	580	590	600	610	620	630	640
AMSLFQITFE	INPLDETVSQ	RCIIEAEPLE	IIYDARTVNS	IVEFFRPPKE	VHLAQLTAAT	LTKLEEFRSK	TATGLLYIIE
650	660	670	680	690	700	710	720
TQKVLDLKIN	LKASYIIVPQ	DGIFSPTSNL	LLLDLGHLKV	TSKSRSELPD	VKQGEANLKE	IMDRAYDSFD	IQLTSVQLLY
730	740	750	760	770	780	790	800
SRVGDNWREA	RKLSVSTQHI	LVPMHFNLEL	SKAMVFMDVR	MPKFKIYGKL	PLISLRISDK	KLQGIMELIE	SIPKPEPVTE
810	820	830	840	850	860	870	880
VSAPVKSFQI	QTSTSLGTSQ	ISQKIIPLLE	LPSVSEDDSE	EEFFDAPCSP	LEEPLQFPTG	VKSIRTRKLQ	KQDCSVNMTT
890	900	910	920	930	940	950	960
FKIRFEVPKV	LIEFYHLVGD	CELSVVEILV	LGLGAEIEIR	TYDLKANAFL	KEFCLKCPEY	LDENKKPVYL	VTTLDNTMED
970	980	990	1000	1010	1020	1030	1040
LLTLEYVKAE	KNVPDLKSTY	NNVLQLIKVN	FSSLDIHLHT	EALLNTINYL	HNILPQSEEK	SAPVSTTETE	DKGDVIKKLA
1050	1060	1070	1080	1090	1100	1110	1120
LKLSTNEDII	TLQILAELSC	LQIFIQDQKC	NISEIKIEGL	DSEMIMRPSE	TEINAKLRNI	IVLDSDITAI	YKKAVYITGK
1130	1140	1150	1160	1170	1180	1190	1200
EVFSFKMVSY	MDATAGSAYT	DMNVVDIQVN	LIVGCIEVVF	VTKFLYSILA	FIDNFQAAKQ	ALAEATVQAA	GMAATGVKEL
1210	1220	1230	1240	1250	1260	1270	1280
AQRSSRMALD	INIKAPVVVI	PQSPVSENVF	VADFGLITMT	NTFHMITESQ	SSPPPVIDLI	TIKLSEMRLY	RSRFINDAYQ
1290	1300	1310	1320	1330	1340	1350	1360
EVLDLLLPLN	LEVVVERNLC	WEWYQEVPCF	NVNAQLKPME	FILSQEDITT	IFKTLHGNIW	YEKDGSASPA	VTKDQYSATS
1370	1380	1390	1400	1410	1420	1430	1440
GVTTNASHHS	GGATVVTAAV	VEVHSRALLV	KTTLNISFKT	DDLTMVLYSP	GPKQASFTDV	RDPSLKLAEF	KLENIISTLK
1450	1460	1470	1480	1490	1500	1510	1520
MYTDGSTFSS	FSLKNCILDD	KRPHVKKATP	RMIGLTVGFD	KKDMMDIKYR	KVRDGCVTDA	VFQEMYICAS	VEFLQTVANV
1530	1540	1550	1560	1570	1580	1590	1600
FLEAYTTGTA	VETSVQTWTA	KEEVPTQESV	KWEINVIIKN	PEIVFVADMT	KNDAPALVIT	TQCEICYKGN	LENSTMTAAI
1610	1620	1630	1640	1650	1660	1670	1680
KDLQVRACPF	LPVKRKGKIT	TVLQPCDLFY	QTTQKGTDPQ	VIDMSVKSLT	LKVSPVIINT	MITITSALYT	TKETIPEETA
1690	1700	1710	1720	1730	1740	1750	1760
SSTAHLWEKK	DTKTLKMWFL	EESNETEKIA	PTTELVPKGE	MIKMNIDSIF	IVLEAGIGHR	TVPMLLAKSR	FSGEGKNWSS
1770	1780	1790	1800	1810	1820	1830	1840
LINLHCQLEL	EVHYYNEMFG	VWEPLLEPLE	IDQTEDFRPW	NLGIKMKKKA	KMAIVESDPE	EENYKVPEYK	TVISFHSKDQ
1850	1860	1870	1880	1890	1900	1910	1920
LNITLSKCGL	VMLNNLVKAF	TEAATGSSAD	FVKDLAPFMI	LNSLGLTISV	SPSDSFSVLN	IPMAKSYVLK	NGESLSMDYI
1930	1940	1950	1960	1970	1980	1990	2000
RTKDNDHFNA	MTSLSSKLFF	ILLTPVNHST	ADKIPLTKVG	RRLYTVRHRE	SGVERSIVCQ	IDTVEGSKKV	TIRSPVQIRN
2010	2020	2030	2040	2050	2060	2070	2080
HFSVPLSVYE	GDTLLGTASP	ENEFNIPLGS	YRSFIFLKPE	DENYQMCEGI	DFEEIIKNDG	ALLKKKCRSK	NPSKESFLIN
2090	2100	2110	2120	2130	2140	2150	2160
IVPEKDNLTS	LSVYSEDGWD	LPYIMHLWPP	ILLRNLLPYK	IAYYIEGIEN	SVFTLSEGHS	AQICTAQLGK	ARLHLKLLDY
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
731	1	698.3535	13.36	3	39.1	12.3	1	1970-1988	R.ESGVERSIVCQIDTVEGSK.K	Carbamidomethyl: 10	
1997	2	648.7895	-184.44	2	53.5	13.3	2	1989-1999	K.KVTIRSPVQIR.N		QD:QU 0.62

Detailed Protein Report

Protein 135: ubiquitin carboxyl-terminal hydrolase 6 [Homo sapiens]

Accession:	gi|109638751	**Score:**	39.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	158.6
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	3

Quantitation

QD:QU	**Median:** 0.83	**CV:** 0.00 %	**No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|530410741	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ubiquitin carboxyl-terminal hydrolase 6 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MDMVENADSL	QAQERKDILM	KYDKGHRAGL	PEDKGPEPVG	INSSIDRFGI	LHETELPPVT	AREAKKIRRE	MTRTSKWMEM
90	100	110	120	130	140	150	160
LGEWETYKHS	SKLIDRVYKG	IPMNIRGPVW	SVLLNIQEIK	LKNPGRYQIM	KERGKRSSEH	IHHIDLDVRT	TLRNHVFFRD
170	180	190	200	210	220	230	240
RYGAKQRELF	YILLAYSEYN	PEVGYCRDLS	HITALFLLYL	PEEDAFWALV	QLLASERHSL	PGFHSPNGGT	VQGLQDQQEH
250	260	270	280	290	300	310	320
VVPKSQPKTM	WHQDKEGLCG	QCASLGCLLR	NLIDGISLGL	TLRLWDVYLV	EGEQVLMPIT	SIALKVQQKR	LMKTSRCGLW
330	340	350	360	370	380	390	400
ARLRNQFFDT	WAMNDDTVLK	HLRASTKKLT	RKQGDLPPPA	KREQGSLAPR	PVPASRGGKT	LCKGYRQAPP	GPPAQFQRPI
410	420	430	440	450	460	470	480
CSASPPWASR	FSTPCPGGAV	REDTYPVGTQ	GVPSLALAQG	GPQGSWRFLE	WKSMPRLPTD	LDIGGPWFPH	YDFEWSCWVR
490	500	510	520	530	540	550	560
AISQEDQLAT	CWQAEHCGEV	HNKDMSWPEE	MSFTANSSKI	DRQKVPTEKG	ATGLSNLGNT	CFMNSSIQCV	SNTQPLTQYF
570	580	590	600	610	620	630	640
ISGRHLYELN	RTNPIGMKGH	MAKCYGDLVQ	ELWSGTQKSV	APLKLRRTIA	KYAPKFDGFQ	QQDSQELLAF	LLDGLHEDLN
650	660	670	680	690	700	710	720
RVHEKPYVEL	KDSDGRPDWE	VAAEAWDNHL	RRNRSIIVDL	FHGQLRSQVK	CKTCGHISVR	FDPFNFLSLP	LPMDSYMDLE
730	740	750	760	770	780	790	800
ITVIKLDGTT	PVRYGLRLNM	DEKYTGLKKQ	LRDLCGLNSE	QILLAEVHDS	NIKNFPQDNQ	KVQLSVSGFL	CAFEIPVPSS
810	820	830	840	850	860	870	880
PISASSPTQI	DFSSSPSTNG	MFTLTTNGDL	PKPIFIPNGM	PNTVVPCGTE	KNFTNGMVNG	HMPSLPDSPF	TGYIIAVHRK
890	900	910	920	930	940	950	960
MMRTELYFLS	PQENRPSLFG	MPLIVPCTVH	TRKKDLYDAV	WIQVSWLARP	LPPQEASIHA	QDRDNCMGYQ	YPFTLRVVQK
970	980	990	1000	1010	1020	1030	1040
DGNSCAWCPQ	YRFCRGCKID	CGEDRAFIGN	AYIAVDWHPT	ALHLRYQTSQ	ERVVDKHESV	EQSRRAQAEP	INLDSCLRAF
1050	1060	1070	1080	1090	1100	1110	1120
TSEEELGESE	MYYCSKCKTH	CLATKKLDLW	RLPPFLIIHL	KRFQFVNDQW	IKSQKIVRFL	RESFDPSAFL	VPRDPALCQH
1130	1140	1150	1160	1170	1180	1190	1200
KPLTPQGDEL	SKPRILAREV	KKVDAQSSAG	KEDMLLSKSP	SSLSANISSS	PKGSPSSSRK	SGTSCPSSKN	SSPNSSPRTL
1210	1220	1230	1240	1250	1260	1270	1280
GRSKGRLRLP	QIGSKNKPSS	SKKNLDASKE	NGAGQICELA	DALSRGHMRG	GSQPELVTPQ	DHEVALANGF	LYEHEACGNG
1290	1300	1310	1320	1330	1340	1350	1360
CGDGYSNGQL	GNHSEEDSTD	DQREDTHIKP	IYNLYAISCH	SGILSGGHYI	TYAKNPNCKW	YCYNDSSCEE	LHPDEIDTDS
1370	1380	1390	1400	1410			
AYILFYEQQG	IDYAQFLPKI	DGKKMADTSS	TDEDSESDYE	KYSMLQ			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2707	4	673.3583	-36.63	2	65.0	13.5	2	89-99	K.HSSKLIDRVYK.G		
2932	1	965.1226	-27.88	3	65.8	10.3	0	218-244	R. HSLPGFHSPNGGTVQGLQDQQE S		

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	1230-1245	K.ENGAGQICELADALSR.G		QD:QU	0.83

Detailed Protein Report

Protein 136: PREDICTED: neuroblastoma breakpoint family member 4 isoform X2 [Homo sapiens]

Accession:	gi|578798443	**Score:**	39.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.3
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	7.2
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.99 **CV:** 0.00 % **No. of Peptides:** 1

```
        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	Ratios
2547	3	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		QD:QU 0.99

Detailed Protein Report

Protein 137: beta/gamma crystallin domain-containing protein 3 [Homo sapiens]

Accession:	gi|390979647	**Score:**	39.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	330.4
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MSSGRRRGSA	PWHSFSRFFA	PRSPSRDKEE	EEEERPGTSP	PPAPGRSAAS	VENEPMSTSQ	KKENVLSSEA	VKIRQSEDKR
90	100	110	120	130	140	150	160
NHAEKPVTLP	VQEDPKKAYD	LSSSTSDTKI	GESDRQPKES	FFQFLGNLFN	ISGKSSLGEA	KQSSFKDDQD	KTEKDLQNPS
170	180	190	200	210	220	230	240
DHHEDGIKRE	REIFSGSLRT	QTHPTEEQDS	NSSELSDAFS	LDTTQDSDQE	TTNLLKQIDG	KPEKPSVTYA	TYRGPRHIGK
250	260	270	280	290	300	310	320
YLKQQTGLAT	VNTLDRENES	SDSSTNRHID	PGSEIEAGVL	PLLLSASTDS	SMKGNLLEGP	LEDSDCSKTS	FNKENSLTNN
330	340	350	360	370	380	390	400
PELQNIASSN	NLLNKNAWGS	IERNRSSPSS	VTNSSYDGES	DSQHHLSCEP	VSQTNRNLVC	SALLTGSNHR	KVPCSPDFQR
410	420	430	440	450	460	470	480
VTTTENTIKE	NSTVMSNRTL	VQREELVEPQ	GPAISDFSCS	KSDGSDTTEQ	ESTNLPSPNK	SIRHEHLQLP	ESECSDKQTI
490	500	510	520	530	540	550	560
DSSSKQAATH	TNIIALQRHA	VTDTEFVNEG	KRLSAQDSQK	NVAVREIRRE	TESASAGESI	ASSHVKAPED	KIESLPKDTD
570	580	590	600	610	620	630	640
QYFETKAKKL	DFRSHDKIPH	IRMNKKDLAS	LNYISESAVV	ASLGNENAPE	LKFELNRSHI	SETPLDSESP	QQAEVSPDAK
650	660	670	680	690	700	710	720
TSLSLDCKKL	NFSISPPTFV	SGVGMLSKLD	IPDLMNEGSP	VPIETGNVNI	VGISYQPRKC	KEENVKNHVE	AAGRKSPPPS
730	740	750	760	770	780	790	800
FCLEYTSAIF	EFKEVLSNSE	KCQVLPGSEA	SGPHLTGLEL	LSFDSGNLSK	DCSSILSQDP	NRVELVSSNT	KANMSIIEKS
810	820	830	840	850	860	870	880
DSLSLEAKTA	NIVSKAEIDG	QNNVLVESHS	GRGKTISLSK	VSLSKVEPRN	ISQDKMSSFP	LKITHVPEKP	ILSELTFLEV
890	900	910	920	930	940	950	960
EQGKRFQSIN	HNEIGEKCSD	AGLKENCQAE	LSPAASKYED	KPEPEVDALG	SPPALLKSNI	SWILPPIHDE	KISRQMAQNC
970	980	990	1000	1010	1020	1030	1040
EAHTCVFHQS	LDICGTKKIS	GHSEMAELSL	TNISPKFQET	GSMKVNSPFL	DSDSSLEKNS	SASEDSSFLK	VPSVLKLEKK
1050	1060	1070	1080	1090	1100	1110	1120
SSSYRKKENI	HFLNGGIDSV	SSSSSYPEEV	SMIVNSHKPQ	NNLDSIQVTK	DLTHEGTSVT	NLLYPTTSYL	EFETSVSIGT
1130	1140	1150	1160	1170	1180	1190	1200
EVTPFQEHFG	IYTGKISIDF	PTAAQFDNLV	EAETGAVAGP	AASVNSSGQQ	CSEASAEHIE	ARRRAHDQLL	DLKSSLLKKA
1210	1220	1230	1240	1250	1260	1270	1280
DTLIGEIFNS	VREELKFKHT	VSTCQEHIAI	EGIMNLGTLK	EDISEKNPSE	VTLTEIQQTE	GLEEQGMENM	SEVKEKPCVS
1290	1300	1310	1320	1330	1340	1350	1360
PTVGEKNLLV	DPNSMNVSCL	LEDKARELVN	EIIYVAQEKL	RNDTFEDTED	TWDSELQANT	SKILNSDSVK	PHDVVREFLV
1370	1380	1390	1400	1410	1420	1430	1440
SEQPVNQSTQ	ISENKVLNEF	FSLSNLASGT	ESIKGGEIVL	YQKSLFSGNG	SGLSDSINLQ	ESDTVLLAED	MSHKRLDDRV
1450	1460	1470	1480	1490	1500	1510	1520
KTHLFRSEDC	NETMEIENVD	NNKTETEDRR	TLVLNFKWPP	LVNDDIHAPG	TSKSSLSDSL	VCISEKNLPG	HSKNTPLAMS
1530	1540	1550	1560	1570	1580	1590	1600
DVGKVHKKDN	EINIGKIELI	PSMLETGKTN	KKDAELNILK	YEAVPPMIEM	GRIHKMDAEL	NVTKTEPKAN	VFKMGEVYQM
1610	1620	1630	1640	1650	1660	1670	1680
DAESCIEKTE	GSAVILGMEK	AYKMKDTEGD	IGKIEVIPMM	PEVKNIHQKD	AEGDIVKTEM	TPVTVDMENI	YQTHAEGDIG
1690	1700	1710	1720	1730	1740	1750	1760
KTGTIALSEV	ENIHQKGGEG	ISEKAEVIPV	TLAMENTYQK	DAEGDIGKAE	VMPVRLEMEN	TYPKDTERDG	GKTEVMPLAL
1770	1780	1790	1800	1810	1820	1830	1840
EVVNTYQKNA	KGFTGNTEGS	VLKMEATYRK	TAEEVIKNTE	IVPCVLKVKE	AHETAPAPLE	MEKACKRDVK	ETIGATVSTP
1850	1860	1870	1880	1890	1900	1910	1920
SVIEMEKISP	EDRGENIGKH	KVLPAVVDIE	KIHGTGLELT	TKQGEAMLPA	FESKTPQEYA	EGSVEETKEE	PTEIKEGLIA
1930	1940	1950	1960	1970	1980	1990	2000
HENRLPTYFR	GYESPTLSKD	YEGYPAPAMP	DFQPGDTTVR	LDKRMSLTAI	YDKRRETDYS	DKGYNLAFVS	QDEQENSSFT
2010	2020	2030	2040	2050	2060	2070	2080
ILYEEPLQEE	DKYASAEARQ	TQSVLFHDTS	ADSMPVLACE	RSESRTDLVH	HFEKGTKLGE	TFDSDSSEMF	LSVEAKRYKI
2090	2100	2110	2120	2130	2140	2150	2160
YPLALSPIYE	DDSSQEDILS	SEVSPGHHGP	RKSRDSENQS	SSVLSLLQSV	SERLKMNFDE	DDREAADEEE	EEEEAAVLHK
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
2896	1	1012.4872	-151.04	1	65.4	13.7	1	1031-1039	K.VPSVLKLEK.K	

Detailed Protein Report

Protein 138: **PREDICTED: sushi, nidogen and EGF-like domain-containing protein 1 isoform X4 [Homo sapiens]**

Accession: gi|578804038

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 39.0

MW [kDa]: 142.7

pI: 6.4

Sequence Coverage [%]: 4.4

No. of unique Peptides: 2

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			
ENMEEAPKRV	SLALQLPEHG	SKDIGSLDLL	LAPVSTRRTG	LCIRRRE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1017	1	788.6695	-45.57	3	41.2	10.3	2	570-590	R.GFHGKHCEKARPHLCSSGPCR.N	Carbamidomethyl: 15
2079	1	1044.9332	12.94	2	56.4	14.4	1	591-609	R.NGGTCKEAGGEYHCSCPYR.F	Carbamidomethyl: 5

Detailed Protein Report

Protein 139: PREDICTED: nebulin-related-anchoring protein isoform X4 [Homo sapiens]

Accession:	gi|530393765	**Score:**	39.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	184.9
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MNVQPCSRCG	YGVYPAEKIS	CIDQIWHKAC	FHCEVCKMML	SVNNFVSHQK	KPYCHAHNPK	NNTFTSVYHT	PLNLNVRTFP
90	100	110	120	130	140	150	160
EAISGIHDQE	DGEQCKSVFH	WDMKSKDKEG	APNRQPLANE	RAYWTGYGEG	NAWCPGALPD	PEIVRMVEAR	KSLGEEYTED
170	180	190	200	210	220	230	240
YEQPRGKGSF	PAMITPAYQR	AKKANQLASQ	VEYKRGHDER	ISRFSTVVDT	PELLRSKAGA	QLQSDVRYTE	DYEQQRGKGS
250	260	270	280	290	300	310	320
FPAMITPAYQ	IAKRANELAS	DVRYHQQYQK	EMRGMAGPAI	GAEGILTREC	ADQYGQGYPE	EYEEHRGKGS	FPAMITPAYQ
330	340	350	360	370	380	390	400
NAKKAHELAS	DIKYRQDFNK	MKGAAHYHSL	PAQDNLVLKQ	AQSVNKLVSE	VEYKKDLESS	RGHSINYCET	PQFRNVSKIS
410	420	430	440	450	460	470	480
KFTSDNKYKE	NYQNHMRGRY	EGVGMDRRTL	HAMKVGSLAS	NVAYKADYKH	DIVDYNYPAT	LTPSYQTAMK	LVPLKDANYR
490	500	510	520	530	540	550	560
QSIDKLKYSS	VTDTPQIVQA	KINAQQLSHV	NYRADYEKNK	LNYTLPQDVP	QLVKAKTNAK	LFSEVKYKEG	WEKTKGKGFE
570	580	590	600	610	620	630	640
MKLDAMSLLA	AKASGELASN	IKYKEEYEKT	KGKAMGTADS	RLLHSLQIAK	MSSEVEYKKG	FEESKTRFHL	PMDMVNIRHA
650	660	670	680	690	700	710	720
KKAQTLASDL	DYRKKLHEYT	VLPEDMKTQW	AKKAYGLQSE	LQYKADLAWM	KGVGWLTEGS	LNLEQAKKAG	QLVSEKNYRQ
730	740	750	760	770	780	790	800
RVDELKFTSV	TDSSQMEHAK	KSQELQSGVA	YKAGNEQSVH	QYTISKDEPL	FLQARANAAN	LSEKLYKSSW	ENQKAKGFEL
810	820	830	840	850	860	870	880
RLDSLTFLAA	KAKRDLASEV	KYKEDYERSR	GKLIGAKDVQ	GDSQMSHSLQ	MSKLQSELEY	KKGFEDTKSQ	CHVSLDMVHL
890	900	910	920	930	940	950	960
VHARKAQHLA	TDVGYKTAEH	HFTALPTDMK	VEWAKKAYGL	QSDNQYRADV	KWMKGMGWVA	TGSLNVEQAK	KAGELISEKK
970	980	990	1000	1010	1020	1030	1040
YRQHPDALKF	TSIKDTPEMV	QARISYTQAV	DRLYREQGEN	IKHHYTPTAD	LPEVLLAKLN	AMNISETRYK	ESWSKLRDGG
1050	1060	1070	1080	1090	1100	1110	1120
YKLRLDALPF	QAAKASGEII	SDYKYKEAFE	KMKGQMLGSR	SLEDDISLAH	SVYATSLQSD	VNYKKGFEHS	KAQFHLPLDM
1130	1140	1150	1160	1170	1180	1190	1200
AALVHAKKAQ	TLASNQDYKH	PLPQYTSLAE	DLRLSCAKKA	HKLQSENLYR	SDLNFMRGVA	CVIPGTLEIE	GRKKASELIS
1210	1220	1230	1240	1250	1260	1270	1280
ESKYRQHPHS	FKYTAVTDTP	NLLHAKFSNQ	ITNERLYKAA	GEDARHEYTM	TLGLPEFIRA	KTNAANLSDA	RYKESWRNLR
1290	1300	1310	1320	1330	1340	1350	1360
AQGYKLTIEA	LPFQAARASG	DIASDLRYKS	DLIGMKGIGW	LALRSPQMES	AKKAGELISE	TKYRKKPDSI	KFTTVVDSPD
1370	1380	1390	1400	1410	1420	1430	1440
LVHAKNSYMH	CNERMYRSGD	AESLHRYTLI	PDHPDFTRAR	LNALHLSDKV	YRNSWEQTRA	GSYDFRLDAI	PFQTARASRE
1450	1460	1470	1480	1490	1500	1510	1520
IASDFRYKEA	FLRDRGLQIG	YRSVDDDPRM	KHFLNVGRLQ	SDNEYKKDFA	KSRSQFHSST	DQPGLLQAKR	SQQLASDVHY
1530	1540	1550	1560	1570	1580	1590	1600
RQPLPQPTCD	PEQLGLRHAQ	KAHQLQSDVK	YKSDLNLTRG	VGWTPPGSYK	VEMARRAAEL	ANARGLGLQG	AYQRGAEAVE
1610	1620	1630					
AGDHQSGEVN	PDATEILHVK	KKKALLL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
16	1	537.2110	-171.55	2	29.8	13.1	0	1045-1054	R.LDALPFQAAK.A	
2951	1	823.4152	-52.46	2	66.1	14.2	1	1310-1324	K.SDLIGMKGIGWLALR.S	Oxidation: 6

Detailed Protein Report

Protein 140: low-density lipoprotein receptor-related protein 2 precursor [Homo sapiens]

Accession:	gi|126012573	**Score:**	38.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	521.6
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	3

Detailed Protein Report

10	20	30	40	50	60	70	80
MDRGPAAVAC	TLLLALVACL	APASGQECDS	AHFRCGSGHC	IPADWRCDGT	KDCSDDADEI	GCAVVTCQQG	YFKCQSEGQC
90	100	110	120	130	140	150	160
IPNSWVCDQD	QDCDDGSDER	QDCSQSTCSS	HQITCSNGQC	IPSEYRCDHV	RDCPDGADEN	DCQYPTCEQL	TCDNGACYNT
170	180	190	200	210	220	230	240
SQKCDWKVDC	RDSSDEINCT	EICLHNEFSC	GNGECIPRAY	VCDHDNDCQD	GSDEHACNYP	TCGGYQFTCP	SGRCIYQNWV
250	260	270	280	290	300	310	320
CDGEDDCKDN	GDEDGCESGP	HDVHKCSPRE	WSCPESGRCI	SIYKVCDGIL	DCPGREDENN	TSTGKYCSMT	LCSALNCQYQ
330	340	350	360	370	380	390	400
CHETPYGGAC	FCPPGYIINH	NDSRTCVEFD	DCQIWGICDQ	KCESRPGRHL	CHCEEGYILE	RGQYCKANDS	FGEASIIFSN
410	420	430	440	450	460	470	480
GRDLLIGDIH	GRSFRILVES	QNRGVAVGVA	FHYHLQRVFW	TDTVQNKVFS	VDINGLNIQE	VLNVSVETPE	NLAVDWVNNK
490	500	510	520	530	540	550	560
IYLVETKVNR	IDMVNLDGSY	RVTLITENLG	HPRGIAVDPT	VGYLFFSDWE	SLSGEPKLER	AFMDGSNRKD	LVKTKLGWPA
570	580	590	600	610	620	630	640
GVTLDMISKR	VYWVDSRFDY	IETVTYDGIQ	RKTVVHGGSL	IPHPFGVSLF	EGQVFFTDWT	KMAVLKANKF	TETNPQVYYQ
650	660	670	680	690	700	710	720
ASLRPYGVTV	YHSLRQPYAT	NPCKDNNGGC	EQVCVLSHRT	DNDGLGFRCK	CTFGFQLDTD	ERHCIAVQNF	LIFSSQVAIR
730	740	750	760	770	780	790	800
GIPFTLSTQE	DVMVPVSGNP	SFFVGIDFDA	QDSTIFFSDM	SKHMIFKQKI	DGTGREILAA	NRVENVESLA	FDWISKNLYW
810	820	830	840	850	860	870	880
TDSHYKSISV	MRLADKTRRT	VVQYLNNPRS	VVVHPFAGYL	FFTDWFRPAK	IMRAWSDGSH	LLPVINTTLG	WPNGLAIDWA
890	900	910	920	930	940	950	960
ASRLYWVDAY	FDKIEHSTFD	GLDRRRLGHI	EQMTHPFGLA	IFGEHLFFTD	WRLGAIIRVR	KADGGEMTVI	RSGIAYILHL
970	980	990	1000	1010	1020	1030	1040
KSYDVNIQTG	SNACNQPTHP	NGDCSHFCFP	VPNFQRVCGC	PYGMRLASNH	LTCEGDPTNE	PPTEQCGLFS	FPCKNGRCVP
1050	1060	1070	1080	1090	1100	1110	1120
NYYLCDGVDD	CHDNSDEQLC	GTLNNTCSSS	AFTCGHGECI	PAHWRCDKRN	DCVDGSDEHN	CPTHAPASCL	DTQYTCDNHQ
1130	1140	1150	1160	1170	1180	1190	1200
CISKNWVCDT	DNDCGDGSDE	KNCNSTETCQ	PSQFNCPNHR	CIDLSFVCDG	DKDCVDGSDE	VGCVLNCTAS	QFKCASGDKC
1210	1220	1230	1240	1250	1260	1270	1280
IGVTNRCDGV	FDCSDNSDEA	GCPTRPPGMC	HSDEFQCQED	GICIPNFWEC	DGHPDCLYGS	DEHNACVPKT	CPSSYFHCDN
1290	1300	1310	1320	1330	1340	1350	1360
GNCIHRAWLC	DRDNDCGDMS	DEKDCPTQPF	RCPSWQWQCL	GHNICVNLSV	VCDGIFDCPN	GTDESPLCNG	NSCSDFNGGC
1370	1380	1390	1400	1410	1420	1430	1440
THECVQEPFG	AKCLCPLGFL	LANDSKTCED	IDECDILGSC	SQHCYNMRGS	FRCSCDTGYM	LESDGRTCKV	TASESLLLLV
1450	1460	1470	1480	1490	1500	1510	1520
ASQNKIIADS	VTSQVHNIYS	LVENGSYIVA	VDFDSISGRI	FWSDATQGKT	WSAFQNGTDR	RVVFDSSIIL	TETIAIDWVG
1530	1540	1550	1560	1570	1580	1590	1600
RNLYWTDYAL	ETIEVSKIDG	SHRTVLISKN	LTNPRGLALD	PRMNEHLLFW	SDWGHHPRIE	RASMDGSMRT	VIVQDKIFWP
1610	1620	1630	1640	1650	1660	1670	1680
CGLTIDYPNR	LLYFMDSYLD	YMDFCDYNGH	HRRQVIASDL	IIRHPYALTL	FEDSVYWTDR	ATRRVMRANK	WHGGNQSVVM
1690	1700	1710	1720	1730	1740	1750	1760
YNIQWPLGIV	AVHPSKQPNS	VNPCAFSRCS	HLCLLSSQGP	HFYSCVCPSG	WSLSPDLLNC	LRDDQPFLIT	VRQHIIFGIS
1770	1780	1790	1800	1810	1820	1830	1840
LNPEVKSNDA	MVPIAGIQNG	LDVEFDDAEQ	YIYWVENPGE	IHRVKTDGTN	RTVFASISMV	GPSMNLALDW	ISRNLYSTNP
1850	1860	1870	1880	1890	1900	1910	1920
RTQSIEVLTL	HGDIRYRKTL	IANDGTALGV	GFPIGITVDP	ARGKLYWSDQ	GTDSGVPAKI	ASANMDGTSV	KTLFTGNLEH
1930	1940	1950	1960	1970	1980	1990	2000
LECVTLDIEE	QKLYWAVTGR	GVIERGNVDG	TDRMILVHQL	SHPWGIAVHD	SFLYYTDEQY	EVIERVDKAT	GANKIVLRDN
2010	2020	2030	2040	2050	2060	2070	2080
VPNLRGLQVY	HRRNAAESSN	GCSNNMNACQ	QICLPVPGGL	FSCACATGFK	LNPDNRSCSP	YNSFIVVSML	SAIRGFSLEL
2090	2100	2110	2120	2130	2140	2150	2160
SDHSETMVPV	AGQGRNALHV	DVDVSSGFIY	WCDFSSSVAS	DNAIRRIKPD	GSSLMNIVTH	GIGENGVRGI	AVDWVAGNLY
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
573	1	656.8903	-140.87	3	35.8	15.5	1	279-295	R.CISIYKVCDGILDCPGR.E	Carbamidomethyl: 1, 8
1012	1	974.7041	-35.28	3	41.2	13.1	1	1173-1199	K.DCVDGSDEVGCVLNCTASQFKCASGDK.C	Carbamidomethyl: 11, 15, 22
936	1	647.6555	-174.87	2	41.8	10.3	0	3696-3706	K.WAVCNGVDDCR.D	Carbamidomethyl: 4

Detailed Protein Report

Protein 141: **PREDICTED: uveal autoantigen with coiled-coil domains and ankyrin repeats isoform X3 [Homo sapiens]**

Accession:	gi|530406156	**Score:**	38.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	160.2
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	2

```
        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
281	2	477.4617	-175.78	3	32.2	22.4	0	189-200	R.TALMLGCEYGCR.D	Carbamidomethyl: 7, 11
1858	2	621.2993	26.87	2	53.6	16.2	1	427-436	R.TFCESAKQDR.L	Carbamidomethyl: 3

Detailed Protein Report

Protein 142: fibrillin-2 precursor [Homo sapiens]

Accession:	gi|66346695	**Score:**	38.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	314.6
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	2

Quantitation

QD:QU	**Median:** 0.70	**CV:** 18.73 %	**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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
472	1	516.1120	-268.37	2	34.5	12.2	0	1884-1893	K.LSPNGACVDR.N		QD:QU 0.84
388	2	642.3201	56.28	2	34.8	15.4	1	2529-2539	K.TCKDLDECQTK.Q		QD:QU 0.58

Detailed Protein Report

Protein 143: **PREDICTED: immunoglobulin-like domain-containing receptor 2 isoform X6 [Homo sapiens]**

Accession:	gi|578800910	**Score:**	38.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.5
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.3
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MDRVLLRWIS	LFWLTAMVEG	LQVTVPDKKK	VAMLFQPTVL	RCHFSTSSHQ	PAVVQWKFKS	YCQDRMGESL	GMSSTRAQSL
90	100	110	120	130	140	150	160
SKRNLEWDPY	LDCLDSRRTV	RVVASKQGST	VTLGDFYRGR	EITIVHDADL	QIGKLMWGDS	GLYYCIITTP	DDLEGKNEDS
170	180	190	200	210	220	230	240
VELLVLGRTG	LLADLLPSFA	VEIMPEWVFV	GLVLLGVFLF	FVLVGICWCQ	CCPHSCCCYV	RCPCCPDSCC	CPQAFRKGYR
250	260	270	280	290	300	310	320
IQADKERDSM	KVLYYVEKEL	AQFDPARRMR	GRYNNTISEL	SSLHEEDSNF	RQSFHQMRSK	QFPVSGDLES	NPDYWSGVMG
330	340	350	360	370	380	390	400
GSSGASRGPS	AMEYNKEDRE	SFRHSQPRSK	SEMLSRKNFA	TGVPAVSMDE	LAAFADSYGQ	RPRRADGNSH	EARGGSRFER
410	420	430	440	450	460	470	480
SESRAHSGFY	QDDSLEEYYG	QRSRSREPLT	DADRGWAFSP	ARRRPAEDAH	LPRLVSRTPG	TAPKYDHSYL	GSARERQARP
490	500	510	520	530	540	550	560
EGASRGGSLE	TPSKRSAQLG	PRSASYYAWS	PPGTYKAGSS	QDDQEDASDD	ALPPYSELEL	TRGPSYRGRD	LPYHSNSEKK
570	580	590					
RKKEPAKKTN	DFPTRMSLVV						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1141	2	902.1920	-134.75	2	42.8	15.4	0	222-236	R.CPCCPDSCCCPQAFR.K	Carbamidomethyl: 3, 4, 8
813	1	625.4938	-120.64	3	38.7	11.2	1	222-237	R.CPCCPDSCCCPQAFRK.G	Carbamidomethyl: 8, 10
1315	1	956.5835	173.01	1	46.6	11.9	0	385-393	R.ADGNSHEAR.G	

Detailed Protein Report

Protein 144: 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 145: ubiquitin carboxyl-terminal hydrolase 34 [Homo sapiens]

Accession:	gi|110347427	**Score:**	38.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	404.0
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

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
597	2	642.8360	18.78	2	36.1	18.4	0	2940-2950	R.SCWTTLISAFR.I	

Detailed Protein Report

Protein 146: GTP-binding nuclear protein Ran [Homo sapiens]

Accession:	gi|5453555	**Score:**	38.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.4
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	13.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAQGEPQVQ	FKLVLVGDGG	TGKTTFVKRH	LTGEFEKKYV	ATLGVEVHPL	VFHTNRGPIK	FNVWDTAGQE	KFGGLRDGYY
90	100	110	120	130	140	150	160
IQAQCAIIMF	DVTSRVTYKN	VPNWHRDLVR	VCENIPIVLC	GNKVDIKDRK	VKAKSIVFHR	KKNLQYYDIS	AKSNYNFEKP
170	180	190	200	210	220		
FLWLARKLIG	DPNLEFVAMP	ALAPPEVVMD	PALAAQYEHD	LEVAQTTALP	DEDDDL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2729	1	671.8236	-44.80	2	63.1	17.4	1	142-152	K.KNLQYYDISAK.S	

Detailed Protein Report

Protein 147: **PREDICTED: zinc finger protein 195 isoform X2 [Homo sapiens]**

Accession:	gi|578820760	**Score:**	38.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.6
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	5.7
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.47 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MNEAGNPAMS	SHFTQDLLPE	QGIQDAFPKR	ILRGYGNCGL	DNLYLRKDWE	SLDECKLQKD	YNGLNQCSST	THSKIFQYNK
90	100	110	120	130	140	150	160
YVKIFDNFSN	LHRRNISNTG	EKPFKCQECG	KSFQMLSFLT	EHQKIHTGKK	FQKCGECGKT	FIQCSHFTEP	ENIDTGEKPY
170	180	190	200	210	220	230	240
KCQECNNVIK	TCSVLTKNRI	YAGGEHYRCE	EFGKVFNQCS	HLTEHEHGTE	EKPCKYEECS	SVFISCSSLS	NQQMILAGEK
250	260	270	280	290	300	310	320
LSKCETWYKG	FNHSPNPSKH	QRNEIGGKPF	KCEECDSIFK	WFSDLTKHKR	IHTGEKPYKC	DECGKAYTQS	SHLSEHRRIH
330	340	350	360	370	380	390	400
TGEKPYQCEE	CGKVFRTCSS	LSNHKRTHSE	EKPYTCEECG	NIFKQLSDLT	KHKKTHTGEK	PYKCDECGKN	FTQSSNLIVH
410	420	430	440	450	460	470	480
KRIHTGEKPY	KCEECGRVFM	WFSDITKHKK	THTGEKPYKC	DECGKNFTQS	SNLIVHKRIH	TGEKPYKCEK	CGKAFTQFSH
490							
LTVHESIHT							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1481	1	727.3860	-18.04	2	48.7	13.2	2	372-383	K.HKKTHTGEKPYK.C		QD:QU	0.47

Detailed Protein Report

Protein 148: **PREDICTED: E3 ubiquitin-protein ligase HECTD1 isoform X2 [Homo sapiens]**

Accession:	gi|578825693	**Score:**	37.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	284.3
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.8
		No. of unique Peptides:	3

10	20	30	40	50	60	70	80
MADVDPDTLL	EWLQMGQGDE	RDMQLIALEQ	LCMLLLMSDN	VDRCFETCPP	RTFLPALCKI	FLDESAPDNV	LEVTARAITY
90	100	110	120	130	140	150	160
YLDVSAECTR	RIVGVDGAIK	ALCNRLVVVE	LNNRTSRDLA	EQCVKVLELI	CTRESGAVFE	AGGLNCVLTF	IRDSGHLVHK
170	180	190	200	210	220	230	240
DTLHSAMAVV	SRLCGKMEPQ	DSSLEICVES	LSSLLKHEDH	QVSDGALRCF	ASLADRFTRR	GVDPAPLAKH	GLTEELLSRM
250	260	270	280	290	300	310	320
AAAGGTVSGP	SSACKPGRST	TGAPSTTADS	KLSNQVSTIV	SLLSTLCRGS	PVVTHDLLRS	ELPDSIESAL	QGDERCVLDT
330	340	350	360	370	380	390	400
MRLVDLLLVL	LFEGRKALPK	SSAGSTGRIP	GLRRLDSSGE	RSHRQLIDCI	RSKDTDALID	AIDTGAFEVN	FMDDVGQTLL
410	420	430	440	450	460	470	480
NWASAFGTQE	MVEFLCERGA	DVNRGQRSSS	LHYAACFGRP	QVAKTLLRHG	ANPDLRDEDG	KTPLDKARER	GHSEVVAILQ
490	500	510	520	530	540	550	560
SPGDWMCPVN	KGDDKKKKDT	NKDEEECNEP	KGDPEMAPIY	LKRLLPVFAQ	TFQQTMLPSI	RKASLALIRK	MIHFCSEALL
570	580	590	600	610	620	630	640
KEVCDSDVGH	NLPTILVEIT	ATVLDQEDDD	DGHLLALQII	RDLVDKGGDI	FLDQLARLGV	ISKVSTLAGP	SSDDENEEES
650	660	670	680	690	700	710	720
KPEKEDEPQE	DAKELQQGKP	YHWRDWSIIR	GRDCLYIWSD	AAALELSNGS	NGWFRFILDG	KLATMYSSGS	PEGGSDSSES
730	740	750	760	770	780	790	800
RSEFLEKLQR	ARGQVKPSTS	SQPILSAPGP	TKLTVGNWSL	TCLKEGEIAI	HNSDGQQATI	LKEDLPGFVF	ESNRGTKHSF
810	820	830	840	850	860	870	880
TAETSLGSEF	VTGWTGKRGR	KLKSKLEKTK	QKVRTMARDL	YDDHFKAVES	MPRGVVVTLR	NIATQLESSW	ELHTNRQCIE
890	900	910	920	930	940	950	960
SENTWRDLMK	TALENLIVLL	KDENTISPYE	MCSSGLVQAL	LTVLNNSMDL	DMKQDCSQLV	ERINVFKTAF	SENEDDESRP
970	980	990	1000	1010	1020	1030	1040
AVALIRKLIA	VLESIERLPL	HLYDTPGSTY	NLQILTRRLR	FRLERAPGET	ALIDRTGRML	KMEPLATVES	LEQYLLKMVA
1050	1060	1070	1080	1090	1100	1110	1120
KQWYDFDRSS	FVFVRKLREG	QNFIFRHQHD	FDENGIIYWI	GTNAKTAYEW	VNPAAYGLVV	VTSSEGRNLP	YGRLEDILSR
1130	1140	1150	1160	1170	1180	1190	1200
DNSALNCHSN	DDKNAWFAID	LGLWVIPSAY	TLRHARGYGR	SALRNWVFQV	SKDGQNWTSL	YTHVDDCSLN	EPGSTATWPL
1210	1220	1230	1240	1250	1260	1270	1280
DPPKDEKQGW	RHVRIKQMGK	NASGQTHYLS	LSGFELYGTV	NGVCEDQLGK	AAKEAEANLR	RQRRLVRSQV	LKYMVPGARV
1290	1300	1310	1320	1330	1340	1350	1360
IRGLDWKWRD	QDGSPQGEGT	VTGELHNGTT	QSWSSLVKNN	CPDKTSAAAG	SSSRKGSSSS	VCSVASSSDI	SLGSTKTERR
1370	1380	1390	1400	1410	1420	1430	1440
SEIVMEHSIV	SGADVHEPIV	VLSSAENVPQ	TEVGSSSSAS	TSTLTAETGS	ENAERKLGPD	SSVRTPGESS	AISMGIVSVS
1450	1460	1470	1480	1490	1500	1510	1520
SPDVSSVSEL	TNKEAASQRP	LSSSASNRLS	VSSLLAAGAP	MSSSASVPNL	SSRETSSLES	FVRRVANIAR	TNATNNMNLS
1530	1540	1550	1560	1570	1580	1590	1600
RSSSDNNTNT	LGRNVMSTAT	SPLMGAQSFP	NLTTPGTTST	VTMSTSSVTS	SSNVATATTV	LSVGQSLSNT	LTTSLTSTSS
1610	1620	1630	1640	1650	1660	1670	1680
ESDTGQEAEY	SLYDFLDSCR	ASTLLAELDD	DEDLPEPDEE	DDENEDDNQE	DQEYEEVMIL	RRPSLQRRAG	SRSDVTHHAV
1690	1700	1710	1720	1730	1740	1750	1760
TSQLPQVPAG	AGSRPIGEQE	EEEYETKGGR	RRTWDDDYVL	KRQFSALVPA	FDPRPGRTNV	QQTTDLEIPP	PGTPHSELLE
1770	1780	1790	1800	1810	1820	1830	1840
EVECTPSPRL	ALTLKVTGLG	TTREVELPLT	NFRSTIFYYV	QKLLQLSCNG	NVKSDKLRRI	WEPTYTIMYR	EMKDSDKEKE
1850	1860	1870	1880	1890	1900	1910	1920
NGKMGCWSIE	HVEQYLGTDE	LPKNDLITYL	QKNADAAFLR	HWKLTGTNKS	IRKNRNCSQL	IAAYKDFCEH	GTKSGLNQGA
1930	1940	1950	1960	1970	1980	1990	2000
ISTLQSSDIL	NLTKEQPQAK	AGNGQNSCGV	EDVLQLLRIL	YIVASDPYSR	ISQEDGDEQP	QFTFPPDEFT	SKKITTKILQ
2010	2020	2030	2040	2050	2060	2070	2080
QIEEPLALAS	GALPDWCEQL	TSKCPFLIPF	ETRQLYFTCT	AFGASRAIVW	LQNRREATVE	RTRTTSSVRR	DDPGEFRVGR
2090	2100	2110	2120	2130	2140	2150	2160
LKHERVKVPR	GESLMEWAEN	VMQIHADRKS	VLEVEFLGEE	GTGLGPTLEF	YALVAAEFQR	TDLGAWLCDD	NFPDDESRHV
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
751	1	765.8890	60.31	2	37.9	11.7	1	2226-2238	K.LMCMGDIKSNMSK.L	Carbamidomethyl: 3; Oxidation: 2
2795	1	729.3498	20.88	2	66.1	14.8	1	2226-2238	K.LMCMGDIKSNMSK.L	
1556	1	502.7809	-70.23	2	49.7	11.3	2	2310-2317	R.ARFLKEIK.D	

Detailed Protein Report

Protein 149: PREDICTED: E3 ubiquitin-protein ligase UBR4 isoform X11 [Homo sapiens]

Accession:	gi|578798772	**Score:**	37.7
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 [%]:**	1.0
		No. of unique Peptides:	3

Detailed Protein Report

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
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 150: histone H4 [Homo sapiens]

Accession: gi|4504301
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 37.5
MW [kDa]: 11.4
pI: 11.8
Sequence Coverage [%]: 7.8
No. of unique Peptides: 1

Quantitation

QD:QU **Median:** 1.78 **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
1451	8	495.2222	-141.96	2	48.3	37.5	0	61-68	K.VFLENVIR.D		QD:QU 1.78

Detailed Protein Report

Protein 151: integrin beta-4 isoform 3 precursor [Homo sapiens]

Accession:	gi|54607033	**Score:**	37.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	194.9
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530412114	refseq_human (refseq_human_20140103.fasta)	PREDICTED: integrin beta-4 isoform X4 [Homo sapiens]

10	20	30	40	50	60	70	80
MAGPRPSPWA	RLLLAALISV	SLSGTLANRC	KKAPVKSCTE	CVRVDKDCAY	CTDEMFRDRR	CNTQAELLAA	GCQRESIVVM
90	100	110	120	130	140	150	160
ESSFQITEET	QIDTTLRRSQ	MSPQGLRVRL	RPGEERHFEL	EVFEPLESPV	DLYILMDFSN	SMSDDLDNLK	KMGQNLARVL
170	180	190	200	210	220	230	240
SQLTSDYTIG	FGKFVDKVSV	PQTDMRPEKL	KEPWPNSDPP	FSFKNVISLT	EDVDEFRNKL	QGERISGNLD	APEGGFDAIL
250	260	270	280	290	300	310	320
QTAVCTRDIG	WRPDSTHLLV	FSTESAFHYE	ADGANVLAGI	MSRNDERCHL	DTTGTYTQYR	TQDYPSVPTL	VRLLAKHNII
330	340	350	360	370	380	390	400
PIFAVTNYSY	SYYEKLHTYF	PVSSLGVLQE	DSSNIVELLE	EAFNRIRSNL	DIRALDSPRG	LRTEVTSKMF	QKTRTGSFHI
410	420	430	440	450	460	470	480
RRGEVGIYQV	QLRALEHVDG	THVCQLPEDQ	KGNIHLKPSF	SDGLKMDAGI	ICDVCTCELQ	KEVRSARCSF	NGDFVCGQCV
490	500	510	520	530	540	550	560
CSEGWSGQTC	NCSTGSLSDI	QPCLREGEDK	PCSGRGECQC	GHCVCYGEGR	YEGQFCEYDN	FQCPRTSGFL	CNDRGRCSMG
570	580	590	600	610	620	630	640
QCVCEPGWTG	PSCDCPLSNA	TCIDSNGGIC	NGRGHCECGR	CHCHQQSLYT	DTICEINYSA	IHPGLCEDLR	SCVQCQAWGT
650	660	670	680	690	700	710	720
GEKKGRTCEE	CNFKVKMVDE	LKRAEEVVVR	CSFRDEDDDC	TYSYTMEGDG	APGPNSTVLV	HKKKDCPPGS	FWWLIPLLLL
730	740	750	760	770	780	790	800
LLPLLALLLL	LCWKYCACCK	ACLALLPCCN	RGHMVGFKED	HYMLRENLMA	SDHLDTPMLR	SGNLKGRDVV	RWKVTNNMQR
810	820	830	840	850	860	870	880
PGFATHAASI	NPTELVPYGL	SLRLARLCTE	NLLKPDTREC	AQLRQEVEEN	LNEVYRQISG	VHKLQQTKFR	QQPNAGKKQD
890	900	910	920	930	940	950	960
HTIVDTVLMA	PRSAKPALLK	LTEKQVEQRA	FHDLKVAPGY	YTLTADQDAR	GMVEFQEGVE	LVDVRVPLFI	RPEDDDEKQL
970	980	990	1000	1010	1020	1030	1040
LVEAIDVPAG	TATLGRRLVN	ITIIKEQARD	VVSFEQPEFS	VSRGDQVARI	PVIRRVLDGG	KSQVSYRTQD	GTAQGNRDYI
1050	1060	1070	1080	1090	1100	1110	1120
PVEGELLFQP	GEAWKELQVK	LLELQEVDSL	LRGRQVRRFH	VQLSNPKFGA	HLGQPHSTTI	IIRDPDELDR	SFTSQMLSSQ
1130	1140	1150	1160	1170	1180	1190	1200
PPPHGDLGAP	QNPNAKAAGS	RKIHFNWLPP	SGKPMGYRVK	YWIQGDSESE	AHLLDSKVPS	VELTNLYPYC	DYEMKVCAYG
1210	1220	1230	1240	1250	1260	1270	1280
AQGEGPYSSL	VSCRTHQEVP	SEPGRLAFNV	VSSTVTQLSW	AEPAETNGEI	TAYEVCYGLV	NDDNRPIGPM	KKVLVDNPKN
1290	1300	1310	1320	1330	1340	1350	1360
RMLLIENLRE	SQPYRYTVKA	RNGAGWGPER	EAIINLATQP	KRPMSIPIIP	DIPIVDAQSG	EDYDSFLMYS	DDVLRSPSGS
1370	1380	1390	1400	1410	1420	1430	1440
QRPSVSDDTE	HLVNGRMDFA	FPGSTNSLHR	MTTTSAAAYG	THLSPHVPHR	VLSTSSTLTR	DYNSLTRSEH	SHSTTLPRDY
1450	1460	1470	1480	1490	1500	1510	1520
STLTSVSSHD	SRLTAGVPDT	PTRLVFSALG	PTSLRVSWQE	PRCERPLQGY	SVEYQLLNGG	ELHRLNIPNP	AQTSVVVEDL
1530	1540	1550	1560	1570	1580	1590	1600
LPNHSYVFRV	RAQSQEGWGR	EREGVITIES	QVHPQSPLCP	LPGSAFTLST	PSAPGPLVFT	ALSPDSLQLS	WERPRRPNGD
1610	1620	1630	1640	1650	1660	1670	1680
IVGYLVTCEM	AQGGGPATAF	RVDGDSPESR	LTVPGLSENV	PYKFKVQART	TEGFGPEREG	IITIESQDGG	PFPQLGSRAG
1690	1700	1710	1720	1730	1740	1750	1760
LFQHPLQSEY	SSITTTHTSA	TEPFLVDGLT	LGAQHLEAGG	SLTRHVTQEF	VSRTLTTSGT	LSTHMDQQFF	QT

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
522	1	678.9701	154.68	2	36.5	13.0	1	368-379	R.SNLDIRALDSPR.G	

Detailed Protein Report

Protein 152:	**eukaryotic peptide chain release factor GTP-binding subunit ERF3A isoform 3 [Homo sapiens]**

Accession:	gi|194018522	**Score:**	37.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.7
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MELSEPIVEN	GETEMSPEES	WEHKEEISEA	EPGGGSLGDG	RPPEESAHEM	MEEEEEIPKP	KSVVAPPGAP	KKEHVNVVFI
90	100	110	120	130	140	150	160
GHVDAGKSTI	GGQIMYLTGM	VDKRTLEKYE	REAKEKNRET	WYLSWALDTN	QEERDKGKTV	EVGRAYFETE	KKHFTILDAP
170	180	190	200	210	220	230	240
GHKSFVPNMI	GGASQADLAV	LVISARKGEF	ETGFEKGGQT	REHAMLAKTA	GVKHLIVLIN	KMDDPTVNWS	NERYEECKEK
250	260	270	280	290	300	310	320
LVPFLKKVGF	NPKKDIHFMP	CSGLTGANLK	EQSDFCPWYI	GLPFIPYLDN	LPNFNRSVDG	PIRLPIVDKY	KDMGTVVLGK
330	340	350	360	370	380	390	400
LESGSICKGQ	QLVMMPNKHN	VEVLGILSDD	VETDTVAPGE	NLKIRLKGIE	EEEILPGFIL	CDPNNLCHSG	RTFDAQIVII
410	420	430	440	450	460	470	480
EHKSIICPGY	NAVLHIHTCI	EEVEITALIC	LVDKKSGEKS	KTRPRFVKQD	QVCIARLRTA	GTICLETFKD	FPQMGRFTLR
490	500						
DEGKTIAIGK	VLKLVPEKD						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
668	1	488.2507	-95.56	2	36.9	37.4	1	304-311	R.LPIVDKYK.D	

Detailed Protein Report

Protein 153: PREDICTED: HEAT repeat-containing protein 5B isoform X3 [Homo sapiens]

Accession:	gi|578802960	**Score:**	37.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	222.9
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MELAHSLLLN	EEALAQITEA	KRPVFIFEWL	RFLDKVLVAA	NKTDVKEKQK	KLVEQLTGLI	SSSPGPPTRK	LLAKNLAALY
90	100	110	120	130	140	150	160
SIGDTFTVFQ	TLDKCNDIIR	NKDDTAAYLP	TKLAAVACVG	AFYEKMGRML	GSAFPETSQG	RSEILMSLQK	VLSGLGGAAA
170	180	190	200	210	220	230	240
SSHRDIYKNA	RSLLTDRSMA	VRCAVAKCLL	ELQNEAVFMW	TAELENIATL	CFKALENSNY	GVRVAVSKLL	GTVMATALMP
250	260	270	280	290	300	310	320
KQATVMRQNV	KRATFDEVLE	LMATGFLRGG	SGFLKSGGEM	LKVGGSVNRE	VRVGVTQAYV	VFVTTLGGQW	LERSFATFLS
330	340	350	360	370	380	390	400
HVLDLVSHPR	ATQTHVEAVY	SRRCVSFILR	ATVGSLLGEK	AQIAAAKEIC	QAIGKQMKAV	EAVVNDTSGE	NKSGAADIAA
410	420	430	440	450	460	470	480
SQHVMVCALQ	ELGSLVQSLN	ATASPLIQEA	SIGLLEIVTS	VLLHPSMAAR	LAAAWCLRCV	AVALPFQLTP	FLDRCAERLN
490	500	510	520	530	540	550	560
NLKTSPEAVS	GYSFAMAALL	GGVHQCPLGI	PHAKGKMVVS	IAEDLLRTAA	QNSRLSLQRT	QAGWLLLGAL	MTLGPSVVRY
570	580	590	600	610	620	630	640
HLPKMLLLWR	NVFPRSLKEL	EAEKARGDSF	TWQVTLEGRA	GALCAMRSFV	AHCPELLTED	VIRKLMTPIE	CAMTMMSHIP
650	660	670	680	690	700	710	720
SVMKAHGAHL	KASAAMVRLR	LYDILALLPP	KTYEGSFNAL	LRELVAEFTL	TDNSANTTTS	LLRSLCHYDD	SVLLGSWLQE
730	740	750	760	770	780	790	800
TDHKSIEDQL	QPNSASGSGA	LEHDPSSIYL	RIPAGEAVPG	PLPLGVSVID	ASVALFGVVF	PHVSYKHRLQ	MLDHFAECVK
810	820	830	840	850	860	870	880
QAKGVRQQAV	QLNIFTAVLS	ALKGLAENKS	TLGPEEVRKS	ALTLVMGPLD	NPNPILRCAA	GEALGRMAQV	VGEATFIARM
890	900	910	920	930	940	950	960
AQYSFDKLKS	ARDVVSRTGH	SLALGCLHRY	VGGIGSGQHL	KTSVSILLAL	AQDGTSPEVQ	TWSLHSLALI	VDSSGPMYRG
970	980	990	1000	1010	1020	1030	1040
YVEPTLSLVL	TLLLTVPPSH	TEVHQCLGRC	LGAIITTVGP	ELQGNGATTS	TIRSSCLVGC	AITQDHSDSL	VQAAAISCLQ
1050	1060	1070	1080	1090	1100	1110	1120
QLHMFAPRHV	NLSSLVPSLC	VHLCSSHLLL	RRAAVACLRQ	LAQREAAEVC	EYAMSLAKNT	GDKESSSANV	SPFAPGVSSR
1130	1140	1150	1160	1170	1180	1190	1200
TDIHCRHQGV	NITETGLEGL	LFGMLDRETD	RKLCSDIHDT	LGHMLSSLAV	EKLSHWLMLC	KDVLAASSDM	STATLLSSGK
1210	1220	1230	1240	1250	1260	1270	1280
DEEAEKKDEM	DDDTMFTTLG	EEDKSKPFVA	PRWATRVFAA	DCLCRIINLC	ENADQAHFDL	ALARSAKLRN	PTNDLLVLHL
1290	1300	1310	1320	1330	1340	1350	1360
SDLIRMAFMA	ATDHSNQLRM	AGLQALEDII	KKFASVPEPE	FPGHVILEQY	QANVGAALRP	AFSQDTPSDI	IAKACQVCST
1370	1380	1390	1400	1410	1420	1430	1440
WIGSGVVSDL	NDLRRVHNLL	VSSLDKVQAG	KGSSSQLYRE	SATTMEKLAV	LKAWAEVYVV	AMNIKKEAES	KPKRAIKNTD
1450	1460	1470	1480	1490	1500	1510	1520
DDDDDCGTID	ELPPDSLITL	VQPELPTLSR	LWLAALKDYA	LLTLPAEFSS	QLPPDGGAFY	TPETIDTARL	HYRNSWAPIL
1530	1540	1550	1560	1570	1580	1590	1600
HAVALWLNST	GFTCSESTEA	AAISGLQKRS	TSVNLNQASG	AVGSAKSLPE	INKDRMHLIL	GVSIQFLCSP	RPEEPIEHVT
1610	1620	1630	1640	1650	1660	1670	1680
ACLQALHTLL	DSPYARVHIA	EDQLIGVELL	SVLHRLLLTW	NPSSVQLLVT	GVVQQIVRAA	QDYLQEKRNT	LNEDDMEKEA
1690	1700	1710	1720	1730	1740	1750	1760
CTVLGEGGDS	GGLIPGKSLV	FATMELLMFI	LVRHMPHLST	KVSDSPSHIA	TKTRLSEESA	RLVAATVTIL	SDLPSLCSPA
1770	1780	1790	1800	1810	1820	1830	1840
GCMTILPTIL	FLIARILKDT	AIKSADNQVP	PPVSAALQGI	KSIVTLSMAK	TEAGVQKQWT	ALIRSTLACI	LEYSQPEDSV
1850	1860	1870	1880	1890	1900	1910	1920
PTPDEVSMLT	AIALFLWSAS	NEIIGVQSLQ	NGCMNRFKNA	LNSCDPWVQA	KCYQLLLSVF	QHSNRALSTP	YIHSLAPIVV
1930	1940	1950	1960	1970	1980	1990	2000
EKLKAVERNR	PASNIELLAV	QEGIKVLETL	VALGEEQNRV	QLLALLVPTL	ISYLLDENSF	ASASSASKDL	HEFALQNLMH
2010	2020	2030	2040	2050	2060		
IGPLYPHAFK	TVMGAAPELK	VRLETAVRAS	QASKAKAAAR	QPAPAIHSAP	TIKLKTSFF		

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
284	1	635.8126	-19.46	2	32.3	12.1	0	672-682	K.TYEGSFNALLR.E	
1278	1	644.3427	-23.92	2	46.1	14.2	1	2011-2022	K.TVMGAAPELKVR.L	Oxidation: 3

Detailed Protein Report

Protein 154: sortilin isoform 2 [Homo sapiens]

Accession:	gi|327315343	**Score:**	37.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.3
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl	**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 155: protein SOGA1 isoform 1 [Homo sapiens]

Accession:	gi|257467639	**Score:**	37.3
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:	2

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

Detailed Protein Report

Protein 156: PREDICTED: regulator of G-protein signaling 3 isoform X2 [Homo sapiens]

Accession:	gi|578817733	**Score:**	37.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	120.1
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	2

```
        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	4	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	

Detailed Protein Report

Protein 157: **histone-lysine N-methyltransferase 2C [Homo sapiens]**

Accession:	gi|91718902	**Score:**	37.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	541.0
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	0.9
		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 158: protein Jade-2 [Homo sapiens]

Accession: gi|40556370

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 37.2

MW [kDa]: 87.4

pI: 5.0

Sequence Coverage [%]: 6.1

No. of unique Peptides: 2

Quantitation

QD:QU **Median:** 0.42 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEEKRRKYSI	SSDNSDTTDS	HATSTSASRC	SKLPSSTKSG	WPRQNEKKPS	EVFRTDLITA	MKIPDSYQLS	PDDYYILADP
90	100	110	120	130	140	150	160
WRQEWEKGVQ	VPAGAEAIPE	PVVRILPPLE	GPPAQASPSS	TMLGEGSQPD	WPGGSRYDLD	EIDAYWLELI	NSELKEMERP
170	180	190	200	210	220	230	240
ELDELTLERV	LEELETLCHQ	NMARAIETQE	GLGIEYDEDV	VCDVCRSPEG	EDGNEMVFCD	KCNVCVHQAC	YGILKVPTGS
250	260	270	280	290	300	310	320
WLCRTCALGV	QPKCLLCPKR	GGALKPTRSG	TKWVHVSCAL	WIPEVSIGCP	EKMEPITKIS	HIPASRWALS	CSLCKECTGT
330	340	350	360	370	380	390	400
CIQCSMPSCV	TAFHVTCAFD	HGLEMRTILA	DNDEVKFKSF	CQEHSDGGPR	NEPTSEPTEP	SQAGEDLEKV	TLRKQRLQQL
410	420	430	440	450	460	470	480
EEDFYELVEP	AEVAERLDLA	EALVDFIYQY	WKLKRKANAN	QPLLTPKTDE	VDNLAQQEQD	VLYRRLKLFT	HLRQDLERVR
490	500	510	520	530	540	550	560
NLCYMVTRRE	RTKHAICKLQ	EQIFHLQMKL	IEQDLCRGLS	TSFPIDGTFF	NSWLAQSVQI	TAENMAMSEW	PLNNGHREDP
570	580	590	600	610	620	630	640
APGLLSEELL	QDEETLLSFM	RDPSLRPGDP	ARKARGRTRL	PAKKKPPPPP	PQDGPGSRTT	PDKAPKKTWG	QDAGSGKGGQ
650	660	670	680	690	700	710	720
GPPTRKPPRR	TSSHLPSSPA	AGDCPILATP	ESPPPLAPET	PDEAASVAAD	SDVQVPGPAA	SPKPLGRLRP	PRESKVTRRL
730	740	750	760	770	780	790	800
PGARPDAGMG	PPSAVAERPK	VSLHFDTETD	GYFSDGEMSD	SDVEAEDGGV	QRGPREAGAE	EVVRMGVLAS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2789	1	863.0890	-25.83	3	66.0	12.9	2	293-315	K. MEPITKISHIPASRWALSCSLCK. E	Oxidation: 1	
256	1	715.8400	-46.05	2	33.2	12.5	2	624-637	K.APKKTWGQDAGSGK.G		QD:QU 0.42

Detailed Protein Report

Protein 159: tripartite motif-containing protein 65 isoform 2 [Homo sapiens]

Accession:	gi|371122551	**Score:**	37.0
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:	3

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
2836	11	973.5061	53.53	2	64.6	14.4	2	46-62	K.ACPECREPFPDGAELRR.N	
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	

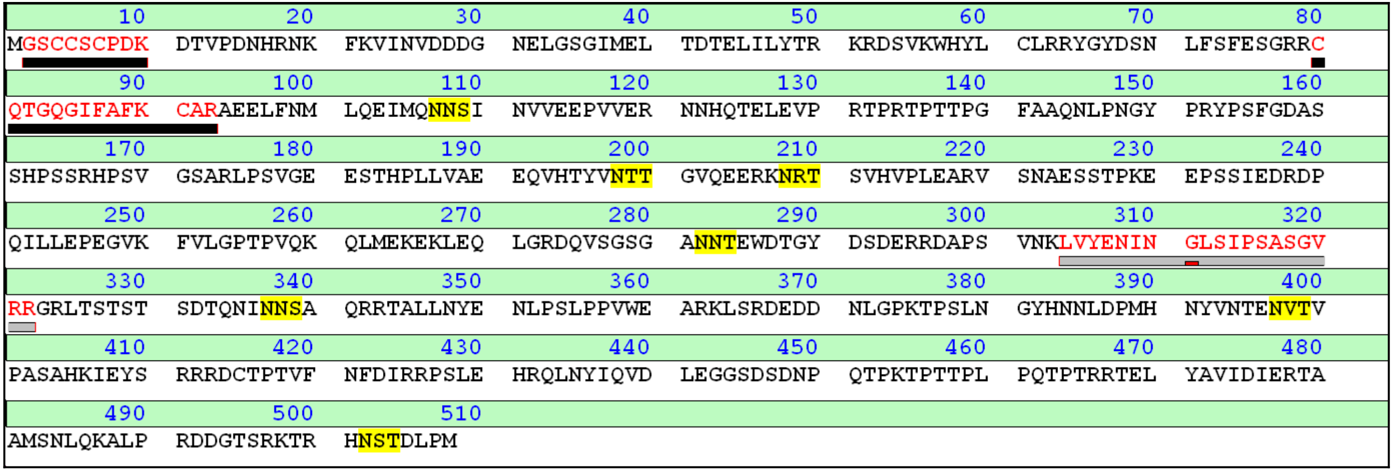
Detailed Protein Report

Protein 160: fibroblast growth factor receptor substrate 2 [Homo sapiens]

Accession:	gi|110347408	**Score:**	37.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.0
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.3
		No. of unique Peptides:	3

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]



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        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	
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 161: PREDICTED: pericentrin isoform X6 [Homo sapiens]

Accession:	gi|530419254	**Score:**	36.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	355.7
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

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	2	1044.5270	3.44	2	65.0	25.0	2	1173-1189	R.FEKEFSFKNEETAQVVR.K	

Detailed Protein Report

Protein 162: retinal dehydrogenase 1 [Homo sapiens]

Accession: gi|21361176
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 36.7
MW [kDa]: 54.8
pI: 6.3
Sequence Coverage [%]: 6.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSSSGTPDLP	VLLTDLKIQY	TKIFINNEWH	DSVSGKKFPV	FNPATEEELC	QVEEGDKEDV	DKAVKAARQA	FQIGSPWRTM
90	100	110	120	130	140	150	160
DASERGRLLY	KLADLIERDR	LLLATMESMN	GGKLYSNAYL	NDLAGCIKTL	RYCAGWADKI	QGRTIPIDGN	FFTYTRHEPI
170	180	190	200	210	220	230	240
GVCGQIIPWN	FPLVMLIWKI	GPALSCGNTV	VVKPAEQTPL	TALHVASLIK	EAGFPPGVVN	IVPGYGPTAG	AAISSHMDID
250	260	270	280	290	300	310	320
KVAFTGSTEV	GKLIKEAAGK	SNLKRVTLEL	GGKSPCIVLA	DADLDNAVEF	AHHGVFYHQG	QCCIAASRIF	VEESIYDEFV
330	340	350	360	370	380	390	400
RRSVERAKKY	ILGNPLTPGV	TQGPQIDKEQ	YDKILDLIES	GKKEGAKLEC	GGGPWGNKGY	FVQPTVFSNV	TDEMRIAKEE
410	420	430	440	450	460	470	480
IFGPVQQIMK	FKSLDDVIKR	ANNTFYGLSA	GVFTKDIDKA	ITISSALQAG	TVWVNCYGVV	SAQCPFGGFK	MSGNGRELGE
490	500	510					
YGFHEYTEVK	TVTVKISQKN	S					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
499	1	587.8106	70.58	2	34.9	13.0	0	368-378	K.LECGGGPWGNK.G	Carbamidomethyl: 3

Detailed Protein Report

Protein 163: PREDICTED: inositol 1,4,5-trisphosphate receptor type 2 isoform X1 [Homo sapiens]

Accession:	gi|578822836	**Score:**	36.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	212.9
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	1.8
		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	6	648.2368	-188.91	2	51.4	14.8	2	1199-1208	K.CRNQHQRLLK.N	

Detailed Protein Report

Protein 164: myeloid zinc finger 1 isoform 1 [Homo sapiens]

Accession:	gi|37622341	**Score:**	36.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.0
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.2
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|578834840	refseq_human (refseq_human_20140103.fasta)	PREDICTED: myeloid zinc finger 1 isoform X5 [Homo sapiens]
gi|578834838	refseq_human (refseq_human_20140103.fasta)	PREDICTED: myeloid zinc finger 1 isoform X4 [Homo sapiens]
gi|37622345	refseq_human (refseq_human_20140103.fasta)	myeloid zinc finger 1 isoform 1 [Homo sapiens]

10	20	30	40	50	60	70	80
MRPAVLGSPD	RAPPEDEGPV	MVKLEDSEEE	GEAALWDPGP	EAARLRFRCF	RYEEATGPQE	ALAQLRELCR	QWLRPEVRSK
90	100	110	120	130	140	150	160
EQMLELLVLE	QFLGALPPEI	QARVQGQRPG	SPEEAAALVD	GLRREPGGPR	RWVTVQVQGQ	EVLSEKMEPS	SFQPLPETEP
170	180	190	200	210	220	230	240
PTPEPGPKTP	PRTMQESPLG	LQVKEESEVT	EDSDFLESGP	LAATQESVPT	LLPEEAQRCG	TVLDQIFPHS	KTGPEGPSWR
250	260	270	280	290	300	310	320
EHPRALWHEE	AGGIFSPGFA	LQLGSISAGP	GSVSPHLHVP	WDLGMAGLSG	QIQSPSREGG	FAHALLLPSD	LRSEQDPTDE
330	340	350	360	370	380	390	400
DPCRGVGPAL	ITTRWRSPRG	RSRGRPSTGG	GVVRGGRCDV	CGKVFSQRSN	LLRHQKIHTG	ERPFVCSECG	RSFSRSSHLL
410	420	430	440	450	460	470	480
RHQLTHTEER	PFVCGDCGQG	FVRSARLEEH	RRVHTGEQPF	RCAECGQSFR	QRSNLLQHQR	IHGDPPGPGA	KPPAPPGAPE
490	500	510	520	530	540	550	560
PPGPFPCSEC	RESFARRAVL	LEHQAVHTGD	KSFGCVECGE	RFGRRSVLLQ	HRRVHSGERP	FACAECGQSF	RQRSNLTQHR
570	580	590	600	610	620	630	640
RIHTGERPFA	CAECGKAFRQ	RPTLTQHLRV	HTGEKPFACP	ECGQRFSQRL	KLTRHQRTHT	GEKPYHCGEC	GLGFTQVSRL
650	660	670	680	690	700	710	720
TEHQRIHTGE	RPFACPECGQ	SFRQHANLTQ	HRRIHTGERP	YACPECGKAF	RQRPTLTQHL	RTHRREKPFA	CQDCGRRFHQ
730	740						
STKLIQHQRV	HSAE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
254	1	977.7698	-46.68	3	31.9	12.1	2	219-244	R.CGTVLDQIFPHSKTGPEGPSWREHPR.A	
2819	1	937.4520	9.17	2	64.4	12.8	1	673-688	R.RIHTGERPYACPECGK.A	Carbamidomethyl: 11

BRUKER

Detailed Protein Report

Protein 165: DNA-directed RNA polymerase, mitochondrial precursor [Homo sapiens]

Accession:	gi|110618253	**Score:**	36.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	138.5
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.69 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSALCWGRGA	AGLKRALRPC	GRPGLPGKEG	TAGGVCGPRR	SSSASPQEQD	QDRRKDWGHV	ELLEVLQARV	RQLQAESVSE
90	100	110	120	130	140	150	160
VVVNRVDVAR	LPECGSGDGS	LQPPRKVQMG	AKDATPVPCG	RWAKILEKDK	RTQQMRMQRL	KAKLQMPFQS	GEFKALTRRL
170	180	190	200	210	220	230	240
QVEPRLLSKQ	MAGCLEDCTR	QAPESPWEEQ	LARLLQEAPG	KLSLDVEQAP	SGQHSQAQLS	GQQQRLLAFF	KCCLLTDQLP
250	260	270	280	290	300	310	320
LAHHLLVVHH	GQRQKRKLLT	LDMYNAVMLG	WARQGAFKEL	VYVLFMVKDA	GLTPDLLSYA	AALQCMGRQD	QDAGTIERCL
330	340	350	360	370	380	390	400
EQMSQEGLKL	QALFTAVLLS	EEDRATVLKA	VHKVKPTFSL	PPQLPPPVNT	SKLLRDVYAK	DGRVSYPKLH	LPLKTLQCLF
410	420	430	440	450	460	470	480
EKQLHMELAS	RVCVVSVEKP	TLPSKEVKHA	RKTLKTLRDQ	WEKALCRALR	ETKNRLEREV	YEGRFSLYPF	LCLLDEREVV
490	500	510	520	530	540	550	560
RMLLQVLQAL	PAQGESFTTL	ARELSARTFS	RHVVQRQRVS	GQVQALQNHY	RKYLCLLASD	AEVPEPCLPR	QYWEELGAPE
570	580	590	600	610	620	630	640
ALREQPWPLP	VQMELGKLLA	EMLVQATQMP	CSLDKPHRSS	RLVPVLYHVY	SFRNVQQIGI	LKPHPAYVQL	LEKAAEPTLT
650	660	670	680	690	700	710	720
FEAVDVPMLC	PPLPWTSPHS	GAFLLSPTKL	MRTVEGATQH	QELLETCPPT	ALHGALDALT	QLGNCAWRVN	GRVLDLVLQL
730	740	750	760	770	780	790	800
FQAKGCPQLG	VPAPPSEAPQ	PPEAHLPHSA	APARKAELRR	ELAHCQKVAR	EMHSLRAEAL	YRLSLAQHLR	DRVFWLPHNM
810	820	830	840	850	860	870	880
DFRGRTYPCP	PHFNHLGSDV	ARALLEFAQG	RPLGPHGLDW	LKIHLVNLTG	LKKREPLRKR	LAFAEEVMDD	ILDSADQPLT
890	900	910	920	930	940	950	960
GRKWWMGAEE	PWQTLACCME	VANAVRASDP	AAYVSHLPVH	QDGSCNGLQH	YAALGRDSVG	AASVNLEPSD	VPQDVYSGVA
970	980	990	1000	1010	1020	1030	1040
AQVEVFRRQD	AQRGMRVAQV	LEGFITRKVV	KQTVMTVVYG	VTRYGGRLQI	EKRLRELSDF	PQEFVWEASH	YLVRQVFKSL
1050	1060	1070	1080	1090	1100	1110	1120
QEMFSGTRAI	QHWLTESARL	ISHMGSVVEW	VTPLGVPVIQ	PYRLDSKVKQ	IGGGIQSITY	THNGDISRKP	NTRKQKNGFP
1130	1140	1150	1160	1170	1180	1190	1200
PNFIHSLDSS	HMMLTALHCY	RKGLTFVSVH	DCYWTHAADV	SVMNQVCREQ	FVRLHSEPIL	QDLSRFLVKR	FCSEPQKILE
1210	1220	1230	1240				
ASQLKETLQA	VPKPGAFDLE	QVKRSTYFFS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
390	1	685.3636	4.04	2	34.8	10.5	0	992-1003	K.QTVMTVVYGVTR.Y	Oxidation: 4	QD:QU	0.69

Detailed Protein Report

Protein 166: pleckstrin homology domain-containing family G member 4B [Homo sapiens]

Accession:	gi|148529025	**Score:**	36.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	139.6
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 1.10 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEALRNPMPL	GSSEEALGDL	ACSSLTGASR	DLGTGAVASG	TQEETSGPRG	DPQQTPSLEK	ERHTPSRTGP	GAAGRTLPRR
90	100	110	120	130	140	150	160
SRSWERAPRS	SRGAQAAACH	TSHHSAGSRP	GGHLGGQAVG	TPNCVPVEGP	GCTKEEDVLA	SSACVSTDGG	SLHCHNPSGP
170	180	190	200	210	220	230	240
SDVPARQPHP	EQEGWPPGTG	DFPSQVPKQV	LDVSQELLQS	GVVTLPGTRD	RHGRAVVQVR	TRSLLWTREH	SSCAELTRLL
250	260	270	280	290	300	310	320
LYFHSIPRKE	VRDLGLVVLV	DARRSPAAPA	VSQALSGLQN	NTSPIIHSIL	LLVDKESAFR	PDKDAIIQCE	VVSSLKAVHK
330	340	350	360	370	380	390	400
FVDSCQLTAD	LDGSFPYSHG	DWICFRQRLE	HFAANCEEAI	IFLQNSFCSL	NTHRTPRTAQ	EVAELIDQHE	TMMKLVLEDP
410	420	430	440	450	460	470	480
LLVSLRLEGG	TVLARLRREE	LGTEDSRDTL	EAATSLYDRV	DEEVHRLVLT	SNNRLQQLEH	LRELASLLEG	NDQQSCQKGL
490	500	510	520	530	540	550	560
QLAKENPQRT	EEMVQDFRRG	LSAVVSQAEC	REGELARWTR	SSELCETVSS	WMGPLDPEAC	PSSPVAECLR	SCHQEATSVA
570	580	590	600	610	620	630	640
AEAFPGAGVA	VLKPHALGKP	WASQQDLWLQ	YPQTRLRLEE	ALSEAAPDPS	LPPLAQSPPK	HERAQEAMRR	HQKPPSFPST
650	660	670	680	690	700	710	720
DSGGGAWEPA	QPLSGLPGRA	LLCGQDGETL	RPGLCALWDP	LSLLRGLPGA	GATTAHLEDS	SACSSEPTQT	LASRPRKHPQ
730	740	750	760	770	780	790	800
KKMIKKTQSF	EIPQPDSGPR	DSCQPDHTSV	FSKGLEVTST	VATEKKLPLW	QHARSPPVTQ	SRSLSSPSGL	HPAEEDGRQQ
810	820	830	840	850	860	870	880
VGSSRLRHIM	AEMIATEREY	IRCLGYVIDN	YFPEMERMDL	PQGLRGKHHV	IFGNLEKLHD	FHQQHFLREL	ERCQHCPLAV
890	900	910	920	930	940	950	960
GRSFLRHEEQ	FGMYVIYSKN	KPQSDALLSS	HGNAFFKDKQ	RELGDKMDLA	SYLLRPVQRV	AKYALLLQDL	LKEASCGLAQ
970	980	990	1000	1010	1020	1030	1040
GQELGELRAA	EVVVCFQLRH	GNDLLAMDAI	RGCDVNLKEQ	GQLRCRDEFI	VCCGRKKYLR	HVFLFEDLIL	FSKTQKVEGS
1050	1060	1070	1080	1090	1100	1110	1120
HDVYLYKQSF	KTAEIGMTEN	VGDSGLRFEI	WFRRRRKSQD	TYILQASSAE	VKSAWTDVIG	RILWRQALKS	RELRIQEMAS
1130	1140	1150	1160	1170	1180	1190	1200
MGIGNQPFMD	VKPRDRTPDC	AVISDRAPKC	AVMSDRVPDS	IVKGTESQMR	GSTAVSSSDH	AAPFKRPHST	ISDSSTSSSS
1210	1220	1230	1240	1250	1260	1270	1280
SQSSSILGSL	GLLVSSSPAH	PGLWSPAHSP	WSSDIRACVE	EDEPEPELET	GTQAAVCEGA	PAVLLSRTRQ	A

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
373	2	627.3450	-10.69	2	34.6	17.1	1	479-489	K.GLQLAKENPQR.T		
2311	4	953.4263	-3.01	2	57.6	19.4	0	823-837	R.CLGYVIDNYFPEMER.M	Carbamidomethyl: 1	QD:QU 1.10

Detailed Protein Report

Protein 167: PREDICTED: rho guanine nucleotide exchange factor 18 isoform X6 [Homo sapiens]

Accession:	gi|578833130	**Score:**	36.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	149.7
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	3

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	
1380	1	683.3455	-90.52	2	45.8	10.4	2	1270-1281	R.NRRSLSPILPGR.H	

Detailed Protein Report

Protein 168: PREDICTED: neuroblastoma breakpoint family member 6 isoform X2 [Homo sapiens]

Accession:	gi|530363207	**Score:**	36.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.3
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTPPPSNSVI	ATADRYLVHW	LLPPSLLSES	ELQAVPSALS	SGIPVPVFAV	KDSKVLCRVH	QLFLNLPGST	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	VQESPAPREV	QKTEEKEVPQ	DSLEECAVTC	SNSHNPSNSN	QPHRSTKITF	KEHEVDSALV
330	340	350	360	370	380	390	400
VESEHPHDEE	EEALNIPPEN	QNDHEEEEGK	APVPPRHHDK	SNSYRHREVS	FLALDEQKVC	SAQDVARDYS	NPKWDETSLG
410	420	430	440	450	460	470	480
FLEKQSDLEE	VKGQETVAPR	LSRGPLRVDK	HEIPQESLDG	CCLTPSILPD	LTPSYHPYWS	TLYSFEDKQV	SLALVDKIKK
490	500	510	520	530	540	550	560
DQEEIEDQSP	PCPRLSQELP	EVKEQEVPED	SVNEVYLTPS	VHHDVSDCHQ	PYSSTLSSLE	DQLACSALDV	ASPTEAACPQ
570	580	590	600	610	620	630	640
GTWSGDLSHH	RSEVQISQAQ	LEPSTLVPSC	LRLQLDQGFH	CGNGLAQRGL	SSTTCSFSAN	ADSGNQWPFQ	ELVLEPSLGM
650	660	670	680	690	700	710	720
KNPPQLEDDA	LEGSASNTQG	RQVTGRIRAS	LVLILKTIRR	RLPFSKWRLA	FRFAGPHAES	AEIPNTAERM	QRMIG

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	710-715	R.MQRMIG.-	Oxidation: 1, 4

Detailed Protein Report

Protein 169: F-box only protein 41 [Homo sapiens]

Accession:	gi|289803020	**Score:**	35.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	94.4
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.7
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578802734	refseq_human (refseq_human_20140103.fasta)	PREDICTED: F-box only protein 41 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MASLDLPYRC	PRCGEHKRFR	SLSSLRAHLE	YSHTYETLYI	LSKTNSICDG	AAAAAAAAAA	ASGFPLAPEP	AALLAVPGAR
90	100	110	120	130	140	150	160
REVFESTSFQ	GKEQAAGPSP	AAPHLLHHHH	HHAPLAHFPG	DLVPASLPCE	ELAEPGLVPA	AAARYALREI	EIPLGELFAR
170	180	190	200	210	220	230	240
KSVASSACST	PPPGPGPGPC	PGPASASPAS	PSPADVAYEE	GLARLKIRAL	EKLEVDRRLE	RLSEEVEQKI	AGQVGRLQAE
250	260	270	280	290	300	310	320
LERKAAELET	ARQESARLGR	EKEELEERAS	ELSRQVDVSV	ELLASLKQDL	VHKEQELSRK	QQEVVQIDQF	LKETAAREAS
330	340	350	360	370	380	390	400
AKLRLQQFIE	ELLERADRAE	RQLQVISSSC	GSTPSASLGR	GGGGGGAGPN	ARGPGRMREH	HVGPAVPNTY	AVSRHGSSPS
410	420	430	440	450	460	470	480
TGASSRVPAA	SQSSGCYDSD	SLELPRPEEG	APEDSGPGGL	GTRAQAANGG	SERSQPPRSS	GLRRQAIQNW	QRRPRRHSTE
490	500	510	520	530	540	550	560
GEEGDVSDVG	SRTTESEAEG	PLDAPRPGPA	MAGPLSSCRL	SARPEGGSGR	GRRAERVSPS	RSNEVISPEI	LKMRAALFCI
570	580	590	600	610	620	630	640
FTYLDTRTLL	HAAEVCRDWR	FVARHPAVWT	RVLLENARVC	SKFLAMLAQW	CTQAHSLTLQ	NLKPRQRGKK	ESKEEYARST
650	660	670	680	690	700	710	720
RGCLEAGLES	LLKAAGGNLL	ILRISHCPNI	LTDRSLWLAS	CYCRALQAVT	YRSATDPVGH	EVIWALGAGC	REIVSLQVAP
730	740	750	760	770	780	790	800
LHPCQQPTRF	SNRCLQMIGR	CWPHLRALGV	GGAGCGVQGL	ASLARNCMRL	QVLELDHVSE	ITQEVAAEVC	REGLKGLEML
810	820	830	840	850	860	870	880
VLTATPVTPK	ALLHFNSICR	NLKSIVVQIG	IADYFKEPSS	PEAQKLFEDM	VTKLQALRRR	PGFSKILHIK	VEGGC

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2879	2	813.9356	28.83	2	65.2	12.4	1	568-580	R.TLLHAAEVCRDWR.F	Carbamidomethyl: 9

Detailed Protein Report

Protein 170: **ral GTPase-activating protein subunit alpha-2 [Homo sapiens]**

Accession: gi|118600961
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 35.6
MW [kDa]: 210.6
pI: 5.7
Sequence Coverage [%]: 2.3
No. of unique Peptides: 1

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				
EAIIQNHREV	MTFEDFAAQV	FSPSPSYSLS	GTD				

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
2089	1	1023.9303	-87.12	2	56.5	14.8	1	433-448	K.WILQDKPVFMEEPDRK.D	Oxidation: 10

Detailed Protein Report

Protein 171:	**PREDICTED: mediator of RNA polymerase II transcription subunit 13-like isoform X2 [Homo sapiens]**		
Accession:	gi|578823479	**Score:**	35.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	241.6
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MLESRKAIAP	SRRKAELTGI	KWRRYNFGGH	GDCGPIISAP	AQDDPILLSF	IRCLQANLLC	VWRRDVKPDC	KELWIFWWGD
90	100	110	120	130	140	150	160
EPNLVGVIHH	ELQVVEEGLW	ENGLSYECRT	LLFKAIHNLL	ERCLMDKNFV	RIGKWFVRPY	EKDEKPVNKS	EHLSCAFTFF
170	180	190	200	210	220	230	240
LHGESNVCTS	VEIAQHQPIY	LINEEHIHMA	QSSPAPFQVL	VSPYGLNGTL	TGQAYKMSDP	ATRKLIEEWQ	YFYPMVLKKK
250	260	270	280	290	300	310	320
EESKEEDELG	YDDDFPVAVE	VIVGGVRMVY	PSAFVLISQN	DIPVPQSVAS	AGGHIAVGQQ	GLGSVKDPSN	CGMPLTPPTS
330	340	350	360	370	380	390	400
PEQAILGESG	GMQSAASHLV	SQDGGMITMH	SPKRSGKIPP	KLHNHMVHRV	WKECILNRTQ	SKRSQMSTPT	LEEEPASNPA
410	420	430	440	450	460	470	480
TWDFVDPTQR	VSCSCSRHKL	LKRCAVGPNR	PPTVSQPGFS	AGPSSSSSLP	PPASSKHKTA	ERQEKGDKLQ	KRPLIPFHHR
490	500	510	520	530	540	550	560
PSVAEELCME	QDTPGQKLGL	AGIDSSLEVS	SSRKYDKQMA	VPSRNTSKQM	NLNPMDSPHS	PISPLPPTLS	PQPRGQETES
570	580	590	600	610	620	630	640
LDPPSVPVNP	ALYGNGLELQ	QLSTLDDRTV	LVGQRLPLMA	EVSETALYCG	IRPSNPESSE	KWWHSYRLPP	SDDAEFRPPE
650	660	670	680	690	700	710	720
LQGERCDAKM	EVNSESTALQ	RLLAQPNKRF	KIWQDKQPQL	QPLHFLDPLP	LSQQPGDSLG	EVNDPYTFED	GDIKYIFTAN
730	740	750	760	770	780	790	800
KKCKQGTEKD	SLKKNKSEDG	FGTKDVTTPG	HSTPVPDGKN	AMSIFSSATK	TDVRQDNAAG	RAGSSSLTQV	TDLAPSLHDL
810	820	830	840	850	860	870	880
DNIFDNSDDD	ELGAVSPALR	SSKMPAVGTE	DRPLGKDGRA	AVPYPPTVAD	LQRMFPTPPS	LEQHPAFSPV	MNYKDGISSE
890	900	910	920	930	940	950	960
TVTALGMMES	PMVSMVSTQL	TEFKMEVEDG	LGSPKPEEIK	DFSYVHKVPS	FQPFVGSSMF	APLKMLPSHC	LLPLKIPDAC
970	980	990	1000	1010	1020	1030	1040
LFRPSWAIPP	KIEQLPMPPA	ATFIRDGYNN	VPSVGSLADP	DYLNTPQMNT	PVTLNSAAPA	SNSGAGVLPS	PATPRFSVPT
1050	1060	1070	1080	1090	1100	1110	1120
PRTPRTPRTP	RGGGTASGQG	SVKYDSTDQG	SPASTPSTTR	PLNSVEPATM	QPIPEAHSLY	VTLILSDSVM	NIFKDRNFDS
1130	1140	1150	1160	1170	1180	1190	1200
CCICACNMNI	KGADVGLYIP	DSSNEDQYRC	TCGFSAIMNR	KLGYNSGLFL	EDELDIFGKN	SDIGQAAERR	LMMCQSTFLP
1210	1220	1230	1240	1250	1260	1270	1280
QVEGTKKPQE	PPISLLLLLQ	NQHTQPFASL	NFLDYISSNN	RQTLPCVSWS	YDRVQADNND	YWTECFNALE	QGRQYVDNPT
1290	1300	1310	1320	1330	1340	1350	1360
GGKVDEALVR	SATVHSWPHS	NVLDISMLSS	QDVVRMLLSL	QPFLQDAIQK	KRTGRTWENI	QHVQGPLTWQ	QFHKMAGRGT
1370	1380	1390	1400	1410	1420	1430	1440
YGSEESPEPL	PIPTLLVGYD	KDFLTISPFS	LPFWERLLLD	PYGGHRDVAY	IVVCPENEAL	LEGAKTFFRD	LSAVYEMCRL
1450	1460	1470	1480	1490	1500	1510	1520
GQHKPICKVL	RDGIMRVGKT	VAQKLTDELV	SEWFNQPWSG	EENDNHSRLK	LYAQVCRHHL	APYLATLQLD	SSLLIPPKYQ
1530	1540	1550	1560	1570	1580	1590	1600
TPPAAAQGQA	TPGNAGPLAP	NGSAAPPAGS	AFNPTSNSSS	TNPAASSSAS	GSSVPPVSSS	ASAPGISQIS	TTSSSGFSGS
1610	1620	1630	1640	1650	1660	1670	1680
VGGQNPSTGG	ISADRTQGNI	GCGGDTDPGQ	SSSQPSQDGQ	ESVTERERIG	IPTEPDSADS	HAHPPAVVIY	MVDPFTYAAE
1690	1700	1710	1720	1730	1740	1750	1760
EDSTSGNFWL	LSLMRCYTEM	LDNLPEHMRN	SFILQIVPCQ	YMLQTMKDEQ	VFYIQYLKSM	AFSVYCQCRR	PLPTQIHIKS
1770	1780	1790	1800	1810	1820	1830	1840
LTGFGPAASI	EMTLKNPERP	SPIQLYSPPF	ILAPIKDKQT	ELGETFGEAS	QKYNVLFVGY	CLSHDQRWLL	ASCTDLHGEL
1850	1860	1870	1880	1890	1900	1910	1920
LETCVVNIAL	PNRSRRSKVS	ARKIGLQKLW	EWCIGIVQMT	SLPWRVVIGR	LGRLGHGELK	DWSILLGECS	LQTISKKLKD
1930	1940	1950	1960	1970	1980	1990	2000
VCRMCGISAA	DSPSILSACL	VAMEPQGSFV	VMPDAVTMGS	VFGRSTALNM	QSSQLNTPQD	ASCTHILVFP	TSSTIQVAPA
2010	2020	2030	2040	2050	2060	2070	2080
NYPNEDGFSP	NNDDMFVDLP	FPDDMDNDIG	ILMTGNLHSS	PNSSPVPSPG	SPSGIGVGSH	FQHSRSQGER	LLSREAPEEL
2090	2100	2110	2120	2130	2140	2150	2160
KQQPLALGYF	VSTAKAENLP	QWFWSSCPQA	QNQCPLFLKA	SLHHHISVAQ	TDELLPARNS	QRVPHPLDSK	TTSDVLRFVL
2170	2180	2190	2200	2210			

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2594	2	1044.5480	2.20	2	63.1	15.8	2	115-131	K.AIHNLLERCLMDKNFVR.I	Oxidation: 11
2308	1	892.3159	-67.35	2	57.5	19.8	0	1696-1709	R.CYTEMLDNLPEHMR.N	Oxidation: 5, 13

Detailed Protein Report

Protein 172: PREDICTED: insulin-like growth factor 1 receptor isoform X2 [Homo sapiens]

Accession:	gi|530407102	**Score:**	35.6
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 [%]:**	3.7
		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
1982	1	1044.8814	-23.69	2	55.2	11.7	0	56-73	K.ECGDLCPGTMEEKPMCEK.T	Carbamidomethyl: 16; Oxidation: 10, 15
1529	1	669.8325	-70.94	2	49.3	13.1	0	271-282	R.HSHALVSLSFLK.N	
2019	1	660.9088	-130.71	3	53.8	10.8	1	325-340	K.MYFAFNPKLCVSEIYR.M	

Detailed Protein Report

Protein 173: **PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial isoform X2 [Homo sapiens]**

Accession:	gi|530364809	**Score:**	35.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.8
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MELSGEMVRK	CDPHIGLLHR	GTEKLIEYKT	YLQALPYFDR	LDYVSMMCNE	QAYSLAVEKL	LNIRPPPRAQ	WIRVLFGEIT
90	100	110	120	130	140	150	160
RLLNHIMAVT	THALDLGAMT	PFFWLFEERE	KMFEFYERVS	GARMHAAYIR	PGGVHQDLPL	GLMDDIYQFS	KNFSLRLDEL
170	180	190	200	210	220	230	240
EELLTNNRIW	RNRTIDIGVV	TAEEALNYGF	SGVMLRGSGI	QWDLRKTQPY	DVYDQVEFDV	PVGSRGDCYD	RYLCRVEEMR
250	260	270	280	290	300	310	320
QSLRIIAQCL	NKMPPGEIKV	DDAKVSPPKR	AEMKTSMESL	IHHFKLYTEG	YQVPPGATYT	AIEAPKGEFG	VYLVSDGSSR
330	340	350	360	370			
PYRCKIKAPG	FAHLAGLDKM	SKGHMLADVV	AIIGTQDIVF	GEVDR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1905	1	673.3043	-41.33	2	54.2	17.5	0	275-285	K.TSMESLIHHFK.L	Oxidation: 3

Detailed Protein Report

Protein 174: pumilio domain-containing protein KIAA0020 [Homo sapiens]

Accession: gi|109948283

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 35.0

MW [kDa]: 73.5

pI: 10.2

Sequence Coverage [%]: 5.1

No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MEVKGKKQFT	GKSTKTAQEK	NRFHKNSDSG	SSKTFPTRKV	AKEGGPKVTS	RNFEKSITKL	GKKGVKQFKN	KQQGDKSPKN
90	100	110	120	130	140	150	160
KFQPANKFNK	KRKFQPDGRS	DESAAKKPKW	DDFKKKKKEL	KQSRQLSDKT	NYDIVVRAKQ	MWEILRRKDC	DKEKRVKLMS
170	180	190	200	210	220	230	240
DLQKLIQGKI	KTIAFAHDST	RVIQCYIQYG	NEEQRKQAFE	ELRDDLVELS	KAKYSRNIVK	KFLMYGSKPQ	IAEIIRSFKG
250	260	270	280	290	300	310	320
HVRKMLRHAE	ASAIVEYAYN	DKAILEQRNM	LTEELYGNTF	QLYKSADHRT	LDKVLEVQPE	KLELIMDEMK	QILTPMAQKE
330	340	350	360	370	380	390	400
AVIKHSLVHK	VFLDFFTYAP	PKLRSEMIEA	IREAVVYLAH	THDGARVAMH	CLWHGTPKDR	KVIVKTMKTY	VEKVANGQYS
410	420	430	440	450	460	470	480
HLVLLAAFDC	IDDTKLVKQI	IISEIISSLP	SIVNDKYGRK	VLLYLLSPRD	PAHTVREIIE	VLQKGDGNAH	SKKDTEVRRR
490	500	510	520	530	540	550	560
ELLESISPAL	LSYLQEHAQE	VVLDKSACVL	VSDILGSATG	DVQPTMNAIA	SLAATGLHPG	GKDGELHIAE	HPAGHLVLKW
570	580	590	600	610	620	630	640
LIEQDKKMKE	NGREGCFAKT	LVEHVGMKNL	KSWASVNRGA	IILSSLLQSC	DLEVANKVKA	ALKSLIPTLE	KTKSTSKGIE
650							
ILLEKLST							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2240	1	569.1603	-210.52	2	56.7	10.9	0	302-310	K.LELIMDEMK.Q	Oxidation: 8
2534	1	698.3342	-3.44	2	60.4	11.9	0	367-378	R.VAMHCLWHGTPK.D	Oxidation: 3

Detailed Protein Report

Protein 175: 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 176: phenylalanine--tRNA ligase alpha subunit [Homo sapiens]

Accession:	gi|4758340	**Score:**	34.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.5
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.7
		No. of unique 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
2536	1	1044.5961	47.08	2	62.3	24.4	2	128-144	R.VVDSMEDEVQRRLQLVR.G	Oxidation: 5

Detailed Protein Report

Protein 177: PREDICTED: zinc finger protein 708 isoform X1 [Homo sapiens]

Accession:	gi|578833563	**Score:**	34.7
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

QD:QU **Median:** 0.30 **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
328	2	605.6684	-199.06	2	32.8	13.8	2	102-111	K.NPFKCKECGK.S	Carbamidomethyl: 8	QD:QU 0.30
1258	6	586.7739	28.23	2	45.9	20.9	1	330-339	K.CEECGKAFTK.S	Carbamidomethyl: 4	

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Detailed Protein Report

Protein 178: PREDICTED: centlein isoform X2 [Homo sapiens]

Accession:	gi|578816553	**Score:**	34.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	155.6
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
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
848	1	512.1520	-290.70	2	40.7	15.4	1	1084-1091	K.RHLIEDLK.F	

Detailed Protein Report

Protein 179: protein MROH8 isoform 3 [Homo sapiens]

Accession:	gi|538260586	**Score:**	34.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.5
Database Date:	2015-11-30	**pI:**	8.0
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPLSRRGRGS	RLAGSRAATS	NLPRATALSP	KSAGRGALSI	SHAQLLTRRR	HSSEQVPPES	EPRADFRSGK	WLQEPATGDA
90	100	110	120	130	140	150	160
RDSRQALRAR	MSSKHRICSQ	EEVVIPCAYD	SDSESVDLEL	SNLEIIKKGS	SSIELTDLDI	PDIPGLHCEP	LSHSPRHLTQ
170	180	190	200	210	220	230	240
QDPLSEAIVE	KLIQSIQKVF	NGELKGELEK	LKFLGDLSSL	SQALPYDETA	KSFIHSHIAD	IVHTLNVLVQ	EERPHSLSSS
250	260	270	280	290	300	310	320
MRQEVFVTIA	DLSYQDVHLL	LGSEDRAELF	SLTIKSIITL	PSVRTLTQIQ	EIMPNGTCNT	ECLYRQTFQA	FSEMLQSLVV
330	340	350	360	370	380	390	400
KDPHLENLDT	IIKLPLRFQR	LGHLVALMAL	LCGDPQEKVA	EEAAEGIHSL	LHITLRLKYI	THDKKDQQNL	KRALTKCREF
410	420	430	440	450	460	470	480
LELHSSAAKC	FYNCPFRIAQ	VFEGFLDSNE	LCQFIMTTFD	TLKTLKHPCI	QRSAGELLLT	LAKNTESQFE	KVPEIMGVIC
490	500	510	520	530	540	550	560
AQLSIISQPR	VRQQIINTVS	LFISRPKYTD	IVLSFLLCHP	VPYNRHLAEV	WRMLSVELPS	TTWILWRLLR	KLQKCHNEPA
570	580						
QEKMAYVAVA	VSP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
222	1	493.5794	24.80	3	32.8	11.1	0	51-63	R.HSSEQVPPESEPR.A	

Detailed Protein Report

Protein 180: uncharacterized protein LOC284677 [Homo sapiens]

Accession:	gi|197116396	**Score:**	34.2
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
2167	3	1051.4380	-62.66	2	57.5	23.3	1	187-205	R.ALPSPDCPGLRTTGEQMQK.L	Carbamidomethyl: 7; Oxidation: 17
2182	1	682.2713	-87.72	3	57.7	10.9	1	187-205	R.ALPSPDCPGLRTTGEQMQK.L	Oxidation: 17

Detailed Protein Report

Protein 181: PREDICTED: uncharacterized protein LOC101929108 [Homo sapiens]

Accession:	gi|578795301	**Score:**	34.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.1
Database Date:	2015-11-30	**pI:**	12.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	16.9
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MTKTLSLQAF PQLRSLLGLG PFLLLSKGVA ANQPCPPALL TPSFSSVPEL CMGSELWLPP GVPVLPQFSQ RSMGPSTPPL
        90        100        110        120        130        140        150        160
AAMHWGLRRV PGPLPPPWPG LPAPGRSCAR FSASRVCVAC SAQRPPPRSA PCRTPRCCGR GGSVAVRAVS VRPHRLPSAD
       170        180        190        200        210        220
FLRRGPELPA RSDAAECRNG LPVCQSGLPR TPSEATRSSR GVSVALLKQK QQLHSPASV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
278	1	998.9505	-45.38	2	33.5	21.2	1	72-89	R.SMGPSTPPLAAMHWGLRR.V	Oxidation: 2, 12
2912	1	1012.4649	-62.98	2	65.6	13.0	2	137-155	R.CCGRGGSVAVRAVSVRPHR.L	Carbamidomethyl: 1

Detailed Protein Report

Protein 182: PREDICTED: uncharacterized protein C11orf85 isoform X7 [Homo sapiens]

Accession:	gi|578821305	**Score:**	34.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.4
Database Date:	2015-11-30	**pI:**	10.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	14.9
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MSLKPFTYPF PETRFLHAGP NVYKFKIRYG KSIRGEEIEN KEVITQELEL VLKVAFGSLR MGSFLHCAFM NCEQLWKGGV
        90        100        110        120        130        140        150        160
TGICFLLKVP VEKKAVGAVM RKRKHMDEPS SPSRPGLDRA KIGTSSQGPS KKKPPVETRR NRERKTQQGL QETLASDITD
       170        180        190        200        210        220
VQKQDSEWGH SLPGRIVPPL QHNSPPPKER AATGFFGFLS SLFPFRYFFR KSSHS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2875	1	922.9828	-58.69	2	65.1	22.3	2	78-94	K.GGVTGICFLLKVPVEKK.A	Carbamidomethyl: 7
930	1	848.9319	50.50	2	41.7	11.9	0	105-119	K.HMDEPSSPSRPGLDR.A	Oxidation: 2

Detailed Protein Report

Protein 183: PREDICTED: ATP-dependent RNA helicase DDX55 isoform X1 [Homo sapiens]

Accession: gi|530401708
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 34.1
MW [kDa]: 50.9
pI: 9.9
Sequence Coverage [%]: 6.0
No. of unique Peptides: 2

```
        10         20         30         40         50         60         70         80
MEHVTEGSWE SLPVPLHPQV LGALRELGFP YMTPVQSATI PLFMRNKDVA AEAVTGSGKT LAFVIPILEI LLRREEKLKK
        90        100        110        120        130        140        150        160
SQVGAIIITP TRELAIQIDE VLSHFTKHFP EFSQILWIGG RNPGEDVERF KQQGGNIIVA TPGRLEDMFR RKAEGLDLAS
       170        180        190        200        210        220        230        240
CVRSLDVLVL DEADRLLDMG FEASINTILE FLPKQRRTGL FSATQTQEVE NLVRAGLRNP VRVSVKEKGV AASSAQKTPS
       250        260        270        280        290        300        310        320
RLENYYMVCK ADEKFNQLVH FLRNHKQEKH LVFFSTCACV EYYGKALEVL VKGVKIMCIH GKMKYKRNKI FMEFRKLQSG
       330        340        350        360        370        380        390        400
ILVCTDVMAR GIDIPEVNWV LQYDPPSNAS AFVHRCGRTA RIGHGGSALV FLLPMEESYI NFLAINQKCP LQEMKPQRNT
       410        420        430        440        450        460
ADLLPKLKSM ALADRAVFEK GMKAFVSYVQ AYAKHECNLI FRLKALLEVL PC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
408	1	655.8392	-35.43	2	35.1	10.7	0	132-144	K.QQGGNIIVATPGR.L	
2795	1	874.5325	120.22	1	64.0	11.6	0	296-302	K.IMCIHGK.M	Carbamidomethyl: 3; Oxidation: 2

Detailed Protein Report

Protein 184:	**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):	Oxidation	**Sequence Coverage [%]:**	0.5
		No. of unique 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
MASLPYEYRL	QHRTVAELNH	MAEVLVPATL	RFLTCQGVSS	LLQVHGQQAV	CAGVAEVTSM	ARILHSLLDL	HLRLKEEKAP
2250	2260	2270	2280	2290	2300	2310	2320
GPEDLSYSDP	VAQSFRSSKS	SFLNRSQVDS	DDVPDKCREH	LLAVSSFLFA	LIWGFGAHLP	SRFWPIFDTF	IRDSISRLSN
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
2087	1	753.3822	17.22	2	56.5	20.7	1	2058-2071	K.VLRAAGQCNNMGQK.R	Oxidation: 11

Detailed Protein Report

Protein 185: **PREDICTED: putative Polycomb group protein ASXL2 isoform X2 [Homo sapiens]**

Accession:	gi|578802980	**Score:**	34.0
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:	2

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	
2134	8	937.3539	-101.03	2	55.3	23.7	2	874-889	R.GSESFRRTHSVNPEDR.F	

Detailed Protein Report

Protein 186: PREDICTED: tau-tubulin kinase 2 isoform X5 [Homo sapiens]

Accession:	gi|578826647	**Score:**	34.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.8
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

```
        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
2024	1	694.3465	21.44	2	55.7	10.8	1	1119-1132	R.SKSPPSHSGSSSSR.R	

Detailed Protein Report

Protein 187: fibrillin-1 precursor [Homo sapiens]

Accession:	gi|281485550	**Score:**	34.0
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 [%]:**	1.3
		No. of unique Peptides:	2

Quantitation

QD:QU	**Median:** 0.71	**CV:** 0.00 %	**No. of Peptides:** 1

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	Ratios
1872	1	1057.6895	-79.32	3	53.8	11.0	2	610-636	R. YCKDINECETPGICMNGRCVNTD C	Carbamidomethyl: 2, 19; Oxidation: 15	
976	6	635.1635	-177.36	2	40.7	23.1	1	2482-2492	R.SCKDLDECATK.Q	Carbamidomethyl: 8	QD:QU 0.71

Detailed Protein Report

Protein 188: SCO-spondin precursor [Homo sapiens]

Accession:	gi|134031945	**Score:**	34.0
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

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	
1675	2	1136.5319	16.36	2	49.5	14.8	1	2854-2875	R.GRSCSSLAPGDTTCPGPHSQTR.D	Carbamidomethyl: 4

Detailed Protein Report

Protein 189:	**PREDICTED: leucine-rich repeat serine/threonine-protein kinase 2 isoform X1 [Homo sapiens]**		
Accession:	gi|530399725	**Score:**	33.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	285.2
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:** 4.52	**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		QD:QU	4.52

Detailed Protein Report

Protein 190: collagen alpha-6(IV) chain isoform 5 precursor [Homo sapiens]

Accession: gi|567757604
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 33.7
MW [kDa]: 158.0
pI: 10.0
Sequence Coverage [%]: 1.8
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MHPGLWLLLV	TLCLTEELAA	AGEKSYGKPC	GGQDCSGSCQ	CFPEKGARGR	PGPIGIQGPT	GPQGFTGSTG	LSGLKGERGF
90	100	110	120	130	140	150	160
PGLLGPYGPK	GDKGPMGVPG	FLGINGIPGH	PGQPGPRGPP	GLDGCNGTQG	AVGFPGPDGY	PGLLGPPGLP	GQKGSKGDPV
170	180	190	200	210	220	230	240
LAPGSFKGMK	GDPGLPGLDG	ITGPQGAPGF	PGAVGPAGPP	GLQGPPGPPG	PLGPDGNMGL	GFQGEKGVKG	DVGLPGPAGP
250	260	270	280	290	300	310	320
PPSTGELEFM	GFPKGKKGSK	GEPGPKGFPG	ISGPPGFPGL	GTTGEKGEKG	EKGIPGLPGP	RGPMGSEGVQ	GPPGQQGKKG
330	340	350	360	370	380	390	400
TLGFPGLNGF	QGIEGQKGDI	GLPGPDVFID	IDGAVISGNP	GDPGVPGLPG	LKGDEGIQGL	RGPSGVPGLP	ALSGVPGALG
410	420	430	440	450	460	470	480
PQGFPGLKGD	QGNPGRTTIG	AAGLPGRDGL	PGPPGPPGPP	SPEFETETLH	NKESGFPGLR	GEQGPKGNLG	LKGIKGDSGF
490	500	510	520	530	540	550	560
CACDGGVPNT	GPPGEPGPPG	PWGLIGLPGL	KGARGDRGSG	GAQGPAGAPG	LVGPLGPSGP	KGKKGEPILS	TIQGMPGDRG
570	580	590	600	610	620	630	640
DSGSQGFRGV	IGEPGKDGVP	GLPGLPGLPG	DGGQGFPGEK	GLPGLPGEKG	HPGPPGLPGN	GLPGLPGPRG	LPGDKGKDGL
650	660	670	680	690	700	710	720
PGQQGLPGSK	GITLPCIIPG	SYGPSGFPGT	PGFPGPKGSR	GLPGTPGQPG	SSGSKGEPGS	PGLVHLPELP	GFPGPRGEKG
730	740	750	760	770	780	790	800
LPGFPGLPGK	DGLPGMIGSP	GLPGSKGATG	DIFGAENGAP	GEQGLQGLTG	HKGFLGDSGL	PGLKGVHGKP	GLLGPKGERG
810	820	830	840	850	860	870	880
SPGTPGQVGQ	PGTPGSSGPY	GIKGKSGLPG	APGFPGISGH	PGKKGTRGKK	GPPGSIVKKG	LPGLKGLPGN	PGLVGLKGSP
890	900	910	920	930	940	950	960
GSPGVAGLPA	LSGPKGEKGS	VGFVGFPGIP	GLPGIPGTRG	LKGIPGSTGK	MGPSGRAGTP	GEKGDRGNPG	PVGIPSPRRP
970	980	990	1000	1010	1020	1030	1040
MSNLWLKGDK	GSQGSAGSNG	FPGPRGDKGE	AGRPGPPGLP	GAPGLPGIIK	GVSGKPGPPG	FMGIRGLPGL	KGSSGITGFP
1050	1060	1070	1080	1090	1100	1110	1120
GMPGESGSQG	IRGSPGLPGA	SGLPGLKGDN	GQTVEISGSP	GPKGQPGESG	FKGTKGRDGL	IGNIGFPGNK	GEDGKVGVSG
1130	1140	1150	1160	1170	1180	1190	1200
DVGLPGAPGF	PGVAGMRGEP	GLPGSSGHQG	AIGPLGSPGL	IGPKGPSITG	VPGPAGLPGP	KGEKGYPGIG	IGAPGKPGLR
1210	1220	1230	1240	1250	1260	1270	1280
GQKGDRGFPG	LQGPAGLPGA	PGISLPSLIA	GQPGDPGRPG	LDGERGRPGP	AGPPGPPGPS	SNQGDTGDPG	FPGIPGPKGP
1290	1300	1310	1320	1330	1340	1350	1360
KGDQGIPGFS	GLPGELGLKG	SSGLQGDPGQ	TPTAEAVQVP	PGPLGLPGID	GIPGLTGDPG	AQGPVGLQGS	KGLPGIPGKD
1370	1380	1390	1400	1410	1420	1430	1440
GPSGLPGPPG	ALGDPGLPGL	QGPPGFEGAP	GQQGPFGMPG	MPGQSMRVGY	TLVKHSQSEQ	VPPCPIGMSQ	LWVGYSLLFV
1450	1460	1470	1480	1490	1500	1510	1520
EGQEKAHNQD	LGFAGSCLPR	FSTMPFIYCN	INEVCHYARR	NDKSYWLSTT	APIPMMPVSQ	TQIPQYISRC	SVCEAPSQAI
1530	1540	1550	1560	1570	1580	1590	1600
AVHSQDITIP	QCPLGWRSLW	IGYSFLMHTA	AGAEGGGQSL	VSPGSCLEDF	RATPFIECSG	ARGTCHYFAN	KYSFWLTTVE
1610	1620	1630	1640				
ERQQFGELPV	SETLKAGQLH	TRVSRCQVCM	KSL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2734	2	710.3788	14.25	2	63.1	11.1	1	157-170	K.GDPVLAPGSFKGMK.G	Oxidation: 13
2485	1	821.9375	56.09	2	61.6	11.5	0	1446-1460	K.AHNQDLGFAGSCLPR.F	Carbamidomethyl: 12

Detailed Protein Report

Protein 191: semaphorin-3A precursor [Homo sapiens]

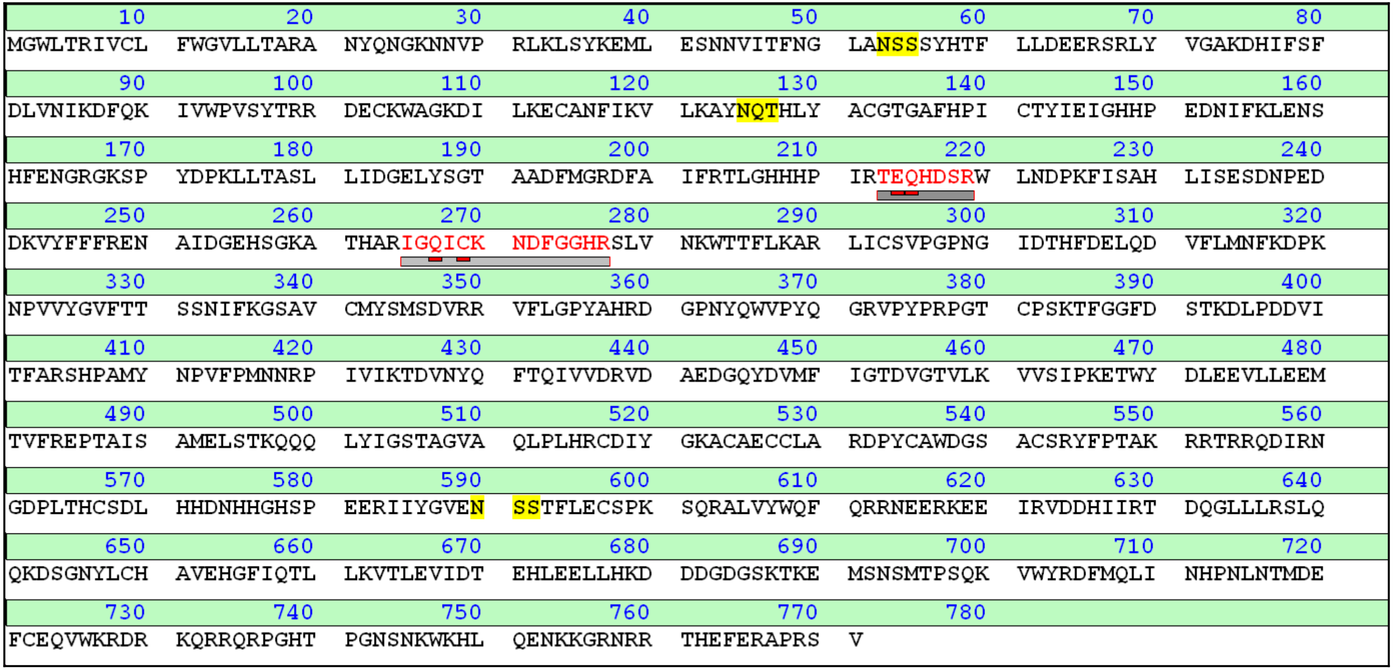
Accession:	gi|5174673	**Score:**	33.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	88.8
Database Date:	2015-11-30	**pI:**	7.2
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.59 **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]



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        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		QD:QU 0.59
2058	1	722.8469	-17.26	2	56.1	14.8	1	265-277	R.IGQICKNDFGGHR.S		

Detailed Protein Report

Protein 192: **tenascin-N precursor [Homo sapiens]**

Accession:	gi|62988324	**Score:**	33.4
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:	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
2573	1	590.4386	252.94	1	62.8	11.4	0	516-521	R.GNQGSK.K	

Detailed Protein Report

Protein 193: 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

QD:QU **Median:** 1.11 **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		QD:QU 1.11
1835	3	599.2683	-138.16	2	53.3	22.4	0	160-171	K.DAGVIAGLNVLR.I		

Detailed Protein Report

Protein 194: **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 195: PREDICTED: thyroglobulin isoform X9 [Homo sapiens]

Accession:	gi|530389281	**Score:**	33.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	232.1
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	2

Quantitation

QD:QU	**Median:** 0.78	**CV:** 0.00 %	**No. of Peptides:** 1

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
1580	1	502.6699	-218.64	2	50.0	19.9	0	467-475	R.LQQNLFGGK.F		
1861	1	719.7564	-125.05	2	51.8	13.2	2	1537-1550	R.GSGKAFCVDGEGRR.L		QD:QU 0.78

Detailed Protein Report

Protein 196: PREDICTED: rho GTPase-activating protein 36 isoform X1 [Homo sapiens]

Accession:	gi|578838609	**Score:**	33.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.2
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MQVEEATGQA	AGRRRGNVVR	RVFGRIRRFF	SRRRNEPTLP	REFTRRGRRG	AVSVDSLAEL	EDGALLLQTL	QLSKISFPIG
90	100	110	120	130	140	150	160
QRLLGSKRKM	SLNPIAKQIP	QVVEACCQFI	EKHGLSAVGI	FTLEYSVQRV	RQLREEFDQG	LDVVLDDNQN	VHDVAALLKE
170	180	190	200	210	220	230	240
FFRDMKDSLL	PDDLYMSFLL	TATLKPQDQL	SALQLLVYLM	PPCHSDTLER	LLKALHKITE	NCEDSIGIDG	QLVPGNRMTS
250	260	270	280	290	300	310	320
TNLALVFGSA	LLKKGKFGKR	ESRKTKLGID	HYVASVNVVR	AMIDNWDVLF	QVPPHIQRQV	AKRVWKSSPE	ALDFIRRRNL
330	340	350	360	370	380	390	400
RKIQSARIKM	EEDALLSDPV	ETSAEARAAV	LAQSKPSDEG	SSEEPAVPSG	TARSHDDEEG	AGNPPIPEQD	RPLLRVPREK
410	420						
EAKTGVSYFF	P						

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	75-82	K.ISFPIGQR.L	
2474	1	822.4025	-186.55	1	61.5	16.1	1	211-217	R.LLKALHK.I	

Detailed Protein Report

Protein 197: **zinc finger protein 90 [Homo sapiens]**

Accession:	gi|209862791	**Score:**	33.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.0
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.3
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 1.73 **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	
1760	1	568.7537	-99.49	2	52.3	21.4	1	592-601	K.AYIVKNMANL.-		QD:QU 1.73

Detailed Protein Report

Protein 198: 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 199: crooked neck-like protein 1 isoform c [Homo sapiens]

Accession:	gi|520975425	**Score:**	32.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.6
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.3
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|520975430	refseq_human(refseq_human_20140103.fasta)	crooked neck-like protein 1 isoform c [Homo sapiens]

10	20	30	40	50	60	70	80
MEMKNRQVNH	ARNIWDRAIT	TLPRVNQFWY	KYTYMEEMLG	NVAGARQVFE	RWMEWQPEEQ	AWHSYINFEL	RYKEVDRART
90	100	110	120	130	140	150	160
IYERFVLVHP	DVKNWIKYAR	FEEKHAYFAH	ARKVYERAVE	FFGDEHMDEH	LYVAFAKFEE	NQKEFERVRV	IYKYALDRIS
170	180	190	200	210	220	230	240
KQDAQELFKN	YTIFEKKFGD	RRGIEDIIVS	KRRFQYEEEV	KANPHNYDAW	FDYLRLVESD	AEAEAVREVY	ERAIANVPPI
250	260	270	280	290	300	310	320
QEKRHWKRYI	YLWINYALYE	ELEAKDPERT	RQVYQASLEL	IPHKKFTFAK	MWILYAQFEI	RQKNLSLARR	ALGTSIGKCP
330	340	350	360	370	380	390	400
KNKLFKVYIE	LELQLREFDR	CRKLYEKFLE	FGPENCTSWI	KFAELETILG	DIDRARAIYE	LAISQPRLDM	PEVLWKSYID
410	420	430	440	450	460	470	480
FEIEQEETER	TRNLYRRLLQ	RTQHVKVWIS	FAQFELSSGK	EGSLTKCRQI	YEEANKTMRN	CEEKEERLML	LESWRSFEEE
490	500	510	520	530	540	550	560
FGTASDKERV	DKLMPEKVKK	RRKVQTDDGS	DAGWEEYFDY	IFPEDAANQP	NLKLLAMAKL	WKKQQQEKED	AEHHPDEDVD
570							
ESES							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2727	1	698.3840	-35.80	2	63.0	10.6	2	148-158	R.VRVIYKYALDR.I	
1986	1	687.3345	-69.29	2	55.2	22.3	2	311-323	R.ALGTSIGKCPKNK.L	Carbamidomethyl: 9

Detailed Protein Report

Protein 200: PREDICTED: diacylglycerol kinase delta isoform X3 [Homo sapiens]

Accession: gi|530371455
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 32.8
MW [kDa]: 104.0
pI: 9.2
Sequence Coverage [%]: 2.9
No. of unique Peptides: 2

Quantitation

QD:QU **Median:** 0.45 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAAAAGAPPP	GPPQPPPPPP	PEESSDSEPE	AEPGSPQKLI	RKVSTSGQIR	QKTIIKEGML	TKQNNSFQRS	KRRYFKLRGR
90	100	110	120	130	140	150	160
TLYYAKTAKS	IIFDEVDLTD	ASVAESSTKN	VNNSFTVITP	CRKLILCADN	RKEMEDWIAA	LKTVQNREHF	EPTQYSMDHF
170	180	190	200	210	220	230	240
SGMHNWYACS	HARPTYCNVC	REALSGVTSH	GLSCEVCKFK	AHKRCAVRAT	NNCKWTTLAS	IGKDIIEDAD	GIAMPHQWLE
250	260	270	280	290	300	310	320
GNLPVSAKCT	VCDKTCGSVL	RLQDWRCLWC	KAMVHTSCKE	SLLTKCPLGL	CKVSVIPPTA	LNSIDSDGFW	KASCPPSCTS
330	340	350	360	370	380	390	400
PLLVFVNSKS	GDNQGVKFLR	RFKQLLNPAQ	VFDLMNGGPH	LGLRLFQKFD	TFRILVCGGD	GSVGWVLSEI	DSLNLHKQCQ
410	420	430	440	450	460	470	480
LGVLPLGTGN	DLARVLGWGS	ACDDDTQLPQ	ILEKLERAST	KMLDRWSVMA	YEAKLPRQAS	SSTVTEDFSE	DSEVQQILFY
490	500	510	520	530	540	550	560
EDSVAAHLSK	ILTSDQHSVV	ISSAKVLCET	VKDFVARVGK	AYEKTTESSE	ESEVMAKKCS	VLKEKLDSLL	KTLDDESQAS
570	580	590	600	610	620	630	640
SSLPNPPPTI	AEEAEDGDGS	GSICGSTGDR	LVASACPARP	QIFRPREQLM	LRANSLKKAI	RQIIEHTEKA	VDEQNAQTQE
650	660	670	680	690	700	710	720
QEGFVLGLSE	SEEKMDHRVC	PPLSHSESFG	VPKGRSQRKV	SKSPCEKLIS	KGSLSLGSSA	SLPPQPGSRD	GLPALNTKIL
730	740	750	760	770	780	790	800
YPNVRAGMSG	SLPGGSVISR	LLINADPFNS	EPETLEYYTE	KCVMNNYFGI	GLDAKISLDF	NNKRDEHPEK	CRSRTKNMMW
810	820	830	840	850	860	870	880
YGVLGTKELL	HRTYKNLEQK	VLLECDGRPI	PLPSLQGIAV	LNIPSYAGGT	NFWGGTKEDD	TFAAPSFDDK	ILEVVAVFGS
890	900	910	920	930	940	950	
MQMAVSRVIR	LQHHRIAQCR	TVKISILGDE	GVPVQVDGEA	WVQPPGYIRI	VHKNRAQTLT	RDRL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1745	1	917.3940	-36.10	2	50.3	17.0	0	182-198	R.EALSGVTSHGLSCEVCK.F	Carbamidomethyl: 13, 16	
22	1	657.3901	130.41	2	28.9	15.8	2	785-794	R.DEHPEKCRSR.T	Carbamidomethyl: 7	QD:QU 0.45

Detailed Protein Report

Protein 201: cystatin-B [Homo sapiens]

Accession: gi|4503117
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 32.7
MW [kDa]: 11.1
pI: 7.9
Sequence Coverage [%]: 12.2
No. of unique Peptides: 1

Quantitation

QD:QU **Median:** 1.47 **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	
953	2	663.8439	-18.59	2	40.4	32.7	0	45-56	K.SQVVAGTNYFIK.V		QD:QU	1.47

Detailed Protein Report

Protein 202: coiled-coil domain-containing protein 88B precursor [Homo sapiens]

Accession:	gi|262118216	**Score:**	32.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	164.7
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	1.9
		No. of unique 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	KKGSWLADKV	KRLMRPRREG	GPPGGLRLGA	DGAGSTESLG	GPPETELPEG
1370	1380	1390	1400	1410	1420	1430	1440
READGTGSPS	PAPMRRAQSS	LCLRDETLAG	GQRRKLSSRF	PVGRSSESFS	PGDTPRQRFR	QRHPGPLGAP	VSHSKGPGVG
1450	1460	1470	1480				
WENSAETLQE	HETDANREGP	EVQEPEKRPL	TPSLSQ				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
245	1	715.7361	-205.90	2	33.1	13.1	1	755-767	K.LEAQNTEAARLSK.E	

Detailed Protein Report

Protein 203: laminin subunit alpha-2 isoform b precursor [Homo sapiens]

Accession:	gi|119466532	**Score:**	32.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	343.3
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:** 1.08	**CV:** 0.00 %	**No. of Peptides:** 1

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
2430	1	531.0471	-454.49	1	60.8	17.8	0	2291-2295	K.ADAVR.V		QD:QU	1.08

Detailed Protein Report

Protein 204: **protein FAM194B [Homo sapiens]**

Accession:	gi|210147567	**Score:**	32.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.6
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	4.3
		No. of unique Peptides:	2

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	
2977	23	710.3760	-33.01	2	66.5	22.0	1	625-636	K.FVIPEVLSEMKK.K	

Detailed Protein Report

Protein 205: probable ATP-dependent RNA helicase DDX10 [Homo sapiens]

Accession:	gi|13514831	**Score:**	32.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.8
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	4.3
		No. of unique Peptides:	1

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
2761	1	713.3401	-111.86	2	65.7	11.2	2	638-649	K.VKRHNVFGLDLK.D	

Detailed Protein Report

Protein 206: **protein MON2 homolog isoform 5 [Homo sapiens]**

Accession:	gi|510937041	**Score:**	32.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	182.4
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGCGTKEPKI	TQLCLAAIQR	LMSHEVVSET	AAGNIINMLW	QLMENSLEEL	KLLQTVLVLL	TTNTVVHDEA	LSKAIVLCFR
90	100	110	120	130	140	150	160
LHFTKDNITN	NTAAATVRQV	VTVVFERMVA	EDERHRDIIE	QPVLVQGNSN	RRSVSTLKPC	AKDAYMLFQD	LCQLVNADAP
170	180	190	200	210	220	230	240
YWLVGMTEMT	RTFGLELLES	VLNDFPQVFL	QHQEFSFLLK	ERVCPLVIKL	FSPNIKFRQG	SSTSSSPAPV	EKPYFPICMR
250	260	270	280	290	300	310	320
LLRVVSVLIK	QFYSLLVTEC	EIFLSLLVKF	LDADKPQWLR	AVAVESIHRF	CVQPQLLRSF	CQSYDMKQHS	TKVFRDIVNA
330	340	350	360	370	380	390	400
LGSFIQSLFL	VPPTGNPATS	NQAGNNNLGG	SVSAPANSGM	VGIGGGVTLL	PAFEYRGTWI	PILTITVQGS	AKATYLEMLD
410	420	430	440	450	460	470	480
KVEPPTIPEG	YAMSVAFHCL	LDLVRGITSM	IEGELGELET	ECQTTTEEGS	SPTQSTEQQD	LQSTSDQMDK	EIVSRAVWEE
490	500	510	520	530	540	550	560
MVNACWCGLL	AALSLLLDAS	TDEAATENIL	KAELTMAALC	GRLGLVTSRD	AFITAICKGS	LPPHYALTVL	NTTTAATLSN
570	580	590	600	610	620	630	640
KSYSVQGQSV	MMISPSSESH	QQVVAVGQPL	AVQPQGTVML	TSKNIQCMRT	LLNLAHCHGA	VLGTSWQLVL	ATLQHLVWIL
650	660	670	680	690	700	710	720
GLKPSSGGAL	KPGRAVEGPS	TVLTTAVMTD	LPVISNILSR	LFESSQYLDD	VSLHHLINAL	CSLSLEAMDM	AYGNNKEPSL
730	740	750	760	770	780	790	800
FAVAKLLETG	LVNMHRIEIL	WRPLTGHLLE	VCQHPNSRMR	EWGAEALTSL	IKAGLTFNHD	PPLSQNQRLQ	LLLLNPLKEM
810	820	830	840	850	860	870	880
SNINHPDIRL	KQLECVLQIL	QSQGDSLGPG	WPLVLGVMGA	IRNDQGESLI	RTAFQCLQLV	VTDFLPTMPC	TCLQIVVDVA
890	900	910	920	930	940	950	960
GSFGLHNQEL	NISLTSIGLL	WNISDYFFQR	GETIEKELNK	EEAAQQKQAE	EKGVVLNRPF	HPAPPFDCLW	LCLYAKLGEL
970	980	990	1000	1010	1020	1030	1040
CVDPRPAVRK	SAGQTLFSTI	GAHGTLLQHS	TWHTVIWKVL	FHLLDRVRES	STTADKEKIE	SGGGNILIHH	SRDTAEKQWA
1050	1060	1070	1080	1090	1100	1110	1120
ETWVLTLAGV	ARIFNTRRYL	LQPLGDFSRA	WDVLLDHIQS	AALSKNNEVS	LAALKSFQEI	LQIVSPVRDS	DKPETPPVVN
1130	1140	1150	1160	1170	1180	1190	1200
VPVPVLIGPI	SGMSRPFVRT	DSIGEKLGRY	SSSEPPIVTD	ELEDLNLWWA	AWNTWYRIGS	ESTKPPITFD	KLTFIPSQPF
1210	1220	1230	1240	1250	1260	1270	1280
LTALIQIFPA	LYQHIKTGFN	MDDLQKLGVI	LHSAISVPIS	SDASPFILPS	YTEAVLTSLQ	EAVLTALDVL	QKAICVGPEN
1290	1300	1310	1320	1330	1340	1350	1360
MQIMYPAIFD	QLLAFVEFSC	KPPQYGQLET	KHIANAKYNQ	IQLFAPAEWV	ALNYVPFAER	SLEVVVDLYQ	KTACHKAVVN
1370	1380	1390	1400	1410	1420	1430	1440
EKVLQNIIKT	LRVPLSLKYS	CPSESTWKLA	VSSLLRVLSI	GLPVARQHAS	SGKFDSMWPE	LANTFEDFLF	TKSIPPDNLS
1450	1460	1470	1480	1490	1500	1510	1520
IQEFQRNENI	DVEVVQLISN	EILPYANFIP	KEFVGQIMTM	LNKGSIHSQS	SSFTEAEIDI	RLREEFSKMC	FETLLQFSFS
1530	1540	1550	1560	1570	1580	1590	1600
NKVTTPQEGY	ISRMALSVLL	KRSQDVLHRY	IEDERLSGKC	PLPRQQVTEI	IFVLKAVSTL	IDSLKKTQPE	NVDGNTWAQV
1610	1620	1630	1640	1650			
IALYPTLVEC	ITCSSSEVCS	ALKEALVPFK	DFMQPPASRV	QNGES			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2422	1	1044.2014	136.78	2	60.8	16.5	2	2-20	M.GCGTKEPKITQLCLAAIQR.L	Carbamidomethyl: 13

Detailed Protein Report

Protein 207: PREDICTED: alpha-actinin-4 isoform X1 [Homo sapiens]

Accession:	gi|530417302	**Score:**	32.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	104.3
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	2

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
875	1	648.3760	9.03	2	41.0	11.8	2	337-346	R.DYRRVHKPPK.V	
2706	1	693.8970	9.14	2	64.9	20.3	0	734-745	R.VGWEQLLTTIAR.T	

Detailed Protein Report

Protein 208: 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

Protein 209: **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 210: 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 211: oligodendrocyte transcription factor 3 [Homo sapiens]

Accession:	gi|28411948	**Score:**	31.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.3
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	11.4
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.84 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MNSDSSSVSS RASSPDMDEM YLRDHHHRHH HHQESRLNSV SSTQGDMMQK MPGESLSRAG AKAAGESSKY KIKKQLSEQD
        90        100        110        120        130        140        150        160
LQQLRLKING RERKRMHDLN LAMDGLREVM PYAHGPSVRK LSKIATLLLA RNYILMLTSS LEEMKRLVGE IYGGHHSAFH
       170        180        190        200        210        220        230        240
CGTVGHSAGH PAHAANSVHP VHPILGGALS SGNASSPLSA ASLPAIGTIR PPHSLLKAPS TPPALQLGSG FQHWAGLPCP
       250        260        270        280
CTICQMPPPP HLSALSTANM ARLSAESKDL LK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1287	1	611.9489	-43.61	3	46.2	14.1	2	51-69	K.MPGESLSRAGAKAAGESSK.Y		
399	1	701.3413	9.92	2	35.0	17.8	0	96-107	R.MHDLNLAMDGLR.E	Oxidation: 1	QD:QU 0.84

Detailed Protein Report

Protein 212: PREDICTED: myotubularin-related protein 10 isoform X2 [Homo sapiens]

Accession:	gi|530406109	**Score:**	31.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.0
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	6.6
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|578840990	refseq_human(refseq_human_20140103.fasta)	PREDICTED: myotubularin-related protein 10 isoform X2 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MFSLKPPKPT FRSYLLPPPQ TDDKINSEPK IKKLEPVLLP GEIVVNEVNF VRKCIATDTS QYDLWGKLIC SNFKISFITD
        90        100        110        120        130        140        150        160
DPMPLQKFHY RNLLLGEHDV PLTCIEQIVT VNDHKRKQKV LGPNQKLKFN PTELIIYCKD FRIVRFRFDE SGPESAKKVC
       170        180        190        200        210        220        230        240
LAIAHYSQPT DLQLLFAFEY VGKKYHNSAN KINGIPSGDG GGGGGGGNGA GGGSSQKTPL FETYSDWDRE IKRTGASGWR
       250        260        270        280        290        300        310        320
VCSINEGYMI STCLPEYIVV PSSLADQDLK IFSHSFVGRR MPLWCWSHSN GSALVRMALI KDVLQQRKID QRICNAITKS
       330        340        350        360        370        380        390        400
HPQRSDVYKS DLDKTLPNIQ EVQAAFVKLK QLCVNEPFEE TEEKWLSSLE NTRWLEYVRA FLKHSAELVY MLESKHLSVV
       410        420        430        440        450        460        470        480
LQEEEGRDLS CCVASLVQVM LDPYFRTITG FQSLIQKEWV MAGYQFLDRC NHLKRSEKES PLFLLFLDAT WQLLEQYPAA
       490        500        510        520        530        540        550        560
FEFSETYLAV LYDSTRISLF GTFLFNSPHQ RVKQSTKIWR VLKGTEQRIR HFPSSSDFVS GVISSSELLC IHCCGSLLPS
       570
IS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2250	1	752.7461	-190.38	2	56.8	15.6	0	75-87	K.ISFITDDPMPLQK.F	
1260	1	903.4372	-43.14	3	45.9	16.3	2	325-348	R.SDVYKSDLDKTLPNIQEVQAAFVK.L	

BRUKER

Detailed Protein Report

Protein 213: PREDICTED: Bloom syndrome protein isoform X1 [Homo sapiens]

Accession: gi|578827270
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 31.5
MW [kDa]: 85.6
pI: 10.0
Sequence Coverage [%]: 5.2
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MMKIFHKKFG	LHNFRTNQLE	AINAALLGED	CFILMPTGGG	KSLCYQLPAC	VSPGVTVVIS	PLRSLIVDQV	QKLTSLDIPA
90	100	110	120	130	140	150	160
TYLTGDKTDS	EATNIYLQLS	KKDPIIKLLY	VTPEKICASN	RLISTLENLY	ERKLLARFVI	DEAHCVSQWG	HDFRQDYKRM
170	180	190	200	210	220	230	240
NMLRQKFPSV	PVMALTATAN	PRVQKDILTQ	LKILRPQVFS	MSFNRHNLKY	YVLPKKPKKV	AFDCLEWIRK	HHPYDSGIIY
250	260	270	280	290	300	310	320
CLSRRECDTM	ADTLQRDGLA	ALAYHAGLSD	SARDEVQQKW	INQDGCQVIC	ATIAFGMGID	KPDVRFVIHA	SLPKSVEGYY
330	340	350	360	370	380	390	400
QESGRAGRDG	EISHCLLFYT	YHDVTRLKRL	IMMEKDGNHH	TRETHFNNLY	SMVHYCENIT	ECRRIQLLAY	FGENGFNPDF
410	420	430	440	450	460	470	480
CKKHPDVSCD	NCCKTKDYKT	RDVTDDVKSI	VRFVQEHSSS	QGMRNIKHVG	PSGRFTMNML	VDIFLGSKSA	KIQSGIFGKG
490	500	510	520	530	540	550	560
SAYSRHNAER	LFKKLILDKI	LDEDLYINAN	DQAIAYVMLG	NKAQTVLNGN	LKVDFMETEN	SSSVKKQKAL	VAKVSQREEM
570	580	590	600	610	620	630	640
VKKCLGELTE	VCKSLGKVFG	VHYFNIFNTV	TLKKLAESLS	SDPEVLLQID	GVTEDKLEKY	GAEVISVLQK	YSEWTSPAED
650	660	670	680	690	700	710	720
SSPGISLSSS	RGPGRSAAEE	LDEEIPVSSH	YFASKTRNER	KRKKMPASQR	SKRRKTASSG	SKAKGGSATC	RKISSKTKSS
730	740	750	760	770			
SIIGSSSASH	TSQATSGANS	KLGIMAPPKP	INRPFLKPSY	AFS			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2797	1	937.4532	-7.25	2	64.1	14.4	1	231-245	K.HHPYDSGIIYCLSRR.E	Carbamidomethyl: 11
1181	1	955.7839	-9.69	3	44.9	17.1	2	656-680	R.SAAEELDEEIPVSSHYFASKTRNER.K	

Detailed Protein Report

Protein 214: eukaryotic initiation factor 4A-III [Homo sapiens]

Accession:	gi|7661920	**Score:**	31.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.8
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MATTATMATS GSARKRLLKE EDMTKVEFET SEEVDVTPTF DTMGLREDLL RGIYAYGFEK PSAIQQRAIK QIIKGRDVIA
        90        100        110        120        130        140        150        160
QSQSGTGKTA TFSISVLQCL DIQVRETQAL ILAPTRELAV QIQKGLLALG DYMNVQCHAC IGGTNVGEDI RKLDYGQHVV
       170        180        190        200        210        220        230        240
AGTPGRVFDM IRRRSLRTRA IKMLVLDEAD EMLNKGFKEQ IYDVYRYLPP ATQVVLISAT LPHEILEMTN KFMTDPIRIL
       250        260        270        280        290        300        310        320
VKRDELTLEG IKQFFVAVER EEWKFDTLCD LYDTLTITQA VIFCNTKRKV DWLTEKMREA NFTVSSMHGD MPQKERESIM
       330        340        350        360        370        380        390        400
KEFRSGASRV LISTDVWARG LDVPQVSLII NYDLPNNREL YIHRIGRSGR YGRKGVAINF VKNDDIRILR DIEQYYSTQI
       410        420
DEMPMNVADL I
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1883	2	621.2961	4.72	2	53.9	17.2	0	2-14	M.ATTATMATSGSAR.K	Oxidation: 6

Detailed Protein Report

Protein 215: PREDICTED: uncharacterized protein LOC100996842 isoform X2 [Homo sapiens]

Accession:	gi|530438094	**Score:**	31.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.7
Database Date:	2015-11-30	**pI:**	12.0
		Sequence Coverage [%]:	7.0
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 4.73 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	**Name**	**Description**
gi|578830177	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein LOC102724164 isoform X2 [Homo sapiens]
gi|578797315	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein LOC102724164 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MSAPATAGPG	TVKQRRRWGR	RAQVGEGQHL	NHPWGPDPQE	SPGSRGLARQ	SRDSPPPRWP	EGAPRAGQRL	RRGRVDPAAL
90	100	110	120	130	140	150	160
LGKGHLGLPG	GGVVLRYRPP	GRQPTVPTRA	SFRCGSALWR	PPSKVYKVTR	MSAGRGGIGA	CQVLRGFNRA	LLLALNMVDR
170	180	190	200	210	220	230	240
TGHSHCSGAT	GAAFGNEVPQ	PPTHCFGCLL	HLKLYEGQEE	GCGDEWLYRL	ATDGELEQPV	APRGGRKGGT	ADPTPAVPGF
250							
GG							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1852	1	612.7877	-44.99	2	53.5	10.4	1	59-69	R.WPEGAPRAGQR.L		QD:QU 4.73

Detailed Protein Report

Protein 216: **PREDICTED: estrogen receptor isoform X1 [Homo sapiens]**

Accession:	gi|578812488	**Score:**	31.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.7
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTMTLHTKAS	GMALLHQIQG	NELEPLNRPQ	LKIPLERPLG	EVYLDSSKPA	VYNYPEGAAY	EFNAAAAANA	QVYGQTGLPY
90	100	110	120	130	140	150	160
GPGSEAAAFG	SNGLGGFPPL	NSVSPSPLML	LHPPPQLSPF	LQPHGQQVPY	YLENEPSGYT	VREAGPPAFY	RPNSDNRRQG
170	180	190	200	210	220	230	240
GRERLASTND	KGSMAMESAK	ETRYCAVCND	YASGYHYGVW	SCEGCKAFFK	RSIQGHNDYM	CPATNQCTID	KNRRKSCQAC
250	260	270	280	290	300	310	320
RLRKCYEVGM	MKGGIRKDRR	GGRMLKHKRQ	RDDGEGRGEV	GSAGDMRAAN	LWPSPLMIKR	SKKNSLALSL	TADQMVSALL
330	340	350	360	370	380	390	400
DAEPPILYSE	YDPTRPFSEA	SMMGLLTNLA	DRELVHMINW	AKRVPGFVDL	TLHDQVHLLE	CAWLEILMIG	LVWRSMEHPG
410	420	430	440	450	460	470	
KLLFAPNLLL	DRNQGKCVEG	MVEIFDMLLA	TSSRFRMMNL	QGEEFVCLKS	IILLNSVTKA	WSICTA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2049	1	812.3468	12.24	2	56.0	10.2	1	272-287	R.DDGEGRGEVGSAGDMR.A	Oxidation: 15

Detailed Protein Report

Protein 217: **caspase-10 isoform 6 preproprotein [Homo sapiens]**

Accession: gi|330864823

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 30.9

MW [kDa]: 51.8

pI: 5.4

Sequence Coverage [%]: 7.0

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MKSQGQHWYS	SSDKNCKVSF	REKLLIIDSN	LGVQDVENLK	FLCIGLVPNK	KLEKSSSASD	VFEHLLAEDL	LSEEDPFFLA
90	100	110	120	130	140	150	160
ELLYIIRQKK	LLQHLNCTKE	EVERLLPTRQ	RVSLFRNLLY	ELSEGIDSEN	LKDMIFLLKD	SLPKTEMTSL	SFLAFLEKQG
170	180	190	200	210	220	230	240
KIDEDNLTCL	EDLCKTVVPK	LLRNIEKYKR	EKAIQIVTPP	VDKEAESYQG	EEELVSQTDV	KTFLEALPQE	SWQNKHAGSN
250	260	270	280	290	300	310	320
EILSHVFQWL	GFTVHIHNNV	TKVEMEMVLQ	KQKCNPAHAD	GDCFVFCILT	HGRFGAVYSS	DEALIPIREI	MSHFTALQCP
330	340	350	360	370	380	390	400
RLAEKPKLFF	IQACQGEEIQ	PSVSIEADAL	NPEQAPTSLQ	DSIPAEADFL	LGLATVPGYV	SFRHVEEGSW	YIQSLCNHLK
410	420	430	440	450	460		
KLVPRHEDIL	SILTAVNDDV	SRRVDKQGTK	KQMPQPAFTL	RKKLVFPVPL	DALSL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2646	1	1145.5422	35.87	2	61.8	11.6	0	274-293	K.CNPAHADGDCFVFCILTHGR.F	Carbamidomethyl: 10, 14

Detailed Protein Report

Protein 218: LIM/homeobox protein Lhx1 [Homo sapiens]

Accession:	gi|30410785	**Score:**	30.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.8
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVHCAGCKRP	ILDRFLLNVL	DRAWHVKCVQ	CCECKCNLTE	KCFSREGKLY	CKNDFFRCFG	TKCAGCAQGI	SPSDLVRRAR
90	100	110	120	130	140	150	160
SKVFHLNCFT	CMMCNKQLST	GEELYIIDEN	KFVCKEDYLS	NSSVAKENSL	HSATTGSDPS	LSPDSQDPSQ	DDAKDSESAN
170	180	190	200	210	220	230	240
VSDKEAGSNE	NDDQNLGAKR	RGPRTTIKAK	QLETLKAAFA	ATPKPTRHIR	EQLAQETGLN	MRVIQVWFQN	RRSKERRMKQ
250	260	270	280	290	300	310	320
LSALGARRHA	FFRSPRRMRP	LVDRLEPGEL	IPNGPFSFYG	DYQSEYYGPG	GNYDFFPQGP	PSSQAQTPVD	LPFVPSSGPS
330	340	350	360	370	380	390	400
GTPLGGLEHP	LPGHHPSSEA	QRFTDILAHP	PGDSPSPEPS	LPGPLHSMSA	EVFGPSPPFS	SLSVNGGASY	GNHLSHPPEM
410							
NEAAVW							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2236	1	916.4377	77.30	2	56.6	12.2	1	28-41	K.CVQCCECKCNLTEK.C	Carbamidomethyl: 4, 5, 7, 9

Detailed Protein Report

Protein 219: pre-mRNA 3' end processing protein WDR33 isoform 1 [Homo sapiens]

Accession: gi|56243590

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 30.8

MW [kDa]: 145.8

pI: 9.9

Sequence Coverage [%]: 2.5

No. of unique 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
2698	1	937.4703	7.09	2	62.7	13.8	1	1-16	-.MATEIGSPPRFFHMPR.F	

Detailed Protein Report

Protein 220: PREDICTED: arginine/serine-rich protein PNISR isoform X3 [Homo sapiens]

Accession:	gi|530383562	**Score:**	30.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	99.0
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	4.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MVWLQMTNGC YYSLLPGETN RAPSCLVPEE VEASKALERC YRNGGDKGVP ELEWKIKYIL KEGMWDQGGQ PWQQWPLNQQ
        90        100        110        120        130        140        150        160
QWMQSFQHQQ DPSQIDWAAL AQAWIAQREA SGQQSMVEQP PGMMPNGQDM STMESGPNNH GNFQGDSNFN RMWQPEWGMH
       170        180        190        200        210        220        230        240
QQPPHPPPDQ PWMPPTPGPM DIVPPSEDSN SQDSGEFAPD NRHIFNQNNH NFGGPPDNFA VGPVNQFDYQ HGAAFGPPQG
       250        260        270        280        290        300        310        320
GFHPPYWQPG PPGPPAPPQN RRERPSSFRD RQRSPIALPV KQEPPQIDAV KRRTLPAWIR EGLEKMEREK QKKLEKERME
       330        340        350        360        370        380        390        400
QQRSQLSKKE KKATEDAEGG DGPRLPQRSK FDSDEEEEDT ENVEAASSGK VTRSPSPVPQ EEHSDPEMTE EEKEYQMMLL
       410        420        430        440        450        460        470        480
TKMLLTEILL DVTDEEIYYV AKDAHRKATK GGLGGYGSGD SEDERSDRGS ESSDTDDEEL RHRIRQKQEA FWRKEKEQQL
       490        500        510        520        530        540        550        560
LHDKQMEEEK QQTERVTKEM NEFIHKEQNS LSLLEAREAD GDVVNEKKRT PNETTSVLEP KKEHKEKEKQ GRSRSGSSSS
       570        580        590        600        610        620        630        640
GSSSSNSRTS STSSTVSSSS YSSSSGSSRT SSRSSSPKRK KRHSRSRSPT IKARRSRSRS YSRRIKIESN RARVKIRDRR
       650        660        670        680        690        700        710        720
RSNRNSIERE RRRNRSPSRE RRRSRSRSRD RRTNRASRSR SRDRRKIDDQ RGNLSGNSHK HKGEAKEQER KKERSRSIDK
       730        740        750        760        770        780        790        800
DRKKKDKERE REQDKRKEKQ KREEKDFKFS SQDDRLKRKR ESERTFSRSG SISVKIIRHD SRQDSKKSTT KDSKKHSGSD
       810        820        830        840        850        860
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	446-461	R.SDRGSESSDTDDEELR.H	

Detailed Protein Report

Protein 221: **PREDICTED: leucine-rich PPR motif-containing protein, mitochondrial isoform X2 [Homo sapiens]**

Accession:	gi|578802653	**Score:**	30.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.1
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
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
1368	1	428.2118	-70.40	3	47.2	12.4	1	673-683	K.AENQPIRDVLK.Q	

Detailed Protein Report

Protein 222: PREDICTED: protein prune homolog 2 isoform X10 [Homo sapiens]

Accession:	gi|530390628	**Score:**	30.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	337.3
Database Date:	2015-11-30	**pI:**	4.2
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:** 0.95	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEEFLQRAKS	KLNRSKRLEK	VHVVIGPKSC	DLDSLISTFT	YAYFLDKVSP	PGVLCLPVLN	IPRTEFNYFT	ETRFILEELN
90	100	110	120	130	140	150	160
ISESFHIFRD	EINLHQLNDE	GKLSITLVGS	SVLASEDKTL	ESAVVKVINP	VEQSDANVEF	RESSSSLVLK	EILQEAPELI
170	180	190	200	210	220	230	240
TEQLAHRLRG	SILFKWMTME	SEKISEKQEE	ILSILEEKFP	NLPPREDIIN	VLQETQFSAQ	GLSIEQTMLK	DLKELSDGEI
250	260	270	280	290	300	310	320
KVAISTVSMN	LENCLFHSNI	TSDLKAFTDK	FGFDVLILFS	SYLSEEQQPR	RQIAVYSENM	ELCSQICCEL	EECQNPCLEL
330	340	350	360	370	380	390	400
EPFDCGCDEI	LVYQQEDPSV	TCDQVVLVVK	EVINRRCPEM	VSNSRTSSTE	AVAGSAPLSQ	GSSGIMELYG	SDIEPQPSSV
410	420	430	440	450	460	470	480
NFIENPPDLN	DSNQAQVDAN	VDLVSPDSGL	ATIRSSRSSK	ESSVFLSDDS	PVGEGAGPHH	TLLPGLDSYS	PIPEGAVAEE
490	500	510	520	530	540	550	560
HAWSGEHGEH	FDLFNFDPAP	MASGQSQQSS	HSADYSPADD	FFPNSDLSEG	QLPAGPEGLD	GMGTNMSNYS	SSSLLSGAGK
570	580	590	600	610	620	630	640
DSLVEHDEEF	VQRQDSPRDN	SERNLSLTDF	VGDESPSPER	LKNTGKRIPP	TPMNSLVESS	PSTEEPASLY	TEDMTQKATD
650	660	670	680	690	700	710	720
TGHMGPPQTH	ARCSSWWGGL	EIDSKNIADA	WSSSEQESVF	QSPESWKEHK	PSSIDRRASD	SVFQPKSLEF	TKSGPWESEF
730	740	750	760	770	780	790	800
GQPELGSNDI	QDKNEESLPF	QNLPMEKSPL	PNTSPQGTNH	LIEDFASLWH	SGRSPTAMPE	PWGNPTDDGE	PAAVAPFPAW
810	820	830	840	850	860	870	880
SAFGKEDHDE	ALKNTWNLHP	TSSKTPSVRD	PNEWAMAKSG	FAFSSSELLD	NSPSEINNEA	APEIWGKKNN	DSRDHIFAPG
890	900	910	920	930	940	950	960
NPSSDLDHTW	TNSKPPKEDQ	NGLVDPKTRG	KVYEKVDSWN	LFEENMKKGG	SDVLVPWEDS	FLSYKCSDYS	ASNLGEDSVP
970	980	990	1000	1010	1020	1030	1040
SPLDTNYSTS	DSYTSPTFAG	DEKETEHKPF	AKEEGFESKD	GNSTAEETDI	PPQSLQQSSR	NRISSGPGNL	DMWASPHTDN
1050	1060	1070	1080	1090	1100	1110	1120
SSEINTTHNL	DENELKTEHT	DGKNISMEDD	VGESSQSSYD	DPSMMQLYNE	TNRQLTLLHS	STNSRQTAPD	SLDLWNRVIL
1130	1140	1150	1160	1170	1180	1190	1200
EDTQSTATIS	DMDNDLDWDD	CSGGAAIPSD	GQTEGYMAEG	SEPETRFTVR	QLEPWGLEYQ	EANQVDWELP	ASDEHTKDSA
1210	1220	1230	1240	1250	1260	1270	1280
PSEHHTLNEK	SGQLIANSIW	DSVMRDKDMS	SFMLPGSSHI	TDSEQRELPP	EIPSHSANVK	DTHSPDAPAA	SGTSESEALI
1290	1300	1310	1320	1330	1340	1350	1360
SHLDKQDTER	ETLQSDAASL	ATRLENPGYF	PHPDPWKGHG	DGQSESEKEA	QGATDRGHLD	EEEVIASGVE	NASGISEKGQ
1370	1380	1390	1400	1410	1420	1430	1440
SDQELSSLVA	SEHQEICIKS	GKISSLAVTF	SPQTEEPEEV	LEYEEGSYNL	DSRDVQTGMS	ADNLQPKDTH	EKHLMSQRNS
1450	1460	1470	1480	1490	1500	1510	1520
GETTETSDGM	NFTKYVSVPE	KDLEKTEECN	FLEPENVGGG	PPHRVPRSLD	FGDVPIDSDV	HVSSTCSEIT	KNLDVKGSEN
1530	1540	1550	1560	1570	1580	1590	1600
SLPGAGSSGN	FDRDTISSEY	THSSASSPEL	NDSSVALSSW	GQQPSSGYQE	ENQGNWSEQN	HQESELITTD	GQVEIVTKVK
1610	1620	1630	1640	1650	1660	1670	1680
DLEKNRINEF	EKSFDRKTPT	FLEIWNDSVD	GDSFSSLSSP	ETGKYSEHSG	THQESNLIAS	YQEKNEHDIS	ATVQPEDARV
1690	1700	1710	1720	1730	1740	1750	1760
ISTSSGSDDD	SVGGEESIEE	EIQVANCHVA	EDESRAWDSL	NESNKFLVTA	DPKSENIYDY	LDSSEPAENE	NKSNPFCDNQ
1770	1780	1790	1800	1810	1820	1830	1840
QSSPDPWTFS	PLTETEMQIT	AVEKEKRSSP	ETGTTGDVAW	QISPKASFPK	NEDNSQLEML	GFSADSTEWW	KASPQEGRLI
1850	1860	1870	1880	1890	1900	1910	1920
ESPFERELSD	SSGVLEINSS	VHQNASPWGV	PVQGDIEPVE	THYTNPFSDN	HQSPFLEGNG	KNSHEQLWNI	QPRQPDPDAD
1930	1940	1950	1960	1970	1980	1990	2000
KFSQLVKLDQ	IKEKDSREQT	FVSAAGDELT	PETPTQEQCQ	DTMLPVCDHP	DTAFTHAEEN	SCVTSNVSTN	EGQETNQWEQ
2010	2020	2030	2040	2050	2060	2070	2080
EKSYLGEMTN	SSIATENFPA	VSSPTQLIMK	PGSEWDGSTP	SEDSRGTFVP	DILHGNFQEG	GQLASAAPDL	WIDAKKPFSL
2090	2100	2110	2120	2130	2140	2150	2160
KADGENPDIL	THCEHDSNSQ	ASDSPDICHD	SEAKQETEKH	LSACMGPEVE	SSELCLTEPE	IDEEPIYEPG	REFVPSNAEL
2170	2180	2190	2200	2210	2220	2230	2240
DSENATVLPP	IGYQADIKGS	SQPASHKGSP	EPSEINGDNS	TGLQVSEKGA	SPDMAPILEP	VDRRIPRIEN	VATSIFVTHQ
2250	2260	2270	2280	2290	2300	2310	2320
EPTPEGDGSW	ISDSFSPESQ	PGARALFDGD	PHLSTENPAL	VPDALLASDT	CLDISEAAFD	HSFSDASGLN	TSTGTIDDMS
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	
797	1	534.6313	-269.15	2	40.0	10.3	0	688-696	K.EHKPSSIDR.R		QD:QU	0.95

Detailed Protein Report

Protein 223: PREDICTED: unconventional myosin-XVIIIb isoform X4 [Homo sapiens]

Accession:	gi|578837445	**Score:**	30.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	272.3
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Detailed Protein Report

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        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
2500	1	937.1908	150.69	2	60.0	17.9	1	1124-1139	R.VQLAGFHILEALRLHR.T	

Detailed Protein Report

Protein 224: hypoxia up-regulated protein 1 precursor [Homo sapiens]

Accession: gi|5453832
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 30.5
MW [kDa]: 111.3
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

Protein 225: splicing factor, proline- and glutamine-rich [Homo sapiens]

Accession:	gi|4826998	**Score:**	30.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.1
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:**	0.54	**CV:**	0.00 %		**No. of Peptides:**	1

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
284	1	671.3405	5.90	2	33.5	10.1	0	667-681	R.FGQGGAGPVGGQGPR.G		QD:QU 0.54

Detailed Protein Report

Protein 226: PREDICTED: synaptojanin-1 isoform X6 [Homo sapiens]

Accession:	gi|530419130	**Score:**	30.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	139.8
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	2

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	
PPQSSLPPPA	QRLQEPLVPV	AAPMPQSGPQ	PNLETPPQPP	PRSRSSHSLP	SEASSQPQQE	QPSG	

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

Detailed Protein Report

Protein 227: N-alpha-acetyltransferase 10 isoform 2 [Homo sapiens]

Accession:	gi|371121601	**Score:**	30.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.8
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	10.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNIRNARPED	LMNMQHCNLL	CLPENYQMKY	YFYHGLSWPQ	LSYIAEDENG	KIVGYVLAKM	EEDPDDVPHG	HITSLAVKRS
90	100	110	120	130	140	150	160
HRRLGLAQKL	MDQASRAMIE	NFNAKYVSLH	VRKRISEVEP	KYYADGEDAY	AMKRDLTQMA	DELRRHLELK	EKGRHVVLGA
170	180	190	200	210	220	230	
IENKVESKGN	SPPSSGEACR	EEKGLAAEDS	GGDSKDLSEV	SETTESTDVK	DSSEASDSAS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
223	1	636.6401	-38.73	3	32.8	18.5	1	97-112	R.AMIENFNAKYVSLHVR.K	Oxidation: 2

Detailed Protein Report

Protein 228: mitogen-activated protein kinase kinase kinase 5 [Homo sapiens]

Accession:	gi|5174547	**Score:**	30.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	154.4
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 1.82 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSTEADEGIT	FSVPPFAPSG	FCTIPEGGIC	RRGGAAAVGE	GEEHQLPPPP	PGSFWNVESA	AAPGIGCPAA	TSSSSATRGR
90	100	110	120	130	140	150	160
GSSVGGGSRR	TTVAYVINEA	SQGQLVVAES	EALQSLREAC	ETVGATLETL	HFGKLDFGET	TVLDRFYNAD	IAVVEMSDAF
170	180	190	200	210	220	230	240
RQPSLFYHLG	VRESFSMANN	IILYCDTNSD	SLQSLKEIIC	QKNTMCTGNY	TFVPYMITPH	NKVYCCDSSF	MKGLTELMQP
250	260	270	280	290	300	310	320
NFELLLGPIC	LPLVDRFIQL	LKVAQASSSQ	YFRESILNDI	RKARNLYTGK	ELAAELARIR	QRVDNIEVLT	ADIVINLLLS
330	340	350	360	370	380	390	400
YRDIQDYDSI	VKLVETLEKL	PTFDLASHHH	VKFHYAFALN	RRNLPGDRAK	ALDIMIPMVQ	SEGQVASDMY	CLVGRIYKDM
410	420	430	440	450	460	470	480
FLDSNFTDTE	SRDHGASWFK	KAFESEPTLQ	SGINYAVLLL	AAGHQFESSF	ELRKVGVKLS	SLLGKKGNLE	KLQSYWEVGF
490	500	510	520	530	540	550	560
FLGASVLAND	HMRVIQASEK	LFKLKTPAWY	LKSIVETILI	YKHFVKLTTE	QPVAKQELVD	FWMDFLVEAT	KTDVTVVRFP
570	580	590	600	610	620	630	640
VLILEPTKIY	QPSYLSINNE	VEEKTISIWH	VLPDDKKGIH	EWNFSASSVR	GVSISKFEER	CCFLYVLHNS	DDFQIYFCTE
650	660	670	680	690	700	710	720
LHCKKFFEMV	NTITEEKGRS	TEEGDCESDL	LEYDYEYDEN	GDRVVLGKGT	YGIVYAGRDL	SNQVRIAIKE	IPERDSRYSQ
730	740	750	760	770	780	790	800
PLHEEIALHK	HLKHKNIVQY	LGSFSENGFI	KIFMEQVPGG	SLSALLRSKW	GPLKDNEQTI	GFYTKQILEG	LKYLHDNQIV
810	820	830	840	850	860	870	880
HRDIKGDNVL	INTYSGVLKI	SDFGTSKRLA	GINPCTETFT	GTLQYMAPEI	IDKGPRGYGK	AADIWSLGCT	IIEMATGKPP
890	900	910	920	930	940	950	960
FYELGEPQAA	MFKVGMFKVH	PEIPESMSAE	AKAFILKCFE	PDPDKRACAN	DLLVDEFLKV	SSKKKKTQPK	LSALSAGSNE
970	980	990	1000	1010	1020	1030	1040
YLRSISLPVP	VLVEDTSSSS	EYGSVSPDTE	LKVDPFSFKT	RAKSCGERDV	KGIRTLFLGI	PDENFEDHSA	PPSPEEKDSG
1050	1060	1070	1080	1090	1100	1110	1120
FFMLRKDSER	RATLHRILTE	DQDKIVRNLM	ESLAQGAEEP	KLKWEHITTL	IASLREFVRS	TDRKIIATTL	SKLKLELDFD
1130	1140	1150	1160	1170	1180	1190	1200
SHGISQVQVV	LFGFQDAVNK	VLRNHNIKPH	WMFALDSIIR	KAVQTAITIL	VPELRPHFSL	ASESDTADQE	DLDVEDDHEE
1210	1220	1230	1240	1250	1260	1270	1280
QPSNQTVRRP	QAVIEDAVAT	SGVSTLSSTV	SHDSQSAHRS	LNVQLGRMKI	ETNRLLEELV	RKEKELQALL	HRAIEEKDQE
1290	1300	1310	1320	1330	1340	1350	1360
IKHLKLKSQP	IEIPELPVFH	LNSSGTNTED	SELTDWLRVN	GADEDTISRF	LAEDYTLLDV	LYYVTRDDLK	CLRLRGGMLC
1370	1380						
TLWKAIIDFR	NKQT						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2651	1	993.9806	1.15	2	64.1	16.5	0	536-551	K.QELVDFWMDFLVEATK.T	Oxidation: 8	
2925	1	1018.9798	-57.02	2	65.7	13.8	2	927-944	R.ACANDLLVDEFLKVSSKK.K	Carbamidomethyl: 2	QD:QU 1.82

Detailed Protein Report

Protein 229: DNA-directed RNA polymerase I subunit RPA49 isoform 2 [Homo sapiens]

Accession:	gi|544346178	**Score:**	30.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.8
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.3
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.52 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MMLNCSTCSH	YFQVFHQESK	IIFWKEPRTC	FLILSLPLPG	ELTWDVSVES	ELALESQTKT	YREKMDSCIE	AFGTTKQKRA
90	100	110	120	130	140	150	160
LNTRRMNRVG	NESLNRAVAK	AAETIIDTKG	VTALVSDAIH	NDLQDDSLYL	PPCYDDAAKP	EDVYKFEDLL	SPAEYEALQS
170	180	190	200	210	220	230	240
PSEAFRNVTS	EEILKMIEEN	SHCTFVIEAL	KSLPSDVESR	DRQARCIWFL	DTLIKFRAHR	VVKRKSALGP	GVPHIINTKL
250	260	270	280	290	300	310	320
LKHFTCLTYN	NGRLRNLISD	SMKAKITAYV	IILALHIHDF	QIDLTVLQRD	LKLSEKRMME	IAKAMRLKIS	KRRVSVAAGS
330	340	350					
EEDHKLGTLS	LPLPPAQTSD	RLAKRRKIT					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
182	1	688.3002	4.63	2	31.0	12.9	0	65-76	K.MDSCIEAFGTTK.Q	Carbamidomethyl: 4; Oxidation: 1	QD:QU	0.52

Detailed Protein Report

Protein 230: **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; Oxidation: 1

Detailed Protein Report

Protein 231: ataxin-2 [Homo sapiens]

Accession: gi|171543895
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 30.2
MW [kDa]: 140.2
pI: 10.2
Sequence Coverage [%]: 2.4
No. of unique Peptides: 2

10	20	30	40	50	60	70	80
MRSAAAAPRS	PAVATESRRF	AAARWPGWRS	LQRPARRSGR	GGGGAAPGPY	PSAAPPPPGP	GPPPSRQSSP	PSASDCFGSN
90	100	110	120	130	140	150	160
GNGGGAFRPG	SRRLLGLGGP	PRPFVVLLLP	LASPGAPPAA	PTRASPLGAR	ASPPRSGVSL	ARPAPGCPRP	ACEPVYGPLT
170	180	190	200	210	220	230	240
MSLKPQQQQQ	QQQQQQQQQQ	QQQQQQQQPP	PAAANVRKPG	GSGLLASPAA	APSPSSSSVS	SSSATAPSSV	VAATSGGGRP
250	260	270	280	290	300	310	320
GLGRGRNSNK	GLPQSTISFD	GIYANMRMVH	ILTSVVGSKC	EVQVKNGGIY	EGVFKTYSPK	CDLVLDAAHE	KSTESSSGPK
330	340	350	360	370	380	390	400
REEIMESILF	KCSDFVVVQF	KDMDSSYAKR	DAFTDSAISA	KVNGEHKEKD	LEPWDAGELT	ANEELEALEN	DVSNGWDPND
410	420	430	440	450	460	470	480
MFRYNEENYG	VVSTYDSSLS	SYTVPLERDN	SEEFLKREAR	ANQLAEEIES	SAQYKARVAL	ENDDRSEEEK	YTAVQRNSSE
490	500	510	520	530	540	550	560
REGHSINTRE	NKYIPPGQRN	REVISWGSGR	QNSPRMGQPG	SGSMPSRSTS	HTSDFNPNSG	SDQRVVNGGV	PWPSPCPSPS
570	580	590	600	610	620	630	640
SRPPSRYQSG	PNSLPPRAAT	PTRPPSRPPS	RPSRPPSHPS	AHGSPAPVST	MPKRMSSEGP	PRMSPKAQRH	PRNHRVSAGR
650	660	670	680	690	700	710	720
GSISSGLEFV	SHNPPSEAAT	PPVARTSPSG	GTWSSVVSGV	PRLSPKTHRP	RSPRQNSIGN	TPSGPVLASP	QAGIIPTEAV
730	740	750	760	770	780	790	800
AMPIPAASPT	PASPASNRAV	TPSSEAKDSR	LQDQRQNSPA	GNKENIKPNE	TSPSFSKAEN	KGISPVVSEH	RKQIDDLKKF
810	820	830	840	850	860	870	880
KNDFRLQPSS	TSESMDQLLN	KNREGEKSRD	LIKDKIEPSA	KDSFIENSSS	NCTSGSSKPN	SPSISPSILS	NTEHKRGPEV
890	900	910	920	930	940	950	960
TSQGVQTSSP	ACKQEKDDKE	EKKDAAEQVR	KSTLNPNAKE	FNPRSFSQPK	PSTTPTSPRP	QAQPSPSMVG	HQQPTPVYTQ
970	980	990	1000	1010	1020	1030	1040
PVCFAPNMMY	PVPVSPGVQP	LYPIPMTPMP	VNQAKTYRAV	PNMPQQRQDQ	HHQSAMMHPA	SAAGPPIAAT	PPAYSTQYVA
1050	1060	1070	1080	1090	1100	1110	1120
YSPQQFPNQP	LVQHVPHYQS	QHPHVYSPVI	QGNARMMAPP	THAQPGLVSS	SATQYGAHEQ	THAMYACPKL	PYNKETSPSF
1130	1140	1150	1160	1170	1180	1190	1200
YFAISTGSLA	QQYAHPNATL	HPHTPHPQPS	ATPTGQQQSQ	HGGSHPAPSP	VQHHQHQAAQ	ALHLASPQQQ	SAIYHAGLAP
1210	1220	1230	1240	1250	1260	1270	1280
TPPSMTPASN	TQSPQNSFPA	AQQTVFTIHP	SHVQPAYTNP	PHMAHVPQAH	VQSGMVPSHP	TAHAPMMLMT	TQPPGGPQAA
1290	1300	1310	1320				
LAQSALQPIP	VSTTAHFPYM	THPSVQAHHQ	QQL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
67	2	1018.8972	-98.75	2	29.5	14.3	1	438-455	R.EARANQLAEEIESSAQYK.A	
536	1	786.8751	-28.43	2	36.7	16.0	1	502-515	R.EVISWGSGRQNSPR.M	

Detailed Protein Report

Protein 232: 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

QD:QU **Median:** 1.15 **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	QD:QU 1.15

Detailed Protein Report

Protein 233: ATP-dependent DNA helicase Q1 [Homo sapiens]

Accession: gi|14591902
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 30.1
MW [kDa]: 73.4
pI: 9.0
Sequence Coverage [%]: 3.9
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
2931	1	753.8886	104.41	2	65.8	11.5	0	600-613	R.AESSQTCHSEQGDK.K	

Detailed Protein Report

Protein 234: structural maintenance of chromosomes protein 4 isoform 2 [Homo sapiens]

Accession:	gi|570700827	**Score:**	30.1
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
452	3	862.8266	-126.10	2	34.3	30.1	2	457-471	R.EKELMGFSKSVNEAR.S	

Detailed Protein Report

Protein 235: **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; Oxidation: 7
1552	3	993.4662	70.96	2	49.6	13.4	2	202-218	R.ACYHCGVMCRCCGGKHK.A	Carbamidomethyl: 2, 5; Oxidation: 8

Detailed Protein Report

Protein 236: 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

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
906	1	676.2230	-177.87	2	41.4	13.2	1	560-570	R.GVHFIFNKENF.-	

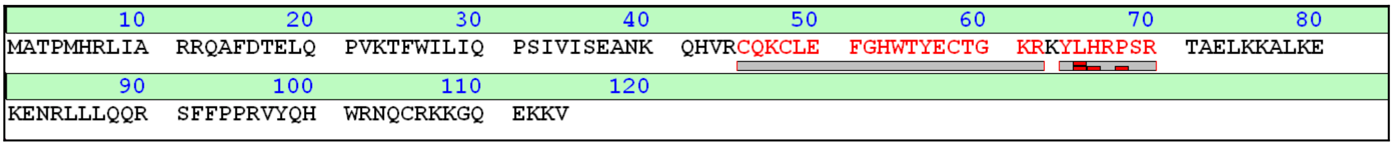
Detailed Protein Report

Protein 237: **PREDICTED: zinc finger CCHC domain-containing protein 10 isoform X4 [Homo sapiens]**

Accession:	gi|530380033	**Score:**	30.0
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

QD:QU **Median:** 0.41 **CV:** 13.14 % **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		QD:QU	0.36
493	1	464.6529	-228.72	2	34.8	14.5	0	64-70	K.YLHRPSR.T		QD:QU	0.46

Detailed Protein Report

Protein 238: uncharacterized protein C5orf55 precursor [Homo sapiens]

Accession:	gi|156523054	**Score:**	30.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	12.7
Database Date:	2015-11-30	**pI:**	12.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	27.7
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MPAVFMLASS SALQCGRGVP RFPRTEVGAG HSVNEETKAE KVGNQTSVIP ATSRQAALGT SWTQRRTQPL QERSHWHPRG
         90        100        110        120
NNASGMGGHR MFPGPLRGPA AQVLENECGS LGRAAEGRS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1854	1	829.2700	-158.89	2	51.7	10.9	0	98-113	R.GPAAQVLENECGSLGR.A	Carbamidomethyl: 11

Detailed Protein Report

Protein 239: 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	

Detailed Protein Report

Protein 240: folate receptor gamma precursor [Homo sapiens]

Accession:	gi|112382370	**Score:**	29.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.9
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	11.0
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.07 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MDMAWQMMQL	LLLALVTAAG	SAQPRSARAR	TDLLNVCMNA	KHHKTQPSPE	DELYGQCSPW	KKNACCTAST	SQELHKDTSR
90	100	110	120	130	140	150	160
LYNFNWDHCG	KMEPTCKRHF	IQDSCLYECS	PNLGPWIRQV	NQSWRKERIL	NVPLCKEDCE	RWWEDCRTSY	TCKSNWHKGW
170	180	190	200	210	220	230	240
NWTSGINECP	AGALCSTFES	YFPTPAALCE	GLWSHSFKVS	NYSRGSGRCI	QMWFDSAQGN	PNEEVAKFYA	AAMNAGAPSR
250							
GIIDS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
2968	1	937.4525	-14.98	2	66.3	16.9	2	127-141	K.ERILNVPLCKEDCER.W	Carbamidomethyl: 9	QD:QU	0.07
782	1	1105.5604	108.49	2	39.8	12.9	2	137-153	K.EDCERWWEDCRTSYTCK.S			

Detailed Protein Report

Protein 241: **1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase epsilon-1 isoform 2 [Homo sapiens]**

Accession:	gi|260166694	**Score:**	29.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	223.7
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:**	0.57	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MVSEGSAAGR	DFAGMEEVRQ	LHVRFCKGIK	IWHQAWFLCS	LLGREPQERE	AGCQLWLCTL	SAVLKVGWLF	PLSEVPNFTL
90	100	110	120	130	140	150	160
LKDGCGCWRL	KEDQIYNAVR	REETENTVGS	LLHFLTKLPA	SETAHGRISV	GPCLKQCVRD	TVCEYRATLQ	RTSISQYITG
170	180	190	200	210	220	230	240
SLLEATTSLG	ARSGLLSTFG	GSTGRMMLKE	RQPGPSVANS	NALPSSSAGI	SKELIDLQPL	IQFPEEVASI	LMEQEQTIYR
250	260	270	280	290	300	310	320
RVLPVDYLCF	LTRDLGTPEC	QSSLPCLKAS	ISASILTTQN	GEHNALEDLV	MRFNEVSSWV	TWLILTAGSM	EEKREVFSYL
330	340	350	360	370	380	390	400
VHVAKCCWNM	GNYNAVMEFL	AGLRSRKVLK	MWQFMDQSDI	ETMRSLKDAM	AQHESSCEYR	KVVTRALHIP	GCKVVPFCGV
410	420	430	440	450	460	470	480
FLKELCEVLD	GASGLMKLCP	RYNSQEETLE	FVADYSGQDN	FLQRVGQNGL	KNSEKESTVN	SIFQVIRSCN	RSLETDEEDS
490	500	510	520	530	540	550	560
PSEGNSSRKS	SLKDKSRWQF	IIGDLLDSDN	DIFEQSKEYD	SHGSEDSQKA	FDHGTELIPW	YVLSIQADVH	QFLLQGATVI
570	580	590	600	610	620	630	640
HYDQDTHLSA	RCFLQLQPDN	STLTWVKPTT	ASPASSKAKL	GVLNNTAEPG	KFPLLGNAGL	SSLTEGVLDL	FAVKAVYMGH
650	660	670	680	690	700	710	720
PGIDIHTVCV	QNKLGSMFLS	ETGVTLLYGL	QTTDNRLLHF	VAPKHTAKML	FSGLLELTRA	VRKMRKFPDQ	RQQWLRKQYV
730	740	750	760	770	780	790	800
SLYQEDGRYE	GPTLAHAVEL	FGGRRWSARN	PSPGTSAKNA	EKPNMQRNNT	LGISTTKKKK	KILMRGESGE	VTDDEMATRK
810	820	830	840	850	860	870	880
AKMHKECRSR	SGSDPQDINE	QEESEVNAIA	NPPNPLPSRR	AHSLTTAGSP	NLAAGTSSPI	RPVSSPVLSS	SNKSPSSAWS
890	900	910	920	930	940	950	960
SSSWHGRIKG	GMKGFQSFMV	SDSNMSFVEF	VELFKSFSVR	SRKDLKDLFD	VYAVPCNRSG	SESAPLYTNL	TIDENTSDLQ
970	980	990	1000	1010	1020	1030	1040
PDLDLLTRNV	SDLGLFIKSK	QQLSDNQRQI	SDAIAAASIV	TNGTGIESTS	LGIFGVGILQ	LNDFLVNCQG	EHCTYDEILS
1050	1060	1070	1080	1090	1100	1110	1120
IIQKFEPSIS	MCHQGLMSFE	GFARFLMDKE	NFASKNDESQ	ENIKELQLPL	SYYYIESSHN	TYLTGHQLKG	ESSVELYSQV
1130	1140	1150	1160	1170	1180	1190	1200
LLQGCRSVEL	DCWDGDDGMP	IIYHGHTLTT	KIPFKEVVEA	IDRSAFINSD	LPIIISIENH	CSLPQQRKMA	EIFKTVFGEK
1210	1220	1230	1240	1250	1260	1270	1280
LVTKFLFETD	FSDDPMLPSP	DQLRKKVLLK	NKKLKAHQTP	VDILKQKAHQ	LASMQVQAYN	GGNANPRPAN	NEEEEDEEDE
1290	1300	1310	1320	1330	1340	1350	1360
YDYDYESLSD	DNILEDRPEN	KSCNDKLQFE	YNEEIPKRIK	KADNSACNKG	KVYDMELGEE	FYLDQNKKES	RQIAPELSDL
1370	1380	1390	1400	1410	1420	1430	1440
VIYCQAVKFP	GLSTLNASGS	SRGKERKSRK	SIFGNNPGRM	SPGETASFNK	TSGKSSCEGI	RQTWEESSSP	LNPTTSLSAI
1450	1460	1470	1480	1490	1500	1510	1520
IRTPKCYHIS	SLNENAAKRL	CRRYSQKLTQ	HTACQLLRTY	PAATRIDSSN	PNPLMFWLHG	IQLVALNYQT	DDLPLHLNAA
1530	1540	1550	1560	1570	1580	1590	1600
MFEANGGCGY	VLKPPVLWDK	NCPMYQKFSP	LERDLDSMDP	AVYSLTIVSG	QNVCPSNSMG	SPCIEVDVLG	MPLDSCHFRT
1610	1620	1630	1640	1650	1660	1670	1680
KPIHRNTLNP	MWNEQFLFHV	HFEDLVFLRF	AVVENNSSAV	TAQRIIPLKA	LKRGYRHLQL	RNLHNEVLEI	SSLFINSRRM
1690	1700	1710	1720	1730	1740	1750	1760
EENSSGNTMS	ASSMFNTEER	KCLQTHRVTV	HGVPGPEPFT	VFTINGGTKA	KQLLQQILTN	EQDIKPVTTD	YFLMEEKYFI
1770	1780	1790	1800	1810	1820	1830	1840
SKEKNECRKQ	PFQRAIGPEE	EIMQILSSWF	PEEGYMGRIV	LKTQQENLEE	KNIVQDDKEV	ILSSEEESFF	VQVHDVSPEQ
1850	1860	1870	1880	1890	1900	1910	1920
PRTVIKAPRV	STAQDVIQQT	LCKAKYSYSI	LSNPNPSDYV	LLEEVVKDTT	NKKTTTPKSS	QRVLLDQECV	FQAQSKWKGA
1930	1940	1950	1960	1970	1980	1990	2000
GKFILKLKEQ	VQASREDKKK	GISFASELKK	LTKSTKQPRG	LTSPSQLLTS	ESIQTKEEKP	VGGLSSSDTM	DYRQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
547	1	624.6856	-218.06	2	35.5	11.3	2	1319-1329	R.IKKADNSACNK.G	Carbamidomethyl: 9	QD:QU 0.57

Detailed Protein Report

Protein 242: PREDICTED: MAX gene-associated protein isoform X16 [Homo sapiens]

Accession:	gi|578826753	**Score:**	29.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	290.2
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	2

Quantitation

QD:QU	**Median:** 0.84	**CV:** 0.00 %	**No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MFKLDTGKMP VVYLEPCAVT RSTVKISELP DNMLSTSRKD KSSMLAELEY LPTYIENSNE TAFCLGKESE NGLRKHSPDL
        90        100        110        120        130        140        150        160
RVVQKYPLLK EPQWKYPDIS DSISTERILD DSKDSVGDSL SGKEDLGRKR TTMLKIATAA KVVNANQNAS PNVPGKRGRP
       170        180        190        200        210        220        230        240
RKLKLCKAGR PPKNTGKSLI STKNTPVSPG STFPDVKPDL EDVDGVLFVS FESKEALDIH AVDGTTEESS SLQASTTNDS
       250        260        270        280        290        300        310        320
GYRARISQLE KELIEDLKTL RHKQVIHPGL QEVGLKLNSV DPTMSIDLKY LGVQLPLAPA TSFPFWNLTG TNPASPDAGF
       330        340        350        360        370        380        390        400
PFVSRTGKTN DFTKIKGWRG KFHSASASRN EGGNSESSLK NRSAFCSDKL DEYLENEGKL METSMGFSSN APTSPVVYQL
       410        420        430        440        450        460        470        480
PTKSTSYVRT LDSVLKKQST ISPSTSYSLK PHSVPPVSRK AKSQNRQATF SGRTKSSYKS ILPYPVSPKQ KYSHVILGDK
       490        500        510        520        530        540        550        560
VTKNSSGIIS ENQANNFVVP TLDENIFPKQ ISLRQAQQQQ QQQQGSRPPG LSKSQVKLMD LEDCALWEGK PRTYITEERA
       570        580        590        600        610        620        630        640
DVSLTTLLTA QASLKTKPIH TIIRKRAPPC NNDFCRLGCV CSSLALEKRQ PAHCRRPDCM FGCTCLKRKV VLVKGGSKTK
       650        660        670        680        690        700        710        720
HFQRKAAHRD PVFYDTLGEE AREEEEGIRE EEEQLKEKKK RKKLEYTICE TEPEQPVRHY PLWVKVEGEV DPEPVYIPTP
       730        740        750        760        770        780        790        800
SVIEPMKPLL LPQPEVLSPT VKGKLLTGIK SPRSYTPKPN PVIREEDKDP VYLYFESMMT CARVRVYERK KEDQRQPSSS
       810        820        830        840        850        860        870        880
SSPSPSFQQQ TSCHSSPENH NNAKEPDSEQ QPLKQLTCDL EDDSDKLQEK SWKSSCNEGE SSSTSYMHQR SPGGPTKLIE
       890        900        910        920        930        940        950        960
IISDCNWEED RNKILSILSQ HINSNMPQSL KVGSFIIELA SQRKSRGEKN PPVYSSRVKI SMPSCQDQDD MAEKSGSETP
       970        980        990       1000       1010       1020       1030       1040
DGPLSPGKME DISPVQTDAL DSVRERLHGG KGLPFYAGLS PAGKLVAYKR KPSSSTSGLI QVNGKSYPQA KLLLGQMGAL
      1050       1060       1070       1080       1090       1100       1110       1120
HPANRLAAYI TGRLRPSVLD LSTLSTVISK VASNAKVAAS RKPRTLLPST SNSKMASSSG TATNRPGKNL KAFVPAKRPI
      1130       1140       1150       1160       1170       1180       1190       1200
AARPSPGGVF TQFVMSKVGA LQQKIPGVST PQTLAGTQKF SIRPSPVMVV TPVVSSEPVQ VCSPVTAAVT TTTPQVFLEN
      1210       1220       1230       1240       1250       1260       1270       1280
TTAVTPMTAI SDVETKETTY SSGATTTGVV EVSETNTSTS VTSTQSTATV NLTKTTGITT PVASVAFPKS LVASPSTITL
      1290       1300       1310       1320       1330       1340       1350       1360
PVASTASTSL VVVTAAASSS MVTTPTSSLG SVPIILSGIN GSPPVSQRPE NAAQIPVATP QVSPNTVKRA GPRLLLIPVQ
      1370       1380       1390       1400       1410       1420       1430       1440
QGSPTLRPVS NTQLQGHRMV LQPVRSPSGM NLFRHPNGQI VQLLPLHQLR GSNTQPNLQP VMFRNPGSVM GIRLPAPSKP
      1450       1460       1470       1480       1490       1500       1510       1520
SETPPSSTSS SAFSVMNPVI QAVGSSSAVN VITQAPSLLS SGASFVSQAG TLTLRISPPE PQSFASKTGS ETKITYSSGG
      1530       1540       1550       1560       1570       1580       1590       1600
QPVGTASLIP LQSGSFALLQ LPGQKPVPSS ILQHVASLQM KRESQNPDQK DETNSIKREQ ETKKVLQSEG EAVDPEANVI
      1610       1620       1630       1640       1650       1660       1670       1680
KQNSGAATSE ETLNDSLEDR GDHLDEECLP EEGCATVKPS EHSCITGSHT DQDYKDVNEE YGARNRKSSK EKVAVLEVRT
      1690       1700       1710       1720       1730       1740       1750       1760
ISEKASNKTV QNLSKVQHQK LGDVKVEQQK GFDNPEENSS EFPVTFKEES KFELSGSKVM EQQSNLQPEA KEKECGDSLE
      1770       1780       1790       1800       1810       1820       1830       1840
KDRERWRKHL KGPLTRKCVG ASQECKKEAD EQLIKETKTC QENSDVFQQE QGISDLLGKS GITEDARVLK TECDSWSRIS
      1850       1860       1870       1880       1890       1900       1910       1920
NPSAFSIVPR RAAKSSRGNG HFQGHLLLPG EQIQPKQEKK GGRSSADFTV LDLEEDDEDD NEKTDDSIDE IVDVVSDYQS
      1930       1940       1950       1960       1970       1980       1990       2000
EEVDDVEKVN NCVEYIEDDE EHVDIETVEE LSEEINVAHL KTTAAHTQSF KQPSCTHISA DEKAAERSRK APPIPLKLKP
      2010       2020       2030       2040       2050       2060       2070       2080
DYWSDKLQKE AEAFAYYRRT HTANERRRRG EMRDLFEKLK ITLGLLHSSK VSKSLILTRA FSEIQGLTDQ ADKLIGQKNL
      2090       2100       2110       2120       2130       2140       2150       2160
LTRKRNILIR KVSSLSGKTE EVVLKKLEYI YAKQQALEAQ KRKKKMGSDE FDISPRISKQ QEGSSASSVD LGQMFINNRR
      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	597-608	R.LGCVCSSLALEK.R		
238	1	897.4097	-91.61	2	31.7	17.0	1	2603-2620	K.VMPCLAPIAAKVGSVGHK.M	Oxidation: 2	QD:QU 0.84

Detailed Protein Report

Protein 243: **SH3 and multiple ankyrin repeat domains protein 3 [Homo sapiens]**

Accession:	gi|380748963	**Score:**	29.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	184.6
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDGPGASAVV	VRVGIPDLQQ	TKCLRLDPAA	PVWAAKQRVL	CALNHSLQDA	LNYGLFQPPS	RGRAGKFLDE	ERLLQEYPPN
90	100	110	120	130	140	150	160
LDTPLPYLEF	RYKRRVYAQN	LIDDKQFAKL	HTKANLKKFM	DYVQLHSTDK	VARLLDKGLD	PNFHDPDSGE	CPLSLAAQLD
170	180	190	200	210	220	230	240
NATDLLKVLK	NGGAHLDFRT	RDGLTAVHCA	TRQRNAAALT	TLLDLGASPD	YKDSRGLTPL	YHSALGGGDA	LCCELLLHDH
250	260	270	280	290	300	310	320
AQLGITDENG	WQEIHQACRF	GHVQHLEHLL	FYGADMGAQN	ASGNTALHIC	ALYNQESCAR	VLLFRGANRD	VRNYNSQTAF
330	340	350	360	370	380	390	400
QVAIIAGNFE	LAEVIKTHKD	SDVVPFRETP	SYAKRRRLAG	PSGLASPRPL	QRSASDINLK	GEAQPAASPG	PSLRSLPHQL
410	420	430	440	450	460	470	480
LLQRLQEEKD	RDRDADQESN	ISGPLAGRAG	QSKISPSGPG	GPGPAPGPGP	APPAPPAPPP	RGPKRKLYSA	VPGRKFIAVK
490	500	510	520	530	540	550	560
AHSPQGEGEI	PLHRGEAVKV	LSIGEGGFWE	GTVKGRTGWF	PADCVEEVQM	RQHDTRPETR	EDRTKRLFRH	YTVGSYDSLT
570	580	590	600	610	620	630	640
SHSDYVIDDK	VAVLQKRDHE	GFGFVLRGAK	AETPIEEFTP	TPAFPALQYL	ESVDVEGVAW	RAGLRTGDFL	IEVNGVNVVK
650	660	670	680	690	700	710	720
VGHKQVVALI	RQGGNRLVMK	VVSVTRKPEE	DGARRRAPPP	PKRAPSTTLT	LRSKSMTAEL	EELASIRRRK	GEKLDEMLAA
730	740	750	760	770	780	790	800
AAEPTLRPDI	ADADSRAATV	KQRPTSRRIT	PAEISSLFER	QGLPGPEKLP	GSLRKGIPRT	KSVGEDEKLA	SLLEGRFPRS
810	820	830	840	850	860	870	880
TSMQDPVREG	RGIPPPPQTA	PPPPPAPYYF	DSGPPPAFSP	PPPPGRAYDT	VRSSFKPGLE	ARLGAGAAGL	YEPGAALGPL
890	900	910	920	930	940	950	960
PYPERQKRAR	SMIILQDSAP	ESGDAPRPPP	AATPPERPKR	RPRPPGPDSP	YANLGAFSAS	LFAPSKPQRR	KSPLVKQLQV
970	980	990	1000	1010	1020	1030	1040
EDAQERAALA	VGSPGPGGGS	FAREPSPTHR	GPRPGGLDYG	AGDGPGLAFG	GPGPAKDRRL	EERRRSTVFL	SVGAIEGSAP
1050	1060	1070	1080	1090	1100	1110	1120
GADLPSLQPS	RSIDERLLGT	GPTAGRDLLL	PSPVSALKPL	VSGPSLGPSG	STFIHPLTGK	PLDPSSPLAL	ALAARERALA
1130	1140	1150	1160	1170	1180	1190	1200
SQAPSRSPTP	VHSPDADRPG	PLFVDVQARD	PERGSLASPA	FSPRSPAWIP	VPARREAEKV	PREERKSPED	KKSMILSVLD
1210	1220	1230	1240	1250	1260	1270	1280
TSLQRPAGLI	VVHATSNGQE	PSRLGGAEEE	RPGTPELAPA	PMQSAAVAEP	LPSPRAQPPG	GTPADAGPGQ	GSSEEEPELV
1290	1300	1310	1320	1330	1340	1350	1360
FAVNLPPAQL	SSSDEETREE	LARIGLVPPP	EEFANGVLLA	TPLAGPGPSP	TTVPSPASGK	PSSEPPPAPE	SAADSGVEEA
1370	1380	1390	1400	1410	1420	1430	1440
DTRSSSDPHL	ETTSTISTVS	SMSTLSSESG	ELTDTHTSFA	DGHTFLLEKP	PVPPKPKLKS	PLGKGPVTFR	DPLLKQSSDS
1450	1460	1470	1480	1490	1500	1510	1520
ELMAQQHHAA	SAGLASAAGP	ARPRYLFQRR	SKLWGDPVES	RGLPGPEDDK	PTVISELSSR	LQQLNKDTRS	LGEEPVGGLG
1530	1540	1550	1560	1570	1580	1590	1600
SLLDPAKKSP	IAAARLFSSL	GELSSISAQR	SPGGPGGGAS	YSVRPSGRYP	VARRAPSPVK	PASLERVEGL	GAGAGGAGRP
1610	1620	1630	1640	1650	1660	1670	1680
FGLTPPTILK	SSSLSIPHEP	KEVRFVVRSV	SARSRSPSPS	PLPSPASGPG	PGAPGPRRPF	QQKPLQLWSK	FDVGDWLESI
1690	1700	1710	1720	1730	1740		
HLGEHRDRFE	DHEIEGAHLP	ALTKDDFVEL	GVTRVGHRMN	IERALRQLDG	S		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
498	1	546.2697	-47.83	2	34.8	13.2	0	853-862	R.SSFKPGLEAR.L	

Detailed Protein Report

Protein 244: cGMP-specific 3',5'-cyclic phosphodiesterase isoform 3 [Homo sapiens]

Accession: gi|61744432
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 29.6
MW [kDa]: 93.6
pI: 5.7
Sequence Coverage [%]: 4.1
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MVNAWFAERV HTIPVCKEGI RGHTESCSCP LQQSPRADNS APGTPTRKIS ASEFDRPLRP IVVKDSEGTV SFLSDSEKKE
        90        100        110        120        130        140        150        160
QMPLTPPRFD HDEGDQCSRL LELVKDISSH LDVTALCHKI FLHIHGLISA DRYSLFLVCE DSSNDKFLIS RLFDVAEGST
       170        180        190        200        210        220        230        240
LEEVSNNCIR LEWNKGIVGH VAALGEPLNI KDAYEDPRFN AEVDQITGYK TQSILCMPIK NHREEVVGVA QAINKKSGNG
       250        260        270        280        290        300        310        320
GTFTEKDEKD FAAYLAFCGI VLHNAQLYET SLLENKRNQV LLDLASLIFE EQQSLEVILK KIAATIISFM QVQKCTIFIV
       330        340        350        360        370        380        390        400
DEDCSDSFSS VFHMECEELE KSSDTLTREH DANKINYMYA QYVKNTMEPL NIPDVSKDKR FPWTTENTGN VNQQCIRSLL
       410        420        430        440        450        460        470        480
CTPIKNGKKN KVIGVCQLVN KMEENTGKVK PFNRNDEQFL EAFVIFCGLG IQNTQMYEAV ERAMAKQMVT LEVLSYHASA
       490        500        510        520        530        540        550        560
AEEETRELQS LAAAVVPSAQ TLKITDFSFS DFELSDLETA LCTIRMFTDL NLVQNFQMKH EVLCRWILSV KKNYRKNVAY
       570        580        590        600        610        620        630        640
HNWRHAFNTA QCMFAALKAG KIQNKLTDLE ILALLIAALS HDLDHRGVNN SYIQRSEHPL AQLYCHSIME HHHFDQCLMI
       650        660        670        680        690        700        710        720
LNSPGNQILS GLSIEEYKTT LKIIKQAILA TDLALYIKRR GEFFELIRKN QFNLEDPHQK ELFLAMLMTA CDLSAITKPW
       730        740        750        760        770        780        790        800
PIQQRIAELV ATEFFDQGDR ERKELNIEPT DLMNREKKNK IPSMQVGFID AICLQLYEAL THVSEDCFPL LDGCRKNRQK
       810        820        830
WQALAEQQEK MLINGESGQA KRN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2072	1	1071.4033	-85.02	2	56.3	13.5	1	18-36	K.EGIRGHTESCSCPLQQSPR.A	Carbamidomethyl: 10

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Detailed Protein Report

Protein 245: transport and Golgi organization protein 6 homolog [Homo sapiens]

Accession:	gi|153791502		**Score:**	29.6
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:	1

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
1030	1	809.4708	-1.60	3	43.0	11.9	2	1029-1050	R.GLSQKATEVLSAVLKDLYHLLK.H	

Detailed Protein Report

Protein 246: 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

QD:QU	**Median:** 1.00	**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; Oxidation: 4	
421	1	846.3629	-53.88	2	35.2	13.6	2	416-429	R.KEFNGSDAKYFCII.-	Carbamidomethyl: 12	QD:QU 1.00

Detailed Protein Report

Protein 247: 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:	1

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
TIVTPNIVIS	VVRLDKGNFA	GAKLPRYEAL	RGEQPPDLET	TVILPESVFR	ETPPVVRPAG	PGEAQEPEEL	ARRQRRHPEL
2250	2260	2270	2280	2290	2300	2310	2320
SQGEAVASVI	IYRTLAGLLP	HNYDPDKRSL	RVPKRPIINT	PVVSISVHDD	EELLPRALDK	PVTVQFRLLE	TEERTKPICV
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
2164	1	937.1664	148.30	2	57.5	14.0	2	129-144	K.LTLPEEHPCLKAPRLR.C	

Detailed Protein Report

Protein 248: centrosomal protein of 55 kDa [Homo sapiens]

Accession:	gi|187608537	**Score:**	29.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|187608545	refseq_human (refseq_human_20140103.fasta)	centrosomal protein of 55 kDa [Homo sapiens]

10	20	30	40	50	60	70	80
MSSRSTKDLI	KSKWGSKPSN	SKSETTLEKL	KGEIAHLKTS	VDEITSGKGK	LTDKERHRLL	EKIRVLEAEK	EKNAYQLTEK
90	100	110	120	130	140	150	160
DKEIQRLRDQ	LKARYSTTAL	LEQLEETTRE	GERREQVLKA	LSEEKDVLKQ	QLSAATSRIA	ELESKTNTLR	LSQTVAPNCF
170	180	190	200	210	220	230	240
NSSINNIHEM	EIQLKDALEK	NQQWLVYDQQ	REVYVKGLLA	KIFELEKKTE	TAAHSLPQQT	KKPESEGYLQ	EEKQKCYNDL
250	260	270	280	290	300	310	320
LASAKKDLEV	ERQTITQLSF	ELSEFRRKYE	ETQKEVHNLN	QLLYSQRRAD	VQHLEDDRHK	TEKIQKLREE	NDIARGKLEE
330	340	350	360	370	380	390	400
EKKRSEELLS	QVQFLYTSLL	KQQEEQTRVA	LLEQQMQACT	LDFENEKLDR	QHVQHQLHVI	LKELRKARNQ	ITQLESLKQL
410	420	430	440	450	460	470	
HEFAITEPLV	TFQGETENRE	KVAASPKSPT	AALNESLVEC	PKCNIQYPAT	EHRDLLVHVE	YCSK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1005	1	423.6388	-147.47	2	41.1	17.5	0	309-315	R.EENDIAR.G	

Detailed Protein Report

Protein 249: OTU domain-containing protein 7A [Homo sapiens]

Accession:	gi|18702331	**Score:**	29.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.6
Database Date:	2015-11-30	**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	3	1068.4771	-72.42	2	30.4	13.9	2	737-761	R.AAAGGTASPGGGARRASASGPVPGR.S	

Detailed Protein Report

Protein 250: SPOC domain-containing protein 1 isoform 3 [Homo sapiens]

Accession:	gi|530354695	**Score:**	29.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.5
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.2
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MEVSSPSPAQ	RLRRKKRPMV	QGPAGCQVFQ	PSPSGGTAGD	PGGLSDPFYP	PRSGSLALGD	PSSDPACSQS	GPMEAEEDSL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
PEQPEDSAQL	QQEKPSLYIG	VRGTVVRSMQ	EVLWTRLREL	PDPVLSEEVV	EGIAAGIEAA	LWDLTQGTNG	RYKTKYRSLL
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
FNLRDPRNLD	LFLKVVHGDV	TPYDLVRMSS	MQLAPQELAR	WRDQEEKRGL	NIIEQQQKEP	CRLPASKMTH	KGEVEIQRDM
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
DQTLTLEDLV	GPQMFMDCSP	QALPIASEDT	TGQHDHHFLD	PNCHICKDWE	PSNELLGSFE	AAKSCGDNIF	QKALSQTPMP
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
APEMPKTREL	SPTEPQDRVP	PSGLHVPAAP	TKALPCLPPW	EGVLDMFSIK	RFRARAQLVS	GHSCRLVQAL	PTVIRSAGCI
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
PSNIVWDLLA	SICPAKAKDV	CVVRLCPHGA	RDTQNCRLLY	SYLNDRQRHG	LASVEHMGMV	LLPLPAFQPL	PTRLRPLGGP
490	**500**	**510**	**520**	**530**	**540**	**550**	**560**
GLEVTHSSLL	LAVLLPKEGL	PDTAGSSPWL	GKVQKMVSFN	SKVEKRYYQP	DDRRPNVPLK	GTPPPGGAWQ	QSQGRGSIAP
570	**580**	**590**	**600**	**610**	**620**	**630**	**640**
RGISAWQRPP	RGRGRLWPEP	ENWQHPGRGQ	WPPEPGLRQS	QHPYSVAPAG	HGFGRGQHFH	RDSCPHQALL	RHLESLATMS
650	**660**	**670**	**680**	**690**	**700**		
HQLQALLCPQ	TKSSIPRPLQ	RLSSALAAPE	PPGPARDSSL	GPTDEAGSEC	PFPRKA		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1959	1	757.2595	-164.75	2	54.9	16.2	2	219-231	K.EPCRLPASKMTHK.G	Oxidation: 10
78	1	877.8658	-95.96	2	30.9	13.3	1	313-328	K.ALSQTPMPAPEMPKTR.E	

Detailed Protein Report

Protein 251: PREDICTED: protein TANC1 isoform X8 [Homo sapiens]

Accession: gi|578805065
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 29.5
MW [kDa]: 183.3
pI: 9.8
Sequence Coverage [%]: 2.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MTVSYKQVLK	MLKAVLKKSR	EGGKGGKKEA	GSDFGPETSP	VLHLDHSADS	PVSSLPTAED	TYRVSLAKGV	SMSLPSSPLL
90	100	110	120	130	140	150	160
PRQSHLVQSR	VNKKSPGPVR	KPKYVESPRV	PGDAVIMPFR	EVAKPTEPDE	HATSSTKLED	LSYLDGQRNA	PLRTSIRLPW
170	180	190	200	210	220	230	240
HNTAGGRAQE	VKARFAPYKP	QDILLKPLLF	EVPSITTDSV	FVGRDWLFHQ	IEENLRNTEL	AENRGAVVVG	NVGFGKTAII
250	260	270	280	290	300	310	320
SKLVALSCHG	SRMRQIASNS	PGSSPKTSDP	TQDLHFTPLL	SPSSSTSASS	TAKTPLGSIS	AENQRPREDA	VKYLASKVVA
330	340	350	360	370	380	390	400
YHYCQADNTY	TCLVPEFVHS	IAALLCRSHQ	LAAYRDLLIK	EPQLQSMLSL	RSCVQDPVAA	FKRGVLEPLT	NLRNEQKIPE
410	420	430	440	450	460	470	480
EEYIILIDGL	NEAEFHKPDY	GDTLSSFITK	IISKFPAWLK	LIVTVRANFQ	EIISALPFVK	LSLDDFPDNK	DIHSDLHAYV
490	500	510	520	530	540	550	560
QHRVHSSQDI	LSNISLNGKA	DATLIGKVSS	HLVLRSLGSY	LYLKLTLDLF	QRGHLVIKSA	SYKVVPVSLS	ELYLLQCNMK
570	580	590	600	610	620	630	640
FMTQSAFERA	LPILNVALAS	LHPMTDEQIF	QAINAGHIQG	EQGWEDFQQR	MDALSCFLIK	RRDKTRMFCH	PSFREWLVWR
650	660	670	680	690	700	710	720
ADGENTAFLC	EPRNGHALLA	FMFSRQEGKL	NRQQTMELGH	HILKAHIFKG	LSKKTGISSS	HLQALWIGYS	TEGLSAALAS
730	740	750	760	770	780	790	800
LRNLYTPNVK	VSRLLILGGA	NVNYRTEVLN	NAPILCVQSH	LGHEEVVTLL	LEFGACLDGT	SENGMTALCY	AAAAGHMKLV
810	820	830	840	850	860	870	880
CLLTKKGVRV	DHLDKKGQCA	LVHSALRGHG	DILQYLLTCE	WSPGPPQPGT	LRKSHALQQA	LTAAASMGHS	SVVQCLLGME
890	900	910	920	930	940	950	960
KEHEVEVNGT	DTLWGETALT	AAAGRGKLEV	CELLLGHGAA	VSRTNRRGVP	PLFCAARQGH	WQIVRLLLER	GCDVNLSDKQ
970	980	990	1000	1010	1020	1030	1040
GRTPLMVAAC	EGHLSTVEFL	LSKGAALSSL	DKEGLSALSW	ACLKGHRAVV	QYLVEEGAAI	DQTDKNGRTP	LDLAAFYGDA
1050	1060	1070	1080	1090	1100	1110	1120
ETVLYLVEKG	AVIEHVDHSG	MRPLDRAIGC	RNTSVVVALL	RKGAKLGNAA	WAMATSKPDI	LIILLQKLME	EGNVMYKKGK
1130	1140	1150	1160	1170	1180	1190	1200
MKEAAQRYQY	ALRKFPREGF	GEDMRPFNEL	RVSLYLNLSR	CRRKTNDFGM	AEEFASKALE	LKPKSYEAFY	ARARAKRNSR
1210	1220	1230	1240	1250	1260	1270	1280
QFVAALADLQ	EAVKLCPTNQ	EVKRLLARVE	EECKQLQRSQ	QQKQQGPLPA	PLNDSENEED	TPTPGLSDHF	HSEETEEEET
1290	1300	1310	1320	1330	1340	1350	1360
SPQEESVSPT	PRSQPSSSVP	SSYIRNLQEG	LQSKGRPVSP	QSRAGIGKSL	REPVAQPGLL	LQPSKQAQIV	KTSQHLGSGQ
1370	1380	1390	1400	1410	1420	1430	1440
SAVRNGSMKV	QISSQNPPPS	PMPGRIAATP	AGSRTQHLEG	TGTFTTRAGC	GHFGDRLGPS	QNVRLQCGEN	GPAHPLPSKT
1450	1460	1470	1480	1490	1500	1510	1520
KTTERLLSHS	SVAVDAAPPN	QGGLATCSDV	RHPASLTSSG	SSGSPSSSIK	MSSSTSSLTS	SSSFSDGFKV	QGPDTRIKDK
1530	1540	1550	1560	1570	1580	1590	1600
VVTHVQSGTA	EHRPRNTPFM	GIMDKTARFQ	QQSNPPSRSW	HCPAPEGLLT	NTSSAAGLQS	ANTEKPSLMQ	VGGYNNQAKT
1610	1620	1630	1640	1650	1660	1670	1680
CSVSTLSASV	HNGAQVKELE	ESKCQIPVHS	QENRITKTVS	HLYQESISKQ	QPHISNEAHR	SHLTAAKPKR	SFIESNV

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2803	2	973.5138	96.14	2	64.1	10.3	0	1491-1509	K.MSSSTSSLTSSSSFSDGFK.V	Oxidation: 1

Detailed Protein Report

Protein 252: PREDICTED: alpha-tubulin N-acetyltransferase isoform X9 [Homo sapiens]

Accession:	gi|530382649	**Score:**	29.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.8
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	11.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530429736	refseq_human(refseq_human_20140103.fasta)	PREDICTED: alpha-tubulin N-acetyltransferase isoform X9 [Homo sapiens]
gi|530429452	refseq_human(refseq_human_20140103.fasta)	PREDICTED: alpha-tubulin N-acetyltransferase isoform X9 [Homo sapiens]
gi|530429087	refseq_human(refseq_human_20140103.fasta)	PREDICTED: alpha-tubulin N-acetyltransferase isoform X9 [Homo sapiens]
gi|530428827	refseq_human(refseq_human_20140103.fasta)	PREDICTED: alpha-tubulin N-acetyltransferase isoform X9 [Homo sapiens]
gi|530428535	refseq_human(refseq_human_20140103.fasta)	PREDICTED: alpha-tubulin N-acetyltransferase isoform X9 [Homo sapiens]
gi|530428190	refseq_human(refseq_human_20140103.fasta)	PREDICTED: alpha-tubulin N-acetyltransferase isoform X9 [Homo sapiens]

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        10         20         30         40         50         60         70         80
MEFPFDVDAL FPERITVLDQ HLRPPARRPG TTTPARVDLQ QQIMTIIDEL GKASAKAQNL SAPITSASRM QSNRHVVYIL
        90        100        110        120        130        140        150        160
KDSSARPAGK GAIIGFIKVG YKKLFVLDDR EAHNEVEPLC ILDFYIHESV QRHGHGRELF QYMLQKERVE PHQLAIDRPS
       170        180        190        200        210        220        230
QKLLKFLNKH YNLETTVPQV NNFVIFEGFF AHQHPPARKL PPKRAEGDIK PYSSSDREWG LPQVW
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
109	1	712.4379	47.78	3	30.1	12.9	2	82-102	K.DSSARPAGKGAIIGFIKVGYK.K	

Detailed Protein Report

Protein 253: **calmodulin-regulated spectrin-associated protein 1 [Homo sapiens]**

Accession:	gi|186659512	**Score:**	29.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	177.9
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVDASGRAAA	EGWRKMEAPP	DGAADLVPLD	RYDAARAKIA	ANLQWICAKA	YGRDNIPEDL	RDPFYVDQYE	QEHIKPPVIK
90	100	110	120	130	140	150	160
LLLSSELYCR	VCSLILKGDQ	VAALQGHQSV	IQALSRKGIY	VMESDDTPVT	ESDLSRAPIK	MSAHMAMVDA	LMMAYTVEMI
170	180	190	200	210	220	230	240
SIEKVVASVK	RFSTFSASKE	LPYDLEDAMV	FWINKVNLKM	REITEKEVKL	KQQLLESPAH	QKVRYRREHL	SARQSPYFPL
250	260	270	280	290	300	310	320
LEDLMRDGSD	GAALLAVIHY	YCPEQMKLDD	ICLKEVTSMA	DSLYNIRLLR	EFSNEYLNKC	FYLTLEDMLY	APLVLKPNVM
330	340	350	360	370	380	390	400
VFIAELFWWF	ENVKPDFVQP	RDVQELKDAK	TVLHQKSSRP	PVPISNATKR	SFLGSPAAGT	LAELQPPVQL	PAEGCHRHYL
410	420	430	440	450	460	470	480
HPEEPEYLGK	GTAAFSPSHP	LLPLRQKQQK	SIQGEDIPDQ	RHRSNSLTRV	DGQPRGAAIA	WPEKKTRPAS	QPTPFALHHA
490	500	510	520	530	540	550	560
ASCEVDPSSG	DSISLARSIS	KDSLASNIVN	LTPQNQPHPT	ATKSHGKSLL	SNVSIEDEEE	ELVAIVRADV	VPQQADPEFP
570	580	590	600	610	620	630	640
RASPRALGLT	ANARSPQGQL	DTSESKPDSF	FLEPLMPAVL	KPAKEKQVIT	KEDERGEGRP	RSIVSRRPSE	GPQPLVRRKM
650	660	670	680	690	700	710	720
TGSRDLNRTF	TPIPCSEFPM	GIDPTETGPL	SVETAGEVCG	GPLALGGFDP	FPQGPSTDGF	FLHVGRADED	TEGRLYVSCS
730	740	750	760	770	780	790	800
KSPNSHDSEP	WTLLRQDSDS	DVVDIEEAEH	DFMGEAHPVV	FSRYIGEEES	AKLQEDMKVK	EHEDKDDASG	RSSPCLSTAS
810	820	830	840	850	860	870	880
QMSSVSMASG	SVKMTSFAER	KLQRLNSCET	KSSTSSSQKT	TPDASESCPA	PLTTWRQKRE	QSPSQHGKDP	ASLLASELVQ
890	900	910	920	930	940	950	960
LHMQLEEKRR	AIEAQKKKME	ALSARQRLKL	GKAAFLHVVK	KGKAEAAPPL	RPEHFAKEYS	QHNGEDCGDA	VSKTEDFLVK
970	980	990	1000	1010	1020	1030	1040
EEQREELLHE	PQDVDKESLA	FAQQHKAKDP	VALHELERNK	VISAALLEDT	VGEVVDVNEC	DLSIEKLNET	ISTLQQAILK
1050	1060	1070	1080	1090	1100	1110	1120
ISQQQEQLLM	KSPTVPVPGS	KNNSQDHKVK	APVHFVEPLS	PTGVAGHRKA	PRLGQGRNSR	SGRPAELKVP	KDRPQGSSRS
1130	1140	1150	1160	1170	1180	1190	1200
KTPTPSVETL	PHLRPFPASS	HPRTPTDPGL	DSALEPSGDP	HGKCLFDSYR	LHDESNQRTL	TLSSSKDANI	LSEQMSLKEV
1210	1220	1230	1240	1250	1260	1270	1280
LDASVKEVGS	SSSDVSGKES	VPVEEPLRSR	ASLIEVDLSD	LKAPDEDGEL	VSLDGSADLV	SEGDQKPGVG	FFFKDEQKAE
1290	1300	1310	1320	1330	1340	1350	1360
DELAKKRAAF	LLKQQRKAEE	ARVRKQQLEA	EVELKRDEAR	RKAEEDRVRK	EEEKARRELI	KQEYLRRKQQ	QILEEQGLGK
1370	1380	1390	1400	1410	1420	1430	1440
PKSKPKKPRP	KSVHREESCS	DSGTKCSSTP	DNLSRTQSGS	SLSLASAATT	EPESVHSGGT	PSQRVESMEA	LPILSRNPSR
1450	1460	1470	1480	1490	1500	1510	1520
STDRDWETAS	AASSLASVAE	YTGPKLFKEP	SSKSNKPIIH	NAISHCCLAG	KVNEPHKNSI	LEELEKCDAN	HYIILFRDAG
1530	1540	1550	1560	1570	1580	1590	1600
CQFRALYCYY	PDTEEIYKLT	GTGPKNITKK	MIDKLYKYSS	DRKQFNLIPA	KTMSVSVDAL	TIHNHLWQPK	RPAVPKKAQT
1610							
RK							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2677	1	862.3965	-106.85	2	64.6	15.1	1	1348-1362	R.KQQQILEEQGLGKPK.S	

Detailed Protein Report

Protein 254: PREDICTED: zinc finger protein 845 isoform X3 [Homo sapiens]

Accession:	gi|578835119	**Score:**	29.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.9
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALSQGLLTF	RDVAIEFSQE	EWKCLDPAQR	TLYRDVMLEN	YRNLVSLDIS	SKCMMKEFSS	TAQGNTEVIH	TGTLQRHERH
90	100	110	120	130	140	150	160
HIGDFCFQEM	EKDIHDFEFQ	WKEDERNSHE	APMTEIKQLT	GSTNRHDQRH	AGNKPIKDQL	GSSFHSHLPE	LHMFQTEGKI
170	180	190	200	210	220	230	240
GNQVEKSINS	ASLVSTSQRI	SCRPKTHISK	NYGNNFLNSS	LLTQKQEVHM	REKSFQCNES	GKAFNYSSVL	RKHQIIHLGA
250	260	270	280	290	300	310	320
KQYKCDVCGK	VFNQKRYLAC	HRRCHTGKKP	YKCNDCGKTF	SQELTLTCHH	RLHTGEKHYK	CSECGKTFSR	NSALVIHKAI
330	340	350	360	370	380	390	400
HTGEKSYKCN	ECGKTFSQTS	YLVYHRRLHT	GEKPYKCEEC	DKAFSFKSNL	ERHRKIHTGE	KPYKCNECSR	TFSRKSSLTR
410	420	430	440	450	460	470	480
HRRLHTGEKP	YKCNDCGKTF	SQMSSLVYHR	RLHTGEKPYK	CEECDEAFSF	KSNLQRHRRI	HTGEKPYRCN	ECGKTFSRKS
490	500	510	520	530	540	550	560
YLTCHRRLHT	GEKPYKCNEC	GKTFGRNSAL	IIHKAIHTGE	KPYKCNECGK	AFSQKSSLTC	HLRLHTGEKP	YKCEECDKVF
570	580	590	600	610	620	630	640
SRKSSLEKHR	RIHTGEKPYK	CKVCDKAFGR	DSHLAQHTRI	HTGEKPYKCN	ECGKNFRHNS	ALVIHKAIHS	GEKPYKCNEC
650	660	670	680	690	700	710	720
GKTFRHNSAL	EIHKAIHTGE	KPYKCSECGK	VFNRKANLSR	HHRLHTGEKP	YKCNKCGKVF	NQQAHLACHH	RIHTGEKPYK
730	740	750	760	770	780		
CNECGKTFRH	NSVLVIHKTI	HTGEKPYKCN	ECGKVFNRKA	KLARHHRIHT	GKKH		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2753	1	920.1206	31.91	3	65.6	17.8	1	53-76	K.CMMKEFSSTAQGNTEVIHTGTLQR.H	Carbamidomethyl: 1; Oxidation: 2, 3

Detailed Protein Report

Protein 255: 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:	2

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
1084	2	530.7982	-0.72	2	43.7	16.4	1	73-80	R.KDIRPEFR.E	
392	1	874.3959	-106.40	3	34.9	13.0	0	419-443	K.VPGSFLLPPPPPVARPVPLPMPDSK.S	Oxidation: 21

Detailed Protein Report

Protein 256: collagen alpha-1(XXVIII) chain precursor [Homo sapiens]

Accession:	gi|154759255	**Score:**	29.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	116.6
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	3.4
		No. of unique 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
201	1	714.3696	-12.54	3	32.5	18.4	2	667-689	K.GEPGVRGPPGPSGPRGVGTQGPK.G	

Detailed Protein Report

Protein 257: 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

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
585	1	537.7782	-18.47	2	37.3	11.4	2	172-179	K.TRHEEFKK.Y	
1116	1	701.1743	-178.79	1	44.1	17.9	0	180-184	K.YEMMK.E	

Detailed Protein Report

Protein 258: **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 259: **phosphatidylinositol 4-phosphate 5-kinase type-1 alpha isoform 4 [Homo sapiens]**

Accession:	gi|208431776	**Score:**	29.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.0
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	5.2
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 1.88 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MASASSGPSS	SVGFSSFDPA	VPSCTLSSAS	GIKRPMASEV	PYASGMPIKK	IGHRSVDSSG	ETTYKKTTSS	ALKGAIQLGI
90	100	110	120	130	140	150	160
THTVGSLSTK	PERDVLMQDF	YVVESIFFPS	EGSNLTPAHH	YNDFRFKTYA	PVAFRYFREL	FGIRPDDYLY	SLCSEPLIEL
170	180	190	200	210	220	230	240
CSSGASGSLF	YVSSDDEFII	KTVQHKEAEF	LQKLLPGYYM	NLNQNPRTLL	PKFYGLYCVQ	AGGKNIRIVV	MNNLLPRSVK
250	260	270	280	290	300	310	320
MHIKYDLKGS	TYKRRASQKE	REKPLPTFKD	LDFLQDIPDG	LFLDADMYNA	LCKTLQRDCL	VLQSFKIMDY	SLLMSIHNID
330	340	350	360	370	380	390	400
HAQREPLSSE	TQYSVDTRRP	APQKALYSTA	MESIQGEARR	GGTMETDDHM	GGIPARNSKG	ERLLLYIGII	DILQSYRFVK
410	420	430	440	450	460	470	480
KLEHSWKALV	HDGDTVSVHR	PGFYAERFQR	FMCNTVFKKI	PCVHLGRPDV	LPQTPPLEEI	SEGSPIPDPS	FSPLVGETLQ
490	500	510					
MLTTSTTLEK	LEVAESEFTH						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2199	1	933.6289	74.91	2	56.1	14.3	2	225-240	K.NIRIVVMNNLLPRSVK.M		
989	3	581.1819	-159.70	2	42.5	14.9	0	491-500	K.LEVAESEFTH.-		QD:QU 1.88

Detailed Protein Report

Protein 260: **leukocyte receptor cluster member 9 [Homo sapiens]**

Accession:	gi|206725452	**Score:**	29.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.1
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	8.2
		No. of unique Peptides:	2

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	
2744	6	673.3579	-72.57	2	65.4	18.8	1	385-397	R.RALLAPGLNAPPR.L	

Detailed Protein Report

Protein 261: putative uncharacterized zinc finger protein 814 [Homo sapiens]

Accession:	gi|222418585	**Score:**	29.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.3
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.60 **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	
417	1	564.5160	-156.98	3	35.2	11.2	1	653-667	R.VHTTERPFKCGECGK.C		QD:QU 0.60

Detailed Protein Report

Protein 262: **PREDICTED: uncharacterized protein C17orf85 isoform X2 [Homo sapiens]**

Accession:	gi|578829984	**Score:**	29.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.0
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSTQDVFSYF	KEYPPAHIEW	LDDTSCNVVW	LDEMTATRAL	INMSSLPAQD	KIRSRDASED	KSAEKRKKDK	QEDSSDDDEA
90	100	110	120	130	140	150	160
EEGEVEDENS	SDVELDTLSQ	VEEESLLRND	LRPANKLAKG	NRLFMRFATK	DDKKELGAAR	RSQYYMKYGN	PNYGGMKGIL
170	180	190	200	210	220	230	240
SNSWKRRYHS	RRIQRDVIKK	RALIGDDVGL	TSYKHRHSGL	VNVPEEPIEE	EEEEEEEEEE	EEEEDQDMDA	DDRVVVEYHE
250	260	270	280	290	300	310	320
ELPALKQPRE	RSASRRSSAS	SSDSDEMDYD	LELKMISTPS	PKKSMKMTMY	ADEVESQLKN	IRNSMRADSV	SSSNIKNRIG
330	340	350	360	370	380	390	400
NKLPPEKFAD	VRHLLDEKRQ	HSRPRPPVSS	TKSDIRQRLG	KRPHSPEKAF	SSNPVVRREP	SSDVHSRLGV	PRQDSKGLYA
410	420	430	440	450	460	470	480
DTREKKSGNL	WTRLGSAPKT	KEKNTKKVDH	RAPGAEEDDS	ELQRAWGALI	KEKEQSRQKK	SRCYQHPFPK	KSQFPGAYWT
490	500						
SFEGEEEGSG	QLTLPGP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2116	1	945.7998	-143.91	2	56.8	14.7	1	284-299	K.SMKMTMYADEVESQLK.N	

Detailed Protein Report

Protein 263: **plakophilin-1 isoform 1a [Homo sapiens]**

Accession: gi|53729344
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 29.1
MW [kDa]: 80.4
pI: 10.0
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 264: myosin-10 isoform 2 [Homo sapiens]

Accession:	gi|367460087	**Score:**	29.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	228.9
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	1.5
		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	

Detailed Protein Report

Protein 265: hemicentin-1 precursor [Homo sapiens]

Accession:	gi|118572606	**Score:**	29.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	613.0
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MISWEVVHTV	FLFALLYSSL	AQDASPQSEI	RAEEIPEGAS	TLAFVFDVTG	SMYDDLVQVI	EGASKILETS	LKRPKRPLFN
90	100	110	120	130	140	150	160
FALVPFHDPE	IGPVTITTDP	KKFQYELREL	YVQGGGDCPE	MSIGAIKIAL	EISLPGSFIY	VFTDARSKDY	RLTHEVLQLI
170	180	190	200	210	220	230	240
QQKQSQVVFV	LTGDCDDRTH	IGYKVYEEIA	STSSGQVFHL	DKKQVNEVLK	WVEEAVQASK	VHLLSTDHLE	QAVNTWRIPF
250	260	270	280	290	300	310	320
DPSLKEVTVS	LSGPSPMIEI	RNPLGKLIKK	GFGLHELLNI	HNSAKVVNVK	EPEAGMWTVK	TSSSGRHSVR	ITGLSTIDFR
330	340	350	360	370	380	390	400
AGFSRKPTLD	FKKTVSRPVQ	GIPTYVLLNT	SGISTPARID	LLELLSISGS	SLKTIPVKYY	PHRKPYGIWN	ISDFVPPNEA
410	420	430	440	450	460	470	480
FFLKVTGYDK	DDYLFQRVSS	VSFSSIVPDA	PKVTMPEKTP	GYYLQPGQIP	CSVDSLLPFT	LSFVRNGVTL	GVDQYLKESA
490	500	510	520	530	540	550	560
SVNLDIAKVT	LSDEGFYECI	AVSSAGTGRA	QTFFDVSEPP	PVIQVPNNVT	VTPGERAVLT	CLIISAVDYN	LTWQRNDRDV
570	580	590	600	610	620	630	640
RLAEPARIRT	LANLSLELKS	VKFNDAGEYH	CMVSSEGGSS	AASVFLTVQE	PPKVTVMPKN	QSFTGGSEVS	IMCSATGYPK
650	660	670	680	690	700	710	720
PKIAWTVNDM	FIVGSHRYRM	TSDGTLFIKN	AAPKDAGIYG	CLASNSAGTD	KQNSTLRYIE	APKLMVVQSE	LLVALGDITV
730	740	750	760	770	780	790	800
MECKTSGIPP	PQVKWFKGDL	ELRPSTFLII	DPLLGLLKIQ	ETQDLDAGDY	TCVAINEAGR	ATGKITLDVG	SPPVFIQEPA
810	820	830	840	850	860	870	880
DVSMEIGSNV	TLPCYVQGYP	EPTIKWRRLD	NMPIFSRPFS	VSSISQLRTG	ALFILNLWAS	DKGTYICEAE	NQFGKIQSET
890	900	910	920	930	940	950	960
TVTVTGLVAP	LIGISPSVAN	VIEGQQLTLP	CTLLAGNPIP	ERRWIKNSAM	LLQNPYITVR	SDGSLHIERV	QLQDGGEYTC
970	980	990	1000	1010	1020	1030	1040
VASNVAGTNN	KTTSVVVHVL	PTIQHGQQIL	STIEGIPVTL	PCKASGNPKP	SVIWSKKGEL	ISTSSAKFSA	GADGSLYVVS
1050	1060	1070	1080	1090	1100	1110	1120
PGGEESGEYV	CTATNTAGYA	KRKVQLTVYV	RPRVFGDQRG	LSQDKPVEIS	VLAGEEVTLP	CEVKSLPPPI	ITWAKETQLI
1130	1140	1150	1160	1170	1180	1190	1200
SPFSPRHTFL	PSGSMKITET	RTSDSGMYLC	VATNIAGNVT	QAVKLNVHVP	PKIQRGPKHL	KVQVGQRVDI	PCNAQGTPLP
1210	1220	1230	1240	1250	1260	1270	1280
VITWSKGGST	MLVDGEHHVS	NPDGTLSIDQ	ATPSDAGIYT	CVATNIAGTD	ETEITLHVQE	PPTVEDLEPP	YNTTFQERVA
1290	1300	1310	1320	1330	1340	1350	1360
NQRIEFPCPA	KGTPKPTIKW	LHNGRELTGR	EPGISILEDG	TLLVIASVTP	YDNGEYICVA	VNEAGTTERK	YNLKVHVPPV
1370	1380	1390	1400	1410	1420	1430	1440
IKDKEQVTNV	SVLLNQLTNL	FCEVEGTPSP	IIMWYKDNVQ	VTESSTIQTV	NNGKILKLFR	ATPEDAGRYS	CKAINIAGTS
1450	1460	1470	1480	1490	1500	1510	1520
QKYFNIDVLV	PPTIIGTNFP	NEVSVVLNRD	VALECQVKGT	PFPDIHWFKD	GKPLFLGDPN	VELLDRGQVL	HLKNARRNDK
1530	1540	1550	1560	1570	1580	1590	1600
GRYQCTVSNA	AGKQAKDIKL	TIYIPPSIKG	GNVTTDISVL	INSLIKLECE	TRGLPMPAIT	WYKDGQPIMS	SSQALYIDKG
1610	1620	1630	1640	1650	1660	1670	1680
QYLHIPRAQV	SDSATYTCHV	ANVAGTAEKS	FHVDVYVPPM	IEGNLATPLN	KQVVIAHSLT	LECKAAGNPS	PILTWLKDGV
1690	1700	1710	1720	1730	1740	1750	1760
PVKANDNIRI	EAGGKKLEIM	SAQEIDRGQY	ICVATSVAGE	KEIKYEVDVL	VPPAIEGGDE	TSYFIVMVNN	LLELDCHVTG
1770	1780	1790	1800	1810	1820	1830	1840
SPPPTIMWLK	DGQLIDERDG	FKILLNGRKL	VIAQAQVSNT	GLYRCMAANT	AGDHKKEFEV	TVHVPPTIKS	SGLSERVVVK
1850	1860	1870	1880	1890	1900	1910	1920
YKPVALQCIA	NGIPNPSITW	LKDDQPVNTA	QGNLKIQSSG	RVLQIAKTLL	EDAGRYTCVA	TNAAGETQQH	IQLHVHEPPS
1930	1940	1950	1960	1970	1980	1990	2000
LEDAGKMLNE	TVLVSNPVQL	ECKAAGNPVP	VITWYKDNRL	LSGSTSMTFL	NRGQIIDIES	AQISDAGIYK	CVAINSAGAT
2010	2020	2030	2040	2050	2060	2070	2080
ELFYSLQVHV	APSISGSNNM	VAVVVNNPVR	LECEARGIPA	PSLTWLKDGS	PVSSFSNGLQ	VLSGGRILAL	TSAQISDTGR
2090	2100	2110	2120	2130	2140	2150	2160
YTCVAVNAAG	EKQRDIDLRV	YVPPNIMGEE	QNVSVLISQA	VELLCQSDAI	PPPTLTWLKD	GHPLLKKPGL	SISENRSVLK
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
1025	1	676.6792	37.90	3	41.3	16.6	2	5247-5264	K.NTRGGYKCIDLCPNGMTK.A	Carbamidomethyl: 8

Detailed Protein Report

Protein 266: PREDICTED: notchless protein homolog 1 isoform X5 [Homo sapiens]

Accession: gi|578831085
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 28.9
MW [kDa]: 42.7
pI: 10.1
Sequence Coverage [%]: 4.1
No. of unique Peptides: 1

```
         10          20          30          40          50          60          70          80
MRAGSCWVPR  STCPWTSPRT  GCSSCATRYW  PRYLASGSGD  TTVRFWDLST  ETPHFTCKGH  RHWVLSISWS  PDGRKLASGC
         90         100         110         120         130         140         150         160
KNGQILLWDP  STGKQVGRTL  AGHSKWITGL  SWEPLHANPE  CRYVASSSKD  GSVRIWDTTA  GRCERILTGH  TQSVTCLRWG
        170         180         190         200         210         220         230         240
GDGLLYSASQ  DRTIKVWRAH  DGVLCRTLQG  HGHWVNTMAL  STDYALRTGA  FEPAEASVNP  QDLQGSLQEL  KERALSRYNL
        250         260         270         280         290         300         310         320
VRGQGPERLV  SGSDDFTLFL  WSPAEDKKPL  TRMTGHQALI  NQVLFSPDSR  IVASASFDKS  IKLWDGRTGK  YLASLRGHVA
        330         340         350         360         370         380         390
AVYQIAWSAD  SRLLVSGSSD  STLKVWDVKA  QKLAMDLPGH  ADEVYAVDWS  PDGQRVASGG  KDKCLRM
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2764	1	937.4600	-13.04	2	63.6	12.4	1	143-158	R.CERILTGHTQSVTCLR.W	Carbamidomethyl: 1

Detailed Protein Report

Protein 267: rap guanine nucleotide exchange factor 4 isoform e [Homo sapiens]

Accession:	gi|544583481	**Score:**	28.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.9
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIRDRKYHLK	TYRQCCVGTE	LVDWMMQQTP	CVHSRTQAVG	MWQVLLEDGV	LNHVDQEHHF	QDKYLFYRFL	DDEHEDAPLP
90	100	110	120	130	140	150	160
TEEEKKECDE	ELQDTMLLLS	QMGPDAHMRM	ILRKPPGQRT	VDDLEIIYEE	LLHIKALSHL	STTVKRELAG	VLIFESHAKG
170	180	190	200	210	220	230	240
GTVLFNQGEE	GTSWYIILKG	SVNVVIYGKG	VVCTLHEGDD	FGKLALVNDA	PRAASIVLRE	DNCHFLRVDK	EDFNRILRDV
250	260	270	280	290	300	310	320
EANTVRLKEH	DQDVLVLEKV	PAGNRASNQG	NSQPQQKYTV	MSGTPEKILE	HFLETIRLEA	TLNEATDSVL	NDFIMMHCVF
330	340	350	360	370	380	390	400
MPNTQLCPAL	VAHYHAQPSQ	GTEQEKMDYA	LNNKRRVIRL	VLQWAAMYGD	LLQEDDVSMA	FLEEFYVSVS	DDARMIAALK
410	420	430	440	450	460	470	480
EQLPELEKIV	KQISEDAKAP	QKKHKVLLQQ	FNTGDERAQK	RQPIRGSDEV	LFKVYCMDHT	YTTIRVPVAT	SVKEVISAVA
490	500	510	520	530	540	550	560
DKLGSGEGLI	IVKMSSGGEK	VVLKPNDVSV	FTTLTINGRL	FACPREQFDS	LTPLPEQEGP	TVGTVGTFEL	MSSKDLAYQM
570	580	590	600	610	620	630	640
TIYDWELFNC	VHELELIYHT	FGRHNFKKTT	ANLDLFLRRF	NEIQFWVVTE	ICLCSQLSKR	VQLLKKFIKI	AAHCKEYKNL
650	660	670	680	690	700	710	720
NSFFAIVMGL	SNVAVSRLAL	TWEKLPSKFK	KFYAEFESLM	DPSRNHRAYR	LTVAKLEPPL	IPFMPLLIKD	MTFTHEGNKT
730	740	750	760	770	780	790	800
FIDNLVNFEK	MRMIANTART	VRYYRSQPFN	PDAAQANKNH	QDVRSYVRQL	NVIDNQRTLS	QMSHRLEPRR	P

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2090	2	917.8279	107.57	3	54.7	15.4	0	87-109	K.ECDEELQDTMLLLSQMGPDAHMR.M	Carbamidomethyl: 2; Oxidation: 10, 22

Detailed Protein Report

Protein 268: **ras-related protein Rab-44 [Homo sapiens]**

Accession:	gi|390635651	**Score:**	28.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.8
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.0
		No. of unique Peptides:	2

```
        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
2821	1	914.4775	-18.24	2	64.4	14.6	1	198-213	R.LQEAQADKEALELTLR.K	

Detailed Protein Report

Protein 269: **tripartite motif-containing protein 46 isoform 4 [Homo sapiens]**

Accession:	gi|375298680	**Score:**	28.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.8
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGAKGNGLTS MKNMEKELLC PVCQEMYKQP LVLPCTHNVC QACAREVLGQ QGYIGHGGDP SSEPTSPAST PSTRSPRLSR
        90        100        110        120        130        140        150        160
RTLPKPDRLD RLLKSGFGTY PGRKRGALHP QVIMFPCPAC QGDVELGERG LAGLFRNLTL ERVVERYRQS VSVGGAILCQ
       170        180        190        200        210        220        230        240
LCKPPPLEAT KGCTECRATF CNECFKLFHP WGTQKAQHEP TLPTLSFRPK GLMCPDHKEE VTHYCKTCQR LVCQLCRVRR
       250        260        270        280        290        300        310        320
THSGHKITPV LSAYQALKDK LTKSLTYILG NQDTVQTQIC ELEEAVRHTE VSGQQAKEEV SQLVRGLGAV LEEKRASLLQ
       330        340        350        360        370        380        390        400
AIEECQQERL ARLSAQIQEH RSLLDGSGLV GYAQEVLKET DQPCFVQAAK QLHNRIARAT EALQTFRPAA SSSFRHCQLD
       410        420        430        440        450        460        470        480
VGREMKLLTE LNFLRVPEAP VIDTQRTFAY DQIFLCWRLP PHSPPAWHYT VEFRRTDVPA QPGPTRWQRR EEVRGTSALL
       490        500        510        520        530        540        550        560
ENPDTGSVYV LRVRGCNKAG YGEYSEDVHL HTPPAPVLHF FLDSRWGASR ERLAISKDQR AVRSVPGLPL LLAADRLLTG
       570        580        590        600        610        620        630        640
CHLSVDVVLG DVAVTQGRSY WACAVDPASY LVKVGVGLES KLQESFQGAP DVISPRYDPD SGHDSGAEDA TVEASPPFAF
       650        660        670        680        690        700        710        720
LTIGMGKILL GSGASSNAGL TGRDGPTAGC TVPLPPRLGI CLDYERGRVS FLDAVSFRGL LECPLDCSGP VCPAFCFIGG
       730        740        750
GAVQLQEPVG TKPERKVTIG GFAKLD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1590	1	945.6946	-76.21	3	48.4	12.7	2	5-28	K.GNGLTSMKNMEKELLCPVCQEMYK.Q	Carbamidomethyl: 16; Oxidation: 7, 22

Detailed Protein Report

Protein 270: PREDICTED: zinc finger protein 675 isoform X4 [Homo sapiens]

Accession: gi|530414624
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 28.8
MW [kDa]: 57.4
pI: 10.2
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 271: 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
		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
2405	1	904.4370	-16.87	2	60.5	15.9	1	206-221	R.DVYRAGIATHFVDSEK.L	

Detailed Protein Report

Protein 272: plastin-2 [Homo sapiens]

Accession:	gi|167614506	**Score:**	28.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.2
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	4.1
		No. of unique Peptides:	2

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
2609	1	658.3945	34.02	2	61.3	14.5	1	77-88	K.IFHGLKSTDVAK.T	
2231	1	793.3805	-58.93	2	56.5	14.2	0	597-610	R.VYALPEDLVEVNPK.M	

Detailed Protein Report

Protein 273: collagen alpha-1(IV) chain preproprotein [Homo sapiens]

Accession:	gi|148536825	**Score:**	28.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	160.5
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

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	

Detailed Protein Report

Protein 274: ATP-sensitive inward rectifier potassium channel 1 isoform a [Homo sapiens]

Accession:	gi|4504837	**Score:**	28.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.8
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNASSRNVFD	TLIRVLTESM	FKHLRKWVVT	RFFGHSRQRA	RLVSKDGRCN	IEFGNVEAQS	RFIFFVDIWT	TVLDLKWRYK
90	100	110	120	130	140	150	160
MTIFITAFLG	SWFFFGLLWY	AVAYIHKDLP	EFHPSANHTP	CVENINGLTS	AFLFSLETQV	TIGYGFRCVT	EQCATAIFLL
170	180	190	200	210	220	230	240
IFQSILGVII	NSFMCGAILA	KISRPKKRAK	TITFSKNAVI	SKRGGKLCLL	IRVANLRKSL	LIGSHIYGKL	LKTTVTPEGE
250	260	270	280	290	300	310	320
TIILDQININ	FVVDAGNENL	FFISPLTIYH	VIDHNSPFFH	MAAETLLQQD	FELVVFLDGT	VESTSATCQV	RTSYVPEEVL
330	340	350	360	370	380	390	400
WGYRFAPIVS	KTKEGKYRVD	FHNFSKTVEV	ETPHCAMCLY	NEKDVRARMK	RGYDNPNFIL	SEVNETDDTK	M

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2895	1	859.1037	-1.61	3	65.4	17.8	2	1-22	-.MNASSRNVFDTLIRVLTESMFK.H	Oxidation: 20

Detailed Protein Report

Protein 275: calmodulin-like protein 3 [Homo sapiens]

Accession:	gi|4885111	**Score:**	28.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.9
Database Date:	2015-11-30	**pI:**	4.1
		Sequence Coverage [%]:	8.1
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.35 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MADQLTEEQV	TEFKEAFSLF	DKDGDGCITT	RELGTVMRSL	GQNPTEAELR	DMMSEIDRDG	NGTVDFPEFL	GMMARKMKDT
90	**100**	**110**	**120**	**130**	**140**	**150**	
DNEEEIREAF	RVFDKDGNGF	VSAAELRHVM	TRLGEKLSDE	EVDEMIRAAD	TDGDGQVNYE	EFVRVLVSK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
245	2	657.8057	-46.21	2	31.8	28.6	0	39-50	R.SLGQNPTEAELR.D		QD:QU	0.35

Detailed Protein Report

Protein 276: A disintegrin and metalloproteinase with thrombospondin motifs 16 preproprotein [Homo sapiens]

Accession:	gi|110735441	**Score:**	28.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	136.1
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	2

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
1728	1	636.2813	0.97	2	51.9	15.9	2	1214-1224	K.QCCKTCSKSNL.-	Carbamidomethyl: 2

Detailed Protein Report

Protein 277: **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 278: PREDICTED: replication initiator 1 isoform X5 [Homo sapiens]

Accession:	gi|578814165	**Score:**	28.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.8
Database Date:	2015-11-30	**pI:**	12.1
		Sequence Coverage [%]:	2.7
		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
1480	1	555.1330	-245.75	2	47.0	11.1	2	112-120	R.AHRCAHCRR.H	

Detailed Protein Report

Protein 279: 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: 28.4
MW [kDa]: 122.8
pI: 10.2
Sequence Coverage [%]: 2.3
No. of unique Peptides: 2

```
        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
2690	5	698.3734	-42.95	2	62.6	16.9	0	2-13	M.PVVWPTLLDLSR.D	
2683	2	822.4436	13.69	2	64.6	11.5	1	1054-1068	R.KIDPPAVPATGQFMR.I	Oxidation: 14

Detailed Protein Report

Protein 280: **NF-kappa-B inhibitor zeta isoform a [Homo sapiens]**

Accession:	gi|13899229	**Score:**	28.4
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 281: FERM and PDZ domain-containing protein 1 [Homo sapiens]

Accession:	gi|239582741	**Score:**	28.4
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 [%]:**	1.5
		No. of unique Peptides:	2

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
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

Protein 282: **PREDICTED: T-complex protein 11-like protein 1 isoform X2 [Homo sapiens]**

Accession:	gi|578820625	**Score:**	28.3
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:	2

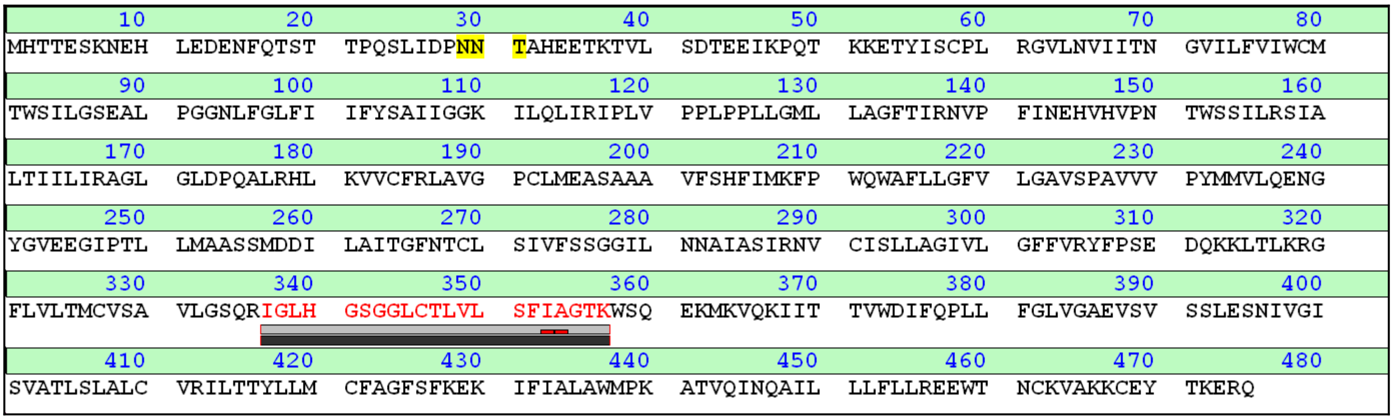
10	20	30	40	50	60	70	80
MMGTLCAPAR	DEEVKKLKDI	KEIVPLFREI	FSVLDLMKVD	MANFAISSIR	PHLMQQSVEY	ERKKFQEILE	RQPNSLDFVT
90	100	110	120	130	140	150	160
QWLEEASEDL	MTQKYKHALP	VGGMAAGSGD	MPRLSPVAVQ	NYAYLKLLKW	DHLQRPFPET	VLMDQSRFHE	LQLQLEQLTI
170	180	190	200	210	220	230	240
LGAVLLVTFS	MAAPGISSQA	DFAEKLKMIV	KILLTDMHLP	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
117	1	1096.9944	-98.96	2	30.2	18.2	2	236-255	K.ETVLKGQIQAVASPDDPIRR.I	

Detailed Protein Report

Protein 283: sodium/hydrogen exchanger 9B1 isoform 2 [Homo sapiens]

Accession:	gi|154937338	**Score:**	28.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.2
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Carbamidomethyl	**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 284: **PREDICTED: serine/threonine-protein kinase ULK2 isoform X1 [Homo sapiens]**

Accession:	gi|578830126	**Score:**	28.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.3
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 4.25 **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
2179	1	766.3372	-117.94	2	55.9	10.0	2	32-44	K.TDWEVAIKSINKK.N		QD:QU 4.25
1434	1	458.6103	-303.83	2	48.1	18.1	0	231-238	R.SLMPSIPR.E	Oxidation: 3	

Detailed Protein Report

Protein 285: mitochondrial ornithine transporter 1 [Homo sapiens]

Accession:	gi|7657585	**Score:**	28.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.7
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	11.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKSNPAIQAA	IDLTAGAAGG	TACVLTGQPF	DTMKVKMQTF	PDLYRGLTDC	CLKTYSQVGF	RGFYKGTSPA	LIANIAENSV
90	100	110	120	130	140	150	160
LFMCYGFCQQ	VVRKVAGLDK	QAKLSDLQNA	AAGSFASAFA	ALVLCPTELV	KCRLQTMYEM	ETSGKIAKSQ	NTVWSVIKSI
170	180	190	200	210	220	230	240
LRKDGPLGFY	HGLSSTLLRE	VPGYFFFFGG	YELSRSFFAS	GRSKDELGPV	PLMLSGGVGG	ICLWLAVYPV	DCIKSRIQVL
250	260	270	280	290	300	310	
SMSGKQAGFI	RTFINVVKNE	GITALYSGLK	PTMIRAFPAN	GALFLAYEYS	RKLMMNQLEA	Y	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1595	1	932.5310	29.48	2	50.2	10.2	0	259-275	K.NEGITALYSGLKPTMIR.A	

Detailed Protein Report

Protein 286: 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

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
662	1	593.6995	-211.24	2	38.3	11.3	1	513-523	R.ELEAKAGELAR.A	

Detailed Protein Report

Protein 287: PREDICTED: otoferlin isoform X1 [Homo sapiens]

Accession:	gi|530368284	**Score:**	28.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	225.9
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

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
1211	2	839.3736	-36.62	2	45.3	13.7	2	181-195	R.DDEHKAGRSVFSAMK.L	

Detailed Protein Report

Protein 288: PREDICTED: YLP motif-containing protein 1 isoform X1 [Homo sapiens]

Accession:	gi|530404193	**Score:**	28.0
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

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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
44	1	767.2360	-155.99	2	30.4	11.8	1	1673-1685	R.STFETEHAGQRDR.Y	
2554	2	746.4789	26.21	1	62.6	16.2	0	1835-1840	R.IVVIMR.G	Oxidation: 5

Detailed Protein Report

Protein 289: PREDICTED: CLIP-associating protein 1 isoform X9 [Homo sapiens]

Accession:	gi|578803955	**Score:**	27.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	162.2
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

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

Detailed Protein Report

Protein 290: **PREDICTED: peregrin isoform X6 [Homo sapiens]**

Accession:	gi|530373123	**Score:**	27.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.0
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	4.3
		No. of unique 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
1974	1	757.2741	-191.30	2	55.1	10.7	0	506-520	R.AAAPVVSVPCIPPHR.L	

Detailed Protein Report

Protein 291: trinucleotide repeat-containing gene 18 protein [Homo sapiens]

Accession:	gi|169658378	**Score:**	27.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	314.3
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	0.8
		No. of unique 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]

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
1643	1	713.3402	-67.63	2	50.8	15.8	2	2464-2476	K.LDHEGVTSPKSKK.A	

Detailed Protein Report

Protein 292: uncharacterized protein C12orf60 [Homo sapiens]

Accession:	gi|157389009	**Score:**	27.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.6
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	11.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530399044	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein C12orf60 isoform X2 [Homo sapiens]
gi|530399042	refseq_human (refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein C12orf60 isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MSSESEKDKE RLIQAAKMFF FHVQDLASVI NTLTELFSRS MNTQILLMAV KNNSYIKDFF EQMLKIFKEM QSVVDARHDK
        90        100        110        120        130        140        150        160
IQKESLCSKV AMAMCSVVQK STNVEELHQS AKEVFKSAHT PVIISVLNSS NILGSLESSL SHLMKFPIMN LQLSDFYTED
       170        180        190        200        210        220        230        240
TKEQSDVTTS ERTRSPPGSS KTTMIDTLKK LQDVLKTEDS KNPTKSAADL LEQIVKAMGP ILEILQKAIK TMEMNISVFK
       250
KASDK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2000	1	918.3556	-135.68	2	55.4	15.0	2	173-189	R.TRSPPGSSKTTMIDTLK.K	Oxidation: 12

Detailed Protein Report

Protein 293: 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 294: **ubiquitin carboxyl-terminal hydrolase 35 [Homo sapiens]**

Accession:	gi|148746183	**Score:**	27.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	113.3
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.2
		No. of unique 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
1261	1	1070.0005	-62.40	2	45.9	12.2	1	131-150	R.TVCERPGPAACAQVARLLAR.H	Carbamidomethyl: 3

Detailed Protein Report

Protein 295: PREDICTED: cullin-9 isoform X3 [Homo sapiens]

Accession:	gi|578811520	**Score:**	27.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	268.2
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MVGERHAGDL MVPLGPRLQA YPEELIRQRP GHDGHPEYLI RWSVLKCGEV GKVGVEEGKA EHILMWLSAP EVYANCPGLL
        90        100        110        120        130        140        150        160
GERALSKGLQ HEPAGVSGSF PRDPGGLDEV AMGEMEADVQ ALVRRAARQL AESGTPSLTA AVLHTIHVLS AYASIGPLTG
       170        180        190        200        210        220        230        240
VFRETGALDL LMHMLCNPEP QIRRSAGKML QALAAHDAGS RAHVLLSLSQ QDGIEQHMDF DSRYTLLELF AETTSSEEHC
       250        260        270        280        290        300        310        320
MAFEGIHLPQ IPGKLLFSLV KRYLCVTSLL DQLNSSPELG AGDQSSPCAT REKSRGQREL EFSMAVGNLI SELVRSMGWA
       330        340        350        360        370        380        390        400
RNLSEQGMSP PRPTRSIFQP YISGPSLLLP TIVTTPRRQG WVFRQRSEFS SRSGYGEYVQ QTLQPGMRVR MLDDYEEISA
       410        420        430        440        450        460        470        480
GDEGEFRQSN NGIPPVQTLG EKALGEISVS VEMAESLLQV LSSRFEGSTL NDLLNSQIYT KYGLLSNEPS SSSTSRNHSC
       490        500        510        520        530        540        550        560
TPDPEEESKS EASFSEEETE SLKAKAEAPK TEAEPTKTRT ETPMAQSDSQ LFNQLLVTEG MTLPTEMKEA ASEMARALRG
       570        580        590        600        610        620        630        640
PGPRSSLDQH VAAVVATVQI SSLDTNLQLS GLSALSQAVE EVTERDHPLV RPDRSLREKL VKMLVELLTN QVGEKMVVVQ
       650        660        670        680        690        700        710        720
ALRLLYLLMT KHEWRPLFAR EGGIYAVLVC MQEYKTSVLV QQAGLAALKM LAVASSSEIP TFVTGRDSIH SLFDAQMTRE
       730        740        750        760        770        780        790        800
IFASIDSATR PGSESLLLTV PAAVILMLNT EGCSSAARNG LLLLNLLLCN HHTLGDQIIT QELRDTLFRH SGIAPRTEPM
       810        820        830        840        850        860        870        880
PTTRTILMML LNRYSEPPGS PERAALETPI IQGQDGSPEL LIRSLVGGPS AELLLDLERV LCREGSPGGA VRPLLKRLQQ
       890        900        910        920        930        940        950        960
ETQPFLLLLR TLDAPGPNKT LLLSVLRVIT RLLDFPEAMV LPWHEVLEPC LNCLSGPSSD SEIVQELTCF LHRLASMHKD
       970        980        990       1000       1010       1020       1030       1040
YAVVLCCLGA KEILSKVLDK HSAQLLLGCE LRDLVTECEK YAQLYSNLTS SILAGCIQMV LGQIEDHRRT HQPINIPFFD
      1050       1060       1070       1080       1090       1100       1110       1120
VFLRHLCQGS SVEVKEDKCW EKVEVSSNPH RASKLTDHNP KTYWESNGST GSHYITLHMH RGVLVRQLTL LVASEDSSYM
      1130       1140       1150       1160       1170       1180       1190       1200
PARVVVFGGD STSCIGTELN TVNVMPSASR VILLENLNRF WPIIQIRIKR CQQGGIDTRV RGVEVLGPKP TFWPLFREQL
      1210       1220       1230       1240       1250       1260       1270       1280
CRRTCLFYTI RAQAWSRDIA EDHRRLLQLC PRLNRVLRHE QNFADRFLPD DEAAQALGKT CWEALVSPLV QNITSPDAEG
      1290       1300       1310       1320       1330       1340       1350       1360
VSALGWLLDQ YLEQRETSRN PLSRAASFAS RVRRLCHLLV HVEPPPGPSP EPSTRPFSKN SKGRDRSPAP SPVLPSSSLR
      1370       1380       1390       1400       1410       1420       1430       1440
NITQCWLSVV QEQVSRFLAA AWRAPDFVPR YCKLYEHLQR AGSELFGPRA AFMLALRSGF SGALLQQSFL TAAHMSEQFA
      1450       1460       1470       1480       1490       1500       1510       1520
RYIDQQIQGG LIGGAPGVEM LGQLQRHLEP IMVLSGLELA TTFEHFYQHY MADRLLSFGS SWLEGAVLEQ IGLCFPNRLP
      1530       1540       1550       1560       1570       1580       1590       1600
QLMLQSLSTS EELQRQFHLF QLQRLDKLFL EQEDEEEKRL EEEEEEEEEE EAEKELFIED PSPAISILVL SPRCWPVSPL
      1610       1620       1630       1640       1650       1660       1670       1680
CYLYHPRKCL PTEFCDALDR FSSFYSQSQN HPVLDMGPHR RLQWTWLGRA ELQFGKQILH VSTVQMWLLL KFNQTEEVSV
      1690       1700       1710       1720       1730       1740       1750       1760
ETLLKDSDLS PELLLQALVP LTSGNGPLTL HEGQDFPHGG VLRLHEPGPQ RSGEALWLIP PQAYLNVEKD EGRTLEQKRN
      1770       1780       1790       1800       1810       1820       1830       1840
LLSCLLVRIL KAHGEKGLHI DQLVCLVLEA WQKGPNPPGT LGHTVAGGVA CTSTDVLSCI LHLLGQGYVK RRDDRPQILM
      1850       1860       1870       1880       1890       1900       1910       1920
YAAPEPMGPC RGQADVPFCG SQSETSKPSP EAVATLASLQ LPAGRTMSPQ EVEGLMKQTV RQVQETLNLE PDVAQHLLAH
      1930       1940       1950       1960       1970       1980       1990       2000
SHWGAEQLLQ SYSEDPEPLL LAAGLCVHQA QAVPVRPDHC PVCVSPLGCD DDLPSLCCMH YCCKSCWNEY LTTRIEQNLV
      2010       2020       2030       2040       2050       2060       2070       2080
LNCTCPIADC PAQPTGAFIR AIVSSPEVIS KYEKALLRGY VESCSNLTWC TNPQGCDRIL CRQGLGCGTT CSKCGWASCF
      2090       2100       2110       2120       2130       2140       2150       2160
NCSFPEAHYP ASCGHMSQWV DDGGYYDGMS VEAQSKHLAK LISKRCPSCQ APIEKNEGCL HMTCAKCNHG FCWRCLKSWK
      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
2528	1	938.1784	46.28	3	60.3	13.1	2	164-188	R.ETGALDLLMHMLCNPEPQIRRSAGK.M	Oxidation: 9, 11
949	1	737.3420	-85.80	1	40.4	14.7	0	790-796	R.HSGIAPR.T	

Detailed Protein Report

Protein 296: **PREDICTED: sterol regulatory element-binding protein 1 isoform X2 [Homo sapiens]**

Accession:	gi|578830023	**Score:**	27.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.1
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 1.31 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MDCTFEDMLQ	LINNQDSDFP	GLFDPPYAGS	GAGGTDPASP	DTSSPGSLSP	PPATLSSSLE	AFLSGPQAAP	SPLSPPQPAP
90	100	110	120	130	140	150	160
TPLKMYPSMP	AFSPGPGIKE	ESVPLSILQT	PTPQPLPGAL	LPQSFPAPAP	PQFSSTPVLG	YPSPPGGFST	GSPPGNTQQP
170	180	190	200	210	220	230	240
LPGLPLASPP	GVPPVSLHTQ	VQSVVPQQLL	TVTAAPTAAP	VTTTVTSQIQ	QVPVLLQPHF	IKADSLLLTA	MKTDGATVKA
250	260	270	280	290	300	310	320
AGLSPLVSGT	TVQTGPLPTL	VSGGTILATV	PLVVDAEKLP	INRLAAGSKA	PASAQSRGEK	RTAHNAIEKR	YRSSINDKII
330	340	350	360	370	380	390	400
ELKDLVVGTE	AKLNKSAVLR	KAIDYIRFLQ	HSNQKLKQEN	LSLRTAVHKS	KSLKDLVSAC	GSGGNTDVLM	EGVKTEVEDT
410	420	430	440	450	460	470	480
LTPPPSDAGS	PFQSSPLSLG	SRGSGSGGSG	SDSEPDSPVF	EDSKAKPEQR	PSLHSRGMLD	RSRLALCTLV	FLCLSCNPLA
490	500	510	520	530	540	550	560
SLLGARGLPS	PSDTTSVYHS	PGRNVLGTES	RDGPGWAQWL	LPPVVWLLNG	LLVLVSLVLL	FVYGEPVTRP	HSGPAVYFWR
570	580	590	600	610	620	630	640
HRKQADLDLA	RGDFAQAAQQ	LWLALRALGR	PLPTSHLDLA	CSLLWNLIRH	LLQRLWVGRW	LAGRAGGLQQ	DCALRVDASA
650	660	670	680	690	700	710	720
SARDAALVYH	KLHQLHTMGK	HTGGHLTATN	LALSALNLAE	CAGDAVSVAT	LAEIYVAAAL	RVKTSLPRAL	HFLTRFFLSS
730	740	750	760	770	780	790	800
ARQACLAQSG	SVPPAMQWLC	HPVGHRFFVD	GDWSVLSTPW	ESLYSLAGNP	VDPLAQVTQL	FREHLLERAL	NCVTQPNPSP
810	820	830	840	850	860	870	880
GSADGDKEFS	DALGYLQLLN	SCSDAAGAPA	YSFSISSSMA	TTTGVDPVAK	WWASLTAVVI	HWLRRDEEAA	ERLCPLVEHL
890	900	910	920	930	940	950	960
PRVLQESERP	LPRAALHSFK	AARALLGCAK	AESGPASLTI	CEKASGYLQD	SLATTPASSS	IDKAVQLFLC	DLLLVVRTSL
970	980	990	1000	1010	1020	1030	1040
WRQQQPPAPA	PAAQGTSSRP	QASALELRGF	QRDLSSLRRL	AQSFRPAMRR	VFLHEATARL	MAGASPTRTH	QLLDRSLRRR
1050	1060	1070	1080	1090	1100	1110	1120
AGPGGKGGAV	AELEPRPTRR	EHAEALLLAS	CYLPPGFLSA	PGQRVGMLAE	AARTLEKLGD	RRLLHDCQQM	LMRLGGGTTV
1130							
TSS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
783	1	676.8811	19.88	2	39.8	12.5	0	1047-1059	K.GGAVAELEPRPTR.R		QD:QU	1.31

Detailed Protein Report

Protein 297: PREDICTED: ubiquitin-protein ligase E3C isoform X3 [Homo sapiens]

Accession:	gi|530387311	**Score:**	27.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	116.7
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFSFEGDFKT	RPKVSLGGAS	RKEEKASLLH	RTQEERRKRE	EERRRLKNAI	IIQSFIRGYR	DRKQQYSIQR	SAFDRCATLS
90	100	110	120	130	140	150	160
QSGGAFPIAN	GPNLTLLVRQ	LLFFYKQNED	SKRLIWLYQN	LIKHSSLFVK	QLDGSERLTC	LFQIKRLMSL	CCRLLQNCND
170	180	190	200	210	220	230	240
DSLNVALPMR	MLEVFSSENT	YLPVLQDASY	VVSVIEQILH	YMIHNGYYRS	LYLLINSKLP	SSIEYSDLSR	VPIAKILLEN
250	260	270	280	290	300	310	320
VLKPLHFTYN	SCPEGARQQV	FTAFTEEFLA	APFTDQIFHF	IIPALADAQT	VFPYEPFLNA	LLLIESRCSR	KSGGAPWLFY
330	340	350	360	370	380	390	400
FVLTVGENYL	GALSEEGLLV	YLRVLQTFLS	QLPVSPASAS	CHDSASDSEE	ESEEADKPSS	PEDGRLSVSY	ITEECLKKLD
410	420	430	440	450	460	470	480
TKQQTNTLLN	LVWRDSASEE	VFTTMASVCH	TLMVQHRMMV	PKVRLLYSLA	FNARFLRHLW	FLISSMSTRM	ITGSMVPLLQ
490	500	510	520	530	540	550	560
VISRGSPMSF	EDSSRIIPLF	YLFSSLFSHS	LISIHDNEFF	GDPIEVVGQR	QSSMMPFTLE	ELIMLSRCLR	DACLGIIKLA
570	580	590	600	610	620	630	640
YPETKPEVRE	EYITAFQSIG	VTTSSEMQQC	IQMEQKRWIQ	LFKVITNLVK	MLKSRDTRRN	FCPPNHWLSE	QEDIKADKIF
650	660	670	680	690	700	710	720
QRLIYADKQE	VQGDGPFLDG	INVTIRRNYI	YEDAYDKLSP	ENEPDLKKRI	RVHLLNAHGL	DEAGIDGGGI	FREFLNELLK
730	740	750	760	770	780	790	800
SGFNPNQGFF	KTTNEGLLYP	NPAAQMLVGD	SFARHYYFLG	RMLGKALYEN	MLVELPFAGF	FLSKLLGTSA	DVDIHHLASL
810	820	830	840	850	860	870	880
DPEVYKNLLF	LKSYEDDVEE	LGLNFTVVNN	DLGEAQVVEL	KFGGKDIPVT	SANRIAYIHL	VADYRLNRQI	RQHCLAFRQG
890	900	910	920	930	940	950	960
LANVVSLEWL	RMFDQQEIQV	LISGAQVPIS	LEDLKSFTNY	SGGYSADHPV	IKVFWRVVEG	FTDEEKRKLL	KFVTSCSRPP
970	980	990	1000	1010	1020	1030	
LLGFKELYPA	FCIHNGGSDL	ERLPTASTCM	NLLKLPEFYD	ETLLRSKLLY	AIECAAGFEL	S	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2489	4	817.4835	32.82	1	61.7	16.0	0	124-130	K.HSSLFVK.Q	

Detailed Protein Report

Protein 298: PREDICTED: protein FAM65C isoform X2 [Homo sapiens]

Accession:	gi|578835791	**Score:**	27.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	105.1
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.99 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVTTMSVRLR	FLSPGDTGAV	GVVGRSASFA	GFSSAQSRRI	ANSVRSRMPA	KSSKMYGTLR	KGSVCADPKP	QQVKKIFEAL
90	100	110	120	130	140	150	160
KRGLKEYLCV	QQAELDHLSG	RHKDTRRNSR	LAFYYDLDKQ	TRCVERHIRK	MEFHISKVDE	LYEDYCIQCR	LRDGASSMQR
170	180	190	200	210	220	230	240
AFARCPPSRA	ARESLQELGR	SLHECAEDMW	LIEGALEVHL	GEFHIRMKGL	VGYARLCPGD	HYEVLMRLGR	QRWKLKGRIE
250	260	270	280	290	300	310	320
SDDSQTWDEE	EKAFIPTLHE	NLDIKVTELR	GLGSLAVGAV	TCDIADFFTT	RPQVIVVDIT	ELGTIKLQLE	VQWNPFDTES
330	340	350	360	370	380	390	400
FLVSPSPTGK	FSMGSRKGSL	YNWTPPSTPS	FRERYYLSVL	QQPTQQALLL	GGPRATSILS	YLSDSDLRGP	SLRSQSQELP
410	420	430	440	450	460	470	480
EMDSFSSEDP	RDTETSTSAS	TSDVGFLPLT	FGPHASIEEE	AREDPLPPGL	LPEMAHLSGG	PFAEQPGWRN	LGGESPSLPQ
490	500	510	520	530	540	550	560
GSLFHSGTAS	SSQNGHEEGA	TGDREDGPGV	ALEGPLQEVL	ELLRPTDSTQ	PQLRELEYQV	LGFRDRLKPC	RARQEHTSAE
570	580	590	600	610	620	630	640
SLMECILESF	AFLNADFALD	ELSLFGGSQG	LRKDRPLPPP	SSLKASSREL	TAGAPELDVL	LMVHLQVCKA	LLQKLASPNL
650	660	670	680	690	700	710	720
SRLVQECLLE	EVAQQKHVLE	TLSVLDFEKV	GKATSIEEII	PQASRTKGCL	KLWRGCTGPG	RVLSCPATTL	LNQLKKTFQH
730	740	750	760	770	780	790	800
RVRGKYPGQL	EIACRRLLEQ	VVSCGGLLPG	AGLPEEQIIT	WFQFHSYLQR	QSVSDLEKHF	TQLTKEVTLI	EELHCAGQAK
810	820	830	840	850	860	870	880
VVRKLQGKRL	GQLQPLPQTL	RAWALLQLDG	TPRVCRAASA	RLAGAVRNRS	FREKALLFYT	NALAENDARL	QQAACLALKH
890	900	910	920	930	940	950	
LKGIESIDQT	ASLCQSDLEA	VRAAARETTL	SFGEKGRLAF	EKMDKLCSEQ	REVFCQEADV	EITIF	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1153	2	583.8250	97.26	2	44.6	14.3	1	923-931	K.MDKLCSEQR.E	Carbamidomethyl: 5	QD:QU 0.99

Detailed Protein Report

Protein 299: prokineticin-2 isoform b precursor [Homo sapiens]

Accession:	gi|17530787	**Score:**	27.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.7
Database Date:	2015-11-30	**pI:**	12.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	15.7
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MRSLCCAPLL LLLLLPPLLL TPRAGDAAVI TGACDKDSQC GGGMCCAVSI WVKSIRICTP MGKLGDSCHP LTRKVPFFGR

        90        100        110
RMHHTCPCLP GLACLRTSFN RFICLAQK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2732	3	937.4633	79.63	2	63.1	12.6	0	37-53	K.DSQCGGGMCCAVSIWVK.S	Carbamidomethyl: 4, 10; Oxidation: 8
2648	2	937.4596	75.76	2	61.9	15.1	0	37-53	K.DSQCGGGMCCAVSIWVK.S	Carbamidomethyl: 4, 9; Oxidation: 8

Detailed Protein Report

Protein 300: PREDICTED: protein angel homolog 2 isoform X1 [Homo sapiens]

Accession:	gi|530366645	**Score:**	27.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.7
Database Date:	2015-11-30	**pI:**	7.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:** 1.13	**CV:** 0.00 %	**No. of 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	Ratios
910	1	866.9745	93.61	2	41.4	12.5	1	28-41	R.HISSCMRWPGHYSR.A	Oxidation: 6	QD:QU 1.13

Detailed Protein Report

Protein 301: EGF domain-specific O-linked N-acetylglucosamine transferase isoform a precursor [Homo sapiens]

Accession: gi|522838254
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 27.6
MW [kDa]: 62.0
pI: 6.6
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 302: SPRY domain-containing SOCS box protein 2 [Homo sapiens]

Accession:	gi|14249178	**Score:**	27.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.6
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.9
		No. of unique Peptides:	2

Quantitation

QD:QU	**Median:** 2.18	**CV:** 483.35 %	**No. of Peptides:** 2

Alias proteins:

Accession	Name	Description
gi|226423903	refseq_human (refseq_human_20140103.fasta)	SPRY domain-containing SOCS box protein 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MGQTALAGGS	SSTPTPQALY	PDLSCPEGLE	ELLSAPPPDL	GAQRRHGWNP	KDCSENIEVK	EGGLYFERRP	VAQSTDGARG
90	100	110	120	130	140	150	160
KRGYSRGLHA	WEISWPLEQR	GTHAVVGVAT	ALAPLQTDHY	AALLGSNSES	WGWDIGRGKL	YHQSKGPGAP	QYPAGTQGEQ
170	180	190	200	210	220	230	240
LEVPERLLVV	LDMEEGTLGY	AIGGTYLGPA	FRGLKGRTLY	PAVSAVWGQC	QVRIRYLGER	RAEPHSLLHL	SRLCVRHNLG
250	260	270					
DTRLGQVSAL	PLPPAMKRYL	LYQ					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
290	2	642.3243	-17.35	2	32.3	15.8	1	233-243	R.LCVRHNLGDTR.L		QD:QU	0.37
2133	2	797.3986	-78.05	2	57.0	11.7	1	244-258	R.LGQVSALPLPPAMKR.Y	Oxidation: 13	QD:QU	13.04

Detailed Protein Report

Protein 303: 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

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
1647	1	524.8144	75.03	2	50.8	12.8	2	12-20	R.QRGRSMASR.G	

Detailed Protein Report

Protein 304: zinc finger protein 622 [Homo sapiens]

Accession:	gi|15529978	**Score:**	27.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.2
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.5
		No. of unique Peptides:	2

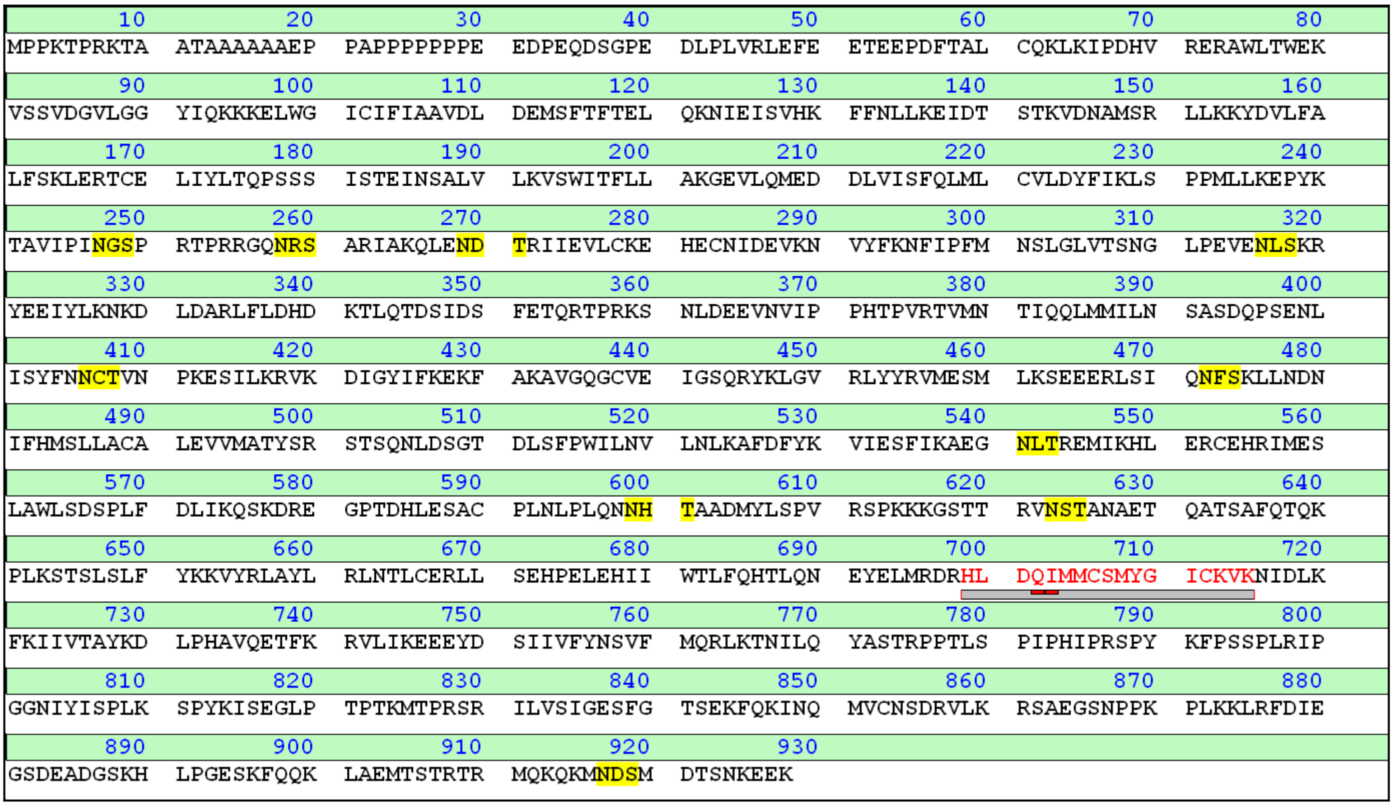
10	20	30	40	50	60	70	80
MATYTCITCR	VAFRDADMQR	AHYKTDWHRY	NLRRKVASMA	PVTAEGFQER	VRAQRAVAEE	ESKGSATYCT	VCSKKFASFN
90	100	110	120	130	140	150	160
AYENHLKSRR	HVELEKKAVQ	AVNRKVEMMN	EKNLEKGLGV	DSVDKDAMNA	AIQQAIKAQP	SMSPKKAPPA	PAKEARNVVA
170	180	190	200	210	220	230	240
VGTGGRGTHD	RDPSEKPPRL	QWFEQQAKKL	AKQQEEDSEE	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
2687	2	973.5040	65.98	2	64.7	14.9	2	15-29	R.DADMQRAHYKTDWHR.Y	Oxidation: 4
1757	1	560.2452	1.92	2	52.3	12.6	0	64-74	K.GSATYCTVCSK.K	

Detailed Protein Report

Protein 305: 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; Oxidation: 6, 10

Detailed Protein Report

Protein 306: **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 307: 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

Protein 308: phosphoglycerate kinase 1 [Homo sapiens]

Accession:	gi|4505763	**Score:**	27.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.6
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 1.26 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSLSNKLTLD	KLDVKGKRVV	MRVDFNVPMK	NNQITNNQRI	KAAVPSIKFC	LDNGAKSVVL	MSHLGRPDGV	PMPDKYSLEP
90	100	110	120	130	140	150	160
VAVELKSLLG	KDVLFLKDCV	GPEVEKACAN	PAAGSVILLE	NLRFHVEEEG	KGKDASGNKV	KAEPAKIEAF	RASLSKLGDV
170	180	190	200	210	220	230	240
YVNDAFGTAH	RAHSSMVGVN	LPQKAGGFLM	KKELNYFAKA	LESPERPFLA	ILGGAKVADK	IQLINNMLDK	VNEMIIGGGM
250	260	270	280	290	300	310	320
AFTFLKVLNN	MEIGTSLFDE	EGAKIVKDLM	SKAEKNGVKI	TLPVDFVTAD	KFDENAKTGQ	ATVASGIPAG	WMGLDCGPES
330	340	350	360	370	380	390	400
SKKYAEAVTR	AKQIVWNGPV	GVFEWEAFAR	GTKALMDEVV	KATSRGCITI	IGGGDTATCC	AKWNTEDKVS	HVSTGGGASL
410	420						
ELLEGKVLPG	VDALSNI						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2285	1	884.8843	-99.45	2	59.0	27.4	0	107-123	K.ACANPAAGSVILLENLR.F	Carbamidomethyl: 2	QD:QU 1.26

BRUKER

Detailed Protein Report

Protein 309: chromodomain-helicase-DNA-binding protein 2 isoform 1 [Homo sapiens]

Accession: gi|118421089
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 27.3
MW [kDa]: 211.2
pI: 8.8
Sequence Coverage [%]: 1.7
No. of unique Peptides: 2

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	m/z meas.	Δ m/z	z	Rt	Score	P	Range	Sequence	Modification

	Cmpds.		[ppm]		[min]					
1777	2	1022.8922	-139.78	2	52.6	14.7	2	932-948	K.KMVLDHLVIQRMDTTGR.T	Oxidation: 2, 12
2192	1	885.2814	-167.85	2	57.8	12.6	0	1221-1234	K.SIIQHEEEFEMLHK.S	

Detailed Protein Report

Protein 310: 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 311: insulin receptor-related protein precursor [Homo sapiens]

Accession:	gi|31657140	**Score:**	27.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	143.6
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.15 **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	QD:QU 0.15

Detailed Protein Report

Protein 312: fibronectin isoform 6 preproprotein [Homo sapiens]

Accession:	gi|47132549	**Score:**	27.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	239.5
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

Detailed Protein Report

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						
CFMPLDVQAD	REDSRE						

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

	Cmpds.		[ppm]		[min]					
2765	1	904.4689	14.28	2	65.7	16.9	0	923-938	K.VTIMWTPPESAVTGYR.V	

Detailed Protein Report

Protein 313: 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 314: syntaxin-binding protein 5 isoform b [Homo sapiens]

Accession:	gi|189217915	**Score:**	27.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	127.5
Database Date:	2015-11-30	**pI:**	7.1
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	2

```
        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
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 315: PREDICTED: serine/threonine-protein kinase WNK2 isoform X12 [Homo sapiens]

Accession:	gi|578817784	**Score:**	27.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	227.1
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:** 2.32	**CV:** 0.00 %	**No. of Peptides:** 1

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	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1286	1	945.9319	-64.24	2	46.2	11.9	2	2129-2147	R.GGQRVGSKTASFAASDPVR.S		QD:QU 2.32

Detailed Protein Report

Protein 316: PREDICTED: cyclin-dependent kinase-like 1 isoform X1 [Homo sapiens]

Accession:	gi|530404810	**Score:**	27.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	108.9
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
MELSTDTGWN	QKSNFPPCDS	RVSKEEAQLP	FPTPSSYGAD	SSNQTYAHKS	QSEREQHKEV	RAVLNHCSGL	DGGEESGLCG
90	100	110	120	130	140	150	160
TSTRIDAGTG	NGTDDKVTDQ	HRHRRCLQGT	KGNNRGSEVW	GLLLQGNVDR	SGGAPSAGVL	LRRRGYSCAL	HGLRKFANLA
170	180	190	200	210	220	230	240
GLLSRQQDSA	RGVSHHSRLK	IHFKKIYSSM	MEKYEKIGKI	GEGSYGVVFK	CRNRDTGQIV	AIKKFLESED	DPVIKKIALR
250	260	270	280	290	300	310	320
EIRMLKAPSP	YAAEPSLCGM	KMVRRGKKEF	LPAVAEKVDA	PSGVGGQGQD	SVTVGSLGRR	STYGRKQEKQ	VRQREGIIYC
330	340	350	360	370	380	390	400
YVAVLLRIYY	FDQGCVAREE	EQFQELVFGP	FCHIGSYFTG	HRTNVRPYIL	LLSRPSPFKT	AAGTYEAGLV	ILECSYFLAE
410	420	430	440	450	460	470	480
QEPYCPTQAL	QQPHPIIGPW	ALEGGGVESK	EDRHPPPKEA	PASCEGFLRS	AVPKQAYTPF	KTSPDKRLSD	CVATPPWAPP
490	500	510	520	530	540	550	560
TPLIISSGVL	VAICSMIDPV	PEFHSEGLLA	KATSGSAGIL	VWIFLCNDAF	IYGKYILRSG	VLWVRGLPGF	KSEAAALCHK
570	580	590	600	610	620	630	640
CYSSADPKRE	QQQDLLQRVK	EQSFHSVNGA	QARHKGSPSP	HQTQEPSWPH	PVDPTPGHRW	SCLPVPCRAP	ALLSPWVVDG
650	660	670	680	690	700	710	720
TGCCGAGGGS	DRGGSAAQEP	TQLKHPNLVN	LLEVFRRKRR	LHLVFEYCDH	TVLHELDRYQ	RGICNIFVCT	GRRLGEHTEA
730	740	750	760	770	780	790	800
LSKKKKKGGG	GPFLKLRAAS	CRITLFKNVG	CGLETTGDLS	LNSGGGAASR	GVAAALRALV	CGTELTSSDS	PQRCIHRDVK
810	820	830	840	850	860	870	880
PENILITKHS	VIKLCDFGFA	RLLTGPSDYY	TDYVATRWYR	SPELLVGDTQ	YGPPVDVWAI	GCVFAELLSG	VPLWPGKSDV
890	900	910	920	930	940	950	960
DQLYLIRKTL	GDLIPRHQQV	FSTNQYFSGV	KIPDPEDMSL	CLSVTLTEGG	LLASGAVKRS	QMGSSVSQAT	SWPHPDIVAE
970	980	990	1000				
TAELDDIAMA	RQTPVMLRFN	RQKEQEKYLS	YGA				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2221	1	1032.3950	-114.27	2	56.4	16.5	2	247-265	K.APSPYAAEPSLCGMKMVRR.G	

Detailed Protein Report

Protein 317: **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

Quantitation

QD:QU **Median:** 0.73 **CV:** 0.00 % **No. of 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	Ratios
1031	1	598.1512	-245.53	2	43.0	26.9	0	281-289	R.FQLMQQQTR.A	Oxidation: 4	QD:QU 0.73

Detailed Protein Report

Protein 318: **E3 ubiquitin-protein ligase TRIP12 isoform c [Homo sapiens]**

Accession:	gi|10863903	**Score:**	26.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	220.3
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	1.7
		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
1915	1	643.3072	-50.38	2	54.3	12.5	2	133-145	K.AHTRKSGATGGSR.S	
2359	1	974.1497	149.86	2	60.0	14.5	2	1067-1086	R.TAGGSGLARAASKDTISNNR.E	

Detailed Protein Report

Protein 319: **PREDICTED: MAM domain-containing glycosylphosphatidylinositol anchor protein 1 isoform X2 [Homo sapiens]**

Accession:	gi|578811587	**Score:**	26.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.5
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEVTCLLLLA	LIPFHCRGQG	VYAPAQAQIV	HAGQACVVKE	DNISERVYTI	REGDTLMLQC	LVTGHPRPQV	RWTKTAGSAS
90	100	110	120	130	140	150	160
DKFQETSVFN	ETLRIERIAR	TQGGRYYCKA	ENGVGVPAIK	SIRVDVQYLD	EPMLTVHQTV	SDVRGNFYQE	KTVFLRCTVN
170	180	190	200	210	220	230	240
SNPPARFIWK	RGSDTLSHSQ	DNGVDIYEPL	YTQGETKVLK	LKNLRPQDYA	SYTCQVSVRN	VCGIPDKAIT	FRLTNTTAPP
250	260	270	280	290	300	310	320
ALKLSVNETL	VVNPGENVTV	QCLLTGGDPL	PQLQWSHGPG	PLPLGALAQG	GTLSIPSVQA	RDSGYYNCTA	TNNVGNPAKK
330	340	350	360	370	380	390	400
TVNLLVRSMK	NATFQITPDV	IKESENIQLG	QDLKLSCHVD	AVPQEKVTYQ	WFKNGKPARM	SKRLLVTRND	PELPAVTSSL
410	420	430	440	450	460	470	480
ELIDLHFSDY	GTYLCMASFP	GAPVPDLSVE	VNISSETVPP	TISVPKGRAV	VTVREGSPAE	LQCEVRGKPR	PPVLWSRVDK
490	500	510	520	530	540		
EAALLPSGLP	LEETPDGKLR	LERVSRDMSG	TYRCQTARYN	GFNVRPREAQ	VQLNVQWTR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1451	1	652.4568	150.96	3	46.7	16.5	0	2-17	M.EVTCLLLLALIPFHCR.G	Carbamidomethyl: 4, 15

Detailed Protein Report

Protein 320: PREDICTED: probable E3 ubiquitin-protein ligase HECTD2 isoform X2 [Homo sapiens]

Accession:	gi|530393122	**Score:**	26.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.8
Database Date:	2015-11-30	**pI:**	8.4
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDASSSEMKA	PVLPEPILPI	QPKTVKDFQE	DVEKVKSSGD	WKAVHDFYLT	TFDSFPELNA	AFKKDATASF	NTIEDSGINA
90	100	110	120	130	140	150	160
KFVNAVYDTL	LNTPQDVQKT	VLKGIINSLL	REWKGPRTKD	DLRAYFILLQ	NPQFNNTSTY	VIYAHLLRQI	ATLVEADHHF
170	180	190	200	210	220	230	240
LVHWFKKLSQ	KRFKQLVERL	LQFISLRLFP	AKPEEFPPIT	KCSWWIPSAA	KVLALLNTAN	NLVHPPLIPY	TDFYNSTLDH
250	260	270	280	290	300	310	320
IDLMEEYHTW	QNFGNSHRFS	FCQYPFVISV	AAKKIIIQRD	SEQQMINIAR	QSLVDKVSRR	QRPDMNILFL	NMKVRRTHLV
330	340	350	360	370	380	390	400
SDSLDELTRK	RADLKKKLKV	TFVGEAGLDM	GGLTKEWFLL	LIRQIFHPDY	GMFTYHKDSH	CHWFSSFKCD	NYSEFRLVGI
410	420	430	440	450	460	470	480
LMGLAVYNSI	TLDIRFPPCC	YKKLLSPPII	PSDQNIPVGI	CNVTVDDLCQ	IMPELAHGLS	ELLSHEGNVE	EDFYSTFQVF
490	500	510	520	530	540	550	560
QEEFGIIKSY	NLKPGGDKIS	VTNQNRKEYV	QLYTDFLLNK	SIYKQFAAFY	YGFHSVCASN	ALMLLRPEEV	EILVCGSPDL
570	580	590	600	610	620	630	640
DMHALQRSTQ	YDGYAKTDLT	IKYFWDVVLG	FPLDLQKKLL	HFTTGSDRVP	VGGMADLNFK	ISKNETSTNC	LPVAHTCFNQ
650	660	670					
LCLPPYKSKK	DLKQKLIIGI	SNSEGFGLE					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2703	1	724.8604	-34.28	2	64.9	13.1	0	656-669	K.LIIGISNSEGFGLE.-	

Detailed Protein Report

Protein 321: ERC protein 2 [Homo sapiens]

Accession:	gi|34577114	**Score:**	26.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.5
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	2.7
		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
790	1	572.7630	-120.83	2	38.4	14.6	0	747-756	K.IAELESLTLR.H	

Detailed Protein Report

Protein 322: 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

Detailed Protein Report

Protein 323: 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 324: 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 325: tyrosine-protein kinase SYK isoform 2 [Homo sapiens]

Accession: gi|205277435
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 26.7
MW [kDa]: 69.5
pI: 7.8
Sequence Coverage [%]: 4.9
No. of unique Peptides: 2

Alias proteins:

Accession	Name	Description
gi|293332611	refseq_human (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	
1940	2	643.2750	-142.67	2	54.6	11.3	0	476-486	R.NVLLVTQHYAK.I	

Detailed Protein Report

Protein 326: 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; Oxidation: 2
2247	1	1017.5903	-9.72	2	58.5	14.5	2	884-902	R.KQLAAGRPHTRSTVITAVK.F	

Detailed Protein Report

Protein 327: PREDICTED: sperm flagellar protein 2 isoform X5 [Homo sapiens]

Accession:	gi|578810001	**Score:**	26.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	176.7
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 2.59 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSEILCQWLN	KELKVSRTVS	PKSFAKAFSS	GYLLGEVLHK	FELQDDFSEF	LDSRVSSAKL	NNFSRLEPTL	NLLGVQFDQN
90	100	110	120	130	140	150	160
VAHGIITEKP	GVATKLLYQL	YIALQKKKKS	GLTGVEMQTM	QRLTNLRLQN	MKSDTFQERL	RHMIPRQTDF	NLMRITYRFQ
170	180	190	200	210	220	230	240
EKYKHVKEDL	AHLHFEKLER	FQKLKEEQRC	FDIEKQYLNR	RRQNEIMAKI	QAAIIQIPKP	ASNRTLKALE	AQKMMKKKKE
250	260	270	280	290	300	310	320
AEDVADEIKK	FEALIKKDLQ	AKESASKTSL	DTAGQTTTDL	LNTYSDDEYI	KKIQKRLEED	AFAREQREKR	RRKLLMDQLI
330	340	350	360	370	380	390	400
AHEAQEEAYR	EEQLINRLMR	QSQQERRIAV	QLMHVRHEKE	VLWQNRIFRE	KQHEERRLKD	FQDALDREAA	LAKQAKIDFE
410	420	430	440	450	460	470	480
EQFLKEKRFH	DQIAVERAQA	RYEKHYSVCA	EILDQIVDLS	TKVADYRMLT	NNLIPYKLMH	DWKELFFNAK	PIYEQASVKT
490	500	510	520	530	540	550	560
LPANPSREQL	TELEKRDLLD	TNDYEEYKNM	VGEWALPEEM	VDNLPPSNNC	ILGHILHRLA	EKSLPPRAES	TTPELPSFAV
570	580	590	600	610	620	630	640
KGCLLGKTLS	GKTTILRSLQ	KDFPIQILSI	DTLVQEAIQA	FHDNEKVSEV	LPIQKNDEED	ALPVLQEEIK	ESQDPQHVFS
650	660	670	680	690	700	710	720
AGPVSDEVLP	ETEGETMLSA	NADKTPKAEE	VKSSDSFLKL	TTRAQLGAKS	EQLLKKGKSI	PDVLLVDIIV	NAINEIPVNQ
730	740	750	760	770	780	790	800
DCILDGFPMT	LNQAQLLEEA	LTGCNRNLTE	VERKKAQKST	LAIDPATSKE	IPLPSPAFDF	VILLDVSDTS	SMSRMNDIIA
810	820	830	840	850	860	870	880
EELSYKTAHE	DISQRVAAEN	QDKDGDQNLR	DQIQHRIIGF	LDNWPLLEQW	FSEPENILIK	INAEIDKESL	CEKVKEILTT
890	900	910	920	930	940	950	960
EIAKKKNKVE	KKLEEKEAEK	KAAASLAELP	LPTPPPAPPP	EPEKEKEIHQ	SHVASKTPTA	KGKPQSEAPH	GKQESLQEGK
970	980	990	1000	1010	1020	1030	1040
GKKGETALKR	KGSPKGKSSG	GKVPVKKSPA	DSTDTSPVAI	VPQPPKPGSE	EWVYVNEPVP	EEMPLFLVPY	WELIENSYIN
1050	1060	1070	1080	1090	1100	1110	1120
TIKTVLRHLR	EDQHTVLAYL	YEIRTSFQEF	LKRPDHKQDF	VAQWQADFNS	LPDDLWDDEE	TKAELHQRVN	DLRDRLWDIC
1130	1140	1150	1160	1170	1180	1190	1200
DARKEEAEQE	RLDIINESWL	QDTLGMTMNH	FFSLMQAELN	RFQDTKRLLQ	DYYWGMESKI	PVEDNKRFTR	IPLVQLDSKD
1210	1220	1230	1240	1250	1260	1270	1280
NSESQLRIPL	VPRISISLET	VTPKPKTKSV	LKGKMDNSLE	NVESNFEADE	KLVMDTWQQA	SLAVSHMVAA	EIHQRLMEEE
1290	1300	1310	1320	1330	1340	1350	1360
KENQPADPKE	KSPQMGANKK	VKKEPPKKKQ	EDKKPKGKSP	PMAEATPVIV	TTEEIAEIKR	KNELRVKIKE	EHLAALQFEE
1370	1380	1390	1400	1410	1420	1430	1440
IATQFRLELI	KTKALALLED	LVTKVVDVYK	LMEKWLGERY	LNEMASTEKL	TDVARYHIET	STKIQNELYL	SQEDFFINGN
1450	1460	1470	1480	1490	1500	1510	1520
IKVFPDPPPS	IRPPPVEKEE	DGTLTIEQLD	SLRDQFLDMA	PKECSENCFQ	RPSPSTCDAF	SNRRQEVASW	ITGSPPELSQ
1530	1540						
GISCNCSATA	LSRQRQK						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2407	2	973.4149	-118.32	2	60.6	12.1	2	2-17	M.SEILCQWLNKELKVSR.T		QD:QU 2.59
1569	1	480.6396	-230.14	2	48.1	14.6	1	1292-1300	K.SPQMGANKK.V		

Detailed Protein Report

Protein 328: 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:	2

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
1383	1	1179.1487	-41.33	2	47.4	15.2	0	49-70	R.ILVSLGLCFSKPSVILLLEQGK.A	
17	1	1103.4962	-28.67	2	29.9	11.4	1	144-161	K.ACFKEEIITHEEPLFDER.E	

Detailed Protein Report

Protein 329: small proline-rich protein 3 [Homo sapiens]

Accession:	gi|4885607	**Score:**	26.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.1
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	18.3
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:** 0.84	**CV:** 0.00 %	**No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|148229144	refseq_human(refseq_human_20140103.fasta)	small proline-rich protein 3 [Homo sapiens]

10	20	30	40	50	60	70	80
MSSYQQKQTF	TPPPQLQQQQ	VKQPSQPPPQ	EIFVPTTKEP	CHSKVPQPGN	TKIPEPGCTK	VPEPGCTKVP	EPGCTKVPEP
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
GCTKVPEPGC	TKVPEPGCTK	VPEPGYTKVP	EPGSIKVPDQ	GFIKFPEPGA	IKVPEQGYTK	VPVPGYTKLP	EPCPSTVTPG
170							
PAQQKTKQK							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
828	1	897.4861	12.13	2	40.4	15.1	0	23-38	K.QPSQPPPQEIFVPTTK.E		QD:QU 0.84

Detailed Protein Report

Protein 330: protein phosphatase 1A isoform 3 [Homo sapiens]

Accession:	gi|193211600	**Score:**	26.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.3
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MFCSGRKWVA	EATICTKLMK	REKRRMGKRR	AKKAKREEKK	KGGERRRNEK	RGNQMKRMCE	RKKYETDLED	QDIMGAFLDK
90	100	110	120	130	140	150	160
PKMEKHNAQG	QGNGLRYGLS	SMQGWRVEME	DAHTAVIGLP	SGLESWSFFA	VYDGHAGSQV	AKYCCEHLLD	HITNNQDFKG
170	180	190	200	210	220	230	240
SAGAPSVENV	KNGIRTGFLE	IDEHMRVMSE	KKHGADRSGS	TAVGVLISPQ	HTYFINCGDS	RGLLCRNRKV	HFFTQDHKPS
250	260	270	280	290	300	310	320
NPLEKERIQN	AGGSVMIQRV	NGSLAVSRAL	GDFDYKCVHG	KGPTEQLVSP	EPEVHDIERS	EEDDQFIILA	CDGIWDVMGN
330	340	350	360	370	380	390	400
EELCDFVRSR	LEVTDDLEKV	CNEVVDTCLY	KGSRDNMSVI	LICFPNAPKV	SPEAVKKEAE	LDKYLECRVE	EIIKKQGEGV
410	420	430	440	450	460		
PDLVHVMRTL	ASENIPSLPP	GGELASKRNV	IEAVYNRLNP	YKNDDTDSTS	TDDMW		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2669	1	974.0887	123.98	2	62.2	10.6	2	1-17	-.MFCSGRKWVAEATICTK.L	Oxidation: 1
2937	1	1018.9845	-66.59	2	65.9	15.9	1	409-428	R.TLASENIPSLPPGGELASKR.N	

Detailed Protein Report

Protein 331: zinc finger RNA-binding protein [Homo sapiens]

Accession:	gi|34101286	**Score:**	26.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	116.9
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.96 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MIPICPVVSF	TYVPSRLGED	AKMATGNYFG	FTHSGAAAAA	AAAQYSQQPA	SGVAYSHPTT	VASYTVHQAP	VAAHTVTAAY
90	100	110	120	130	140	150	160
APAAATVAVA	RPAPVAVAAA	ATAAAYGGYP	TAHTATDYGY	TQRQQEAPPP	PPPATTQNYQ	DSYSYVRSTA	PAVAYDSKQY
170	180	190	200	210	220	230	240
YQQPTATAAA	VAAAAQPQPS	VAETYYQTAP	KAGYSQGATQ	YTQAQQTRQV	TAIKPATPSP	ATTTFSIYPV	SSTVQPVAAA
250	260	270	280	290	300	310	320
ATVVPSYTQS	ATYSTTAVTY	SGTSYSGYEA	AVYSAASSYY	QQQQQQQKQA	AAAAAAAAAT	AAWTGTTFTK	KAPFQNKQLK
330	340	350	360	370	380	390	400
PKQPPKPPQI	HYCDVCKISC	AGPQTYKEHL	EGQKHKKKEA	ALKASQNTSS	SNSSTRGTQN	QLRCELCDVS	CTGADAYAAH
410	420	430	440	450	460	470	480
IRGAKHQKVV	KLHTKLGKPI	PSTEPNVVSQ	ATSSTAVSAS	KPTASPSSIA	ANNCTVNTSS	VATSSMKGLT	TTGNSSLNST
490	500	510	520	530	540	550	560
SNTKVSAVPT	NMAAKKTSTP	KINFVGGNKL	QSTGNKAEDI	KGTECVKSTP	VTSAVQIPEV	KQDTVSEPVT	PASLAALQSD
570	580	590	600	610	620	630	640
VQPVGHDYVE	EVRNDEGKVI	RFHCKLCECS	FNDPNAKEMH	LKGRRHRLQY	KKKVNPDLQV	EVKPSIRARK	IQEEKMRKQM
650	660	670	680	690	700	710	720
QKEEYWRRRE	EEERWRMEMR	RYEEDMYWRR	MEEEQHHWDD	RRRMPDGGYP	HGPPGPLGLL	GVRPGMPPQP	QGPAPLRRPD
730	740	750	760	770	780	790	800
SSDDRYVMTK	HATIYPTEEE	LQAVQKIVSI	TERALKLVSD	SLSEHEKNKN	KEGDDKKEGG	KDRALKGVLR	VGVLAKGLLL
810	820	830	840	850	860	870	880
RGDRNVNLVL	LCSEKPSKTL	LSRIAENLPK	QLAVISPEKY	DIKCAVSEAA	IILNSCVEPK	MQVTITLTSP	IIREENMREG
890	900	910	920	930	940	950	960
DVTSGMVKDP	PDVLDRQKCL	DALAALRHAK	WFQARANGLQ	SCVIIIRILR	DLCQRVPTWS	DFPSWAMELL	VEKAISSASS
970	980	990	1000	1010	1020	1030	1040
PQSPGDALRR	VFECISSGII	LKGSPGLLDP	CEKDPFDTLA	TMTDQQREDI	TSSAQFALRL	LAFRQIHKVL	GMDPLPQMSQ
1050	1060	1070	1080				
RFNIHNNRKR	RRDSDGVDGF	EAEGKKDKKD	YDNF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1045	1	839.3856	-82.99	2	41.6	11.3	0	2-16	M.IPICPVVSFTYVPSR.L		QD:QU	0.96
103	1	1240.0318	-79.59	2	31.2	15.2	1	726-746	R.YVMTKHATIYPTEEELQAVQK.I			

Detailed Protein Report

Protein 332: **origin recognition complex subunit 1 isoform 2 [Homo sapiens]**

Accession:	gi|299890795	**Score:**	26.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.7
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAHYPTRLKT	RKTYSWVGRP	LLDRKLHYQT	YREMCVKTEG	CSTEIHIQIG	QFVLIEGDDD	ENPYVAKLLE	LFEDDSDPPP
90	100	110	120	130	140	150	160
KKRARVQWFV	RFCEVPACKR	HLLGRKPGAQ	EIFWYDYPAC	DSNINAETII	GLVRVIPLAP	KDVVPTNLKN	EKTLFVKLSW
170	180	190	200	210	220	230	240
NEKKFRPLSS	ELFAELNKPQ	ESAAKCQKPV	RAKSKSAESP	SWTPAEHVAK	RIESRHSASK	SRQTPTHPLT	PRARKRLELG
250	260	270	280	290	300	310	320
NLGNPQMSQQ	TSCASLDSPG	RIKRKVAFSE	ITSPSKRSQP	DKLQTLSPAL	KAPEKTRETG	LSYTEDDKKA	SPEHRIILRT
330	340	350	360	370	380	390	400
RIAASKTIDI	REERTLTPIS	GGQRSSVVPS	VILKPENIKK	RDAKEAKAQN	EATSTPHRIR	RKSSVLTMNR	IRQQLRFLGN
410	420	430	440	450	460	470	480
SKSDQEEKEI	LPAAEISDSS	SDEEEASTPP	LPRRAPRTVS	RNLRSSLKSS	LHTLTKLKPR	TPRCAAPQIR	SRSLAAQEPA
490	500	510	520	530	540	550	560
SVLEEARLRL	HVSAVPESLP	CREQEFQDIY	NFVESKLLDH	TGGCMYISGV	PGTGKTATVH	EVIRCLQQAA	QANDVPPFQY
570	580	590	600	610	620	630	640
IEVNGMKLTE	PHQVYVQILQ	KLTGQKATAN	HAAELLAKQF	CTRGSPQETT	VLLVDELDLL	WTHKQDIMYN	LFDWPTHKEA
650	660	670	680	690	700	710	720
RLVVLAIANT	MDLPERIMMN	RVSSRLGLTR	MCFQPYTYSQ	LQQILRSRLK	HLKAFEDDAI	QLVARKVAAL	SGDARRCLDI
730	740	750	760	770	780	790	800
CRRATEICEF	SQQKPDSPGL	VTIAHSMEAV	DEMFSSSYIT	AIKNSSVLEQ	SFLRAILAEF	RRSGLEEATF	QQIYSQHVAL
810	820	830	840	850	860		
CRMEGLPYPT	MSETMAVCSH	LGSCRLLLVE	PSRNDLLLRV	RLNVSQDDVL	YALKDE		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1039	1	516.1512	-244.92	2	41.5	10.2	1	327-334	K.TIDIREER.T	

Detailed Protein Report

Protein 333: PREDICTED: PH and SEC7 domain-containing protein 3 isoform X3 [Homo sapiens]

Accession:	gi|578815261	**Score:**	26.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	112.4
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.45 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGNCWSYSNL	CDHGGSTLLP	PNVTNEFPEY	GTMEEGGEGL	RASLEFDGEA	LPCHPQEQQG	VQPLTGCHSG	LDSVTEGPKD
90	100	110	120	130	140	150	160
VREAPSQSHL	KEQSLQPIDS	LISALKATEA	RIISGTLQAT	KVLDQDAVSS	FSVQQVEKEL	DTASRKTQRV	NKTLPAGQKN
170	180	190	200	210	220	230	240
LPEIPLSAEV	TTEESFYLSI	QKDLTALLTG	DTQAEISQIM	NNGRKGAVCV	QEPSCPLASL	GSSAVTCHSA	GSVGFLKEQR
250	260	270	280	290	300	310	320
SALGREHPGG	CDRSSSMGRP	GRVKHVEFQG	VEILWTGGDK	RETQHPIDFE	TSLQRTASPD	SKESSKVPRH	LISSAGLCNS
330	340	350	360	370	380	390	400
SSLTENVWDE	SWKAPSERPG	TSSGTFSPVR	LDESGEDEVF	LQENKQHLEK	TPKPERDRER	ISEQEEHVKG	EDEDILGPGY
410	420	430	440	450	460	470	480
TEDSTDVYSS	QFETILDNTS	LYYSAESLET	LYSEPDSYFS	FEMPLTPMIQ	QRIKEGGQFL	ERTSGGGHQD	ILSVSADGGI
490	500	510	520	530	540	550	560
VMGYSSGVTN	GLNDASDSIY	TKGTPEIAFW	GSNAGVKTTR	LEAHSEMGST	EILEKETPEN	LSNGTSSNVE	AAKRLAKRLY
570	580	590	600	610	620	630	640
QLDRFKRSDV	AKHLGKNNEF	SKLVAEEYLK	FFDFTGMTLD	QSLRYFFKAF	SLVGETQERE	RVLIHFSNRY	FYCNPDTIAS
650	660	670	680	690	700	710	720
QDGVHCLTCA	IMLLNTDLHG	HNIGKKMTCQ	EFIANLQGVN	EGVDFSKDLL	KALYNSIKNE	KLEWAVDDEE	KKKSPSESTE
730	740	750	760	770	780	790	800
EKANGTHPKT	ISRIGSTTNP	FLDIPHDPNA	AVYKSGFLAR	KIHADMDGKK	TPRGKRGWKT	FYAVLKGTVL	YLQKDEYKPE
810	820	830	840	850	860	870	880
KALSEEDLKN	AVSVHHALAS	KATDYEKKPN	VFKLKTADWR	VLLFQTQSPE	EMQGWINKIN	CVAAVFSAPP	FPAAIGSQKK
890	900	910	920	930	940	950	960
FSRPLLPATT	TKLSQEEQLK	SHESKLKQIT	TELAEHRSYP	PDKKVKAKDV	DEYKLKDHYL	EFEKTRYEMY	VSILKEGGKE
970	980	990	1000	1010	1020		
LLSNDESEAA	GLKKSHSSPS	LNPDTSPITA	KVKRNVSERK	DHRPETPSIK	QKVT		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
909	1	578.3188	46.40	3	41.4	13.5	0	334-350	K.APSERPGTSSGTFSPVR.L		QD:QU 0.45
249	1	561.2240	-81.38	2	31.8	12.9	1	713-722	K.KSPSESTEEK.A		

Detailed Protein Report

Protein 334: 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

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
554	1	476.1400	-265.76	2	36.9	12.8	1	1019-1026	K.FSSKNQLK.T	
2539	1	648.3564	69.94	2	62.4	13.6	0	1173-1184	K.SSVSSVLQECEK.K	

Detailed Protein Report

Protein 335: sodium-dependent phosphate transport protein 2B isoform a [Homo sapiens]

Accession:	gi|110611906	**Score:**	26.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.7
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAPWPELGDA	QPNPDKYLEG	AAGQQPTAPD	KSKETNKTDN	TEAPVTKIEL	LPSYSTATLI	DEPTEVDDPW	NLPTLQDSGI
90	100	110	120	130	140	150	160
KWSERDTKGK	ILCFFQGIGR	LILLLGFLYF	FVCSLDILSS	AFQLVGGKMA	GQFFSNSSIM	SNPLLGLVIG	VLVTVLVQSS
170	180	190	200	210	220	230	240
STSTSIVVSM	VSSSLLTVRA	AIPIIMGANI	GTSITNTIVA	LMQVGDRSEF	RRAFAGATVH	DFFNWLSVLV	LLPVEVATHY
250	260	270	280	290	300	310	320
LEIITQLIVE	SFHFKNGEDA	PDLLKVITKP	FTKLIVQLDK	KVISQIAMND	EKAKNKSLVK	IWCKTFTNKT	QINVTVPSTA
330	340	350	360	370	380	390	400
NCTSPSLCWT	DGIQNWTMKN	VTYKENIAKC	QHIFVNFHLP	DLAVGTILLI	LSLLVLCGCL	IMIVKILGSV	LKGQVATVIK
410	420	430	440	450	460	470	480
KTINTDFPFP	FAWLTGYLAI	LVGAGMTFIV	QSSSVFTSAL	TPLIGIGVIT	IERAYPLTLG	SNIGTTTTAI	LAALASPGNA
490	500	510	520	530	540	550	560
LRSSLQIALC	HFFFNISGIL	LWYPIPFTRL	PIRMAKGLGN	ISAKYRWFAV	FYLIIFFFLI	PLTVFGLSLA	GWRVLVGVGV
570	580	590	600	610	620	630	640
PVVFIIILVL	CLRLLQSRCP	RVLPKKLQNW	NFLPLWMRSL	KPWDAVVSKF	TGCFQMRCCC	CCRVCCRACC	LLCGCPKCCR
650	660	670	680	690	700		
CSKCCEDLEE	AQEGQDVPVK	APETFDNITI	SREAQGEVPA	SDSKTECTAL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1700	1	538.2445	-41.77	2	51.5	12.2	0	38-47	K.TDNTEAPVTK.I	

Detailed Protein Report

Protein 336: PREDICTED: dynein intermediate chain 1, axonemal isoform X3 [Homo sapiens]

Accession:	gi|578816466	**Score:**	26.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.4
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.67 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MIPASAKAPH	KQPHKQSISI	GRGTRKRDED	SGTEVGEGTD	EWAQSKATVR	PPDQLELTDA	ELKEEFTRIL	TANNPHAPQN
90	100	110	120	130	140	150	160
IVRYSFKKQW	SLGFIPKLKR	KIPVNYWGQD	EGEISNETEG	TYKPIGFVNQ	LAVHYTQVGN	LIPKDSDEGR	RQHYRDELVA
170	180	190	200	210	220	230	240
VSYQGSQESV	KVISETGNLE	EDEEPKELET	EPGSQTDVPA	AGAAEKVTEE	ELMTPKQPKE	RKLTNQFNFS	ERASQTYNNP
250	260	270	280	290	300	310	320
VRDRECQTEP	PPRTNFSATA	NQWEIYDAYV	EELEKQEKTK	EKEKAKTPVA	KKSGKMAMRK	LTSMESQTDD	LIKLSQAAKI
330	340	350	360	370	380	390	400
MERMVNQNTY	DDIAQDFKYY	DDAADEYRDQ	VGTLLPLWKF	QNDKAKRLSV	TALCWNPKYR	DLFAVGYGSY	DFMKQSRGML
410	420	430	440	450	460	470	480
LLYSLKNPSF	PEYMFSSNSG	VMCLDIHVDH	PYLVAVGHYD	GNVAIYNLKK	PHSQPSFCSS	AKSGKHSDPV	WQVKWQKDDM
490	500	510	520	530	540	550	560
DQNLNFFSVS	SDGRIVSWTL	VKRKLVHIDV	IKLKVEGSTT	EVPEGLQLHP	VGCGTAFDFH	KEIDYMFLVG	TEEGKIYKCS
570	580	590	600	610	620	630	640
KSYSSQFLDT	YDAHNMSVDT	VSWNPYHTKV	FMSCSSDWTV	KIWDHTIKTP	MFIYDLNSAV	GDVAWAPYSS	TVFAAVTTDG
650	660	670	680				
KEKKGQEVQK	GPAVEIAKLD	KLLNLVREVK	IKT				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
255	1	838.3679	-55.82	2	31.9	12.9	1	450-465	K.KPHSQPSFCSSAKSGK.H		QD:QU	0.67

Detailed Protein Report

Protein 337: SPATS2-like protein isoform b [Homo sapiens]

Accession:	gi|154426312	**Score:**	26.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530370155	refseq_human (refseq_human_20140103.fasta)	PREDICTED: SPATS2-like protein isoform X7 [Homo sapiens]
gi|530370153	refseq_human (refseq_human_20140103.fasta)	PREDICTED: SPATS2-like protein isoform X6 [Homo sapiens]

10	20	30	40	50	60	70	80
MAELNTHVNV	KEKIYAVRSV	VPNKSNNEIV	LVLQQFDFNV	DKAVQAFVDG	SAIQVLKEWN	MTGKKKNNKR	KRSKSKQHQG
90	100	110	120	130	140	150	160
NKDAKDKVER	PEAGPLQPQP	PQIQNGPMNG	CEKDSSSTDS	ANEKPALIPR	EKKISILEEP	SKALRGVTGP	NIEKSVKDLQ
170	180	190	200	210	220	230	240
RCTVSLTRYR	VMIKEEVDSS	VKKIKAAFAE	LHNCIIDKEV	SLMAEMDKVK	EEAMEILTAR	QKKAEELKRL	TDLASQMAEM
250	260	270	280	290	300	310	320
QLAELRAEIK	HFVSERKYDE	ELGKAARFSC	DIEQLKAQIM	LCGEITHPKN	NYSSRTPCSS	LLPLLNAHAA	TSGKQSNFSR
330	340	350	360	370	380	390	400
KSSTHNKPSE	GKAANPKMVS	SLPSTADPSH	QTMPANKQNG	SSNQRRRFNP	QYHNNRLNGP	AKSQGSGNEA	EPLGKGNSRH
410	420	430	440	450	460	470	480
EHRRQPHNGF	RPKNKGGAKN	QEASLGMKTP	EAPAHSEKPR	RRQHAADTSE	ARPFRGSVGR	VSQCNLCPTR	IEVSTDAAVL
490							
SVPAVTLVA							

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	14-18	K.IYAVR.S	

Detailed Protein Report

Protein 338: 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

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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 339: 5'-nucleotidase isoform 2 preproprotein [Homo sapiens]

Accession:	gi|325651886	**Score:**	26.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.9
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCPRAARAPA	TLLLALGAVL	WPAAGAWELT	ILHTNDVHSR	LEQTSEDSSK	CVNASRCMGG	VARLFTKVQQ	IRRAEPNVLL
90	100	110	120	130	140	150	160
LDAGDQYQGT	IWFTVYKGAE	VAHFMNALRY	DAMALGNHEF	DNGVEGLIEP	LLKEAKFPIL	SANIKAKGPL	ASQISGLYLP
170	180	190	200	210	220	230	240
YKVLPVGDEV	VGIVGYTSKE	TPFLSNPGTN	LVFEDEITAL	QPEVDKLKTL	NVNKIIALGH	SGFEMDKLIA	QKVRGVDVVV
250	260	270	280	290	300	310	320
GGHSNTFLYT	GNPPSKEVPA	GKYPFIVTSD	DGRKVPVVQA	YAFGKYLGYL	KIEFDERGNV	ISSHGNPILL	NSSIPEDPSI
330	340	350	360	370	380	390	400
KADINKWRIK	LDNYSTQELG	KTIVYLDGSS	QSCRFRECNM	GNLICDAMIN	NNLRHTDEMF	WNHVSMCILN	GGGIRSPIDE
410	420	430	440	450	460	470	480
RNNGIHVVYD	LSRKPGDRVV	KLDVLCTKCR	VPSYDPLKMD	EVYKVILPNF	LANGGDGFQM	IKDELLRHDS	GDQDINVVST
490	500	510	520	530			
YISKMKVIYP	AVEGRIKFST	GSHCHGSFSL	IFLSLWAVIF	VLYQ			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1850	1	727.3153	-15.31	2	51.6	13.1	1	51-63	K.CVNASRCMGGVAR.L	Carbamidomethyl: 1, 7; Oxidation: 8

Detailed Protein Report

Protein 340: 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

QD:QU **Median:** 0.73	**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		QD:QU 0.73

Detailed Protein Report

Protein 341: PREDICTED: coiled-coil domain-containing protein 136 isoform X4 [Homo sapiens]

Accession:	gi|530386309	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	131.9
Database Date:	2015-11-30	**pI:**	4.5
		Sequence Coverage [%]:	1.8
		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 342: PREDICTED: ubiquitin carboxyl-terminal hydrolase 31 isoform X1 [Homo sapiens]

Accession:	gi|530408620	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.3
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578828616	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ubiquitin carboxyl-terminal hydrolase 31 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MMPEGPSFPV	CSTFVQELFQ	AQYRSSLTCP	HCQKQSNTFD	PFLCISLPIP	LPHTRPLYVT	VVYQGKCSHC	MRIGVAVPLS
90	100	110	120	130	140	150	160
GTVARLREAV	SMETKIPTDQ	IVLTEMYYDG	FHRSFCDTDD	LETVHESDCI	FAFETPEIFR	PEGILSQRGI	HLNNNLNHLK
170	180	190	200	210	220	230	240
FGLDYHRLSS	PTQTAAKQGK	MDSPTSRAGS	DKIVLLVCNR	ACTGQQGKRF	GLPFVLHLEK	TIAWDLLQKE	ILEKMKYFLR
250	260	270	280	290	300	310	320
PTVCIQVCPF	SLRVVSVVGI	TYLLPQEEQP	LCHPIVERAL	KSCGPGGTAH	VKLVVEWDKE	TRDFLFVNTE	DEYIPDAESV
330	340	350	360	370	380	390	400
RLQRERHHQP	QTCTLSQCFQ	LYTKEERLAP	DDAWRCPHCK	QLQQGSITLS	LWTLPDVLII	HLKRFRQEGD	RRMKLQNMVK
410	420	430	440	450	460	470	480
FPLTGLDMTP	HVVKRSQSSW	SLPSHWSPWR	RPYGLGRDPE	DYIYDLYAVC	NHHGTMQGGH	YTAYCKNSVD	GLWYCFDDSD
490	500	510	520	530	540	550	560
VQQLSEDEVC	TQTAYILFYQ	RRTAIPSWSA	NSSVAGSTSS	SLCEHWVSRL	PGSKPASVTS	AASSRRTSLA	SLSESVEMTG
570	580	590	600	610	620	630	640
ERSEDDGGFS	TRPFVRSVQR	QSLSSRSSVT	SPLAVNENCM	RPSWSLSAKL	QMRSNSPSRF	SGDSPIHSSA	STLEKIGEAA
650	660	670	680	690	700	710	720
DDKVSISCFG	SLRNLSSSYQ	EPSDSHSRRE	HKAVGRAPLA	VMEGVFKDES	DTRRLNSSVV	DTQSKHSAQG	DRLPPLSGPF
730	740	750	760	770	780	790	800
DNNNQIAYVD	QSDSVDSSPV	KEVKAPSHPG	SLAKKPESTT	KRSPSSKGTS	EPEKSLRKGR	PALASQESSL	SSTSPSSPLP
810	820	830	840	850	860	870	880
VKVSLKPSRS	RSKADSSSRG	SGRHSSPAPA	QPKKESSPKS	QDSVSSPSPQ	KQKSASALTY	TASSTSAKKA	SGPATRSPFP
890	900	910	920	930	940	950	960
PGKSRTSDHS	LSREGSRQSL	GSDRASATST	SKPNSPRVSQ	ARAGEGRGAG	KHVRSSSMAS	LRSPSTSIKS	GLKRDSKSED
970	980	990	1000	1010	1020	1030	1040
KGLSFFKSAL	RQKETRRSTD	LGKTALLSKK	AGGSSVKSVC	KNTGDDEAER	GHQPPASQQP	NANTTGKEQL	VTKDPASAKH
1050	1060	1070	1080	1090			
SLLSARKSKS	SQLDSGVPSS	PGGRQSAEKS	SKKLSSSMQT	SARPSQKPQ			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2244	1	792.8941	-36.04	2	56.7	11.2	2	958-971	K.SEDKGLSFFKSALR.Q	

Detailed Protein Report

Protein 343: zinc finger protein 512 isoform b [Homo sapiens]

Accession:	gi|404501451	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.3
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSRLGAVPA	TSGPTTFKQQ	RSTRIVGAKN	RTQCSIKDNS	FQYTIPHDDS	LSGSSSASSC	EPVSDFPASF	RKSTYWMKMR
90	100	110	120	130	140	150	160
RIKPAATSHV	EGSGGVSAKG	KRKPRQEEDE	DYREFPQKKH	KLYGSLEEQW	YLEIVDKGSV	SCPTCQAVGR	KTIEGLKKHM
170	180	190	200	210	220	230	240
ENCKQEMFTC	HHCGKQLRSL	AGMKYHVMAN	HNSLPILKAG	DEIDEPSERE	RLRTVLKRLG	KLRCMRESCS	SSFTSIMGYL
250	260	270	280	290	300	310	320
YHVRKCGKGA	AELEKMTLKC	HHCGKPYRSK	AGLAYHLRSE	HGPISFFPES	GQPECLKEMN	LESKSGGRVQ	RRSAKIAVYH
330	340	350	360	370	380	390	400
LQELASAELA	KEWPKRKVLQ	DLVPDDRKLK	YTRPGLPTFS	QEVLHKWKTD	IKKYHRIQCP	NQGCEAVYSS	VSGLKAHLGS
410	420	430	440	450	460	470	480
CTLGNFVAGK	YKCLLCQKEF	VSESGVKYHI	NSVHAEDWFV	VNPTTTKSFE	KLMKIKQRQQ	EEEKRRQQHR	SRRSLRRRQQ
490	500	510	520	530	540		
PGIELPETEL	SLRVGKDQRR	NNEELVVSAS	CKEPEQEPVP	AQFQKVKPPK	TNHKRGRK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1367	1	388.0811	-337.50	2	45.6	13.6	1	19-24	K.QQRSTR.I	

Detailed Protein Report

Protein 344: protocadherin gamma-B5 isoform 1 precursor [Homo sapiens]

Accession:	gi|11128031	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	99.8
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:**	0.08	**CV:**	0.00 %	**No. of Peptides:**	1	

10	20	30	40	50	60	70	80
MGSGAGELGR	AERLPVLFLF	LLSLFCPALC	EQIRYRIPEE	MPKGSVVGNL	ATDLGFSVQE	LPTRKLRVSS	EKPYFTVSAE
90	100	110	120	130	140	150	160
SGELLVSSRL	DREEICGKKP	ACALEFEAVA	ENPLNFYHVN	VEIEDINDHT	PKFTQNSFEL	QISESAQPGT	RFILEVAEDA
170	180	190	200	210	220	230	240
DIGLNSLQKY	KLSLNPSFSL	IIKEKQDGSK	YPELALEKTL	DREQQSYHRL	VLTALDGGHP	PLSGTTELRI	QVTDANDNPP
250	260	270	280	290	300	310	320
VFNRDVYRVS	LRENVPPGTT	VLQVSATDQD	EGINSEITYS	FYRTGQIFSL	NSKSGEITTQ	KKLDFEETKE	YSMVVEGRDG
330	340	350	360	370	380	390	400
GGLVAQCTVE	INIQDENDNS	PEVTFHSLLE	MILENAVPGT	LIALIKIHDQ	DSGENGEVNC	QLQGEVPFKI	ISSSKNSYKL
410	420	430	440	450	460	470	480
VTDGTLDREQ	TPEYNVTITA	TDRGKPPLSS	SISVILHIRD	VNDNAPVFHQ	ASYLVSVPEN	NPPGASIAQV	CASDLDLGLN
490	500	510	520	530	540	550	560
GQVSYSIMAS	DLEPLALASY	VSMSAQSGVV	FAQRAFDYEQ	LRTFELTLQA	RDQGSPALSA	NVSLRVLVGD	RNDNAPRVLY
570	580	590	600	610	620	630	640
PALGPDGSAL	FDMVPRAAEP	GYLVTKVVAV	DADSGHNAWL	SYHVLQASEP	GLFSLGLRTG	EVRTARALGD	RDAARQRLLV
650	660	670	680	690	700	710	720
AVRDGGQPPL	SATATLHLVF	ADSLQEVLPD	ITDRPVPSDP	QAELQFYLVV	ALALISVLFL	LAVILAVALR	LRRSSSPAAW
730	740	750	760	770	780	790	800
SCFQPGLCVK	SGPVVPPNYS	QGTLPYSYNL	CVAHTGKTEF	NFLKCSEQLS	SGQDILCGDS	SGALFPLCNS	SESTSHPELQ
810	820	830	840	850	860	870	880
APPNTDWRFS	QAQRPGTSGS	QNGDDTGTWP	NNQFDTEMLQ	AMILASASEA	ADGSSTLGGG	AGTMGLSARY	GPQFTLQHVP
890	900	910	920	930			
DYRQNVYIPG	SNATLTNAAG	KRDGKAPAGG	NGNKKKSGKK	EKK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1752	1	990.9543	-20.48	2	50.4	10.1	1	713-730	R.RSSSPAAWSCFQPGLCVK.S	Carbamidomethyl: 16	QD:QU 0.08

Detailed Protein Report

Protein 345: **PREDICTED: deleted in lung and esophageal cancer protein 1 isoform X6 [Homo sapiens]**

Accession:	gi|578806835	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	160.3
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
METRSSKTRR	SLASRTNECQ	GTMWAPTSPP	AGSSSPSQPT	WKSSLYSSLA	YSEAFHYSFA	ARPRRLTQLA	LAQRPEPQLL
90	100	110	120	130	140	150	160
RLRPSSLRTQ	DISHLLTGVF	RNLYSAEVIG	DEVSASLIKA	RGSENERHEE	FVDQLQQIRE	LYKQRLDEFE	MLERHITQAQ
170	180	190	200	210	220	230	240
ARAIAENERV	MSQAGVQDLE	SLVRLPPVKS	VSRWCIDSEL	LRKHHLISPE	DYYTDTVPFH	SAPKGISLPG	CSKLTFSCEK
250	260	270	280	290	300	310	320
RSVQKKELNK	KLEDSCRKKL	AEFEDELDHT	VDSLTWNLTP	KAKERTREPL	KKASQPRNKN	WMNHLRVPQR	ELDRLLLARM
330	340	350	360	370	380	390	400
ESRNHFLKNP	RFFPPNTRYG	GKSLVFPPKK	PAPIGEFQST	EPEQSCADTP	VFLAKPPIGF	FTDYEIGPVY	EMVIALQNTT
410	420	430	440	450	460	470	480
TTSRYLRVLP	PSTPYFALGL	GMFPGKGGMV	APGMTCQYIV	QFFPDCLGDF	DDFILVETQS	AHTLLIPLQA	RRPPPVLTLS
490	500	510	520	530	540	550	560
PVLDCGYCLI	GGVKMTRFIC	KNVGFSVGRF	CIMPKTSWPP	LSFKAIATVG	FVEQPPFGIL	PSVFELAPGH	AILVEVLFSP
570	580	590	600	610	620	630	640
KSLGKAEQTF	IIMCDNCQIK	ELVTIGIGQL	IALDLIYISG	EKSQPDPGEL	TDLTAQHFIR	FEPENLRSTA	RKQLIIRNAT
650	660	670	680	690	700	710	720
HVELAFYWQI	MKPNLQPLMP	GETFSMDSIK	CYPDKETAFS	IMPRKGVLSP	HTDHEFILSF	SPHELRDFHS	VLQMVLEEVP
730	740	750	760	770	780	790	800
EPVSSEAESL	GHSSYSVDDV	IVLEIEVKGS	VEPFQVLLEP	YALIIPGENY	IGINVKKAFK	MWNNSKSPIR	YLWGKISDCH
810	820	830	840	850	860	870	880
IIEVEPGTGV	IEPSEVGDFE	LNFTGGVPGP	TSQDLLCEIE	DSPSPVVLHI	EAVFKGPALI	INVSALQFGL	LRLGQKATNS
890	900	910	920	930	940	950	960
IQIRNVSQLP	ATWRMKESPV	SLQERPEDVS	PFDIEPSSGQ	LHSLGECRVD	ITLEALHCQH	LETVLELEVE	NGAWSYLPVY
970	980	990	1000	1010	1020	1030	1040
AEVQKPHVYL	QSSQVEVRNL	YLGVPTKTTI	TLINGTLLPT	QFHWGKLLGH	QAEFCMVTVS	PKHGLLGPSE	ECQLKLELTA
1050	1060	1070	1080	1090	1100	1110	1120
HTQEELTHLA	LPCHVSGMKK	PLVLGISGKP	QGLQVAITIS	KESSDCSVFS	TEQWPGHPKE	LRLDFGSAVP	LRTRVTRQLI
1130	1140	1150	1160	1170	1180	1190	1200
LTNRSPIRTR	FSLKFEYFGS	PQNSLSKKTS	LPNMPPALLK	TVRMQEHLAK	REQLDFMESM	LSHGKGAAFF	PHFSQGMLGP
1210	1220	1230	1240	1250	1260	1270	1280
YQQLCIDITG	CANMWGEYWD	NLICTVGDLL	PEVIPVHMAA	VGCPISSLRT	TSYTIDQAQK	EPAMRFGTQV	SGGDTVTRTL
1290	1300	1310	1320	1330	1340	1350	1360
RLNNSSPCDI	RLDWETYVPE	DKEDRLVELL	VFYGPPFPLR	DQAGNELVCP	DTPEGGCLLW	SPGPSSSSEF	SHETDSSVEG
1370	1380	1390	1400	1410	1420	1430	1440
SSSASNRVAQ	KLISVILQAH	EGVPSGHLYC	ISPKQVVVPA	GGSSTIYISF	TPMVLSPEIL	HKVECTGYAL	GFMSLDSK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
34	1	628.3634	65.98	3	29.1	13.9	2	225-241	K.GISLPGCSKLTFSCEKR.S	Carbamidomethyl: 14

Detailed Protein Report

Protein 346: **PREDICTED: conserved oligomeric Golgi complex subunit 4 isoform X1 [Homo sapiens]**

Accession:	gi|578828932	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.7
Database Date:	2015-11-30	**pI:**	5.1
		Sequence Coverage [%]:	4.3
		No. of unique 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
1637	1	993.4172	-42.79	2	50.7	12.5	1	238-255	K.RISSDFEVGDSMASEEVK.Q	

Detailed Protein Report

Protein 347: **PREDICTED: ankyrin repeat domain-containing protein 18A isoform X1 [Homo sapiens]**

Accession:	gi|578816446	**Score:**	26.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	124.6
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRKLFSFGRR	LGQALLSSMD	QEYAGPGYDI	RDWELRKIHR	AAIKGDAAEV	ERCLTRRFRD	LDARDRKDRT	VLHLACAHGR
90	100	110	120	130	140	150	160
VQVVTLLLHR	RCQIDICDRL	NRTPLMKAVH	SQEEACAIVL	LECGANPNIE	DIYGNTALHY	AVYNKGTSLA	ERLLSHHANI
170	180	190	200	210	220	230	240
EALNKEGNTP	LLFAINSRRQ	HMVEFLLKNQ	ANIHAVDNFK	RTALILAVQH	NLSSIVTLLL	QQNIRISSQD	MFGQTAEDYA
250	260	270	280	290	300	310	320
LCSDLRSIRQ	QILEHKNKML	KNHLRNDNQE	AAAMKNESFK	TQGASSKETA	AMKPANLKKR	KERAKAEHNL	KVASEEKQER
330	340	350	360	370	380	390	400
LQRSENKQPQ	DSQSYGKKKD	AMYGNFMLKK	DIAMLKEELY	AIKNDSLRKE	KKYIQEIKSI	TEINANFEKS	VRLNEKMITK
410	420	430	440	450	460	470	480
TVARYSQQLN	DLKAENARLN	SELEKEKHNK	ERLEAEVESL	HSSLATAINE	YNEIVERKDL	ELVLWRADDV	SRHEKMGSNI
490	500	510	520	530	540	550	560
SQLTDKNELL	TEQVHKARVK	FNTLKGKLRE	TRDALREKTL	ALGSVQLDLR	QAQHRIKEMK	QMHPNGEAKE	SQSIGKQNSL
570	580	590	600	610	620	630	640
EERIRQQELE	NLLLERQLED	ARKEGDNKEI	VINIHRDCLE	NGKEDLLEER	NKELMKEYNY	LKEKLLQCEK	EKAEREVIVR
650	660	670	680	690	700	710	720
EFQEELVDHL	KTFSISESPL	EGTSHCHINL	NETWTSKKKL	FQVEIQPEEK	HEEFRKLFEL	ISLLNYTADQ	IRKKNRELEE
730	740	750	760	770	780	790	800
EATGYKKCLE	MTINMLNAFA	NEDFSCHGDL	NTDQLKMDIL	FKKLKQKFND	LVAEKEAVSS	ECVNLAKDNE	VLHQELLSMR
810	820	830	840	850	860	870	880
NVQEKCEKLE	KDKKMLEEEV	LNLKTHMEKD	MVELGKLQEY	KSELDERAVQ	EIEKLEEIHL	QKQAEYEKQL	EQLNKDNTAS
890	900	910	920	930	940	950	960
LKKKELTLKD	VECKFSKMKT	AYEEVTTELE	EFKEAFAGAV	KANNSMSKKL	MKSDKKIAVI	STKLFTEKQR	MKYFLSTLPT
970	980	990	1000	1010	1020	1030	1040
RPEPELPCVE	NLNSIELNRK	YIPKTAIRIP	TSNPQTSNNC	KNFLTEMELD	RVEQIITGTK	KSFAMLSTCS	RLLSFVESTA
1050	1060	1070	1080				
PRKHRRALPI	MRSLVPNRRT	TVASTEVKGT	SQHS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
702	1	733.4640	131.96	3	38.8	12.2	1	788-805	K.DNEVLHQELLSMRNVQEK.C	Oxidation: 12

Detailed Protein Report

Protein 348: catenin alpha-1 [Homo sapiens]

Accession:	gi|55770844	**Score:**	25.9
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 [%]:**	2.9
		No. of unique Peptides:	2

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	1	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; Oxidation: 2

Detailed Protein Report

Protein 349: 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:	2

Quantitation

QD:QU	**Median:**	5.44	**CV:**	0.00 %	**No. of 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	Ratios
377	1	657.6657	-223.40	2	34.7	10.5	1	913-922	R.TMEQQFQKMK.I	Oxidation: 2	QD:QU 5.44
1864	1	612.7893	-8.93	2	53.7	15.4	1	1040-1049	R.RMMLSNQNSK.G	Oxidation: 2	

Detailed Protein Report

Protein 350: serine/threonine-protein kinase WNK3 isoform 2 [Homo sapiens]

Accession:	gi|50845416	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	191.7
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578838231	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serine/threonine-protein kinase WNK3 isoform X2 [Homo sapiens]
gi|578838229	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serine/threonine-protein kinase WNK3 isoform X1 [Homo sapiens]

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Detailed Protein Report

10	20	30	40	50	60	70	80
MATDSGDPAS	TEDSEKPDGI	SFENRVPQVA	ATLTVEARLK	EKNSTFSASG	ETVERKRFFR	KSVEMTEDDK	VAESSPKDER
90	100	110	120	130	140	150	160
IKAAMNIPRV	DKLPSNVLRG	GQEVKYEQCS	KSTSEISKDC	FKEKNEKEME	EEAEMKAVAT	SPSGRFLKFD	IELGRGAFKT
170	180	190	200	210	220	230	240
VYKGLDTETW	VEVAWCELQD	RKLTKAEQQR	FKEEAEMLKG	LQHPNIVRFY	DSWESILKGK	KCIVLVTELM	TSGTLKTYLK
250	260	270	280	290	300	310	320
RFKVMKPKVL	RSWCRQILKG	LQFLHTRTPP	IIHRDLKCDN	IFITGPTGSV	KIGDLGLATL	MRTSFAKSVI	GTPEFMAPEM
330	340	350	360	370	380	390	400
YEEHYDESVD	VYAFGMCMLE	MATSEYPYSE	CQNAAQIYRK	VTSGIKPASF	NKVTDPEVKE	IIEGCIRQNK	SERLSIRDLL
410	420	430	440	450	460	470	480
NHAFFAEDTG	LRVELAEEDD	CSNSSLALRL	WVEDPKKLKG	KHKDNEAIEF	SFNLETDTPE	EVAYEMVKSG	FFHESDSKAV
490	500	510	520	530	540	550	560
AKSIRDRVTP	IKKTREKKPA	GCLEERRDSQ	CKSMGNVFPQ	PQNTTLPLAP	AQQTGAECEE	TEVDQHVRQQ	LLQRKPQQHC
570	580	590	600	610	620	630	640
SSVTGDNLSE	AGAASVIHSD	TSSQPSVAYS	SNQTMGSQMV	SNIPQAEVNV	PGQIYSSQQL	VGHYQQVSGL	QKHSKLTQPQ
650	660	670	680	690	700	710	720
ILPLVQGQST	VLPVHVLGPT	VVSQPQVSPL	TVQKVPQIKP	VSQPVGAEQQ	AALLKPDLVR	SLNQDVATTK	ENVSSPDNPS
730	740	750	760	770	780	790	800
GNGKQDRIKQ	RRASCPRPEK	GTKFQLTVLQ	VSTSGDNMVE	CQLETHNNKM	VTFKFDVDGD	APEDIADYMV	EDNFVLESEK
810	820	830	840	850	860	870	880
EKFVEELRAI	VGQAQEILHV	HFATERATGV	DSITVDSNSS	QTGSSEQVQI	NSTSTQTSNE	SAPQSSPVGR	WRFCINQTIR
890	900	910	920	930	940	950	960
NRETQSPPSL	QHSMSAVPGR	HPLPSPKNTS	NKEISRDTLL	TIENNPCHRA	LFTSKSEHKD	VVDGKISECA	SVETKQPAIL
970	980	990	1000	1010	1020	1030	1040
YQVEDNRQIM	APVTNSSSYS	TTSVRAVPAE	CEGLTKQASI	FIPVYPCHQT	ASQADALMSH	PGESTQTSGN	SLTTLAFDQK
1050	1060	1070	1080	1090	1100	1110	1120
PQTLSVQQPA	MDAEFISQEG	ETTVNTEASS	PKTVIPTQTP	GLEPTTLQPT	TVLESDGERP	PKLEFADNRI	KTLDEKLRNL
1130	1140	1150	1160	1170	1180	1190	1200
LYQEHSISSI	YPESQKDTQS	IDSPFSSSAE	DTLSCPVTEV	IAISHCGIKD	SPVQSPNFQQ	TGSKLLSNVA	ASQPANISVF
1210	1220	1230	1240	1250	1260	1270	1280
KRDLNVITSV	PSELCLHEMS	SDASLPGDPE	AYPAAVSSGG	AIHLQTGVET	EEMRSAIAPD	PIPLTRESTA	DTRALNRCKA
1290	1300	1310	1320	1330	1340	1350	1360
MSGSFQRGRF	QVITIPQQQS	AKMTSFGIEH	ISVFSETNHS	SEEAFIKTAK	SQLVEIEPAT	QNPKTSFSYE	KLQALQETCK
1370	1380	1390	1400	1410	1420	1430	1440
ENKGVPKQGD	NFLSFSAACE	TDVSSVTPEK	EFEETSATGS	SMQSGSELLL	KEREILTAGK	QPSSDSEFSA	SLAGSGKSVA
1450	1460	1470	1480	1490	1500	1510	1520
KTGPESNQCL	PHHEEQAYAQ	TQSSLFYSPS	SPMSSDDESE	IEDEDLKVEL	QRLREKHIQE	VVNLQTQQNK	ELQELYERLR
1530	1540	1550	1560	1570	1580	1590	1600
SIKDSKTQST	EIPLPPASPR	RPRSFKSKLR	SRPQSLTHVD	NGIVATDPLC	VESNAASCQQ	SPASKKGMFT	DDLHKLVDDW
1610	1620	1630	1640	1650	1660	1670	1680
TKEAVGNSLI	KPSLNQLKQS	QHKLETENWN	KVSENTPSTM	GYTSTWISSL	SQIRGAVPTS	LPQGLSLPSF	PGPLSSYGMP
1690	1700	1710	1720	1730	1740	1750	
HVCQYNAVAG	AGYPVQWVGI	SGTTQQSVVI	PAQSGGPFQP	GMNMQAFPTS	SVQNPATIPP	GPK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1472	1	918.1282	-10.85	3	46.9	10.8	2	1414-1441	R.EILTAGKQPSSDSEFSASLAGSGKSVAK.T	

Detailed Protein Report

Protein 351: teneurin-1 isoform 3 [Homo sapiens]

Accession:	gi|110347400	**Score:**	25.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	304.8
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MEQTDCKPYQ	PLPKVKHEMD	LAYTSSSDES	EDGRKPRQSY	NSRETLHEYN	QELRMNYNSQ	SRKRKEVEKS	TQEMEFCETS
90	100	110	120	130	140	150	160
HTLCSGYQTD	MHSVSRHGYQ	LEMGSDVDTE	TEGAASPDHA	LRMWIRGMKS	EHSSCLSSRA	NSALSLTDTD	HERKSDGENG
170	180	190	200	210	220	230	240
FKFSPVCCDM	EAQAGSTQDV	QSSPHNQFTF	RPLPPPPPPP	HACTCARKPP	PAADSLQRRS	MTTRSQPSPA	APAPPTSTQD
250	260	270	280	290	300	310	320
SVHLHNSWVL	NSNIPLETRH	FLFKHGSGSS	AIFSAASQNY	PLTSNTVYSP	PPRPLPRSTF	SRPAFTFNKP	YRCCNWKCTA
330	340	350	360	370	380	390	400
LSATAITVTL	ALLLAYVIAV	HLFGLTWQLQ	PVEGELYANG	VSKGNRGTES	MDTTYSPIGG	KVSDKSEKKV	FQKGRAIDTG
410	420	430	440	450	460	470	480
EVDIGAQVMQ	TIPPGLFWRF	QITIHHPIYL	KFNISLAKDS	LLGIYGRRNI	PPTHTQFDFV	KLMDGKQLVK	QDSKGSDDTQ
490	500	510	520	530	540	550	560
HSPRNLILTS	LQETGFIEYM	DQGPWYLAFY	NDGKKMEQVF	VLTTAIEIMD	DCSTNCNGNG	ECISGHCHCF	PGFLGPDCAR
570	580	590	600	610	620	630	640
DSCPVLCGGN	GEYEKGHCVC	RHGWKGPECD	VPEEQCIDPT	CFGHGTCIMG	VCICVPGYKG	EICEEEDCLD	PMCSNHGICV
650	660	670	680	690	700	710	720
KGECHCSTGW	GGVNCETPLP	VCQEQCSGHG	TFLLDAGVCS	CDPKWTGSDC	STELCTMECG	SHGVCSRGIC	QCEEGWVGPT
730	740	750	760	770	780	790	800
CEERSCHSHC	TEHGQCKDGK	CECSPGWEGD	HCTIAHYLDA	VRDGCPGLCF	GNGRCTLDQN	GWHCVCQVGW	SGTGCNVVME
810	820	830	840	850	860	870	880
MLCGDNLDND	GDGLTDCVDP	DCCQQSNCYI	SPLCQGSPDP	LDLIQQSQTL	FSQHTSRLFY	DRIKFLIGKD	STHVIPPEVS
890	900	910	920	930	940	950	960
FDSRRACVIR	GQVVAIDGTP	LVGVNVSFLH	HSDYGFTISR	QDGSFDLVAI	GGISVILIFD	RSPFLPEKRT	LWLPWNQFIV
970	980	990	1000	1010	1020	1030	1040
VEKVTMQRVV	SDPPSCDISN	FISPNPIVLP	SPLTSFGGSC	PERGTIVPEL	QVVQEEIPIP	SSFVRLSYLS	SRTPGYKTLL
1050	1060	1070	1080	1090	1100	1110	1120
RILLTHSTIP	VGMIKVHLTV	AVEGRLTQKW	FPAAINLVYT	FAWNKTDIYG	QKVWGLAEAL	VSVGYEYETC	PDFILWEQRT
1130	1140	1150	1160	1170	1180	1190	1200
VVLQGFEMDA	SNLGGWSLNK	HHILNPQSGI	IHKGNGENMF	ISQQPPVIST	IMGNGHQRSV	ACTNCNGPAH	NNKLFAPVAL
1210	1220	1230	1240	1250	1260	1270	1280
ASGPDGSVYV	GDFNFVRRIF	PSGNSVSILE	LSTSPAHKYY	LAMDPVSESL	YLSDTNTRKV	YKLKSLVETK	DLSKNFEVVA
1290	1300	1310	1320	1330	1340	1350	1360
GTGDQCLPFD	QSHCGDGGRA	SEASLNSPRG	ITVDRHGFIY	FVDGTMIRKI	DENAVITTVI	GSNGLTSTQP	LSCDSGMDIT
1370	1380	1390	1400	1410	1420	1430	1440
QVRLEWPTDL	AVNPMDNSLY	VLDNNIVLQI	SENRRVRIIA	GRPIHCQVPG	IDHFLVSKVA	IHSTLESARA	ISVSHSGLLF
1450	1460	1470	1480	1490	1500	1510	1520
IAETDERKVN	RIQQVTTNGE	IYIIAGAPTD	CDCKIDPNCD	CFSGDGGYAK	DAKMKAPSSL	AVSPDGTLYV	ADLGNVRIRT
1530	1540	1550	1560	1570	1580	1590	1600
ISRNQAHLND	MNIYEIASPA	DQELYQFTVN	GTHLHTLNLI	TRDYVYNFTY	NSEGDLGAIT	SSNGNSVHIR	RDAGGMPLWL
1610	1620	1630	1640	1650	1660	1670	1680
VVPGGQVYWL	TISSNGVLKR	VSAQGYNLAL	MTYPGNTGLL	ATKSNENGWT	TVYEYDPEGH	LTNATFPTGE	VSSFHSDLEK
1690	1700	1710	1720	1730	1740	1750	1760
LTKVELDTSN	RENVLMSTNL	TATSTIYILK	QENTQSTYRV	NPDGSLRVTF	ASGMEIGLSS	EPHILAGAVN	PTLGKCNISL
1770	1780	1790	1800	1810	1820	1830	1840
PGEHNANLIE	WRQRKEQNKG	NVSAFERRLR	AHNRNLLSID	FDHITRTGKI	YDDHRKFTLR	ILYDQTGRPI	LWSPVSRYNE
1850	1860	1870	1880	1890	1900	1910	1920
VNITYSPSGL	VTFIQRGTWN	EKMEYDQSGK	IISRTWADGK	IWSYTYLEKS	VMLLLHSQRR	YIFEYDQPDC	LLSVTMPSMV
1930	1940	1950	1960	1970	1980	1990	2000
RHSLQTMLSV	GYYRNIYTPP	DSSTSFIQDY	SRDGRLLQTL	HLGTGRRVLY	KYTKQARLSE	VLYDTTQVTL	TYEESSGVIK
2010	2020	2030	2040	2050	2060	2070	2080
TIHLMHDGFI	CTIRYRQTGP	LIGRQIFRFS	EEGLVNARFD	YSYNNFRVTS	MQAVINETPL	PIDLYRYVDV	SGRTEQFGKF
2090	2100	2110	2120	2130	2140	2150	2160
SVINYDLNQV	ITTTVMKHTK	IFSANGQVIE	VQYEILKAIA	YWMTIQYDNV	GRMVICDIRV	GVDANITRYF	YEYDADGQLQ
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
286	1	879.7298	-17.42	3	32.3	12.4	2	15-37	K.VKHEMDLAYTSSSDESEDGRKPR.Q	
2523	1	856.5611	167.23	2	62.1	13.5	0	2222-2236	R.GNDIFEYNSNGLLQK.A	

Detailed Protein Report

Protein 352: PREDICTED: chondroadherin-like protein isoform X2 [Homo sapiens]

Accession: gi|530419599
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 25.9
MW [kDa]: 81.7
pI: 10.9
Sequence Coverage [%]: 4.4
No. of unique Peptides: 2

Quantitation

QD:QU **Median:** 0.73 **CV:** 0.00 % **No. of Peptides:** 1

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        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	QD:QU 0.73
2204	1	1130.1280	10.71	2	58.0	11.7	1	549-569	R.WVYLSGNRITEVSLGALGPAR.E		

Detailed Protein Report

Protein 353: **interferon-induced guanylate-binding protein 2 [Homo sapiens]**

Accession:	gi|38327558	**Score:**	25.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.2
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAPEINLPGP	MSLIDNTKGQ	LVVNPEALKI	LSAITQPVVV	VAIVGLYRTG	KSYLMNKLAG	KKNGFSLGST	VKSHTKGIWM
90	100	110	120	130	140	150	160
WCVPHPKKPE	HTLVLLDTEG	LGDIEKGDNE	NDSWIFALAI	LLSSTFVYNS	MGTINQQAMD	QLHYVTELTD	RIKANSSPGN
170	180	190	200	210	220	230	240
NSVDDSADFV	SFFPAFVWTL	RDFTLELEVD	GEPITADDYL	ELSLKLRKGT	DKKSKSFNDP	RLCIRKFFPK	RKCFVFDWPA
250	260	270	280	290	300	310	320
PKKYLAHLEQ	LKEEELNPDF	IEQVAEFCSY	ILSHSNVKTL	SGGIPVNGPR	LESLVLTYVN	AISSGDLPCM	ENAVLALAQI
330	340	350	360	370	380	390	400
ENSAAVEKAI	AHYEQQMGQK	VQLPTETLQE	LLDLHRDSER	EAIEVFMKNS	FKDVDQMFQR	KLGAQLEARR	DDFCKQNSKA
410	420	430	440	450	460	470	480
SSDCCMALLQ	DIFGPLEEDV	KQGTFSKPGG	YRLFTQKLQE	LKNKYYQVPR	KGIQAKEVLK	KYLESKEDVA	DALLQTDQSL
490	500	510	520	530	540	550	560
SEKEKAIEVE	RIKAESAEAA	KKMLEEIQKK	NEEMMEQKEK	SYQEHVKQLT	EKMERDRAQL	MAEQEKTLAL	KLQEQERLLK
570	580	590	600				
EGFENESKRL	QKDIWDIQMR	SKSLEPICNI	L				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2870	1	1027.5482	62.66	2	65.0	11.1	2	503-518	K.MLEEIQKKNEEMMEQK.E	Oxidation: 12

Detailed Protein Report

Protein 354: zinc finger protein 865 [Homo sapiens]

Accession:	gi|307219238	**Score:**	25.8
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

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
13	1	819.8462	-127.06	2	29.7	15.8	2	260-272	R.TYNHVSSLIRHRR.C	
2279	1	869.2738	-114.47	2	58.9	10.1	0	689-704	K.EVHMAEKPYGCDACGK.T	

Detailed Protein Report

Protein 355: centrosomal protein of 290 kDa [Homo sapiens]

Accession:	gi|109255234	**Score:**	25.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	290.2
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MPPNINWKEI	MKVDPDDLPR	QEELADNLLI	SLSKVEVNEL	KSEKQENVIH	LFRITQSLMK	MKAQEVELAL	EEVEKAGEEQ
90	100	110	120	130	140	150	160
AKFENQLKTK	VMKLENELEM	AQQSAGGRDT	RFLRNEICQL	EKQLEQKDRE	LEDMEKELEK	EKKVNEQLAL	RNEEAENENS
170	180	190	200	210	220	230	240
KLRRENKRLK	KKNEQLCQDI	IDYQKQIDSQ	KETLLSRRGE	DSDYRSQLSK	KNYELIQYLD	EIQTLTEANE	KIEVQNQEMR
250	260	270	280	290	300	310	320
KNLEESVQEM	EKMTDEYNRM	KAIVHQTDNV	IDQLKKENDH	YQLQVQELTD	LLKSKNEEDD	PIMVAVNAKV	EEWKLILSSK
330	340	350	360	370	380	390	400
DDEIIEYQQM	LHNLREKLKN	AQLDADKSNV	MALQQGIQER	DSQIKMLTEQ	VEQYTKEMEK	NTCIIEDLKN	ELQRNKGAST
410	420	430	440	450	460	470	480
LSQQTHMKIQ	STLDILKEKT	KEAERTAELA	EADAREKDKE	LVEALKRLKD	YESGVYGLED	AVVEIKNCKN	QIKIRDREIE
490	500	510	520	530	540	550	560
ILTKEINKLE	LKISDFLDEN	EALRERVGLE	PKTMIDLTEF	RNSKHLKQQQ	YRAENQILLK	EIESLEEERL	DLKKKIRQMA
570	580	590	600	610	620	630	640
QERGKRSATS	GLTTEDLNLT	ENISQGDRIS	ERKLDLLSLK	NMSEAQSKNE	FLSRELIEKE	RDLERSRTVI	AKFQNKLKEL
650	660	670	680	690	700	710	720
VEENKQLEEG	MKEILQAIKE	MQKDPDVKGG	ETSLIIPSLE	RLVNAIESKN	AEGIFDASLH	LKAQVDQLTG	RNEELRQELR
730	740	750	760	770	780	790	800
ESRKEAINYS	QQLAKANLKI	DHLEKETSLL	RQSEGSNVVF	KGIDLPDGIA	PSSASIINSQ	NEYLIHLLQE	LENKEKKLKN
810	820	830	840	850	860	870	880
LEDSLEDYNR	KFAVIRHQQS	LLYKEYLSEK	ETWKTESKTI	KEEKRKLEDQ	VQQDAIKVKE	YNNLLNALQM	DSDEMKKILA
890	900	910	920	930	940	950	960
ENSRKITVLQ	VNEKSLIRQY	TTLVELERQL	RKENEKQKNE	LLSMEAEVCE	KIGCLQRFKE	MAIFKIAALQ	KVVDNSVSLS
970	980	990	1000	1010	1020	1030	1040
ELELANKQYN	ELTAKYRDIL	QKDNMLVQRT	SNLEHLECEN	ISLKEQVESI	NKELEITKEK	LHTIEQAWEQ	ETKLGNESSM
1050	1060	1070	1080	1090	1100	1110	1120
DKAKKSITNS	DIVSISKKIT	MLEMKELNER	QRAEHCQKMY	EHLRTSLKQM	EERNFELETK	FAELTKINLD	AQKVEQMLRD
1130	1140	1150	1160	1170	1180	1190	1200
ELADSVSKAV	SDADRQRILE	LEKNEMELKV	EVSKLREISD	IARRQVEILN	AQQQSRDKEV	ESLRMQLLDY	QAQSDEKSLI
1210	1220	1230	1240	1250	1260	1270	1280
AKLHQHNVSL	QLSEATALGK	LESITSKLQK	MEAYNLRLEQ	KLDEKEQALY	YARLEGRNRA	KHLRQTIQSL	RRQFSGALPL
1290	1300	1310	1320	1330	1340	1350	1360
AQQEKFSKTM	IQLQNDKLKI	MQEMKNSQQE	HRNMENKTLE	MELKLKGLEE	LISTLKDTKG	AQKVINWHMK	IEELRLQELK
1370	1380	1390	1400	1410	1420	1430	1440
LNRELVKDKE	EIKYLNNIIS	EYERTISSLE	EEIVQQNKFH	EERQMAWDQR	EVDLERQLDI	FDRQQNEILN	AAQKFEEATG
1450	1460	1470	1480	1490	1500	1510	1520
SIPDPSLPLP	NQLEIALRKI	KENIRIILET	RATCKSLEEK	LKEKESALRL	AEQNILSRDK	VINELRLRLP	ATAEREKLIA
1530	1540	1550	1560	1570	1580	1590	1600
ELGRKEMEPK	SHHTLKIAHQ	TIANMQARLN	QKEEVLKKYQ	RLLEKAREEQ	REIVKKHEED	LHILHHRLEL	QADSSLNKFK
1610	1620	1630	1640	1650	1660	1670	1680
QTAWDLMKQS	PTPVPTNKHF	IRLAEMEQTV	AEQDDSLSSL	LVKLKKVSQD	LERQREITEL	KVKEFENIKL	QLQENHEDEV
1690	1700	1710	1720	1730	1740	1750	1760
KKVKAEVEDL	KYLLDQSQKE	SQCLKSELQA	QKEANSRAPT	TTMRNLVERL	KSQLALKEKQ	QKALSRALLE	LRAEMTAAAE
1770	1780	1790	1800	1810	1820	1830	1840
ERIISATSQK	EAHLNVQQIV	DRHTRELKTQ	VEDLNENLLK	LKEALKTSKN	RENSLTDNLN	DLNNELQKKQ	KAYNKILREK
1850	1860	1870	1880	1890	1900	1910	1920
EEIDQENDEL	KRQIKRLTSG	LQGKPLTDNK	QSLIEELQRK	VKKLENQLEG	KVEEVDLKPM	KEKNAKEELI	RWEEGKKWQA
1930	1940	1950	1960	1970	1980	1990	2000
KIEGIRNKLK	EKEGEVFTLT	KQLNTLKDLF	AKADKEKLTL	QRKLKTTGMT	VDQVLGIRAL	ESEKELEELK	KRNLDLENDI
2010	2020	2030	2040	2050	2060	2070	2080
LYMRAHQALP	RDSVVEDLHL	QNRYLQEKLH	ALEKQFSKDT	YSKPSISGIE	SDDHCQREQE	LQKENLKLSS	ENIELKFQLE
2090	2100	2110	2120	2130	2140	2150	2160
QANKDLPRLK	NQVRDLKEMC	EFLKKEKAEV	QRKLGHVRGS	GRSGKTIPEL	EKTIGLMKKV	VEKVQRENEQ	LKKASGILTS
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
2146	2	937.4291	-49.48	2	55.4	15.4	2	115-129	R.NEICQLEKQLEQKDR.E	
1648	1	858.4049	-102.70	1	49.1	10.3	0	2438-2444	K.NILLEEK.V	

Detailed Protein Report

Protein 356: zinc finger protein 534 isoform 1 [Homo sapiens]

Accession:	gi|221139777	**Score:**	25.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.7
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALTQGQLSF	SDVAIEFSQE	EWKCLDPGQK	ALYRDVMLEN	YRNLVSLGIC	LPDLSVTSML	EQKRDPWTLQ	SEVKIINNPD
90	100	110	120	130	140	150	160
GRECIKGVNT	EKSSKLGSSA	GNKSLKNQHG	LTLQLHLTEW	QPFQAVRNIY	GCKHVEKSIS	DNSSVSPVQI	SFFSVKTHIF
170	180	190	200	210	220	230	240
NNYRNDFLFS	TLLPQEQKVH	IREKPYGCNE	HGKVFRVSSS	LTNRQVIHIA	DKTYKCSDCG	EIFSSNSNFA	QHQRIHTGEK
250	260	270	280	290	300	310	320
PYKYNECGKV	FNQNSHLAQH	QKIHTGQKPY	NNKECGKVFS	HHAYLAQHRK	IHTGEKPYKC	SECGKAFSVC	SSLTAHLVIH
330	340	350	360	370	380	390	400
TGEKPYDCKE	CGKVFRHKSS	LTTHQTVHTG	ERPYKCNECG	KGFSRIAFLA	RHRKVHTGEK	PYKCNECGKV	FIGNSRLARH
410	420	430	440	450	460	470	480
RKIHTGGRRY	KCNECGKAFR	TCSDLTAHLL	IHTGEKPYEC	IDCGKVFRHK	SSLTYHCRIH	TGEKPYKCNE	CGKVFSQNSN
490	500	510	520	530	540	550	560
LQRHRKIHTG	EKLYKCNECG	KVFRQNSHLA	QHRDIHTGEK	PYSCNECGKV	FRRNSHLVRH	RNVHTGEKPY	SCNECGKVFS
570	580	590	600	610	620	630	640
RNSHLARHRN	IHTGEKPHSC	NECGKVFSRN	SHLARHRKIH	TGEKLYKCNE	CSKVFSRNSR	LAQHRNIHTG	VKPYSCNECG
650	660	670					
KVFSKNSILV	QHCSIHTREK	P					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2242	1	961.4221	-46.22	2	56.7	10.2	2	290-305	R.KIHTGEKPYKCSECGK.A	Carbamidomethyl: 11, 14

Detailed Protein Report

Protein 357: fibrous sheath-interacting protein 2 [Homo sapiens]

Accession:	gi|297206791	**Score:**	25.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	789.4
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	2

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
2211	1	933.6966	-60.77	3	56.3	14.8	0	896-919	K.NSMPHTLDPMCDIAEDMVHAILEK.L	Carbamidomethyl: 11; Oxidation: 3, 10
59	1	841.4513	24.83	3	30.6	11.0	2	5590-5613	K.SGMINLTSGLATGVTNKKEVDENK.V	Oxidation: 3

Detailed Protein Report

Protein 358: short transient receptor potential channel 4 isoform zeta [Homo sapiens]

Accession:	gi|209863032	**Score:**	25.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.2
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQFYYKRNV	NAPYRDRIPL	RIVRAESELS	PSEKAYLNAV	EKGDYASVKK	SLEEAEIYFK	ININCIDPLG	RTALLIAIEN
90	100	110	120	130	140	150	160
ENLELIELLL	SFNVYVGDAL	LHAIRKEVVG	AVELLLNHKK	PSGEKQFVAQ	PNCQQLLASR	WYDEFPGWRR	RHWAVKMVTC
170	180	190	200	210	220	230	240
FIIGLLFPVF	SVCYLIAPKS	PLGLFIRKPF	IKFICHTASY	LTFLFLLLLA	SQHIDRSDLN	RQGPPPTIVE	WMILPWVLGF
250	260	270	280	290	300	310	320
IWGEIKQMWD	GGLQDYIHDW	WNLMDFVMNS	LYLATISLKI	VAFVKYSALN	PRESWDMWHP	TLVAEALFAI	ANIFSSLRLI
330	340	350	360	370	380	390	400
SLFTANSHLG	PLQISLGRML	LDILKFLFIY	CLVLLAFANG	LNQLYFYYEE	TKGLTCKGIR	CEKQNNAFST	LFETLQSLFW
410	420	430	440	450	460	470	480
SIFGLINLYV	TNVKAQHEFT	EFVGATMFGT	YNVISLVVLL	NMLIAMMNNS	YQLIADHADI	EWKFARTKLW	MSYFEEGGTL
490	500	510	520	530	540	550	560
PTPFNVIPSP	KSLWYLIKWI	WTHLCKKKMR	RKPESFGTIG	RRAADNLRRH	HQYQEVMRNL	VKRYVAAMIR	DAKTEEGLTE
570	580	590	600	610	620	630	640
ENFKELKQDI	SSFRFEVLGL	LRGSKLSTIQ	SANASKESSN	SADSDEKSDS	EGNSKDKKKN	FSLFDLTTLI	HPRSAAIASE
650	660	670	680	690	700	710	720
RHNISNGSAL	VVQEPPREKQ	RKVNFVTDIK	NFGLFHRRSK	QNAAEQNANQ	IFSVSEEVAR	QQAAGPLERN	IQLESRGLAS
730	740	750	760	770	780	790	800
RGDLSIPGLS	EQCVLVDHRE	RNTDTLGLQV	GKRVCPFKSE	KVVVEDTVPI	IPKEKHAKEE	DSSIDYDLNL	PDTVTHEDYV
810							
TTRL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
547	1	607.8337	8.15	2	36.8	10.5	1	499-507	K.WIWTHLCKK.K	

Detailed Protein Report

Protein 359: 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

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
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

Detailed Protein Report

Protein 360: squamous cell carcinoma antigen recognized by T-cells 3 [Homo sapiens]

Accession:	gi|7661952	**Score:**	25.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	109.9
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATAAETSAS	EPEAESKAGP	KADGEEDEVK	AARTRRKVLS	RAVAAATYKT	MGPAWDQQEE	GVSESDGDEY	AMASSAESSP
90	100	110	120	130	140	150	160
GEYEWEYDEE	EEKNQLEIER	LEEQLSINVY	DYNCHVDLIR	LLRLEGELTK	VRMARQKMSE	IFPLTEELWL	EWLHDEISMA
170	180	190	200	210	220	230	240
QDGLDREHVY	DLFEKAVKDY	ICPNIWLEYG	QYSVGGIGQK	GGLEKVRSVF	ERALSSVGLH	MTKGLALWEA	YREFESAIVE
250	260	270	280	290	300	310	320
AARLEKVHSL	FRRQLAIPLY	DMEATFAEYE	EWSEDPIPES	VIQNYNKALQ	QLEKYKPYEE	ALLQAEAPRL	AEYQAYIDFE
330	340	350	360	370	380	390	400
MKIGDPARIQ	LIFERALVEN	CLVPDLWIRY	SQYLDRQLKV	KDLVLSVHNR	AIRNCPWTVA	LWSRYLLAME	RHGVDHQVIS
410	420	430	440	450	460	470	480
VTFEKALNAG	FIQATDYVEI	WQAYLDYLRR	RVDFKQDSSK	ELEELRAAFT	RALEYLKQEV	EERFNESGDP	SCVIMQNWAR
490	500	510	520	530	540	550	560
IEARLCNNMQ	KARELWDSIM	TRGNAKYANM	WLEYYNLERA	HGDTQHCRKA	LHRAVQCTSD	YPEHVCEVLL	TMERTEGSLE
570	580	590	600	610	620	630	640
DWDIAVQKTE	TRLARVNEQR	MKAAEKEAAL	VQQEEEKAEQ	RKRARAEKKA	LKKKKKIRGP	EKRGADEDDE	KEWGDDEEEQ
650	660	670	680	690	700	710	720
PSKRRRVENS	IPAAGETQNV	EVAAGPAGKC	AAVDVEPPSK	QKEKAASLKR	DMPKVLHDSS	KDSITVFVSN	LPYSMQEPDT
730	740	750	760	770	780	790	800
KLRPLFEACG	EVVQIRPIFS	NRGDFRGYCY	VEFKEEKSAL	QALEMDRKSV	EGRPMFVSPC	VDKSKNPDFK	VFRYSTSLEK
810	820	830	840	850	860	870	880
HKLFISGLPF	SCTKEELEEI	CKAHGTVKDL	RLVTNRAGKP	KGLAYVEYEN	ESQASQAVMK	MDGMTIKENI	IKVAISNPPQ
890	900	910	920	930	940	950	960
RKVPEKPETR	KAPGGPMLLP	QTYGARGKGR	TQLSLLPRAL	QRPSAAAPQA	ENGPAAAPAV	AAPAATEAPK	MSNADFAKLF
970							
LRK							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1898	1	686.2375	-164.62	2	52.2	12.0	1	670-682	K.CAAVDVEPPSKQK.E	

Detailed Protein Report

Protein 361: **PREDICTED: centromere protein T isoform X3 [Homo sapiens]**

Accession:	gi|578829227	**Score:**	25.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.4
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSWCCLWLCL	SSVGRTGSAG	PSLPFSELCS	LGLLRLRPVF	SPLHSGPGKP	AQFLAGEAEE	VNAFALGFLS	TSSGVSGEDE
90	100	110	120	130	140	150	160
VEPLHDGVEE	AEKKMEEEGV	SVSEMEATGA	QGPSRVEEAE	GHTEVTEAEG	SQGTAEADGP	GASSGDEDAS	GRAASPESAS
170	180	190	200	210	220	230	240
STPESLQARR	HHQFLEPAPA	PGAAVLSSEP	AEPLLVRHPP	RPRTTGPRPR	QDPHKAGLSH	YVKLFSFYAK	MPMERKALEM
250	260	270	280	290	300	310	320
VEKCLDKYFQ	HLCDDLEVFA	AHAGRKTVKP	EDLELLMRRQ	GLVTDQVSLH	VLVERHLPLE	YRQLLIPCAY	SGNSVFPAQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2474	1	965.7758	-154.68	2	59.6	14.1	0	1-15	-.MSWCCLWLCLSSVGR.T	Carbamidomethyl: 4, 5, 9; Oxidation: 1

Detailed Protein Report

Protein 362: 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 363:	**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

Quantitation

QD:QU	**Median:**	0.75	**CV:**	0.00 %	**No. of Peptides:**	1

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	Ratios
193	1	613.7845	-35.89	2	32.4	14.1	0	51-60	R.QCQQLSQHVR.T		QD:QU 0.75
490	1	636.2255	-63.89	3	36.1	11.6	1	4132-4148	R.TTTCFGDGCQNTASRCK.N	Carbamidomethyl: 9, 16	

Detailed Protein Report

Protein 364: PREDICTED: transmembrane protein 255B isoform X13 [Homo sapiens]

Accession:	gi|578825377	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.8
Database Date:	2015-11-30	**pI:**	10.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.4
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 1.06 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MGLRGRKNLT SSLACLPEGL SRRKKTSLWF VGSLLLVSVL IVTVGLAATT RTENVTVGGY YPGIILGFGS FLGIIGINLV
        90        100        110        120        130        140        150        160
ENRRQMLVAA IVFISFGVVA AFCCAIVDGV FAAQHIEPRP LTTGRCQFYS SGVGYLYDVY QTEVTCHSLD GKCQLKRRAL
       170
ARLL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2276	1	873.4565	-8.97	2	58.9	13.3	1	7-22	R.KNLTSSLACLPEGLSR.R	Carbamidomethyl: 9	QD:QU 1.06

Detailed Protein Report

Protein 365: polypeptide N-acetylgalactosaminyltransferase 9 isoform A [Homo sapiens]

Accession:	gi|169790926	**Score:**	25.6
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:	1

Quantitation

QD:QU **Median:** 0.37 **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		QD:QU 0.37

Detailed Protein Report

Protein 366: PREDICTED: alpha-tectorin isoform X1 [Homo sapiens]

Accession:	gi|530398338	**Score:**	25.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	238.8
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:** 0.90	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MNYSSFLRIW	VSFIFALVQH	QAQPRELMYP	FWQNDTKTPK	VDDGSSSEIK	LAIPVFFFGV	PYRTVYVNNN	GVVSFNVLVS
90	100	110	120	130	140	150	160
QFTPESFPLT	DGRAFVAPFW	ADVHNGIRGE	IYYRETMEPA	ILKRATKDIR	KYFKDMATFS	ATWVFIVTWE	EVTFYGGSST
170	180	190	200	210	220	230	240
TPVNTFQAVL	VSDGSYTFTL	FNYYEINWTT	GTASGGDPLT	GLGGVMAQAG	FNGGNLTNFF	SLPGSRTPEI	VNIQETTNVN
250	260	270	280	290	300	310	320
VPGRWAFKVD	GKEIDPANGC	TSRGQFLRRG	EVFWDDLNCT	VKCRCLDFNN	EIYCQEASCS	PYEVCEPKGK	FFYCSAVETS
330	340	350	360	370	380	390	400
TCVVFGEPHY	HTFDGFLFHF	QGSCAYLLAR	QCLQTSSLPF	FSVEAKNEHR	RGSAVSWVKE	LSVEVNGYKI	LIPKGSYGRV
410	420	430	440	450	460	470	480
KVNDLVTSLP	VTLDLGTVKI	YQSGISTAVE	TDFGLLVTFD	GQHYASISVP	GSYINSTCGL	CGNYNKNPLD	DFLRPDGRPA
490	500	510	520	530	540	550	560
MSVLDLGESW	RVYHADWKCD	SGCVDNCTQC	DAATEALYFG	SDYCGFLNKT	DGPLWECGTV	VDPTAFVHSC	VYDLCSVRDN
570	580	590	600	610	620	630	640
GTLLCQAIQA	YALVCQALGI	PIGDWRTQTG	CVSTVQCPSF	SHYSVCTSSC	PDTCSDLTAS	RNCATPCTEG	CECNQGFVLS
650	660	670	680	690	700	710	720
TSQCVPLHKC	GCDFDGHYYT	MGEFFWATAN	CTVQCLCEEG	GDVYCFNKTC	GSGEVCAVED	GYQGCFPKRE	TVCLLSQNQV
730	740	750	760	770	780	790	800
LHTFDGASYA	FPSEFSYTLL	KTCPERPEYL	EIDINKKKPD	AGPAWLRGLR	ILVADQEVKI	GGIGASEVKL	NGQEVELPFF
810	820	830	840	850	860	870	880
HPSGKLEIYR	NKNSTTVESK	GVVTVQYSDI	GLLYIRLSTT	YFNCTGGLCG	FYNANASDEF	CLPNGKCTDN	LAVFLESWTT
890	900	910	920	930	940	950	960
FEEICNGECG	DLLKACNNDS	ELLKFYRSRS	RCGIINDPSN	SSFLECHGVV	NVTAYYRTCL	FRLCQSGGNE	SELCDSVARY
970	980	990	1000	1010	1020	1030	1040
ASACKNADVE	VGPWRTYDFC	PLECPENSHF	EECITCTETC	ETLTLGPICV	DSCSEGCQCD	EGYALLGSQC	VTRSECGCNF
1050	1060	1070	1080	1090	1100	1110	1120
EGHQLATNET	FWVDLDCQIF	CYCSGTDNRV	HCETIPCKDD	EYCMEEGGLY	YCQARTDASC	IVSGYGHYLT	FDGFPFDFQT
1130	1140	1150	1160	1170	1180	1190	1200
SCPLILCTTG	SRPSSDSFPK	FVVTAKNEDR	DPSLALWVKQ	VDVTVFGYSI	VIHRAYKHTV	LVNSERLYLP	LKLGQGKINI
1210	1220	1230	1240	1250	1260	1270	1280
FSFGFHVVVE	TDFGLKVVYD	WKTFLSITVP	RSMQNSTYGL	CGRYNGNPDD	DLEMPMGLLA	SSVNEFGQSW	VKRDTFCQVG
1290	1300	1310	1320	1330	1340	1350	1360
CGDRCPSCAK	VEGFSKVQQL	CSLIPNQNAA	FSKCHSKVNP	TFFYKNCLFD	SCIDGGAVQT	ACSWLQNYAS	TCQTQGITVT
1370	1380	1390	1400	1410	1420	1430	1440
GWRNYTSCTV	TCPPNSHYES	CVSVCQPRCA	AIRLKSDCSH	YCVEGCHCDA	GYVLNGKSCI	LPHSCGCYSD	GKYYEPKQLF
1450	1460	1470	1480	1490	1500	1510	1520
WNSDCTRRCR	CFRRNVIQCD	PRQCKSDEEC	ALRNGVRGCF	STKTSYCLAA	GGGVFRTFDG	AFLRFPANCA	FVLSTICQKL
1530	1540	1550	1560	1570	1580	1590	1600
PDISFQLIIN	FDKWSAPNLT	IISPVYFYIN	EEQILINDRN	TVKVNGTQVN	VPFITGLATK	IYSSEGFLVI	DTSPDIQIYY
1610	1620	1630	1640	1650	1660	1670	1680
NGFNVIKISI	SERLQNKVCG	LCGNFNGDLT	DDYVTLRGKP	VVSSVVLAQS	WKTNGMQKSC	NELQFSQYAA	MCDNVHIQKM
1690	1700	1710	1720	1730	1740	1750	1760
QGDGYCLKLT	DMKGFFQPCY	GLLDPLPFYE	SCYLDGCYSH	KKFQLCGSLA	AYGEACRSFG	ILSTEWIEKE	NCSGVVEDPC
1770	1780	1790	1800	1810	1820	1830	1840
VGADCPNRTC	ELGNGRELCG	CIEPPPYGNN	SHDIIDAEVT	CKAAQMEVSI	SKCKLFQLGF	EREGVRINDR	QCTGIEGEDF
1850	1860	1870	1880	1890	1900	1910	1920
ISFQINNTKG	NCGNIVQSNG	THIMYKNTLW	IESANNTGNI	ITRDRTINVE	FSCAYELDIK	ISLDSVVKPM	LSVINLTVPT
1930	1940	1950	1960	1970	1980	1990	2000
QEGSFITKMA	LYKNASYKHP	YRQGEVVLTT	RDVLYVGVFV	VGADATHLIL	TLNKCYATPT	RDSNDKLRYF	IIEGGCQNLK
2010	2020	2030	2040	2050	2060	2070	2080
DNTIGIEENA	VSLTCRFHVT	VFKFIGDYDE	VHLHCAVSLC	DSEKYSCKIT	CPHNSRIATD	YTKEPKEQII	SVGPIRRKRL
2090	2100	2110	2120	2130	2140	2150	2160
DWCEDNGGCE	QICTSRVDGP	LCSCVTGTLQ	EDGKSCRASN	SSMELQVWTL	LLIMIQISLW	HFVYKSGTTS	

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
132	1	673.3206	73.69	3	30.4	10.7	1	1274-1290	R.DTFCQVGCGDRCPSCAK.V	Carbamidomethyl: 4, 8, 12, 15	QD:QU	0.90

Detailed Protein Report

Protein 367: dynein heavy chain 10, axonemal [Homo sapiens]

Accession:	gi|198442844	**Score:**	25.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	514.5
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.4
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MVPEEVEVEI	DEIPVLSEEG	EEEEETYSQK	VESVDKVRAK	RVSLRTESLG	QPLNREDEEM	DKEISEKLPS	KRTAKHIMEK
90	100	110	120	130	140	150	160
MHLHMLCTPL	PEEFLDQNVV	FFLRNTKEAI	SEATDMKEAM	EIMPETLEYG	IINANVLHFL	KNIICQVFLP	ALSFNQHRTS
170	180	190	200	210	220	230	240
TTVGVTSGEV	SNSSEHESDL	PPMPGEAVEY	HSIQLIRDEF	LMNVQKFASN	IQRTMQQLEG	EIKLEMPIIS	VEGEVSDLAA
250	260	270	280	290	300	310	320
DPETVDILEQ	CVINWLNQIS	TAVEAQLKKT	PQGKGPLAEI	EFWRERNATL	SALHEQTKLP	IVRKVLDVIK	ESDSMLVANL
330	340	350	360	370	380	390	400
QPVFTELFKF	HTEASDNVRF	LSTVERYFKN	ITHGSGFHVV	LDTIPAMMSA	LRMVWIISRH	YNKDERMIPL	MERIAWEIAE
410	420	430	440	450	460	470	480
RVCRVVNLRT	LFKENRASAQ	SKTLEARNTL	RLWKKAYFDT	RAKIEASGRE	DRWEFDRKRL	FERTDYMATI	CQDLSDVLQI
490	500	510	520	530	540	550	560
LEEFYNIFGP	ELKAVTGDPK	RIDDVLCRVD	GLVTPMENLT	FDPFSIKSSQ	FWKYVMDEFK	IEVLIDIINK	IFVQNLENPP
570	580	590	600	610	620	630	640
LYKNHPPVAG	AIYWERSLFF	RIKHTILRFQ	EVQEILDSDR	GQEVKQKYLE	VGRTMKEYED	RKYEQWMEVT	EQVLPALMKK
650	660	670	680	690	700	710	720
SLLTKSSIAT	EEPSTLERGA	VFAINFSPAL	REIINETKYL	EQLGFTVPEL	ARNVALQEDK	FLRYTAGIQR	MLDHYHMLIG
730	740	750	760	770	780	790	800
TLNDAESVLL	KDHSQELLRV	FRSGYKRLNW	NSLGIGDYIT	GCKQAIGKFE	SLVHQIHKNA	DDISSRLTLI	EAINLFKYPA
810	820	830	840	850	860	870	880
AKSEEELPGV	KEFFEHIERE	RASDVDHMVR	WYLAIGPLLT	KVEGLVVHTN	TGKAPKLASY	YKYWEKKIYE	VLTKLILKNL
890	900	910	920	930	940	950	960
QSFNSLILGN	VPLFHTETIL	TAPEIILHPN	TNEIDKMCFH	CVRNCVEITK	HFVRWMNGSC	IECPPQKGEE	EEVVIINFYN
970	980	990	1000	1010	1020	1030	1040
DISLNPQIIE	QAVMIPQNVH	RILINLMKYL	QKWKRYRPLW	KLDKAIVMEK	FAAKKPPCVA	YDEKLQFYSK	IAYEVMRHPL
1050	1060	1070	1080	1090	1100	1110	1120
IKDEHCIRLQ	LRHLANTVQE	NAKSWVISLG	KLLNESAKEE	LYNLHEEMEH	LAKNLRKIPN	TLEDLKFVLA	TIAEIRSKSL
1130	1140	1150	1160	1170	1180	1190	1200
VMELRYRDVQ	ERYRTMAMYN	LFPPDAEKEL	VDKIESIWSN	LFNDSVNVEH	ALGDIKRTFT	ELTRGEIMNY	RVQIEEFAKR
1210	1220	1230	1240	1250	1260	1270	1280
FYSEGPGSVG	DDLDKGVELL	GVYERELARH	EKSRQELANA	EKLFDLPITM	YPELLKVQKE	MSGLRMIYEL	YEGLKVAKEE
1290	1300	1310	1320	1330	1340	1350	1360
WSQTLWINLN	VQILQEGIEG	FLRALRKLPR	PVRGLSVTYY	LEAKMKAFKD	SIPLLLDLKN	EALRDRHWKE	LMEKTSVFFE
1370	1380	1390	1400	1410	1420	1430	1440
MTETFTLENM	FAMELHKHTD	VLNEIVTAAI	KEVAIEKAVK	EILDTWENMK	FTVVKYCKGT	QERGYILGSV	DEIIQSLDDN
1450	1460	1470	1480	1490	1500	1510	1520
TFNLQSISGS	RFVGPFLQTV	HKWEKTLSLI	GEVIEIWMLV	QRKWMYLESI	FIGGDIRSQL	PEEAKKFDNI	DKVFKRIMGE
1530	1540	1550	1560	1570	1580	1590	1600
TLKDPVIKRC	CEAPNRLSDL	QNVSEGLEKC	QKSLNDYLDS	KRNAFPRFFF	ISDDELLSIL	GSSDPLCVQE	HMIKMYDNIA
1610	1620	1630	1640	1650	1660	1670	1680
SLRFNDGDSG	EKLVSAMISA	EGEVMEFRKI	LRAEGRVEDW	MTAVLNEMRR	TNRLITKEAI	FRYCEDRSRV	DWMLLYQGMV
1690	1700	1710	1720	1730	1740	1750	1760
VLAASQVWWT	WEVEDVFHKA	QKGEKQAMKN	YGRKMHRQID	ELVTRITMPL	SKNDRKKYNT	VLIIDVHARD	IVDSFIRGSI
1770	1780	1790	1800	1810	1820	1830	1840
LEAREFDWES	QLRFYWDREP	DELNIRQCTG	TFGYGYEYMG	LNGRLVITPL	TDRIYLTLTQ	ALSMYLGGAP	AGPAGTGKTE
1850	1860	1870	1880	1890	1900	1910	1920
TTKDLAKALG	LLCVVTNCGE	GMDYRAVGKI	FSGLAQCGAW	GCFDEFNRID	ASVLSVISSQ	IQTIRNALIH	QLTTFQFEGQ
1930	1940	1950	1960	1970	1980	1990	2000
EISLDSRMGI	FITMNPGYAG	RTELPESVKA	LFRPVVVIVP	DLQQICEIML	FSEGFLEAKT	LAKKMTVLYK	LAREQLSKQY
2010	2020	2030	2040	2050	2060	2070	2080
HYDFGLRALK	SVLVMAGELK	RGSSDLREDV	VLMRALRDMN	LPKFVFEDVP	LFLGLISDLF	PGLDCPRVRY	PDFNDAVEQV
2090	2100	2110	2120	2130	2140	2150	2160
LEENGYAVLP	IQVDKVVQMF	ETMLTRHTTM	VVGPTRGGKS	VVINTLCQAQ	TKLGLTTKLY	ILNPKAVSVI	ELYGILDPTT
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
2459	1	1045.2266	-235.83	1	61.2	14.2	0	822-830	R.ASDVDHMVR.W	Oxidation: 7

Detailed Protein Report

Protein 368: PREDICTED: centrosomal protein of 192 kDa isoform X12 [Homo sapiens]

Accession:	gi|578832148	**Score:**	25.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	154.9
Database Date:	2015-11-30	**pI:**	4.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.88 **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	QD:QU 0.88
2156	2	955.8889	-44.17	2	55.6	12.5	0	494-509	K.QNLNVSLSDEMNEDFR.S		

Detailed Protein Report

Protein 369: zinc finger protein 471 [Homo sapiens]

Accession:	gi|150170667	**Score:**	25.4
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

Quantitation

QD:QU **Median:** 0.29 **CV:** 0.00 % **No. of 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	Ratios
520	1	690.4558	150.35	2	36.5	14.8	1	357-366	R.YNTSFIRHWR.S		QD:QU 0.29

Detailed Protein Report

Protein 370: ubiquitin-like-conjugating enzyme ATG10 [Homo sapiens]

Accession:	gi|18594496	**Score:**	25.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.3
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	6.8
		No. of unique Peptides:	2

Quantitation

QD:QU	**Median:** 2.86	**CV:** 0.00 %	**No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|530379522	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ubiquitin-like-conjugating enzyme ATG10 isoform X2 [Homo sapiens]
gi|530379520	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ubiquitin-like-conjugating enzyme ATG10 isoform X1 [Homo sapiens]
gi|196162717	refseq_human (refseq_human_20140103.fasta)	ubiquitin-like-conjugating enzyme ATG10 [Homo sapiens]

10	20	30	40	50	60	70	80
MEEDEFIGEK	TFQRYCAEFI	KHSQQIGDSW	EWRPSKDCSD	GYMCKIHFQI	KNGSVMSHLG	ASTHGQTCLP	MEEAFELPLD
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
DCEVIETAAA	SEVIKYEYHV	LYSCSYQVPV	LYFRASFLDG	RPLTLKDIWE	GVHECYKMRL	LQGPWDTITQ	QEHPILGQPF
170	**180**	**190**	**200**	**210**	**220**	**230**	
FVLHPCKTNE	FMTPVLKNSQ	KINKNVNYIT	SWLSIVGPVV	GLNLPLSYAK	ATSQDERNVP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1635	1	576.3013	186.62	2	49.0	10.1	0	37-45	K.DCSDGYMCK.I	Carbamidomethyl: 2, 8; Oxidation: 7	
2921	2	922.9870	83.40	2	65.7	15.3	1	37-51	K.DCSDGYMCKIHFQIK.N	Carbamidomethyl: 2	QD:QU 2.86

Detailed Protein Report

Protein 371: PREDICTED: cysteine-rich with EGF-like domain protein 1 isoform X2 [Homo sapiens]

Accession:	gi|578806578	**Score:**	25.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.9
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.1
		No. of unique Peptides:	2

```
        10          20          30          40          50          60          70          80
MAPWPPKGLV  PAMLWGLSLF  LNLPGPIWLQ  PSPPPQSSPP  PQPHPCHTCR  GLVDSFNKGL  ERTIRDNFGG  GNTAWEEENL
        90         100         110         120         130         140         150         160
SKYKDSETRL  VEVLEGVCSK  SDFECHRLLE  LSEELVESWW  FHKQQEAPDL  FQWLCSDSLK  LCCPAGTFGP  SCLPCPGGTE
       170         180         190         200         210         220         230         240
RPCGGYGQCE  GEGTRGGSGH  CDCQAGYGGE  ACGQCGLGYF  EAERNASHLV  CSACFGPCAR  CSGPEESNCL  QCKKGWALHH
       250         260         270         280         290         300         310         320
LKCVDCAKAC  LGCMGAGPGR  CKKCSPGYQQ  VGSKCLDVDE  CETEVCPGEN  KQCENTEGGY  RCICAEGYKQ  MEGICVKEQI
       330         340         350         360         370         380         390         400
PGAFPILTDL  TPETTRRWKL  GSHPHSTYVK  MKMQRDEATF  PGLYGKQVAK  LGSQSRQSDR  GTRLIHSQQA  SSQR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2830	1	913.4702	92.84	2	64.5	10.8	1	243-260	K.CVDCAKACLGCMGAGPGR.C	Carbamidomethyl: 4, 8
2495	1	607.3216	119.88	2	61.8	14.6	0	292-301	K.QCENTEGGYR.C	Carbamidomethyl: 2

Detailed Protein Report

Protein 372: 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 373: **PREDICTED: pleckstrin homology domain-containing family G member 3 isoform X5 [Homo sapiens]**

Accession: gi|578825697
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 25.4
MW [kDa]: 148.9
pI: 5.3
Sequence Coverage [%]: 2.1
No. of unique Peptides: 2

Quantitation

QD:QU **Median:** 1.18 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MNLPGVPSPG SNARMPVSTS LHQDGSQERP VSLTSTTSSS GSSCDSRSAM EEPSSSEAPA KNGAGSLRSR HLPNSNNNSS
        90        100        110        120        130        140        150        160
SWLNVKGPLS PFNSRAAAGP AHHKLSYLGR VVREIVETER MYVQDLRSIV EDYLLKIIDT PGLLKPEQVS ALFGNIENIY
       170        180        190        200        210        220        230        240
ALNSQLLRDL DSCNSDPVAV ASCFVERSQE FDIYTQYCNN YPNSVAALTE CMRDKQQAKF FRDRQELLQH SLPLGSYLLK
       250        260        270        280        290        300        310        320
PVQRILKYHL LLQEIAKHFD EEEDGFEVVE DAIDTMTCVA WYINDMKRRH EHAVRLQEIQ SLLINWKGPD LTTYGELVLE
       330        340        350        360        370        380        390        400
GTFRVHRVRN ERTFFLFDKT LLITKKRGDH FVYKGNIPCS SLMLIESTRD SLCFTVTHYK HSKQQYSIQA KTVEEKRNWT
       410        420        430        440        450        460        470        480
HHIKRLILEN HHATIPQKAK EAILEMDSYY PNRYRCSPER LKKAWSSQDE VSTNVRQGRR QSEPTKHLLR QLNEKARAAG
       490        500        510        520        530        540        550        560
MKHAGSAGTL LDFGQPSRTR GLQPEAEGAT QEEEEEEEEV VEEEEEEEEE EQAFQVSLED LTGHEGNEKG AGPEPPGSEE
       570        580        590        600        610        620        630        640
EEEEQEESLA VAEQVADFAS SLLAALHCWH YRANALLFSR GAMGKGRRES ESSRSSRRPS GRSPTSTEKR MSFESISSLP
       650        660        670        680        690        700        710        720
EVEPDPEAGS EQEVFSAVEG PSAEETPSDT ESPEVLETQL DAHQGLLGMD PPGDMVDFVA AESTEDLKAL SSEEEEEMGG
       730        740        750        760        770        780        790        800
AAQEPESLLP PSVLDQASVI AERFVSSFSR RSSVAQEDSK SSGFGSPRLV SRSSSVLSLE GSEKGLARHG SATDSLSCQL
       810        820        830        840        850        860        870        880
SPEVDISVGV ATEDSPSVNG MEPPSPGCPV EPDRSSCKKK ESALSTRDRL LLDKIKSYYE NAEHHDAGFS VRRRESLSYI
       890        900        910        920        930        940        950        960
PKGLVRNSIS RFNSLPRPDP EPVPPVGSKR QVGSRPTSWA LFELPGPSQA VKGDPPPISD AEFRPSSEIV KIWEGMESSG
       970        980        990       1000       1010       1020       1030       1040
GSPGKGPGQG QANGFDLHEP LFILEEHELG AITEESATAS PESSSPTEGR SPAHLARELK ELVKELSSST QGELVAPLHP
      1050       1060       1070       1080       1090       1100       1110       1120
RIVQLSHVMD SHVSERVKNK VYQLARQYSL RIKSNKPVMA RPPLQWEKVA PERDGKSPTV PCLQEEAGEP LGGKGKRKPV
      1130       1140       1150       1160       1170       1180       1190       1200
LSLFDYEQLM AQEHSPPKPS SAGEMSPQRF FFNPSAVSQR TTSPGGRPSA RSPLSPTETF SWPDVRELCS KYASRDEARR
      1210       1220       1230       1240       1250       1260       1270       1280
AGGGRPRGPP VNRSHSVPEN MVEPPLSGRV GRCRSLSTKR GRGGGEAAQS PGPLPQSKPD GGETLYVTAD LTLEDNRRVI
      1290       1300       1310       1320       1330       1340       1350       1360
VMEKGPLPSP TAGLEESSGQ GPSSPVALLG QVQDFQQSAE CQPKEEGSRD PADPSQQGRV RNLREKFQAL NSVG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2000	1	698.7973	-80.70	2	53.5	15.3	0	1-14	-.MNLPGVPSPGSNAR.M		QD:QU 1.18
2130	1	789.2959	-119.98	2	57.0	10.1	2	609-622	R.ESESSRSSRRPSGR.S		

Detailed Protein Report

Protein 374: serine/threonine-protein kinase 36 isoform 2 [Homo sapiens]

Accession:	gi|343183344	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	141.6
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEKYHVLEMI	GEGSFGRVYK	GRRKYSAQVV	ALKFIPKLGR	SEKELRNLQR	EIEIMRGLRH	PNIVHMLDSF	ETDKEVVVVT
90	100	110	120	130	140	150	160
DYAEGELFQI	LEDDGKLPED	QVQAIAAQLV	SALYYLHSHR	ILHRDMKPQN	ILLAKGGGIK	LCDFGFARAM	STNTMVLTSI
170	180	190	200	210	220	230	240
KGTPLYMSPE	LVEERPYDHT	ADLWSVGCIL	YELAVGTPPF	YATSIFQLVS	LILKDPVRWP	STISPCFKNF	LQGLLTKDPR
250	260	270	280	290	300	310	320
QRLSWPDLLY	HPFIAGHVTI	ITEPAGPDLG	TPFTSRLPPE	LQVLKDEQAH	RLAPKGNQSR	ILTQAYKRMA	EEAMQKKHQN
330	340	350	360	370	380	390	400
TGPALEQEDK	TSKVAPGTAP	LPRLGATPQE	SSLLAGILAS	ELKSSWAKSG	TGEVPSAPRE	NRTTPDCERA	FPEERPEVLG
410	420	430	440	450	460	470	480
QRSTDVVDLE	NEEPDSDNEW	QHLLETTEPV	PIQLKAPLTL	LCNPDFCQRI	QSQLHEAGGQ	ILKGILEGAS	HILPAFRVLS
490	500	510	520	530	540	550	560
SLLSSCSDSV	ALYSFCREAG	LPGLLLSLLR	HSQESNSLQQ	QSWYGTFLQD	LMAVIQAYFA	CTFNLERSQT	SDSLQVFQEA
570	580	590	600	610	620	630	640
ANLFLDLLGK	LLAQPDDSEQ	TLRRDSLMCF	TVLCEAMDGN	SRAISKAFYS	SLLTTQQVVL	DGLLHGLTVP	QLPVHTPQGA
650	660	670	680	690	700	710	720
PQVSQPLREQ	SEDIPGAISS	ALAAICTAPV	GLPDCWDAKE	QVCWHLANQL	TEDSSQLRPS	LISGLQHPIL	CLHLLKVLYS
730	740	750	760	770	780	790	800
CCLVSEGLCR	LLGQEPLALE	SLFMLIQGKV	KVVDWEESTE	VTLYFLSLLV	FRLQNLPCGM	EKLGSDVATL	FTHSHVVSLV
810	820	830	840	850	860	870	880
SAAACLLGQL	GQQGVTFDLQ	PMEWMAAATH	ALSAPAELLT	EQGKASLIRD	MSSSEMWTVL	WHRFSMVLRL	PEEASAQEGE
890	900	910	920	930	940	950	960
LSLSSPPSPE	PDWTLISPQG	MAALLSLAMA	TFTQEPQLCL	SCLSQHGSIL	MSILKHLLCP	SFLNQLRQAP	HGSEFLPVVV
970	980	990	1000	1010	1020	1030	1040
LSVCQLLCFP	FALDMDADLL	IGVLADLRDS	EVAAHLLQVC	CYHLPLMQVE	LPISLLTRLA	LMDPTSLNQF	VNTVSASPRT
1050	1060	1070	1080	1090	1100	1110	1120
IVSFLSVALL	SDQPLLTSDL	LSLLAHTARV	LSPSHLSFIQ	ELLAGSDESY	RPLRSLLGHP	ENSVRAHTYR	LLGHLLQHSM
1130	1140	1150	1160	1170	1180	1190	1200
ALRGALQSQS	GLLSLLLLGL	GDKDPVVRCS	ASFAVGNAAY	QAGPLGPALA	AAVPSMTQLL	GDPQAGIRRN	VASALGNLGP
1210	1220	1230	1240	1250	1260	1270	1280
EGLGEELLQC	EVPQRLLEMA	CGDPQPNVKE	AALIALRSLQ	QEPGIHQVLV	SLGASEKLSL	LSLGNQSLPH	SSPRPASAKH
1290	1300						
CRKLIHLLRP	AHSM						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
259	1	898.4195	-41.72	3	33.2	13.6	0	1190-1215	R.NVASALGNLGPEGLGEELLQCEVPQR.L	

Detailed Protein Report

Protein 375: PREDICTED: PR domain zinc finger protein 16 isoform X3 [Homo sapiens]

Accession:	gi|530360370	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.7
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRSKARARKL	AKSDGDVVNN	MYEPNRDLLA	SHSAEDEAED	SAMSPIPVGP	PSPFPTSEDF	TPKEGSPYEA	PVYIPEDIPI
90	100	110	120	130	140	150	160
PADFELRESS	IPGAGLGVWA	KRKMEAGERL	GPCVVVPRAA	AKETDFGWEQ	ILTDVEVSPQ	EGCITKQISE	DLGSEKFCVD
170	180	190	200	210	220	230	240
ANQAGAGSWL	KYIRVACSCD	DQNLTMCQIS	EQIYYKVIKD	IEPGEELLVH	VKEGVYPLGT	VPPGLDEEPT	FRCDECDELF
250	260	270	280	290	300	310	320
QSKLDLRRHK	KYTCGSVGAA	LYEGLAEELK	PEGLGGGSGQ	AHECKDCERM	FPNKYSLEQH	MVIHTEEREY	KCDQCPKAFN
330	340	350	360	370	380	390	400
WKSNLIRHQM	SHDSGKRFEC	ENCVKVFTDP	SNLQRHIRSQ	HVGARAHACP	DCGKTFATSS	GLKQHKHIHS	TVKPFICEVC
410	420	430	440	450	460	470	480
HKSYTQFSNL	CRHKRMHADC	RTQIKCKDCG	QMFSTTSSLN	KHRRFCEGKN	HYTPGGIFAP	GLPLTPSPMM	DKAKPSPSLN
490	500	510	520	530	540	550	560
HASLGFNEYF	PSRPHPGSLP	FSTAPPTFPA	LTPGFPGIFP	PSLYPRPPLL	PPTSLLKSPL	NHTQDAKLPS	PLGNPALPLV
570	580	590	600	610	620	630	640
SAVSNSSQGT	TAAAGPEEKF	ESRLEDSCVE	KLKTRSSDMS	DGSDFEDVNT	TTGTDLDTTT	GTGSDLDSDV	DSDPDKDKGK
650	660	670	680	690	700	710	720
GKSAEGQPKF	GGGLAPPGAP	NSVAEVPVFY	SQHSFFPPPD	EQLLTATGAA	GDSIKAIASI	AEKYFGPGFM	GMQEKKLGSL
730	740	750	760	770	780	790	800
PYHSAFPFQF	LPNFPHSLYP	FTDRALAHNL	LVKAEPKSPR	DALKVGGPSA	ECPFDLTTKP	KDVKPILPMP	KGPSAPASGE
810	820	830	840	850	860	870	880
EQPLDLSIGS	RARASQNGGG	REPRKNHVYG	ERKLGAGEGL	PQVCPARMPQ	QPPLHYAKPS	PFFMDPIYSR	VEKRKVTDPV
890	900	910	920	930	940	950	960
GALKEKYLRP	SPLLFHPQMS	AIETMTEKLE	SFAAMKADSG	SSLQPLPHHP	FNFRSPPPTL	SDPILRKGKE	RYTCRYCGKI
970	980	990	1000	1010	1020	1030	1040
FPRSANLTRH	LRTHTGEQPY	RCKYCDRSFS	ISSNLQRHVR	NIHNKEKPFK	CHLCNRCFGQ	QTNLDRHLKK	HEHENAPVSQ
1050	1060	1070	1080	1090	1100	1110	1120
HPGVLTNHLG	TSASSPTSES	DNHALLDEKE	DSYFSEIRNF	IANSEMNQAS	TRTEKRADMQ	IVDGSAQCPG	LASEKQEDVE
1130	1140	1150	1160	1170	1180		
EEDDDDLEED	DEDSLAGKSQ	DDTVSPAPEP	QAAYEDEEDE	EPAASLAVGF	DHTRRHMQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2972	1	646.8226	-64.07	2	66.4	11.8	0	935-946	R.SPPPTLSDPILR.K	

Detailed Protein Report

Protein 376: **brain mitochondrial carrier protein 1 isoform 2 precursor [Homo sapiens]**

Accession:	gi|532524956	**Score:**	25.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.9
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	8.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGIFPGIILI	FLRVKFATAA	VIHQKSTTVS	HEMSGLNWKP	FVYGGLASIV	AEFGTFPVDL	TKTRLQVQGQ	SIDARFKEIK
90	100	110	120	130	140	150	160
YRGMFHALFR	ICKEEGVLAL	YSGIAPALLR	QASYGTIKIG	IYQSLKRLFV	ERLEDETLLI	NMICGVVSGV	ISSTIANPTD
170	180	190	200	210	220	230	240
VLKIRMQAQG	SLFQGSMIGS	FIDIYQQEGT	RGLWRGVVPT	AQRAAIVVGV	ELPVYDITKK	HLILSGMMGD	TILTHFVSSF
250	260	270	280	290	300	310	320
TCGLAGALAS	NPVDVVRTRM	MNQRAIVGHV	DLYKGTVDGI	LKMWKHEGFF	ALYKGFWPNW	LRLGPWNIIF	FITYEQLKRL
330							
QI							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1961	1	656.7950	-145.20	2	54.9	11.0	1	14-25	R.VKFATAAVIHQK.S	

Detailed Protein Report

Protein 377: PREDICTED: disks large homolog 5 isoform X3 [Homo sapiens]

Accession:	gi|578819987	**Score:**	25.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	176.9
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|578839810	refseq_human (refseq_human_20140103.fasta)	PREDICTED: disks large homolog 5 isoform X3 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MEPQRRELLA QCQQSLAQAM TEVEAVLGLL EAAGALSPGE RRQLDEEAGG AKAELLLKLL LAKERDHFQD LRAALEKTQP
        90        100        110        120        130        140        150        160
HLLPILYLNG VVGPPQPAEG AGSTYSVLST MPSDSESSSS LSSVGTTGKA PSPPPLLTDQ QVNEKVENLS IQLRLMTRER
       170        180        190        200        210        220        230        240
NELRKRLAFA THGTAFDKRP YHRLNPDYER LKIQCVRAMS DLQSLQNQHT NALKRCEEVA KETDFYHTLH SRLLSDQTRL
       250        260        270        280        290        300        310        320
KDDVDMLRRE NGQLLRERNL LQQSWEDMKR LHEEDQKEIG DLRAQQQQVL KHNGSSEILN KLYDTAMDKL EVVKKDYDAL
       330        340        350        360        370        380        390        400
RKRYSEKVAI HNADLSRLEQ LGEENQRLLK QTEMLTQQRD TAIQLQHQCA LSLRRFEAIH HELNKATAQN KDLQWEMELL
       410        420        430        440        450        460        470        480
QSELTELRTT QVKTAKESEK YREERDAVYS EYKLIMSERD QVISELDKLQ TEVELAESKL KSSTSEKKAA NEEMEALRQI
       490        500        510        520        530        540        550        560
KDTVTMDAGR ANKEVEILRK QCKALCQELK EALQEADVAK CRRDWAFQER DKIVAERDSI RTLCDNLRRE RDRAVSELAE
       570        580        590        600        610        620        630        640
ALRSLDDTRK QKNDVSRELK ELKEQMESQL EKEARFRQLM AHSSHDSAID TDSMEWETEV VEFERETEDI DLKALGFDMA
       650        660        670        680        690        700        710        720
EGVNEPCFPG DCGIFVTKVD KGSIADGRLR VNDWLLRIND VDLINKDKKQ AIKALLNGEG AINMVVRRRK SLGGKVVTPL
       730        740        750        760        770        780        790        800
HINLSGQKDS GISLENGVYA AAVLPGSPAA KEGSLAVGDR IVAINGIALD NKSLNECESL LRSCQDSLTL SLLKEQKCVP
       810        820        830        840        850        860        870        880
ASGELSPELQ EWAPYSPGHS SRHSNPPLYP SRPSVGTVPR SLTPSTTVSS ILRNPIYTVR SHRVGPCSSP PAARDAGPQG
       890        900        910        920        930        940        950        960
LHPSVQHQGR LSLDLSHRTC SDYSEMRATH GSNSLPSSAR LGSSSNLQFK AERIKIPSTP RYPRSVVGSE RGSVSHSECS
       970        980        990       1000       1010       1020       1030       1040
TPPQSPLNID TLSSCSQSQT SASTLPRIAV NPASLGERRK DRPYVEEPRH VKVQKGSEPL GISIVSGEKG GIYVSKVTVG
      1050       1060       1070       1080       1090       1100       1110       1120
SIAHQAGLEY GDQLLEFNGI NLRSATEQQA RLIIGQQCDT ITILAQYNPH VHQLSSHSRS SSHLDPAGTH STLQGSGTTT
      1130       1140       1150       1160       1170       1180       1190       1200
PEHPSVIDPL MEQDEGPSTP PAKQSSSRIA GDANKKTLEP RVVFIKKSQL ELGVHLCGGN LHGVFVAEVE DDSPAKGPDG
      1210       1220       1230       1240       1250       1260       1270       1280
LVPGDLILEY GSLDVRNKTV EEVYVEMLKP RDGVRLKVQY RPEEFTKAKG LPGDSFYIRA LYDRLADVEQ ELSFKKDDIL
      1290       1300       1310       1320       1330       1340       1350       1360
YVDDTLPQGT FGSWMAWQLD ENAQKIQRGQ IPSKYVMDQE FSRRLSMSEV KDDNSATKTL SAAARRSFFR RKHKHKRSGS
      1370       1380       1390       1400       1410       1420       1430       1440
KDGKDLLALD AFSSDSIPLF EDSVSLAYQR VQKVDCTALR PVLILGPLLD VVKEMLVNEA PGKFCRCPLE VMKASQQAIE
      1450       1460       1470       1480       1490       1500       1510       1520
RGVKDCLFVD YKRRSGHFDV TTVASIKEIT EKNRHCLLDI APHAIERLHH MHIYPIVIFI HYKSAKHIKE QRDPIYLRDK
      1530       1540       1550       1560       1570       1580
VTQRHSKEQF EAAQKLEQEY SRYFTGVIQG GALSSICTQI LAMVNQEQNK VLWIPACPL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2115	1	916.8144	-155.80	2	55.0	10.3	2	257-270	R.ERNLLQQSWEDMKR.L	
1673	1	662.2991	-86.48	2	49.4	14.9	1	1248-	K.AKGLPGDSFYIR.A	

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
								1259		

Detailed Protein Report

Protein 378: PREDICTED: extracellular matrix protein FRAS1 isoform X4 [Homo sapiens]

Accession:	gi|578809385	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	430.3
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGVLKVWLGL	ALALAEFAVL	PHHSEGACVY	QDSLLADATI	WKPDSCQSCR	CHGDIVICKP	AVCRNPQCAF	EKGEVLQIAA
90	100	110	120	130	140	150	160
NQCCPECVLR	TPGSCHHEKK	IHEHGTEWAS	SPCSVCSCNH	GEVRCTPQPC	PPLSCGHQEL	AFIPEGSCCP	VCVGLGKPCS
170	180	190	200	210	220	230	240
YEGHVFQDGE	DWRLSRCAKC	LCRNGVAQCF	TAQCQPLFCN	QDETVVRVPG	KCCPQCSARS	CSAAGQVYEH	GEQWSENACT
250	260	270	280	290	300	310	320
TCICDRGEVR	CHKQACLPLR	CGKGQSRARR	HGQCCEECVS	PAGSCSYDGV	VRYQDEMWKG	SACEFCMCDH	GQVTCQTGEC
330	340	350	360	370	380	390	400
AKVECARDEE	LIHLDGKCCP	ECISRNGYCV	YEETGEFMSS	NASEVKRIPE	GEKWEDGPCK	VCECRGAQVT	CYEPSCPPCP
410	420	430	440	450	460	470	480
VGTLALEVKG	QCCPDCTSVH	CHPDCLTCSQ	SPDHCDLCQD	PTKLLQNGWC	VHSCGLGFYQ	AGSLCLACQP	QCSTCTSGLE
490	500	510	520	530	540	550	560
CSSCQPPLLM	RHGQCVPTCG	DGFYQDRHSC	AVCHESCAGC	WGPTEKHCLA	CRDPLHVLRD	GGCESSCGKG	FYNRQGTCSA
570	580	590	600	610	620	630	640
CDQSCDSCGP	SSPRCLTCTE	KTVLHDGKCM	SECPGGYYAD	ATGRCKVCHN	SCASCSGPTP	SHCTACSPPK	ALRQGHCLPR
650	660	670	680	690	700	710	720
CGEGFYSDHG	VCKACHSSCL	ACMGPAPSHC	TGCKKPEEGL	QVEQLSDVGI	PSGECLAQCR	AHFYLESTGI	CEACHQSCFR
730	740	750	760	770	780	790	800
CAGKSPHNCT	DCGPSHVLLD	GQCLSQCPDG	YFHQEGSCTE	CHPTCRQCHG	PLESDCISCY	PHISLTNGNC	RTSCREEQFL
810	820	830	840	850	860	870	880
NLVGYCADCH	HLCQHCAADL	HNTGSICLRC	QNAHYLLLGD	HCVPDCPSGY	YAERGACKKC	HSSCRTCQGR	GPFSCSSCDT
890	900	910	920	930	940	950	960
NLVLSHTGTC	STTCFPGHYL	DDNHVCQPCN	THCGSCDSQA	SCTSCRDPNK	VLLFGECQYE	SCAPQYYLDF	STNTCKECDW
970	980	990	1000	1010	1020	1030	1040
SCSACSGPLK	TDCLQCMDGY	VLQDGACVEQ	CLSSFYQDSG	LCKNCDSYCL	QCQGPHECTR	CKGPFLLLEA	QCVQECGKGY
1050	1060	1070	1080	1090	1100	1110	1120
FADHAKHKCT	ACPQGCLQCS	HRDRCHLCDH	GFFLKSGLCV	YNCVPGFSVH	TSNETCSGKI	HTPSLHVNGS	LILPIGSIKP
1130	1140	1150	1160	1170	1180	1190	1200
LDFSLLNVQD	QEGRVEDLLF	HVVSTPTNGQ	LVLSRNGKEV	QLDKAGRFSW	KDVNEKKVRF	VHSKEKLRKG	YLFLKISDQQ
1210	1220	1230	1240	1250	1260	1270	1280
FFSEPQLINI	QAFSTQAPYV	LRNEVLHISR	GERATITTQM	LDIRDDDNPQ	DVVIEIIDPP	LHGQLLQTLQ	SPATPIYQFQ
1290	1300	1310	1320	1330	1340	1350	1360
LDELSRGLLH	YAHDGSDSTS	DVAVLQANDG	HSFHNILFQV	KTVPQNDRGL	QLVANSMVWV	PEGGMLQITN	RILQAEAPGA
1370	1380	1390	1400	1410	1420	1430	1440
SAEEIIYKIT	QDYPQFGEVV	LLVNMPADSP	ADEGQHLPDG	RTATPTSTFT	QQDINEGIVW	YRHSGAPAQS	DSFRFEVSSA
1450	1460	1470	1480	1490	1500	1510	1520
SNAQTRLESH	MFNIAILPQT	PEAPKVSLEA	SLHMTAREDG	LTVIQPHSLS	FINSEKPSGK	IVYNITLPLH	PNQGIIEHRD
1530	1540	1550	1560	1570	1580	1590	1600
HPHSPIRYFT	QEDINQGKVM	YRPPPAAPHL	QELMAFSFAG	LPESVKFHFT	VSDGEHTSPE	MVLTIHLLPS	DQQLPVFQVT
1610	1620	1630	1640	1650	1660	1670	1680
APRLAVSPGG	STSVGLQVVV	RDAETAPKEL	FFELRRPPQH	GVLLKHTAEF	RRPMATGDTF	TYEDVEKNAL	QYIHDGSSTR
1690	1700	1710	1720	1730	1740	1750	1760
EDSMEISVTD	GLTVTMLEVR	VEVSLSEDRG	PRLAAGSSLS	ITVASKSTAI	ITRSHLAYVD	DSSPDPEIWI	QLNYLPSYGT
1770	1780	1790	1800	1810	1820	1830	1840
LLRISGSEVE	ELSEVSNFTM	EDINNKKIRY	SAVFETDGHL	VTDSFYFSVS	DMDHNHLDNQ	IFTIMITPAE	NPPPVIAFAD
1850	1860	1870	1880	1890	1900	1910	1920
LITVDEGGRA	PLSFHHFFAT	DDDDNLQRDA	IIKLSALPKY	GCIENTGTGH	VLWRQTASEP	LENGRVLVQG	STFTYQDILA
1930	1940	1950	1960	1970	1980	1990	2000
GLVGYVPSVP	GMVVDEFQFS	LTDGLHVDTG	RMKIYTELPA	SDTPHLAINQ	GLQLSAGSVA	RITEQHLKVT	DIDSDDHQVM
2010	2020	2030	2040	2050	2060	2070	2080
YIMKEDPGAG	RLQMMKHGNL	EQISIKGPIR	SFTQADISQG	HVEYSHGTGE	PGGSFAFKFD	VVDGEGNRLI	DKSFSISILE
2090	2100	2110	2120	2130	2140	2150	2160
DKSPPVITTN	KGLVLDENSV	KKITTLQLSA	TDQDSGPTEL	IYRITRQPQL	GHLEHAASPG	IQISSFTQAD	LTSRNVQYVH
2170	2180	2190	2200	2210	2220	2230	2240
SSEAEKHSDA	FSFTLSDGVS	EVTQTFHITL	HPVDDSLPVV	QNLGMRVQEG	MRKTITEFEL	KAVDADTEAE	SVTFTIVQPP
2250	2260	2270	2280	2290	2300	2310	2320
RHGTIERTSN	GQHFHLTSTF	TMKDIYQNRV	SYSHDGSNSL	KDRFTFTVSD	GTNPFFIIEE	GGKEIMTAAP	QPFRVDILPV
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
2707	1	710.3638	64.25	2	62.8	10.1	1	208-219	R.VPGKCCPQCSAR.S	Carbamidomethyl: 5, 6, 9

Detailed Protein Report

Protein 379: **putative polypeptide N-acetylgalactosaminyltransferase-like protein 3 [Homo sapiens]**

Accession:	gi|22538495	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.7
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.9
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MASLRRVKVL LVLNLIAVAG FVLFLAKCRP IAVRSGDAFH EIRPRAEVAN LSAHSASPIQ DAVLKRLSLL EDIVYRQLNG
        90        100        110        120        130        140        150        160
LSKSLGLIEG YGGRGKGGLP ATLSPAEEEK AKGPHEKYGY NSYLSEKISL DRSIPDYRPT KCKELKYSKD LPQISIIFIF
       170        180        190        200        210        220        230        240
VNEALSVILR SVHSAVNHTP THLLKEIILV DDNSDEEELK VPLEEYVHKR YPGLVKVVRN QKREGLIRAR IEGWKVATGQ
       250        260        270        280        290        300        310        320
VTGFFDAHVE FTAGWAEPVL SRIQENRKRV ILPSIDNIKQ DNFEVQRYEN SAHGYSWELW CMYISPPKDW WDAGDPSLPI
       330        340        350        360        370        380        390        400
RTPAMIGCSF VVNRKFFGEI GLLDPGMDVY GGENIELGIK VWLCGGSMEV LPCSRVAHIE RKKKPYNSNI GFYTKRNALR
       410        420        430        440        450        460        470        480
VAEVWMDDYK SHVYIAWNLP LENPGIDIGD VSERRALRKS LKCKNFQWYL DHVYPEMRRY NNTVAYGELR NNKAKDVCLD
       490        500        510        520        530        540        550        560
QGPLENHTAI LYPCHGWGPQ LARYTKEGFL HLGALGTTTL LPDTRCLVDN SKSRLPQLLD CDKVKSSLYK RWNFIQNGAI
       570        580        590        600
MNKGTGRCLE VENRGLAGID LILRSCTGQR WTIKNSIK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
33	1	1069.0298	-31.46	2	30.2	13.7	1	28-45	K.CRPIAVRSGDAFHEIRPR.A	Carbamidomethyl: 1
2906	1	981.9571	-51.41	2	65.5	11.4	2	551-567	K.RWNFIQNGAIMNKGTGR.C	

Detailed Protein Report

Protein 380: rRNA 2'-O-methyltransferase fibrillarin [Homo sapiens]

Accession:	gi|12056465	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.8
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	10.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKPGFSPRGG	GFGGRGGFGD	RGGRGGRGGF	GGGRGRGGGF	RGRGRGGGGG	GGGGGGGGRG	GGGFHSGGNR	GRGRGGKRGN
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
QSGKNVMVEP	HRHEGVFICR	GKEDALVTKN	LVPGESVYGE	KRVSISEGDD	KIEYRAWNPF	RSKLAAAILG	GVDQIHIKPG
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
AKVLYLGAAS	GTTVSHVSDI	VGPDGLVYAV	EFSHRSGRDL	INLAKKRTNI	IPVIEDARHP	HKYRMLIAMV	DVIFADVAQP
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
DQTRIVALNA	HTFLRNGGHF	VISIKANCID	STASAEAVFA	SEVKKMQQEN	MKPQEQLTLE	PYERDHAVVV	GVYRPPPKVK
330							
N							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2667	1	1057.0851	99.43	2	62.2	13.7	2	46-72	R.GGGGGGGGGGGGGRGGGGFHSGGNRGR.G	

Detailed Protein Report

Protein 381: pleckstrin homology domain-containing family A member 4 isoform 2 [Homo sapiens]

Accession:	gi|238859653	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.2
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.40 **CV:** 37.08 % **No. of Peptides:** 2

```
        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
526	1	711.1747	-209.60	2	35.2	11.2	1	151-163	R.ASRAEGDDYGQPR.S		QD:QU 0.28
489	2	603.8256	17.71	2	36.1	13.9	0	300-312	R.GPPSEAGGGKPPR.S		QD:QU 0.58

Detailed Protein Report

Protein 382: growth/differentiation factor 2 precursor [Homo sapiens]

Accession: gi|7705308
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 25.1
MW [kDa]: 47.3
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 383: sterile alpha motif domain-containing protein 9 [Homo sapiens]

Accession:	gi|38201706	**Score:**	25.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	184.2
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|300863105	refseq_huma (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
1785	1	660.9025	-122.86	3	50.8	11.7	0	714-731	R.LEAMIQNCADSSKPTSTK.I	Carbamidomethyl: 8
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 384: **PREDICTED: probable E3 ubiquitin-protein ligase HERC1 isoform X6 [Homo sapiens]**

Accession:	gi|530406610	**Score:**	25.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	524.9
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

Detailed Protein Report

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
2832	1	923.8157	-4.48	3	64.6	12.0	1	487-513	R.NIPTLVKDISNVGEVSCGSSHTIALSK.D	

Detailed Protein Report

Protein 385: protein LAP2 isoform 7 [Homo sapiens]

Accession: gi|55770895
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 25.0
MW [kDa]: 146.0
pI: 5.0
Sequence Coverage [%]: 1.3
No. of unique Peptides: 1

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
2597	1	913.4719	-133.82	1	63.1	13.2	2	1209-1215	K.LEKIRVR.V	

Detailed Protein Report

Protein 386: vitamin D3 receptor isoform VDRA [Homo sapiens]

Accession:	gi|4507883	**Score:**	25.0
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
2656	1	673.3675	125.73	2	64.2	12.0	0	403-413	R.CLSFQPECSMK.L	Carbamidomethyl: 1; Oxidation: 10
2332	3	665.1572	-192.83	2	59.6	12.9	0	403-413	R.CLSFQPECSMK.L	Carbamidomethyl: 1

Detailed Protein Report

Protein 387: **SKI family transcriptional corepressor 1 [Homo sapiens]**

Accession:	gi|384407369	**Score:**	25.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	93.7
Database Date:	2015-11-30	**pI:**	8.5
		Sequence Coverage [%]:	4.1
		No. of unique Peptides:	2

```
        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
2243	1	945.9550	-39.77	2	58.5	11.7	0	454-477	R.GLGLATGASGPAGPGGPGGGAGVR.S	
2760	1	729.3797	-5.05	2	65.6	13.2	1	759-770	K.DIENLAREELQK.L	

Detailed Protein Report

Protein 388: PREDICTED: tetratricopeptide repeat protein 13 isoform X7 [Homo sapiens]

Accession:	gi|578802328	**Score:**	25.0
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
1705	2	820.8385	-139.02	2	49.9	10.6	1	234-247	R.SLSRGFNNHINLIR.G	

Detailed Protein Report

Protein 389: PREDICTED: coiled-coil domain-containing protein 38 isoform X1 [Homo sapiens]

Accession: gi|578823285
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 25.0
MW [kDa]: 46.1
pI: 6.0
Sequence Coverage [%]: 6.8
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MNLLMTRETG	FCSRAAQETI	NKLQMTAELK	KASMEVQAVK	SEIAKTEFLL	REYMKYGFFL	LQMSPKHWQI	QQALKRAQAS
90	100	110	120	130	140	150	160
KSKANIILPK	ILAKLSLHSS	NKEGILEESG	RTAVLSEDAS	QGRDSQGKPS	RSLTRTPEKK	KSNLAESFGS	EDSLEFLLDD
170	180	190	200	210	220	230	240
EMDVDLEPAL	YFKEPEELLQ	VLRELEEQNL	TLFQYSQDVD	ENLEEVNKRE	KVIQDKTNSN	IEFLLEQEKM	LKANCVREEE
250	260	270	280	290	300	310	320
KAAELQLKSK	LFSFGEFNSD	AQEILIDSLS	KKITQVYKVC	IGDAEDDGLN	PIQKLVKVES	RLVELCDLIE	SIPKENVEAI
330	340	350	360	370	380	390	400
ERMKQKEWRQ	KFRDEKMKEK	QRHQQERLKA	ALEKAVAQPK	KKLGRRLVFH	SKPPSGNKQQ	LPLVNETKTK	SQEEEYFFT

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
353	1	676.4443	133.31	3	33.1	11.6	1	279-297	K.VCIGDAEDDGLNPIQKLVK.V	

BRUKER

Detailed Protein Report

Protein 390: PREDICTED: KN motif and ankyrin repeat domain-containing protein 3 isoform X2 [Homo sapiens]

Accession: gi|530427478

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 25.0

MW [kDa]: 91.0

pI: 4.9

Sequence Coverage [%]: 5.8

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MCGGRWLGGG	ELLGPVCLDS	KAGPRGSSQR	DSAQPHLHPF	CRVPLTAAAG	NMAKFALNQN	LPDLGGPRLC	PVPAAGGARS
90	100	110	120	130	140	150	160
PSSPYSVETP	YGFHLDLDFL	KYIEELERGP	AARRAPGPPT	SRRPRAPRPG	LAGARSPGAW	TSSESLASDD	GGAPGILSQG
170	180	190	200	210	220	230	240
APSGLLMQPL	SPRAPVRNPR	VEHTLRETSR	RLELAQTHER	APSPGRGVPR	SPRGSGRSSP	APNLAPASPG	PAQLQLVREQ
250	260	270	280	290	300	310	320
MAAALRRLRE	LEDQARTLPE	LQEQVRALRA	EKARLLAGRA	QPEPDGEAET	RPDKLAQLRR	LTERLATSER	GGRARASPRA
330	340	350	360	370	380	390	400
DSPDGLAAGR	SEGALQVLDG	EVGSLDGTPQ	TREVAAEAVP	ETREAGAQAV	PETREAGVEA	APETVEADAW	VTEALLGLPA
410	420	430	440	450	460	470	480
AAERELELLR	ASLEHQRGVS	ELLRGRLREL	EEAREAAEEA	AAGARAQLRE	ATTQTPWSCA	EKAAQTESPA	EAPSLTQESS
490	500	510	520	530	540	550	560
PGSMDGDRAV	APAGILKSIM	KKRDGTPGAQ	PSSGPKSLQF	VGVLNGEYES	SSSEDASDSD	GDSENGGAEP	PGSSSSGSGDD
570	580	590	600	610	620	630	640
SGGGSDSGTP	GPPSGGDIRD	PEPEAEAEPQ	QVAQGRCELS	PRLREACVAL	QRQLSRPRGV	ASDGGAVRLV	AQEWFRVSSQ
650	660	670	680	690	700	710	720
RRSQAEPVAR	MLEGVRRLGP	ELLAHVVNLA	DGNGNTALHY	SVSHGNLAIA	SLLLDTGACE	VNRQNRAGYS	ALMLAALTSV
730	740	750	760	770	780	790	800
RQEEEDMAVV	QRLFCMGDVN	AKASQTGQTA	LMLAISHGRQ	DMVATLLACG	ADVNAQDADG	ATALMCASEY	GRLDTVRLLL
810	820	830	840	850	860	870	880
TQPGCDPAIL	DNEGTSALAI	ALEAEQDEVA	ALLHAHLSSG	QPDTQSESPP	GSQTATPGEG	ECGDNGENPQ	VQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
428	1	1293.7593	91.80	2	34.0	12.9	2	1-25	-.MCGGRWLGGGELLGPVCLDSKAGPR.G	Carbamidomethyl: 17

Detailed Protein Report

Protein 391: PREDICTED: E3 ubiquitin-protein ligase UBR5 isoform X5 [Homo sapiens]

Accession:	gi|530389110	**Score:**	24.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	308.4
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:** 0.96	**CV:** 0.00 %	**No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MTSIHFVVHP LPGTEDQLND RLREVSEKLN KYNLNSHPPL NVLEQATIKQ CVVGPNHAAF LLEDGRVCRI GFSVQPDRLE
        90        100        110        120        130        140        150        160
LGKPDNNDGS KLNSNSGAGR TSRPGRTSDS PWFLSGSETL GRLAGNTLGS RWSSGVGGSG GGSSGRSSAG ARDSRRQTRV
       170        180        190        200        210        220        230        240
IRTGRDRGSG LLGSQPQPVI PASVIPEELI SQAQVVLQGK SRSVIIRELQ RTNLDVNLAV NNLLSRDDED GDDGDDTASE
       250        260        270        280        290        300        310        320
SYLPGEDLMS LLDADIHSAH PSVIIDADAM FSEDISYFGY PSFRRSSLSR LGSSRERDSE LLRERESVLR LRERRWLDGA
       330        340        350        360        370        380        390        400
SFDNERGSTS KEGEPNLDKK NTPVQSPVSL GEDLQWWPDK DGTKFICIGA LYSELLAVSS KGELYQWKWS ESEPYRNAQN
       410        420        430        440        450        460        470        480
PSLHHPRATF LGLTNEKIVL LSANSIRATV ATENNKVATW VDETLSSVAS KLEHTAQTYS ELQGERIVSL HCCALYTCAQ
       490        500        510        520        530        540        550        560
LENSLYWWGV VPFSQRKKML EKARAKNKKP KSSAGISSMP NITVGTQVCL RNNPLYHAGA VAFSISAGIP KVGVLMESVW
       570        580        590        600        610        620        630        640
NMNDSCRFQL RSPESLKNME KASKTTEAKP ESKQEPVKTE MGPPPSPAST CSDASSIASS ASMPYKRRRS TPAPKEEEKV
       650        660        670        680        690        700        710        720
NEEQWSLREV VFVEDVKNVP VGKVLKVDGA YVAVKFPGTS SNTNCQNSSG PDADPSSLLQ DCRLLRIDEL QVVKTGGTPK
       730        740        750        760        770        780        790        800
VPDCFQRTPK KLCIPEKTEI LAVNVDSKGV HAVLKTGNWV RYCIFDLATG KAEQENNFPT SSIAFLGQNE RNVAIFTAGQ
       810        820        830        840        850        860        870        880
ESPIILRDGN GTIYPMAKDC MGGIRDPDWL DLPPISSLGM GVHSLINLPA NSTIKKKAAV IIMAVEKQTL MQHILRCDYE
       890        900        910        920        930        940        950        960
ACRQYLMNLE QAVVLEQNLQ MLQTFISHRC DGNRNILHAC VSVCFPTSNK ETKEEEEAER SERNTFAERL SAVEAIANAI
       970        980        990       1000       1010       1020       1030       1040
SVVSSNGPGN RAGSSSSRSL RLREMMRRSL RAAGLGRHEA GASSSDHQDP VSPPIAPPSW VPDPPAMDPD GDIDFILAPA
      1050       1060       1070       1080       1090       1100       1110       1120
VGSLTTAATG TGQGPSTSTI PGPSTEPSVV ESKDRKANAH FILKLLCDSV VLQPYLRELL SAKDARGMTP FMSAVSGRAY
      1130       1140       1150       1160       1170       1180       1190       1200
PAAITILETA QKIAKAEISS SEKEEDVFMG MVCPSGTNPD DSPLYVLCCN DTCSFTWTGA EHINQDIFEC RTCGLLESLC
      1210       1220       1230       1240       1250       1260       1270       1280
CCTECARVCH KGHDCKLKRT SPTAYCDCWE KCKCKTLIAG QKSARLDLLY RLLTATNLVT LPNSRGEHLL LFLVQTVARQ
      1290       1300       1310       1320       1330       1340       1350       1360
TVEHCQYRPP RIREDRNRKT ASPEDSDMPD HDLEPPRFAQ LALERVLQDW NALKSMIMFG SQENKDPLSA SSRIGHLLPE
      1370       1380       1390       1400       1410       1420       1430       1440
EQVYLNQQSG TIRLDCFTHC LIVKCTADIL LLDTLLGTLV KELQNKYTPG RREEAIAVTM RFLRSVARVF VILSVEMASS
      1450       1460       1470       1480       1490       1500       1510       1520
KKKNNFIPQP IGKCKRVFQA LLPYAVEELC NVAESLIVPV RMGIARPTAP FTLASTSIDA MQGSEELFSV EPLPPRPSSD
      1530       1540       1550       1560       1570       1580       1590       1600
QSSSSSQSQS SYIIRNPQQR RISQSQPVRG RDEEQDDIVS ADVEEVEVVE GVAGEEDHHD EQEEHGEENA EAEGQHDEHD
      1610       1620       1630       1640       1650       1660       1670       1680
EDGSDMELDL LAAAETESDS ESNHSNQDNA SGRRSVVTAA TAGSEAGASS VPAFFSEDDS QSNDSSDSDS SSSQSDDIEQ
      1690       1700       1710       1720       1730       1740       1750       1760
ETFMLDEPLE RTTNSSHANG AAQAPRSMQW AVRNTQHQRA ASTAPSSTST PAASSAGLIY IDPSNLRRSG TISTSAAAAA
      1770       1780       1790       1800       1810       1820       1830       1840
AALEASNASS YLTSASSLAR AYSIVIRQIS DLMGLIPKYN HLVYSQIPAA VKLTYQDAVN LQNYVEEKLI PTWNWMVSIM
      1850       1860       1870       1880       1890       1900       1910       1920
DSTEAQLRYG SALASAGDPG HPNHPLHASQ NSARRERMTA REEASLRTLE GRRRATLLSA RQGMMSARGD FLNYALSLMR
      1930       1940       1950       1960       1970       1980       1990       2000
SHNDEHSDVL PVLDVCSLKH VAYVFQALIY WIKAMNQQTT LDTPQLERKR TRELLELGID NEDSEHENDD DTNQSATLND
      2010       2020       2030       2040       2050       2060       2070       2080
KDDDSLPAET GQNHPFFRRS DSMTFLGCIP PNPFEVPLAE AIPLADQPHL LQPNARKEDL FGRPSQGLYS SSASSGKCLM
      2090       2100       2110       2120       2130       2140       2150       2160
EVTVDRNCLE VLPTKMSYAA NLKNVMNMQN RQKKEGEEQP VLPEETESSK PGPSAHDLAA QLKSSLLAEI GLTESEGPPL
      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	
1093	1	647.6752	-180.54	2	42.2	14.8	0	132-146	R.WSSGVGGSGGGSSGR.S		QD:QU	0.96

Detailed Protein Report

Protein 392: dnaJ homolog subfamily C member 14 [Homo sapiens]

Accession:	gi|119943096	**Score:**	24.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.5
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.4
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.77 **CV:** 37.11 % **No. of Peptides:** 2

10	20	30	40	50	60	70	80
MAQKHPGERG	LYGAHHSGGA	SLRTLGPSVD	PEIPSFSGLR	DSAGTAPNGT	RCLTEHSGPK	HTQHPNPAHW	LDPSHGPPGG
90	100	110	120	130	140	150	160
PGPPRDAEDP	DQSETSSEEE	SGVDQELSKE	NETGNQKDGN	SFLSIPSACN	CQGTPGIPEG	PYSEGGNGSS	SNFCHHCTSP
170	180	190	200	210	220	230	240
ALGEDELEEE	YDDEESLKFP	SDFSRVSSGK	KPPSRRQRHR	FPTKEDTREG	GRRDPRSPGR	HRLGRKRSQA	DKRKGLGLWG
250	260	270	280	290	300	310	320
AEELCQLGQA	GFWWLIELLV	LVGEYVETCG	HLIYACRQLK	SSDLDLFRVW	MGVWTGRLGG	WAQVMFQFLS	QGFYCGVGLF
330	340	350	360	370	380	390	400
TRFLKLLGAL	LLLALALFLG	FLQLGWRFLV	GLGDRLGWRD	KATWLFSWLD	SPALQRCLTL	LRDSRPWQRL	VRIVQWGWLE
410	420	430	440	450	460	470	480
LPWVKQNINR	QGNAPVASGR	YCQPEEEVAR	LLTMAGVPED	ELNPFHVLGV	EATASDVELK	KAYRQLAVMV	HPDKNHHPRA
490	500	510	520	530	540	550	560
EEAFKVLRAA	WDIVSNAEKR	KEYEMKRMAE	NELSRSVNEF	LSKLQDDLKE	AMNTMMCSRC	QGKHRRFEMD	REPKSARYCA
570	580	590	600	610	620	630	640
ECNRLHPAEE	GDFWAESSML	GLKITYFALM	DGKVYDITEW	AGCQRVGISP	DTHRVPYHIS	FGSRIPGTRG	RQRATPDAPP
650	660	670	680	690	700	710	
ADLQDFLSRI	FQVPPGQMPN	GNFFAAPQPA	PGAAAASKPN	STVPKGEAKP	KRRKKVRRPF	QR	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
2138	1	661.2888	-106.46	2	55.3	10.6	1	278-288	R.QLKSSDLDLFR.V		QD:QU	0.53
1717	4	820.8378	-35.57	2	50.0	14.3	2	552-564	R.EPKSARYCAECNR.L	Carbamidomethyl: 8, 11	QD:QU	1.10

Detailed Protein Report

Protein 393: krev interaction trapped protein 1 isoform 2 [Homo sapiens]

Accession:	gi|61742817	**Score:**	24.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.6
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	4.5
		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	YVAVIRPKNT	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 394: **PREDICTED: integrin beta-7 isoform X3 [Homo sapiens]**

Accession:	gi|578823673	**Score:**	24.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.0
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MVALPMVLVL	LLVLSRGESE	LDAKIPSTGD	ATEWRNPHLS	MLGSCQPAPS	CQKCILSHPS	CAWCKQLNFT	ASGEAEARRC
90	100	110	120	130	140	150	160
ARREELLARG	CPLEELEEPR	GQQEVLQDQP	LSQGARGEGA	TQLAPQRVRV	TLRPGEPQQL	QVRFLRAEGY	PVDLYYLMDL
170	180	190	200	210	220	230	240
SYSMKDDLER	VRQLGHALLV	RLQEVTHSVR	IGFGSFVDKT	VLPFVSTVPS	KLRHPCPTRL	ERCQSPFSFH	HVLSLTGDAQ
250	260	270	280	290	300	310	320
AFEREVGRQS	VSGNLDSPEG	GFDAILQAAL	CQEQIGWRNV	SRLLVFTSDD	TFHTAGDGKL	GGIFMPSDGH	CHLDSNGLYS
330	340	350	360	370	380	390	400
RSTEFDYPSV	GQVAQALSAA	NIQPIFAVTS	AALPVYQELS	KLIPKSAVGE	LSEDSSNVVQ	LIMDAYNSLS	STVTLEHSSL
410	420	430	440	450	460	470	480
PPGVHISYES	QCEGPEKREG	KAEDRGQCNH	VRINQTVTFW	VSLQATHCLP	EPHLLRLRAL	GFSEELIVEL	HTLCDCNCSD
490	500	510	520	530	540	550	560
TQPQAPHCSD	GQGHLQCGVC	SCAPGRLGRL	CECSVAELSS	PDLESGCRAP	NGTGPLCSGK	GHCQCGRCSC	SGQSSGHLCE
570	580	590	600	610	620	630	640
CDDASCERHE	GILCGGFGRC	QCGVCHCHAN	RTGRACECSG	DMDSCISPEG	GLCSGHGRCK	CNRCQCLDGY	YGALCDQCPG
650	660	670	680	690	700	710	720
CKTPCERHRD	CAECGAFRTG	PLATNCSTAC	AHTNVTLALA	PILDDGWCKE	RTLDNQLFFF	LVEDDARGTV	VLRVRPQEKG
730	740	750	760	770	780	790	
ADHTQAIVLG	CVGGIVAVGL	GLVLAYRLSV	EIYDRREYSR	FEKEQQQLNW	KQLLGFGSRL	AS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2949	1	1019.4212	-21.13	3	66.0	11.9	2	569-594	R.HEGILCGGFGRCQCGVCHCHANRTGR.A	Carbamidomethyl: 6, 12, 14, 17, 19
143	1	722.7732	-4.06	2	30.5	13.0	0	580-591	R.CQCGVCHCHANR.T	Carbamidomethyl: 1, 3

Detailed Protein Report

Protein 395: neuropeptides B/W receptor type 1 [Homo sapiens]

Accession:	gi|53828924	**Score:**	24.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.1
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.5
		No. of unique Peptides:	1

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
42	1	706.9621	-93.24	3	30.4	10.4	1	186-201	R.RQCVLVFPQPEAFWWR.A	Carbamidomethyl: 3

Detailed Protein Report

Protein 396: PREDICTED: ankyrin repeat domain-containing protein 12 isoform X6 [Homo sapiens]

Accession:	gi|578832112	**Score:**	24.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	202.9
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

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
110	1	1083.4576	-80.32	2	31.3	13.6	2	865-884	K.DAVSNRSQSVDTKNVMTLGK.S	Oxidation: 16

Detailed Protein Report

Protein 397: **PREDICTED: plasma membrane calcium-transporting ATPase 2 isoform X9 [Homo sapiens]**

Accession:	gi|578806173	**Score:**	24.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.4
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.6
		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 398: beta-1,4 N-acetylgalactosaminyltransferase 2 isoform c [Homo sapiens]

Accession:	gi|227497758	**Score:**	24.7
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

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
26	1	537.7695	-77.75	2	30.0	13.9	0	299-308	R.NLAISQVTTK.Y	

Detailed Protein Report

Protein 399: leucine-rich repeat and WD repeat-containing protein KIAA1239 [Homo sapiens]

Accession: gi|222418587
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 24.7
MW [kDa]: 197.3
pI: 5.8
Sequence Coverage [%]: 1.3
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MWPAGAGTKL	PCPRDSALRR	AAFSGNLTAL	PSHLVPAGRS	VRVFISANPE	DTGAERQALR	ENVYPKLREF	CRENYGLEFQ
90	100	110	120	130	140	150	160
VIDLYWGVEE	DEWDSPELQK	TRMKLLENCL	KTSAGPCFVG	LLGEKYGNIR	IPGEVEASEF	EMILDAAIEA	KLETKLLEEW
170	180	190	200	210	220	230	240
YCRDENSVPA	AYYLRPKSEM	LRSNRNAMQP	STNAENEKTW	QEISDEIKKI	FKAAVKLLHE	KGKMKHSQAK	RYLFSAIEDE
250	260	270	280	290	300	310	320
FDFALGKQTP	AFLKKCVCYI	RKIANIERFV	KIPEMGKYMD	ITGTEPRIIR	DPEAQEKLIK	LRDEFIPTIV	ASSNLRVYTS
330	340	350	360	370	380	390	400
VTHCDMKLGY	SQEIENHYIE	GLGKQFYEDM	IDIIQATIQQ	NFDTETDTLY	DEILQHSSLC	KTYASFYEYK	CESLNIVHNY
410	420	430	440	450	460	470	480
ILPSKAGHIN	PLIIYGGPCT	GKTLLLAEVA	KKAYGWLHED	TGPESDPVVI	VRFLGTTDMS	SDLRTLLLSV	CEQLAVNYRC
490	500	510	520	530	540	550	560
LVQSYPKKIH	DLCDLFINLL	NESSLQRPLV	IIFDALEQLS	ENDDARKLWW	LPAHLPRFVR	IVLSTLPNKH	GILQKLRCLI
570	580	590	600	610	620	630	640
HEEDNYIELI	PRDRKMCSQV	LKHQLLRVKR	KVTSGQQIYV	NNALSKCTLP	MFVNLTFREV	RHWRSHKDVD	ESSLSVTVHE
650	660	670	680	690	700	710	720
SIEQLFWSLE	KKCGQKLVSR	ALGYITMAKM	GLSEMELEDV	LALDNSVMSE	LKENTRPSNP	LRVPYLYIAR	LKEGLSGYLI
730	740	750	760	770	780	790	800
ERHVKNVTLL	VWANRHLQLI	AQKLYLQDDN	DLREMHTILA	DYFLGVWSGG	RRKAFCLEDP	YLNGCLDLEN	RSLLEEEKHF
810	820	830	840	850	860	870	880
MEQASFDRQA	PDQPWVFQCN	PLEPDIFFVN	HRKMSELLYH	LTRCGKTDDL	LYGIIMNFSW	LYTMIKIGQF	DKVLSDIELA
890	900	910	920	930	940	950	960
YNYSQEKELK	FLANTLRSIK	NKVTAFPGSL	SAELQQRLLP	VVSSLPKLRH	LLLECDKDGP	KYCSIVPLHS	SMDVTYSPER
970	980	990	1000	1010	1020	1030	1040
LPLSSSHLHV	TEILPTCNPS	TVLTALENGS	ISTWDVETRQ	LLRQITTAQS	VILGMKLTSD	EKYLVVATTN	NTLLIYDNVN
1050	1060	1070	1080	1090	1100	1110	1120
SCLLSEVEIK	GTKHGSSATY	INGFTLSANH	ALAWLEASKD	VTVIDLLYGW	PLYQFHCWYE	VTCVQCSLDG	LYAFCGQYLN
1130	1140	1150	1160	1170	1180	1190	1200
TTTIFHLGSG	EKLCTVTSEF	SGGFVKFLLI	LDTAQEMVMV	DSEGSLSVWN	TEDISSPQLT	DDFDCRREDS	EVVSIELSED
1210	1220	1230	1240	1250	1260	1270	1280
QSAVLICKAL	SIELLDTGLW	KVAEKFRAKH	NERFISAVLS	KNGDCIIATM	ENTSAVFFWR	RDTGQCMASL	QEISGSIVKL
1290	1300	1310	1320	1330	1340	1350	1360
VKSSHHNMLL	SLSTSGVLSI	WDIDIITAMS	NIDKTGKPIQ	SLLLPARGEI	IYSLDGSDCV	HKWNFSSGFI	EAVFKHEGIV
1370	1380	1390	1400	1410	1420	1430	1440
EHCVLTSTGD	IMVTSDDKSS	QYVWHTSSGE	NLFRINGQRI	SQLLITHNDQ	FVVSLCEENA	SRVWRLATGH	RVCNILTTLQ
1450	1460	1470	1480	1490	1500	1510	1520
NAFITSANTF	VVGMTKSKVL	AVSLWTGSIT	KKFCCEDGTT	IVNFKLIPDC	PDIIVFITSA	ETVNIWSLTD	EVICRRVQLP
1530	1540	1550	1560	1570	1580	1590	1600
NNFLKNLEDF	EISPNGKLGI	IARGDENINV	LDLYSGKLRV	VHASGIIWRQ	RLSRDGRYLV	YICFRNGEEE	DENGAIFSLI
1610	1620	1630	1640	1650	1660	1670	1680
VMRLADGKNI	GACSLYKTPT	FLALSQRHLN	IIVGFDDGSI	GIYTVVDRVD	AALKIKIATS	NSRQIFNNAT	HTSRPKCNSY
1690	1700	1710	1720	1730	1740	1750	
CFKISVDCLW	RESTEVFARD	SPITVSDSTE	SNEATPSKKH	NSCYERVCSA	LEARGHSYAP	DN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
607	1	766.5212	180.82	2	36.2	10.1	0	1343-1355	K.WNFSSGFIEAVFK.H	

Detailed Protein Report

Protein 400: spectrin beta chain, non-erythrocytic 1 isoform 2 [Homo sapiens]

Accession:	gi|112382252	**Score:**	24.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	251.2
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	2

Quantitation

QD:QU	**Median:** 0.37	**CV:** 0.00 %	**No. of Peptides:** 1

Detailed Protein Report

10	20	30	40	50	60	70	80
MELQRTSSIS	GPLSPAYTGQ	VPYNYNQLEG	RFKQLQDERE	AVQKKTFTKW	VNSHLARVSC	RITDLYTDLR	DGRMLIKLLE
90	100	110	120	130	140	150	160
VLSGERLPKP	TKGRMRIHCL	ENVDKALQFL	KEQRVHLENM	GSHDIVDGNH	RLTLGLIWTI	ILRFQIQDIS	VETEDNKEKK
170	180	190	200	210	220	230	240
SAKDALLLWC	QMKTAGYPNV	NIHNFTTSWR	DGMAFNALIH	KHRPDLIDFD	KLKKSNAHYN	LQNAFNLAEQ	HLGLTKLLDP
250	260	270	280	290	300	310	320
EDISVDHPDE	KSIITYVVTY	YHYFSKMKAL	AVEGKRIGKV	LDNAIETEKM	IEKYESLASD	LLEWIEQTII	ILNNRKFANS
330	340	350	360	370	380	390	400
LVGVQQQLQA	FNTYRTVEKP	PKFTEKGNLE	VLLFTIQSKM	RANNQKVYMP	REGKLISDIN	KAWERLEKAE	HERELALRNE
410	420	430	440	450	460	470	480
LIRQEKLEQL	ARRFDRKAAM	RETWLSENQR	LVSQDNFGFD	LPAVEAATKK	HEAIETDIAA	YEERVQAVVA	VARELEAENY
490	500	510	520	530	540	550	560
HDIKRITARK	DNVIRLWEYL	LELLRARRQR	LEMNLGLQKI	FQEMLYIMDW	MDEMKVLVLS	QDYGKHLLGV	EDLLQKHTLV
570	580	590	600	610	620	630	640
EADIGIQAER	VRGVNASAQK	FATDGEGYKP	CDPQVIRDRV	AHMEFCYQEL	CQLAAERRAR	LEESRRLWKF	FWEMAEEEGW
650	660	670	680	690	700	710	720
IREKEKILSS	DDYGKDLTSV	MRLLSKHRAF	EDEMSGRSGH	FEQAIKEGED	MIAEEHFGSE	KIRERIIYIR	EQWANLEQLS
730	740	750	760	770	780	790	800
AIRKKRLEEA	SLLHQFQADA	DDIDAWMLDI	LKIVSSSDVG	HDEYSTQSLV	KKHKDVAEEI	ANYRPTLDTL	HEQASALPQE
810	820	830	840	850	860	870	880
HAESPDVRGR	LSGIEERYKE	VAELTRLRKQ	ALQDTLALYK	MFSEADACEL	WIDEKEQWLN	NMQIPEKLED	LEVIQHRFES
890	900	910	920	930	940	950	960
LEPEMNNQAS	RVAVVNQIAR	QLMHSGHPSE	KEIKAQQDKL	NTRWSQFREL	VDRKKDALLS	ALSIQNYHLE	CNETKSWIRE
970	980	990	1000	1010	1020	1030	1040
KTKVIESTQD	LGNDLAGVMA	LQRKLTGMER	DLVAIEAKLS	DLQKEAEKLE	SEHPDQAQAI	LSRLAEISDV	WEEMKTTLKN
1050	1060	1070	1080	1090	1100	1110	1120
REASLGEASK	LQQFLRDLDD	FQSWLSRTQT	AIASEDMPNT	LTEAEKLLTQ	HENIKNEIDN	YEEDYQKMRD	MGEMVTQGQT
1130	1140	1150	1160	1170	1180	1190	1200
DAQYMFLRQR	LQALDTGWNE	LHKMWENRQN	LLSQSHAYQQ	FLRDTKQAEA	FLNNQEYVLA	HTEMPTTLEG	AEAAIKKQED
1210	1220	1230	1240	1250	1260	1270	1280
FMTTMDANEE	KINAVVETGR	RLVSDGNINS	DRIQEKVDSI	DDRHRKNRET	ASELLMRLKD	NRDLQKFLQD	CQELSLWINE
1290	1300	1310	1320	1330	1340	1350	1360
KMLTAQDMSY	DEARNLHSKW	LKHQAFMAEL	ASNKEWLDKI	EKEGMQLISE	KPETEAVVKE	KLTGLHKMWE	VLESTTQTKA
1370	1380	1390	1400	1410	1420	1430	1440
QRLFDANKAE	LFTQSCADLD	KWLHGLESQI	QSDDYGKDLT	SVNILLKKQQ	MLENQMEVRK	KEIEELQSQA	QALSQEGKST
1450	1460	1470	1480	1490	1500	1510	1520
DEVDSKRLTV	QTKFMELLEP	LNERKHNLLA	SKEIHQFNRD	VEDEILWVGE	RMPLATSTDH	GHNLQTVQLL	IKKNQTLQKE
1530	1540	1550	1560	1570	1580	1590	1600
IQGHQPRIDD	IFERSQNIVT	DSSSLSAEAI	RQRLADLKQL	WGLLIEETEK	RHRRLEEAHR	AQQYYFDAAE	AEAWMSEQEL
1610	1620	1630	1640	1650	1660	1670	1680
YMMSEEKAKD	EQSAVSMLKK	HQILEQAVED	YAETVHQLSK	TSRALVADSH	PESERISMRQ	SKVDKLYAGL	KDLAEERRGK
1690	1700	1710	1720	1730	1740	1750	1760
LDERHRLFQL	NREVDDLEQW	IAEREVVAGS	HELGQDYEHV	TMLQERFREF	ARDTGNIGQE	RVDTVNHLAD	ELINSGHSDA
1770	1780	1790	1800	1810	1820	1830	1840
ATIAEWKDGL	NEAWADLLEL	IDTRTQILAA	SYELHKFYHD	AKEIFGRIQD	KHKKLPEELG	RDQNTVETLQ	RMHTTFEHDI
1850	1860	1870	1880	1890	1900	1910	1920
QALGTQVRQL	QEDAARLQAA	YAGDKADDIQ	KRENEVLEAW	KSLLDACESR	RVRLVDTGDK	FRFFSMVRDL	MLWMEDVIRQ
1930	1940	1950	1960	1970	1980	1990	2000
IEAQEKPRDV	SSVELLMNNH	QGIKAEIDAR	NDSFTTCIEL	GKSLLARKHY	ASEEIKEKLL	QLTEKRKEMI	DKWEDRWEWL
2010	2020	2030	2040	2050	2060	2070	2080
RLILEVHQFS	RDASVAEAWL	LGQEPYLSSR	EIGQSVDEVE	KLIKRHEAFE	KSAATWDERF	SALERLTTLE	LLEVRRQQEE
2090	2100	2110	2120	2130	2140	2150	2160
EERKRRPPSP	EPSTKVSEEA	ESQQQWDTSK	GEQVSQNGLP	AEQGSPRVSY	RSQTYQNYKN	FNSRRTASDQ	PWSGL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
577	3	607.8304	-55.95	2	35.8	12.5	2	820-829	K.EVAELTRLRK.Q		
601	2	548.1743	-250.21	2	36.1	12.2	0	1087-1095	K.LLTQHENIK.N		QD:QU 0.37

Detailed Protein Report

Protein 401: **RING finger protein 39 isoform 2 [Homo sapiens]**

Accession:	gi|297139767	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.2
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	7.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWWRDLTRLR	LWLKREAIPG	EGRKAAKVNA	GVGEKGIYTA	SSRGGPPSAR	SKAVTVVAEG	AASRSWLSMD	APELGPGLVE
90	100	110	120	130	140	150	160
RLEQLATCPL	CGGSFEDPVL	LACEHSFCRA	CLARRWGTPP	ATGTEASPTA	CPCCGLPCPR	RSLRSNVRLA	VEVRISRELR
170	180	190	200	210	220	230	240
EKLAEPGARA	GRRRGGRIPT	MGCLDLPGED	MRKTWRRFEV	PTSKSSNSED	DLPEDYPVVK	KMLHRLTADL	TLDPGTAHRR
250	260	270	280	290	300	310	320
LLISADRRSV	QLAPPGTPAP	PDGPKRFDQL	PAVLGAQGFG	AGRHCWEVET	ADAASCRDSS	GEDADDEESH	YAVGAAGESV
330	340	350	360				
QRKGCAPGPL	GERIFPLFCT	CDPRAPLRIV	PAES				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
732	1	472.2592	-60.62	2	39.1	11.7	1	241-248	R.LLISADRR.S	

Detailed Protein Report

Protein 402: 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
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	21.2
		No. of unique Peptides:	2

```
        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
2793	1	846.4331	4.83	2	66.1	13.0	2	34-47	R.RSHHPESGCRTVLR.L	Carbamidomethyl: 9
2006	1	1044.9286	-117.90	2	55.5	11.6	1	134-151	R.VYNVSQKLYAEHSLLDLP.-	

Detailed Protein Report

Protein 403: 1-phosphatidylinositol 3-phosphate 5-kinase isoform 2 [Homo sapiens]

Accession:	gi|121583483	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	237.0
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MATDDKTSPT	LDSANDLPRS	PTSPSHLTHF	KPLTPDQDEP	PFKSAYSSFV	NLFRFNKERA	EGGQGEQQPL	SGSWTSPQLP
90	100	110	120	130	140	150	160
SRTQSVRSPT	PYKKQLNEEL	QRRSSALDTR	RKAEPTFGGH	DPRTAVQLRS	LSTVLKRLKE	IMEGKSQDSD	LKQYWMPDSQ
170	180	190	200	210	220	230	240
CKECYDCSEK	FTTFRRRHHC	RLCGQIFCSR	CCNQEIPGKF	MGYTGDLRAC	TYCRKIALSY	AHSTDSNSIG	EDLNALSDSA
250	260	270	280	290	300	310	320
CSVSVLDPSE	PRTPVGSRKA	SRNIFLEDDL	AWQSLIHPDS	SNTPLSTRLV	SVQEDAGKSP	ARNRSASITN	LSLDRSGSPM
330	340	350	360	370	380	390	400
VPSYETSVSP	QANRTYVRTE	TTEDERKILL	DSVQLKDLWK	KICHHSSGME	FQDHRYWLRT	HPNCIVGKEL	VNWLIRNGHI
410	420	430	440	450	460	470	480
ATRAQAIAIG	QAMVDGRWLD	CVSHHDQLFR	DEYALYRPLQ	STEFSETPSP	DSDSVNSVEG	HSEPSWFKDI	KFDDSDTEQI
490	500	510	520	530	540	550	560
AEEGDDNLAN	SASPSKRTSV	SSFQSTVDSD	SAASISLNVE	LDNVNFHIKK	PSKYPHVPPH	PADQKEYLIS	DTGGQQLSIS
570	580	590	600	610	620	630	640
DAFIKESLFN	RRVEEKSKEL	PFTPLGWHHN	NLELLREENG	EKQAMERLLS	ANHNHMMALL	QQLLHSDSLS	SSWRDIIVSL
650	660	670	680	690	700	710	720
VCQVVQTVRP	DVKNQDDDMD	IRQFVHIKKI	PGGKKFDSVV	VNGFVCTKNI	AHKKMSSCIK	NPKILLLKCS	IEYLYREETK
730	740	750	760	770	780	790	800
FTCIDPIVLQ	EREFLKNYVQ	RIVDVRPTLV	LVEKTVSRIA	QDMLLEHGIT	LVINVKSQVL	ERISRMTQGD	LVMSMDQLLT
810	820	830	840	850	860	870	880
KPHLGTCHKF	YMQIFQLPNE	QTKTLMFFEG	CPQHLGCTIK	LRGGSDYELA	RVKEILIFMI	CVAYHSQLEI	SFLMDEFAMP
890	900	910	920	930	940	950	960
PTLMQNPSFH	SLIEGRGHEG	AVQEQYGGGS	IPWDPDIPPE	SLPCDDSSLL	ELRIVFEKGE	QENKNLPQAV	ASVKHQEHST
970	980	990	1000	1010	1020	1030	1040
TACPAGLPCA	FFAPVPESLL	PLPVDDQQDA	LGSEQPETLQ	QTVVLQDPKS	QIRAFRDPLQ	DDTGLYVTEE	VTSSEDKRKT
1050	1060	1070	1080	1090	1100	1110	1120
YSLAFKQELK	DVILCISPVI	TFREPFLLTE	KGMRCSTRDY	FAEQVYWSPL	LNKEFKEMEN	RRKKQLLRDL	SGLQGMNGSI
1130	1140	1150	1160	1170	1180	1190	1200
QAKSIQVLPS	HELVSTRIAE	HLGDSQSLGR	MLADYRARGG	RIQPKNSDPF	AHSKDASSTS	SGQSGSKNEG	DEERGLILSD
1210	1220	1230	1240	1250	1260	1270	1280
AVWSTKVDCL	NPINHQRLCV	LFSSSSAQSS	NAPSACVSPW	IVTMEFYGKN	DLTLGIFLER	YCFRPSYQCP	SMFCDTPMVH
1290	1300	1310	1320	1330	1340	1350	1360
HIRRFVHGQG	CVQIILKELD	SPVPGYQHTI	LTYSWCRICK	QVTPVVALSN	ESWSMSFAKY	LELRFYGHQY	TRRANAEPCG
1370	1380	1390	1400	1410	1420	1430	1440
HSIHHDYHQY	FSYNQMVASF	SYSPIRLLEV	CVPLPKIFIK	RQAPLKVSLL	QDLKDFFQKV	SQVYVAIDER	LASLKTDTFS
1450	1460	1470	1480	1490	1500	1510	1520
KTREEKMEDI	FAQKEMEEGE	FKNWIEKMQA	RLMSSSVDTP	QQLQSVFESL	IAKKQSLCEV	LQAWNNRLQD	LFQQEKGRKR
1530	1540	1550	1560	1570	1580	1590	1600
PSVPPSPGRL	RQGEESKISA	MDASPRNISP	GLQNGEKEDR	FLTTLSSQSS	TSSTHLQLPT	PPEVMSEQSV	GGPPELDTAS
1610	1620	1630	1640	1650	1660	1670	1680
SSEDVFDGHL	LGSTDSQVKE	KSTMKAIFAN	LLPGNSYNPI	PFPFDPDKHY	LMYEHERVPI	AVCEKEPSSI	IAFALSCKEY
1690	1700	1710	1720	1730	1740	1750	1760
RNALEELSKA	TQWNSAEEGL	PTNSTSDSRP	KSSSPIRLPE	MSGGQTNRTT	ETEPQPTKKA	SGMLSFFRGT	AGKSPDLSSQ
1770	1780	1790	1800	1810	1820	1830	1840
KRETLRGADS	AYYQVGQTGK	EGTENQGVEP	QDEVDGGDTQ	KKQLINPHVE	LQFSDANAKF	YCRLYYAGEF	HKMREVILDS
1850	1860	1870	1880	1890	1900	1910	1920
SEEDFIRSLS	HSSPWQARGG	KSGAAFYATE	DDRFILKQMP	RLEVQSFLDF	APHYFNYITN	AVQQKRPTAL	AKILGVYRIG
1930	1940	1950	1960	1970	1980	1990	2000
YKNSQNNTEK	KLDLLVMENL	FYGRKMAQVF	DLKGSLRNRN	VKTDTGKESC	DVVLLDENLL	KMVRDNPLYI	RSHSKAVLRT
2010	2020	2030	2040	2050	2060	2070	2080
SIHSDSHFLS	SHLIIDYSLL	VGRDDTSNEL	VVGIIDYIRT	FTWDKKLEMV	VKSTGILGGQ	GKMPTVVSPE	LYRTRFCEAM
2090	2100						
DKYFLMVPDH	WTGLGLNC						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
596	1	656.3887	96.05	2	36.0	14.0	1	112-123	R.KAEPTFGGHDPR.T	
1652	1	911.3660	-108.75	2	50.9	10.6	0	2024-2039	R.DDTSNELVVGIIDYIR.T	

Detailed Protein Report

Protein 404: 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 405: up-regulator of cell proliferation isoform 2 [Homo sapiens]

Accession:	gi|117968345	**Score:**	24.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.3
Database Date:	2015-11-30	**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
1901	12	698.8088	27.42	2	52.3	14.5	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 406: PREDICTED: protein Shroom4 isoform X2 [Homo sapiens]

Accession: gi|578838225
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 24.6
MW [kDa]: 147.5
pI: 6.0
Sequence Coverage [%]: 1.9
No. of unique Peptides: 2

Quantitation

QD:QU **Median:** 0.25 **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	QD:QU 0.25
2564	1	731.7179	-190.01	2	60.7	10.2	2	822-834	R.KTSQSGREMAHSK.T	Oxidation: 9	

Detailed Protein Report

Protein 407: 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:	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
1604	1	783.2767	-145.45	2	50.3	12.9	0	250-263	K.VSHPQEPMLTASPR.M	Oxidation: 8

Detailed Protein Report

Protein 408: smoothelin isoform e [Homo sapiens]

Accession:	gi|333360860	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	104.8
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.9
		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
2098	2	938.2855	-133.64	2	54.8	13.7	0	1-19	-.MGGMGTPGDLHAACPSTTR.R	Oxidation: 1

Detailed Protein Report

Protein 409: PREDICTED: PDZ domain-containing protein 2 isoform X8 [Homo sapiens]

Accession:	gi|578809880	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	289.4
Database Date:	2015-11-30	**pI:**	7.4
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

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	

Detailed Protein Report

Protein 410: zinc finger protein 99 [Homo sapiens]

Accession:	gi|339418230	**Score:**	24.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.7
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	2.9
		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 411: PREDICTED: protein transport protein Sec16A isoform X5 [Homo sapiens]

Accession:	gi|530426857	**Score:**	24.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	240.9
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	1.0
		No. of unique 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
2846	2	607.3426	-19.17	2	64.7	10.1	2	2001-2011	K.RPGQAAKKETK.E	

Detailed Protein Report

Protein 412: **putative RNA-binding protein 15B [Homo sapiens]**

Accession:	gi|54607124	**Score:**	24.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.1
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
MKRQSERDSS	PSGRGSSSSA	KRPREREREA	EAGGRRAAHK	ASGGAKHPVP	ARARDKPRGS	GSGGGGHRDG	RGTGDANHRA
90	100	110	120	130	140	150	160
SSGRSSGSGA	GGGGRGGKAS	GDPGASGMSP	RASPLPPPPP	PPGAEPACPG	SSAAAPEYKT	LLISSLSPAL	PAEHLEDRLF
170	180	190	200	210	220	230	240
HQFKRFGEIS	LRLSHTPELG	RVAYVNFRHP	QDAREARQHA	LARQLLLYDR	PLKVEPVYLR	GGGGSSRRSS	SSSAAASTPP
250	260	270	280	290	300	310	320
PGPPAPADPL	GYLPLHGGYQ	YKQRSLSPVA	APPLREPRAR	HAAAAFALDA	AAAAAVGLSR	ERALDYYGLY	DDRGRPYGYP
330	340	350	360	370	380	390	400
AVCEEDLMPE	DDQRATRNLF	IGNLDHSVSE	VELRRAFEKY	GIIEEVVIKR	PARGQGGAYA	FLKFQNLDMA	HRAKVAMSGR
410	420	430	440	450	460	470	480
VIGRNPIKIG	YGKANPTTRL	WVGGLGPNTS	LAALAREFDR	FGSIRTIDHV	KGDSFAYIQY	ESLDAAQAAC	AKMRGFPLGG
490	500	510	520	530	540	550	560
PDRRLRVDFA	KAEETRYPQQ	YQPSPLPVHY	ELLTDGYTRH	RNLDADLVRD	RTPPHLLYSD	RDRTFLEGDW	TSPSKSSDRR
570	580	590	600	610	620	630	640
NSLEGYSRSV	RSRSGERWGA	DGDRGLPKPW	EERRKRRSLS	SDRGRTTHSP	YEERSRTKGS	GQQSERGSDR	TPERSRKENH
650	660	670	680	690	700	710	720
SSEGTKESSS	NSLSNSRHGA	EERGHHHHHH	EAADSSHGKK	ARDSERNHRT	TEAEPKPLEE	PKHETKKLKN	LSEYAQTLQL
730	740	750	760	770	780	790	800
GWNGLLVLKN	SCFPTSMHIL	EGDQGVISSL	LKDHTSGSKL	TQLKIAQRLR	LDQPKLDEVT	RRIKQGSPNG	YAVLLATQAT
810	820	830	840	850	860	870	880
PSGLGTEGMP	TVEPGLQRRL	LRNLVSYLKQ	KQAAGVISLP	VGGSKGRDGT	GMLYAFPPCD	FSQQYLQSAL	RTLGKLEEEH
890	900						
MVIVIVRDTA							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
609	1	666.9243	159.05	2	36.2	14.3	1	604-614	R.GRTTHSPYEER.S	

Detailed Protein Report

Protein 413: prolactin-inducible protein precursor [Homo sapiens]

Accession: gi|4505821
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 24.3
MW [kDa]: 16.6
pI: 9.3
Sequence Coverage [%]: 10.3
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MRLLQLLFRA SPATLLLVLC LQLGANKAQD NTRKIIIKNF DIPKSVRPND EVTAVLAVQT ELKECMVVKT YLISSIPLQG
        90        100        110        120        130        140        150
AFNYKYTACL CDDNPKTFYW DFYTNRTVQI AAVVDVIREL GICPDDAAVI PIKNNRFYTI EILKVE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2317	1	805.9036	-28.46	2	57.6	24.3	0	119-133	R.ELGICPDDAAVIPIK.N	Carbamidomethyl: 5

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Detailed Protein Report

Protein 414: xylosyltransferase 1 precursor [Homo sapiens]

Accession:	gi|28269693	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	107.5
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	2

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
87	1	669.7442	115.37	3	29.8	12.8	2	68-91	R.RDLPAEPAAARGGGGGGGGGGGR.G	
2175	1	701.2622	-127.85	3	57.6	11.6	0	388-406	R.MATIWGGASLLSTYLQSMR.D	Oxidation: 18

Detailed Protein Report

Protein 415: PREDICTED: E3 ubiquitin-protein ligase MIB2 isoform X7 [Homo sapiens]

Accession:	gi|578798430	**Score:**	24.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	111.6
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	2

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
2600	1	835.4660	80.35	2	63.2	12.9	0	401-414	R.MAEHHSFWVGDVVR.V	
1170	1	713.1709	-414.81	1	43.1	11.4	0	562-567	R.LLLQAR.A	

Detailed Protein Report

Protein 416: 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

QD:QU **Median:** 2.58 **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		QD:QU	2.58

Detailed Protein Report

Protein 417: PREDICTED: E3 ubiquitin-protein ligase DTX4 isoform X1 [Homo sapiens]

Accession:	gi|578821243	**Score:**	24.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.2
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	3.9
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 2.11 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEVGITIQHA	YEKQHPWIDL	TSIGFSYVID	FNTMGQINRQ	TQRQRRVRRR	LDLIYPMVTG	TLPKAQSWPV	SPGPATSPPM
90	100	110	120	130	140	150	160
SPCSCPQCVL	VMSVKAAVVN	GSTGPLQLPV	TRKNMPPPGV	VKLPPLPGSG	AKPLDSTGTI	RGPLKTAPSQ	VIRRQASSMP
170	180	190	200	210	220	230	240
TGTTMGSPAS	PPGPNSKTGR	VALATLNRTN	LQRLAIAQSR	VLIASGVPTV	PVKNLNGSSP	VNPALAGITG	ILMSAAGLPV
250	260	270	280	290	300	310	320
CLTRPPKLVL	HPPPVSKSEI	KSIPGVSNTS	RKTTKKQAKK	GKTPEEVLKK	YLQKVRHPPD	EDCTICMERL	TAPSGYKGPQ
330	340	350	360	370	380	390	400
PTVKPDLVGK	LSRCGHVYHI	YCLVAMYNNG	NKDGSLQCPT	CKTIYGVKTG	TQPPGKMEYH	LIPHSLPGHP	DCKTIRIIYS
410	420	430	440	450	460	470	480
IPPGIQGPEH	PNPGKSFSAR	GFPRHCYLPD	SEKGRKVLKL	LLVAWDRRLI	FAIGTSSTTG	ESDTVIWNEV	HHKTEFGSNL
490	500	510	520				
TGHGYPDANY	LDNVLAELAA	QGISEDSTAQ	EKD				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
690	1	564.6885	-259.06	2	37.2	10.9	2	280-289	K.KGKTPEEVLK.K		QD:QU 2.11

Detailed Protein Report

Protein 418: **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 419: **PREDICTED: pecanex-like protein 3 isoform X4 [Homo sapiens]**

Accession:	gi|530396772	**Score:**	24.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	115.4
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	2.0
		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
1593	1	1172.1148	-1.72	2	50.1	24.2	2	161-181	R.DIKELVREQGSNNVIVTSADR.E	

Detailed Protein Report

Protein 420: myosin light chain kinase, smooth muscle isoform 3B [Homo sapiens]

Accession:	gi|116008190	**Score:**	24.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	197.3
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	2

Quantitation

QD:QU	**Median:** 0.93	**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		QD:QU 0.93
2643	1	995.0088	-31.93	2	63.9	10.1	1	180-196	R.FSCKITGRPQPQVTWLK.G		

Detailed Protein Report

Protein 421: 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; Oxidation: 7
1854	1	938.8329	-130.94	2	53.5	11.5	1	521-536	K.QIHSVQKPYKCEECGK.A	

Detailed Protein Report

Protein 422: **phosphoserine aminotransferase isoform 2 [Homo sapiens]**

Accession:	gi|10863955	**Score:**	24.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.2
Database Date:	2015-11-30	**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

Protein 423: titin isoform novex-3 [Homo sapiens]

Accession:	gi|110349721	**Score:**	24.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	631.2
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

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
SSHAFLLVQA	KQLITFTQEL	QDVVAKEKDT	MATFECETSE	PFVKVKWYKD	GMEVHEGDKY	RMHSDRKVHF	LSILTIDTSD
2250	2260	2270	2280	2290	2300	2310	2320
AEDYSCVLVE	DENVKTTAKL	IVEGAVVEFV	KELQDIEVPE	SYSGELECIV	SPENIEGKWY	HNDVELKSNG	KYTITSRRGR
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
2534	1	921.5697	156.01	2	62.3	13.8	1	4501-4516	R.ESRSSNLNANMYQAEK.M	

Detailed Protein Report

Protein 424: **PREDICTED: centrosomal protein of 164 kDa isoform X10 [Homo sapiens]**

Accession:	gi|530397903	**Score:**	24.1
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 425: **PREDICTED: zinc finger CCCH domain-containing protein 3 isoform X7 [Homo sapiens]**

Accession:	gi|578815908	**Score:**	24.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	107.0
Database Date:	2015-11-30	**pI:**	12.1
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSIQGTLLSD	VFSSGHTPPW	PAPPRPREKG	RVAMTSWGPG	RPSRTREMEE	KEILRRQIRL	LQGLIDDYKT	LHGNAPAPGT
90	100	110	120	130	140	150	160
PAASGWQPPT	YHSGRAFSAR	YPRPSRRGYS	SHHGPSWRKK	YSLVNRPPGP	SDPPADHAVR	PLHGARGGQP	PVPQQHVLER
170	180	190	200	210	220	230	240
QVQLSQGQNV	VIKVKPPSKS	GSASASGAQR	GSLEEFEETP	WSDQRPREGE	GEPPRGQLQP	SRPTRARGTC	SVEDPLLVCQ
250	260	270	280	290	300	310	320
KEPGKPRMVK	SVGSVGDSPR	EPRRTVSESV	IAVKASFPSS	ALPPRTGVAL	GRKLGSHSVA	SCAPQLLGDR	RVDAGHTDQP
330	340	350	360	370	380	390	400
VPSGSVGGPA	RPASGPRQAR	EASLVVTCRT	NKFRKNNYKW	VAASSKSPRV	ARRALSPRVA	AENVCKASAG	MANKVEKPQL
410	420	430	440	450	460	470	480
IADPEPKPRK	PATSSKPGSA	PSKYKWKASS	PSASSSSSFR	WQSEASSKDH	ASQLSPVLSR	SPSGDRPAVG	HSGLKPLSGE
490	500	510	520	530	540	550	560
TPLSAYKVKS	RTKIIRRRSS	TSLPGDKKSG	TSPAATAKSH	LSLRRRQALR	GKSSPVLKKT	PNKGLVQVTT	HRLCRLPPSR
570	580	590	600	610	620	630	640
AHLPTKEASS	LHAVRTAPTS	KVIKTRYRIV	KKTPASPLSA	PPFPLSLPSW	RARRLSLSRS	LVLNRLRPVA	SGGGKAQPGS
650	660	670	680	690	700	710	720
PWWRSKGYRC	IGGVLYKVSA	NKLSKTSGQP	SDAGSRPLLR	TGRLDPAGSC	SRSLASRAVQ	RSLAIIRQAR	QRREKRKEYC
730	740	750	760	770	780	790	800
MYYNRFGRCN	RGERCPYIHD	PEKVAVCTRF	VRGTCKKTDG	TCPFSHHVSK	EKMPVCSYFL	KGICSNSNCP	YSHVYVSRKA
810	820	830	840	850	860	870	880
EVCSDFLKGY	CPLGAKCKKK	HTLLCPDFAR	RGACPRGAQC	QLLHRTQKRH	SRRAATSPAP	GPSDATARSR	VSASHGPRKP
890	900	910	920	930	940	950	960
SASQRPTRQT	PSSAALTAAA	VAAPPHCPGG	SASPSSSKAS	SSSSSSSSPP	ASLDHEAPSL	QEAALAAACS	NRLCKLPSFI
970	980	990	1000				
SLQSSPSPGA	QPRVRAPRAP	LTKDSGKPLH	IKPRL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2689	1	701.3840	39.36	2	64.7	10.2	0	32-44	R.VAMTSWGPGRPSR.T	

Detailed Protein Report

Protein 426: **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:	1

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	

Detailed Protein Report

Protein 427: PREDICTED: focal adhesion kinase 1 isoform X12 [Homo sapiens]

Accession:	gi|530389222	**Score:**	24.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	108.1
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
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	
2062	1	720.2626	-173.22	2	54.3	10.7	0	922-935	K.QMLTAAHALAVDAK.N	

Detailed Protein Report

Protein 428: **PREDICTED: probable phospholipid-transporting ATPase IIB isoform X6 [Homo sapiens]**

Accession:	gi|530414190	**Score:**	24.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	114.6
Database Date:	2015-11-30	**pI:**	7.3
Modification(s):	Carbamidomethyl	**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 429: **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

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
2294	1	841.8204	-110.73	2	59.1	12.2	0	615-630	R.SVMTQMSSSLVSAAQR.A	

Detailed Protein Report

Protein 430: zinc finger homeobox protein 3 isoform B [Homo sapiens]

Accession:	gi|258613987	**Score:**	24.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	306.5
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MRLGGGQLVS	EELMNLGESF	IQTNDPSLKL	FQCAVCNKFT	TDNLDMLGLH	MNVERSLSED	EWKAVMGDSY	QCKLCRYNTQ
90	100	110	120	130	140	150	160
LKANFQLHCK	TDKHVQKYQL	VAHIKEGGKA	NEWRLKCVAI	GNPVHLKCNA	CDYYTNSLEK	LRLHTVNSRH	EASLKLYKHL
170	180	190	200	210	220	230	240
QQHESGVEGE	SCYYHCVLCN	YSTKAKLNLI	QHVRSMKHQR	SESLRKLQRL	QKGLPEEDED	LGQIFTIRRC	PSTDPEEAIE
250	260	270	280	290	300	310	320
DVEGPSETAA	DPEELAKDQE	GGASSSQAEK	ELTDSPATSK	RISFPGSSES	PLSSKRPKTA	EEIKPEQMYQ	CPYCKYSNAD
330	340	350	360	370	380	390	400
VNRLRVHAMT	QHSVQPMLRC	PLCQDMLNNK	IHLQLHLTHL	HSVAPDCVEK	LIMTVTTPEM	VMPSSMFLPA	AVPDRDGNSN
410	420	430	440	450	460	470	480
LEEAGKQPET	SEDLGKNILP	SASTEQSGDL	KPSPADPGSV	REDSGFICWK	KGCNQVFKTS	AALQTHFNEV	HAKRPQLPVS
490	500	510	520	530	540	550	560
DRHVYKYRCN	QCSLAFKTIE	KLQLHSQYHV	IRAATMCCLC	QRSFRTFQAL	KKHLETSHLE	LSEADIQQLY	GGLLANGDLL
570	580	590	600	610	620	630	640
AMGDPTLAED	HTIIVEEDKE	EESDLEDKQS	PTGSDSGSVQ	EDSGSEPKRA	LPFRKGPNFT	MEKFLDPSRP	YKCTVCKESF
650	660	670	680	690	700	710	720
TQKNILLVHY	NSVSHLHKLK	RALQESATGQ	PEPTSSPDNK	PFKCNTCNVA	YSQSSTLEIH	MRSVLHQTKA	RAAKLEAASG
730	740	750	760	770	780	790	800
SSNGTGNSSS	ISLSSSTPSP	VSTSGSNTFT	TSNPSSAGIA	PSSNLLSQVP	TESVGMPPLG	NPIGANIASP	SEPKEANRKK
810	820	830	840	850	860	870	880
LADMIASRQQ	QQQQQQQQQQ	QQQQQQQAQT	LAQAQAQVQA	HLQQELQQQA	ALIQSQLFNP	TLLPHFPMTT	ETLLQLQQQQ
890	900	910	920	930	940	950	960
HLLFPFYIPS	AEFQLNPEVS	LPVTSGALTL	TGTGPGLLED	LKAQVQVPQQ	SHQQILPQQQ	QNQLSIAQSH	SALLQPSQHP
970	980	990	1000	1010	1020	1030	1040
EKKNKLVIKE	KEKESQRERD	SAEGGEGNTG	PKETLPDALK	AKEKKELAPG	GGSEPSMLPP	RIASDARGNA	TKALLENFGF
1050	1060	1070	1080	1090	1100	1110	1120
ELVIQYNENK	QKVQKKNGKT	DQGENLEKLE	CDSCGKLFSN	ILILKSHQEH	VHQNYFPFKQ	LERFAKQYRD	HYDKLYPLRP
1130	1140	1150	1160	1170	1180	1190	1200
QTPEPPPPPP	PPPPPPLPAA	PPQPASTPAI	PASAPPITSP	TIAPAQPSVP	LTQLSMPMEL	PIFSPLMMQT	MPLQTLPAQL
1210	1220	1230	1240	1250	1260	1270	1280
PPQLGPVEPL	PADLAQLYQH	QLNPTLLQQQ	NKRPRTRITD	DQLRVLRQYF	DINNSPSEEQ	IKEMADKSGL	PQKVIKHWFR
1290	1300	1310	1320	1330	1340	1350	1360
NTLFKERQRN	KDSPYNFSNP	PITSLEELKI	DSRPPSPEPP	KQEYWGSKRS	SRTRFTDYQL	RVLQDFFDAN	AYPKDDEFEQ
1370	1380	1390	1400	1410	1420	1430	1440
LSNLLNLPTR	VIVVWFQNAR	QKARKNYENQ	GEGKDGERRE	LTNDRYIRTS	NLNYQCKKCS	LVFQRIFDLI	KHQKKLCYKD
1450	1460	1470	1480	1490	1500	1510	1520
EDEEGQDDSQ	NEDSMDAMEI	LTPTSSSCST	PMPSQAYSAP	APSANNTASS	AFLQLTAEAE	ELATFNSKTE	AGDEKPKLAE
1530	1540	1550	1560	1570	1580	1590	1600
APSAQPNQTQ	EKQGQPKPEL	QQQEQPEQKT	NTPQQKLPQL	VSLPSLPQPP	PQAPPPQCPL	PQSSPSPSQL	SHLPLKPLHT
1610	1620	1630	1640	1650	1660	1670	1680
STPQQLANLP	PQLIPYQCDQ	CKLAFPSFEH	WQEHQQLHFL	SAQNQFIHPQ	FLDRSLDMPF	MLFDPSNPLL	ASQLLSGAIP
1690	1700	1710	1720	1730	1740	1750	1760
QIPASSATSP	STPTSTMNTL	KRKLEEKASA	SPGENDSGTG	GEEPQRDKRL	RTTITPEQLE	ILYQKYLLDS	NPTRKMLDHI
1770	1780	1790	1800	1810	1820	1830	1840
AHEVGLKKRV	VQVWFQNTRA	RERKGQFRAV	GPAQAHRRCP	FCRALFKAKT	ALEAHIRSRH	WHEAKRAGYN	LTLSAMLLDC
1850	1860	1870	1880	1890	1900	1910	1920
DGGLQMKGDI	FDGTSFSHLP	PSSSDGQGVP	LSPVSKTMEL	SPRTLLSPSS	IKVEGIEDFE	SPSMSSVNLN	FDQTKLDNDD
1930	1940	1950	1960	1970	1980	1990	2000
CSSVNTAITD	TTTGDEGNAD	NDSATGIATE	TKSSSAPNEG	LTKAAMMAMS	EYEDRLSSGL	VSPAPSFYSK	EYDNEGTVDY
2010	2020	2030	2040	2050	2060	2070	2080
SETSSLADPC	SPSPGASGSA	GKSGDSGDRP	GQKRFRTQMT	NLQLKVLKSC	FNDYRTPTML	ECEVLGNDIG	LPKRVVQVWF
2090	2100	2110	2120	2130	2140	2150	2160
QNARAKEKKS	KLSMAKHFGI	NQTSYEGPKT	ECTLCGIKYS	ARLSVRDHIF	SQQHISKVKD	TIGSQLDKEK	EYFDPATVRQ
2170	2180	2190	2200	2210	2220	2230	2240
LMAQQELDRI	KKANEVLGLA	AQQQGMFDNT	PLQALNLPTA	YPALQGIPPV	LLPGLNSPSL	PGFTPSNTAL	TSPKPNLMGL
2250	2260	2270	2280	2290	2300	2310	2320
PSTTVPSPGL	PTSGLPNKPS	SASLSSPTPA	QATMAMGPQQ	PPQQQQQQQQ	PQVQQPPPPP	AAQPPPTPQL	PLQQQQQRKD
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
2629	1	973.4760	-77.59	2	61.6	11.7	1	1730-1745	R.LRTTITPEQLEILYQK.Y	
2712	1	1006.4372	-42.21	3	65.0	12.3	2	2097-2122	K.HFGINQTSYEGPKTECTLCGIKYSAR.L	Carbamidomethyl: 16, 19

Detailed Protein Report

Protein 431: PREDICTED: rotatin isoform X3 [Homo sapiens]

Accession:	gi|578832429	**Score:**	24.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	229.9
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	2

Detailed Protein Report

10	20	30	40	50	60	70	80
MVLAGLIRKL	GHQLAEIRER	ALKSILCKIE	HNLICYADLI	QERQLFLHLL	EWFNFPSVPM	KEEVLNLLSR	LVKYPPAVQH
90	100	110	120	130	140	150	160
LVDVGAVEFL	SKLRSNVEPN	LQAEIDGILD	GLFLLPSEVP	ALSSASYQTN	QTELSKNPEI	LTGYFPQDKS	NFQQMEVPPR
170	180	190	200	210	220	230	240
PVVNQTVKCL	KFSTFPWLPL	TTTDRHVLSS	NESSLRSSNH	TLIWNTCELL	KDVIMQDFPA	EIFLQRPKIV	QSLLSLLKLA
250	260	270	280	290	300	310	320
FGDGKHRLAL	QSVSCLQQLC	MYLRNRLNFH	RDPGFFSNKH	DTVSQNSSLS	YCHEARGTHH	SQNPSPGSSS	PRPSVVGRTG
330	340	350	360	370	380	390	400
QRPRGDGQDW	DAASSSGSSS	HAHVNSRISV	HSPLDMGHID	LPELETEDTL	ELQFQQLSLP	QFCVSILESA	VPLLRTGSRQ
410	420	430	440	450	460	470	480
VIIRVLELLT	EDMTLIGEAI	STDIWDDSSL	FGIDMKEKLL	LVLGALGETM	CYHKSSISLE	QPEVMLVHHR	MAFISISLFA
490	500	510	520	530	540	550	560
VRLLQTLLPV	EKASEFLSEP	MSTALFLLSL	DMPISLEYPN	IHEAVVAYLE	QLNSENYSIY	KRTAEAVYSI	ECTCNFLSDI
570	580	590	600	610	620	630	640
GKEGEKNLLE	LVELADQALR	SFSYHQHFPL	IKEIISICSK	IWKSAQASPL	LQGESQKVLL	HMLSHPLPRV	KAETYHCCLE
650	660	670	680	690	700	710	720
ITKECLGVHN	VTKPVSSLCN	GIHFLLHPKV	LYEISVFGIQ	EPESEQVNTA	AKAILLYLLQ	GRLMMTALTW	NKFIESLCPV
730	740	750	760	770	780	790	800
IPILQGYADT	EDPLGNCILL	LSKASSDTEE	MLPCTTRLKS	MLRLLLVKKP	SVRSLALKLL	AFHLTSEEGA	DTKRPLIDAR
810	820	830	840	850	860	870	880
VLSRVTDLFI	GKKPIELRLD	DRRELVIKLE	TVEKVYEIFT	SDDVDLVLRK	SAAEQLAVIM	QDIKMHAVVK	KLCLIDKIIE
890	900	910	920	930	940	950	960
YLNECVSQDG	KVVECLVQPC	LTLLRKVLCG	DPVMRVSLSQ	QSSLLTVLFR	VSLIFHEDCS	VVTEVGALFC	LLLFDEVSRM
970	980	990	1000	1010	1020	1030	1040
DMWSVNPSNK	PSLPSVFSLP	VSVFRRYHLP	VHVIGHHAVS	PYSIVLPLSA	DCLALKPVSD	MLRIAWNLSW	YHGSDNLLKQ
1050	1060	1070	1080	1090	1100	1110	1120
MNSETKTQEI	LDALKLSTED	ILTLKITHMA	SGLQDCLHSI	VQAATHREVR	AAVTRMSFYL	LNDRLSLKGC	PGPCGVTLKS
1130	1140	1150	1160	1170	1180	1190	1200
LAWHTALNRF	LQVLPACTED	EKLLIDIIHF	LNKLIKEQRK	NSSLELLNWI	LELLLRHSAN	PLLDLLVLTE	SQAREETDDI
1210	1220	1230	1240	1250	1260	1270	1280
RTAVRQQLQK	ELIALFDTLL	LNFMEVTDRK	CSELLYVFQT	QLALKLLQCL	KVTDAPHFYG	LPSLERTLRG	MANLTAFPGW
1290	1300	1310	1320	1330	1340	1350	1360
SSHSPLTKPL	DICVKYLSGL	LEVITSFYVE	RGGNAMSFMG	KGVTKSTILC	LLHLSHEMMA	QAGSLEWMSL	WFLPLGSHSE
1370	1380	1390	1400	1410	1420	1430	1440
EHIPTQQGLA	WLIPLWVDRD	PEVRFTSLGL	GSALTTLETG	CVALANSCQN	ISGGLWGTVV	NILLDQSECS	MVRREAAFIL
1450	1460	1470	1480	1490	1500	1510	1520
QNLLVIPMPT	EIIKDYTWQG	PCVHDEDSGL	SLIGKPALQA	LLYHCHFYEH	LNQMVKHCYL	GRCMFDLNFS	AFDRNSESND
1530	1540	1550	1560	1570	1580	1590	1600
LNGLDDSFKF	WRAPSRTSQD	RDPSSLSTSE	TTVAPSLGST	EFQPLVQSTT	LLPEASHDQF	VAQGHQESTS	PRPPHDSSLS
1610	1620	1630	1640	1650	1660	1670	1680
APLPKLCVFV	TPSLLSAMCS	LLDNLLTIAP	RDTAKAFRQA	HLIELLCSIA	DATLIQTCVQ	ELRALLPSSP	PAEHTQAQVS
1690	1700	1710	1720	1730	1740	1750	1760
FLLEYLSSLS	RLLQSCLLVE	PDLVIQDELV	KPLITNIIGI	LTICTKDVLD	KELISAFYHT	WTHLFNLLAM	LLRKAGAITL
1770	1780	1790	1800	1810	1820	1830	1840
PFVTVALAKH	WTAAIDMFCT	CAGLSATCPA	LYTASLQFLS	VLLTEEAKGH	LQAKSKTHLC	CSPTVASLLD	DSQENQKSLE
1850	1860	1870	1880	1890	1900	1910	1920
QLSDVILQCY	EGKSSKDILK	RVAANALMSL	LAVSRRAQKH	ALKANLIDNC	MEQMKHINAQ	LNLDSLRPGK	AALKKKEDGV
1930	1940	1950	1960	1970	1980	1990	2000
IKELSIAMQL	LRNCLYQNEE	CKEAALEAHL	VPVLHSLWPW	ILMDDSLMQI	SLQLLCVYTA	NFPNGCSSLC	WSSCGQHPVQ
2010	2020	2030	2040	2050	2060		
ATHRGAVSNS	LMLCILKLAS	QMPLENTTVQ	QMVFMLLSNL	ALSHDCKGVI	QKAKINCRS		

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
10	1	1205.0326	-122.89	2	29.6	12.9	1	71-92	R.LVKYPPAVQHLVDVGAVEFLSK.L	
2647	1	753.6332	-97.01	3	61.9	11.1	2	1877-1895	R.AQKHALKANLIDNCMEQMK.H	Carbamidomethyl: 14; Oxidation: 15

Detailed Protein Report

Protein 432: tubulin polyglutamylase TTLL5 [Homo sapiens]

Accession:	gi|50658079	**Score:**	23.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	143.5
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
MPIVMARDLE	ETASSSEDEE	VISQEDHPCI	MWTGGCRRIP	VLVFHADAIL	TKDNNIRVIG	ERYHLSYKIV	RTDSRLVRSI
90	100	110	120	130	140	150	160
LTAHGFHEVH	PSSTDYNLMW	TGSHLKPFLL	RTLSEAQKVN	HFPRSYELTR	KDRLYKNIIR	MQHTHGFKAF	HILPQTFLLP
170	180	190	200	210	220	230	240
AEYAEFCNSY	SKDRGPWIVK	PVASSRGRGV	YLINNPNQIS	LEENILVSRY	INNPLLIDDF	KFDVRLYVLV	TSYDPLVIYL
250	260	270	280	290	300	310	320
YEEGLARFAT	VRYDQGAKNI	RNQFMHLTNY	SVNKKSGDYV	SCDDPEVEDY	GNKWSMSAML	RYLKQEGRDT	TALMAHVEDL
330	340	350	360	370	380	390	400
IIKTIISAEL	AIATACKTFV	PHRSSCFELY	GFDVLIDSTL	KPWLLEVNLS	PSLACDAPLD	LKIKASMISD	MFTVVGFVCQ
410	420	430	440	450	460	470	480
DPAQRASTRP	IYPTFESSRR	NPFQKPQRCR	PLSASDAEMK	NLVGSAREKG	PGKLGGSVLG	LSMEEIKVLR	RVKEENDRRG
490	500	510	520	530	540	550	560
GFIRIFPTSE	TWEIYGSYLE	HKTSMNYMLA	TRLFQDRMTA	DGAPELKIES	LNSKAKLHAA	LYERKLLSLE	VRKRRRRSSR
570	580	590	600	610	620	630	640
LRAMRPKYPV	ITQPAEMNVK	TETESEEEEE	VALDNEDEEQ	EASQEESAGF	LRENQAKYTP	SLTALVENTP	KENSMKVREW
650	660	670	680	690	700	710	720
NNKGGHCCKL	ETQELEPKFN	LMQILQDNGN	LSKMQARIAF	SAYLQHVQIR	LMKDSGGQTF	SASWAAKEDE	QMELVVRFLK
730	740	750	760	770	780	790	800
RASNNLQHSL	RMVLPSRRLA	LLERRRILAH	QLGDFIIVYN	KETEQMAEKK	SKKKVEEEEE	DGVNMENFQE	FIRQASEAEL
810	820	830	840	850	860	870	880
EEVLTFYTQK	NKSASVFLGT	HSKISKNNNN	YSDSGAKGDH	PETIMEEVKI	KPPKQQQTTE	IHSDKLSRFT	TSAEKEAKLV
890	900	910	920	930	940	950	960
YSNSSSGPTA	TLQKIPNTHL	SSVTTSDLSP	GPCHHSSLSQ	IPSAIPSMPH	QPTILLNTVS	ASASPCLHPG	AQNIPSPTGL
970	980	990	1000	1010	1020	1030	1040
PRCRSGSHTI	GPFSSFQSAA	HIYSQKLSRP	SSAKAGSCYL	NKHHSGIAKT	QKEGEDASLY	SKRYNQSMVT	AELQRLAEKQ
1050	1060	1070	1080	1090	1100	1110	1120
AARQYSPSSH	INLLTQQVTN	LNLATGIINR	SSASAPPTLR	PIISPSGPTW	STQSDPQAPE	NHSSSPGSRS	LQTGGFAWEG
1130	1140	1150	1160	1170	1180	1190	1200
EVENNVYSQA	TGVVPQHKYH	PTAGSYQLQF	ALQQLEQQKL	QSRQLLDQSR	ARHQAIFGSQ	TLPNSNLWTM	NNGAGCRISS
1210	1220	1230	1240	1250	1260	1270	1280
ATASGQKPTT	LPQKVVPPPS	SCASLVPKPP	PNHEQVLRRA	TSQKASKGSS	AEGQLNGLQS	SLNPAAFVPI	TSSTDPAHTK
1290							
I							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2086	1	720.2523	-137.01	2	54.7	11.9	0	1024-1035	R.YNQSMVTAELQR.L	

Detailed Protein Report

Protein 433: peroxisome biogenesis factor 1 isoform 3 [Homo sapiens]

Accession:	gi|544186104	**Score:**	23.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.5
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
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
1391	1	1207.8676	86.30	1	45.9	12.7	2	233-242	K.IPRSLKLQPR.E	

Detailed Protein Report

Protein 434: short transient receptor potential channel 7 isoform 3 [Homo sapiens]

Accession:	gi|262399375	**Score:**	23.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.2
Database Date:	2015-11-30	**pI:**	8.4
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLRNSTFKNM	QRRHTTLREK	GRRQAIRGPA	YMFNEKGTSL	TPEEERFLDS	AEYGNIPVVR	KMLEESKTLN	FNCVDYMGQN
90	100	110	120	130	140	150	160
ALQLAVGNEH	LEVTELLLKK	ENLARVGDAL	LLAISKGYVR	IVEAILNHPA	FAQGQRLTLS	PLEQELRDDD	FYAYDEDGTR
170	180	190	200	210	220	230	240
FSHDITPIIL	AAHCQEYEIV	HILLLKGARI	ERPHDYFCKC	NECTEKQRKD	SFSHSRSRMN	AYKGLASAAY	LSLSSEDPVL
250	260	270	280	290	300	310	320
TALELSNELA	RLANIETEFK	LGRTLRSPFM	KFVAHAVSFT	IFLGLLVVNA	SDRFEGVKTL	PNETFTDYPK	QIFRVKTTQF
330	340	350	360	370	380	390	400
SWTEMLIMKW	VLGMIWSECK	EIWEEGPREY	VLHLWNLLDF	GMLSIFVASF	TARFMAFLKA	TEAQLYVDQH	VQDDTLHNVS
410	420	430	440	450	460	470	480
LPPEVAYFTY	ARDKWWPSDP	QIISEGLYAI	AVVLSFSRIA	YILPANESFG	PLQISLGRTV	KDIFKFMVIF	IMVFVAFMIG
490	500	510	520	530	540	550	560
MFNLYSYYRG	AKYNPAFTTV	EESFKTLFWS	IFGLSEVISV	VLKYDHKFIE	NIGYVLYGVY	NVTMVVVLLN	MLIAMINNSY
570	580	590	600	610	620	630	640
QEIEEDADVE	WKFARAKLWL	SYFDEGRTLP	APFNLVPSPK	SFYYLIMRIK	MCLIKLCKSK	AKSCENDLEM	GMLNSKFKKT
650	660	670	680	690	700	710	720
RYQAGMRNSE	NLTANNTLSK	PTRYQKIMKR	LIKRYVLKAQ	VDRENDEVNE	GELKEIKQDI	SSLRYELLEE	KSQATGELAD
730	740	750					
LIQQLSEKFG	KNLNKDHLRV	NKGKDI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
81	1	1120.1328	21.81	2	30.9	11.6	1	117-136	K.GYVRIVEAILNHPAFAQGQR.L	

Detailed Protein Report

Protein 435: phosphoglycolate phosphatase [Homo sapiens]

Accession:	gi|108796653	**Score:**	23.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.0
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	13.4
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAAAEAGGDD	ARCVRLSAER	AQALLADVDT	LLFDCDGVLW	RGETAVPGAP	EALRALRARG	KRLGFITNNS	SKTRAAYAEK
90	100	110	120	130	140	150	160
LRRLGFGGPA	GPGASLEVFG	TAYCTALYLR	QRLAGAPAPK	AYVLGSPALA	AELEAVGVAS	VGVGPEPLQG	EGPGDWLHAP
170	180	190	200	210	220	230	240
LEPDVRAVVV	GFDPHFSYMK	LTKALRYLQQ	PGCLLVGTNM	DNRLPLENGR	FIAGTGCLVR	AVEMAAQRQA	DIIGKPSRFI
250	260	270	280	290	300	310	320
FDCVSQEYGI	NPERTVMVGD	RLDTDILLGA	TCGLKTILTL	TGVSTLGDVK	NNQESDCVSK	KKMVPDFYVD	SIADLLPALQ
330							
G							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
44	1	634.4553	188.58	2	29.2	13.2	0	42-54	R.GETAVPGAPEALR.A	
2202	1	1057.5324	-23.37	3	56.1	10.7	2	81-110	K.LRRLGFGGPAGPGASLEVFGTAYCTALYLR.Q	Carbamidomethyl: 24

Detailed Protein Report

Protein 436: **PREDICTED: probable phospholipid-transporting ATPase IG isoform X3 [Homo sapiens]**

Accession:	gi|578838665	**Score:**	23.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	126.6
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	2

Quantitation

QD:QU	**Median:**	0.67	**CV:**	88.43 %	**No. of Peptides:**	2

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.NAMDGYRTLCVAFKEIAPDDYER.I	Oxidation: 3	QD:QU 1.44
223	1	491.6240	-189.17	2	31.5	12.8	0	782-789	K.CTAVLCCR.M	Carbamidomethyl: 1, 6	QD:QU 0.32

Detailed Protein Report

Protein 437: tubulin-specific chaperone E isoform a [Homo sapiens]

Accession:	gi|4507375	**Score:**	23.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.3
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	4.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|118442828	refseq_human (refseq_human_20140103.fasta)	tubulin-specific chaperone E isoform a [Homo sapiens]

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	VLRCVAGCPG	LEELYLESNN
250	260	270	280	290	300	310	320
IFISERPTDV	LQTVKLLDLS	SNQLIDENQL	YLIAHLPRLE	QLILSDTGIS	SLHFPDAGIG	CKTSMFPSLK	YLVVNDNQIS
330	340	350	360	370	380	390	400
QWSFFNELEK	LPSLRALSCL	RNPLTKEDKE	AETARLLIIA	SIGQLKTLNK	CEILPEERRR	AELDYRKAFG	NEWKQAGGHK
410	420	430	440	450	460	470	480
DPEKNRLSEE	FLTAHPRYQF	LCLKYGAPED	WELKTQQPLM	LKNQLLTLKI	KYPHQLDQKV	LEKQLPGSMT	IQKVKGLLSR
490	500	510	520	530			
LLKVPVSDLL	LSYESPKKPG	REIELENDLK	SLQFYSVENG	DCLLVRW			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
486	1	535.7503	-186.51	2	34.7	13.3	1	443-451	K.NQLLTLKIK.Y	

Detailed Protein Report

Protein 438: **PREDICTED: ankyrin repeat domain-containing protein SOWAHC-like [Homo sapiens]**

Accession:	gi|341914886	**Score:**	23.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.7
Database Date:	2015-11-30	**pI:**	12.2
		Sequence Coverage [%]:	7.8
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.78 **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	
1819	1	719.7489	-178.16	2	51.3	10.6	0	106-120	R.NLCPGGSSLGAPPLR.T		QD:QU	0.78

Detailed Protein Report

Protein 439: reticulon-4 receptor-like 1 precursor [Homo sapiens]

Accession:	gi|30425553	**Score:**	23.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.0
Database Date:	2015-11-30	**pI:**	10.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLRKGCCVEL	LLLLVAAELP	LGGGCPRDCV	CYPAPMTVSC	QAHNFAAIPE	GIPVDSERVF	LQNNRIGLLQ	PGHFSPAMVT
90	100	110	120	130	140	150	160
LWIYSNNITY	IHPSTFEGFV	HLEELDLGDN	RQLRTLAPET	FQGLVKLHAL	YLYKCGLSAL	PAGVFGGLHS	LQYLYLQDNH
170	180	190	200	210	220	230	240
IEYLQDDIFV	DLVNLSHLFL	HGNKLWSLGP	GTFRGLVNLD	RLLLHENQLQ	WVHHKAFHDL	RRLTTLFLFN	NSLSELQGEC
250	260	270	280	290	300	310	320
LAPLGALEFL	RLNGNPWDCG	CRARSLWEWL	QRFRGSSSAV	PCVSPGLRHG	QDLKLLRAED	FRNCTGPASP	HQIKSHTLTT
330	340	350	360	370	380	390	400
TDRAARKEHH	SPHGPTRSKG	HPHGPRPGHR	KPGKNCTNPR	NRNQISKAGA	GKQAPELPDY	APDYQHKFSF	DIMPTARPKR
410	420	430	440	450			
KGKCARRTPI	RAPSGVQQAS	SASSLGASLL	AWTLGLAVTL	R			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2008	1	687.3490	4.76	2	55.5	10.2	0	275-288	R.GSSSAVPCVSPGLR.H	Carbamidomethyl: 8

Detailed Protein Report

Protein 440: 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 441: **PREDICTED: type I inositol 3,4-bisphosphate 4-phosphatase isoform X4 [Homo sapiens]**

Accession:	gi|578804269	**Score:**	23.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.5
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 0.50 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MTAREHSPRH GARARAMQRA STIDVAADML GLSLAGNIQD PDEPILEFSL ACSELHTPSL DRKPNSFVAV SVTTPPQAFW

        90        100        110        120        130        140        150        160
TKHAQTEIIE GTNNPIFLSS IAFFQDSLIN QMTQVKLSVY DVKDRSQGTM YLLGSGTFIV KDLLQDRHHR LHLTLRSAES

       170        180        190        200        210        220        230        240
DRVGNITVIG WQMEEKSDQR PPVTRSVDTV NGRMVLPVDE SLTEALGIRS KYASLRKDTL LKSVFGGAIC RMYRFPTTDG

       250        260        270        280        290        300        310        320
NHLRILEQMA ESVLSLHVPR QFVKLLLEED AARVCELEEL GELSPCWESL RRQIVTQYQT IILTYQENLT DLHQYRGPSF

       330        340        350        360        370        380        390        400
KASSLKADKK LEFVPTNLHI QRMRVQDDGG SDQNYDIVTI GAPAAHCQGF KSGGLRKKLH KFEETKKHSF EECCTSSGCQ

       410        420        430        440        450        460        470        480
SIIYIPQDVV RAKEIIAQIN TLKTQVSYYA ERLSRAAKDR SATGLERTLA ILADKTRQLV TVCDCKLLAN SIHGLNAARP

       490        500        510        520        530        540        550        560
DYIASKASPT STEEEQVMLR NDQDTLMARW TGRNSRSSLQ VDWHEEEWEK VWLNVDKSLE CIIQRVDKLL QKERLHGEGC

       570        580        590        600        610        620        630        640
EDVFPCAGSC TSKKGNPDSH AYWIRPEDPF CDVPSSPCPS TMPSTACHPH LTTREWSEAL YPLLTTLTDC VAMMSDKAKK

       650        660        670        680        690        700        710        720
AMVFLLMQDS APTIATYLSL QYRRDVVFCQ TLTALICGFI IKLRNCLHDD GFLRQLYTIG LLAQFESLLS TYGEELAMLE

       730        740        750        760        770        780        790        800
DMSLGIMDLR NVTFKVTQAT SSASADMLPV ITGNRDGFNV RVPLPGPLFD ALPREIQSGM LLRVQPVLFN VGINEQQTLA

       810        820        830        840        850        860        870        880
ERFGDTSLQE VINVESLVRL NSYFEQFKEV LPEDCLPRSR SQTCLPELLR FLGQNVHARK NKNVDILWQA AEICRRLNGV

       890        900        910        920        930        940        950        960
RFTSCKSAKD RTAMSVTLEQ CLILQHEHGM APQVFTQALE CMRSIGTREV VTQKNLSGLV PIRDLRLDPS LLCSIPLLAL

       970        980        990
SPNLLIVWLF LSIAYLVTKL RCK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2694	1	963.8006	5.32	3	64.8	12.9	1	615-639	R. EWSEALYPLLTTLTDCVAMMSDKA K	Carbamidomethyl: 16; Oxidation: 19	
675	1	562.6665	-233.07	2	37.0	10.7	1	877-886	R.LNGVRFTSCK.S		QD:QU 0.50

Detailed Protein Report

Protein 442: PREDICTED: allograft inflammatory factor 1 isoform X2 [Homo sapiens]

Accession:	gi|530381505	**Score:**	23.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.9
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	8.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530429518	refseq_human (refseq_human_20140103.fasta)	PREDICTED: allograft inflammatory factor 1 isoform X2 [Homo sapiens]
gi|530429177	refseq_human (refseq_human_20140103.fasta)	PREDICTED: allograft inflammatory factor 1 isoform X2 [Homo sapiens]
gi|530428888	refseq_human (refseq_human_20140103.fasta)	PREDICTED: allograft inflammatory factor 1 isoform X2 [Homo sapiens]
gi|530428260	refseq_human (refseq_human_20140103.fasta)	PREDICTED: allograft inflammatory factor 1 isoform X2 [Homo sapiens]
gi|530427928	refseq_human (refseq_human_20140103.fasta)	PREDICTED: allograft inflammatory factor 1 isoform X2 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MSQTRDLQGG KAFGLLKAQQ EERLDEINKQ FLDDPKYSSD EDLPSKLEGF KEKYMEFDLN GNGDIGEKRV ICGGRVVCRP
        90        100        110        120        130        140        150        160
KKTEVSPTCS IPHDLGGGPP TTVGGRRMGM RKWERRERVS PPSPHPHPLP PDIMSLKRML EKLGVPKTHL ELKKLIGEVS
       170        180        190
SGSGETFSYP DFLRMMLGKR SAILKM
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1677	1	619.9559	5.16	3	51.2	23.6	1	54-69	K.YMEFDLNGNGDIGEKR.V	

Detailed Protein Report

Protein 443: probable ubiquitin carboxyl-terminal hydrolase FAF-Y [Homo sapiens]

Accession:	gi|74319833	**Score:**	23.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	290.9
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTAITHGSPV	GGNDSQGQVL	DGQSQHLFQQ	NQTSSPDSSN	ENSVATPPPE	EQGQGDAPPQ	HEDEEPAFPH	TELANLDDMI
90	100	110	120	130	140	150	160
NRPRWVVPVL	PKGELEVLLE	AAIDLSVKGL	DVKSEACQRF	FRDGLTISFT	KILMDEAVSG	WKFEIHRCII	NNTHRLVELC
170	180	190	200	210	220	230	240
VAKLSQDWFP	LLELLAMALN	PHCKFHIYNG	TRPCELISSN	AQLPEDELFA	RSSDPRSPKG	WLVDLINKFG	TLNGFQILHD
250	260	270	280	290	300	310	320
RFFNGSALNI	QIIAALIKPF	GQCYEFLSQH	TLKKYFIPVI	EIVPHLLENL	TDEELKKEAK	NEAKNDALSM	IIKSLKNLAS
330	340	350	360	370	380	390	400
RISGQDETIK	NLEIFRLKMI	LRLLQISSFN	GKMNALNEIN	KVISSVSYYT	HRHSNPEEEE	WLTAERMAEW	IQQNNILSIV
410	420	430	440	450	460	470	480
LQDSLHQPQY	VEKLEKILRF	VIKEKALTLQ	DLDNIWAAQA	GKHEAIVKNV	HDLLAKLAWD	FSPGQLDHLF	DCFKASWTNA
490	500	510	520	530	540	550	560
SKKQREKLLE	LIRRLAEDDK	DGVMAHKVLN	LLWNLAQSDD	VPVDIMDLAL	SAHIKILDYS	CSQDRDAQKI	QWIDHFIEEL
570	580	590	600	610	620	630	640
RTNDKWVIPA	LKQIREICSL	FGEASQNLSQ	TQRSPHIFYR	HDLINQLQQN	HALVTLVAEN	LATYMNSIRL	YAGDHEDYDP
650	660	670	680	690	700	710	720
QTVRLGSRYS	HVQEVQERLN	FLRFLLKDGQ	LWLCAPQAKQ	IWKCLAENAV	YLCDREACFK	WYSKLMGDEP	DLDPDINKDF
730	740	750	760	770	780	790	800
FESNVLQLDP	SLLTENGMKC	FERFFKAVNC	RERKLIAKRR	SYMMDDLELI	GLDYLWRVVI	QSSDEIANRA	IDLLKEIYTN
810	820	830	840	850	860	870	880
LGPRLKANQV	VIHEDFIQSC	FDRLKASYDT	LCVFDGDKNS	INCARQEAIR	MVRVLTVIKE	YINECDSDYH	KERMILPMSR
890	900	910	920	930	940	950	960
AFRGKHLSLI	VRFPNQGRQV	DELDIWSHTN	DTIGSVRRCI	VNRIKANVAH	KKIELFVGGE	LIDSEDDRKL	IGQLNLKDKS
970	980	990	1000	1010	1020	1030	1040
LITAKLTQIN	FNMPSSPDSS	SDSSTASPGN	HRNHYNDGPN	LEVESCLPGV	IMSVHPRYIS	FLWQVADLGS	NLNMPPLRDG
1050	1060	1070	1080	1090	1100	1110	1120
ARVLMKLMPP	DRTAVEKLRA	VCLDHAKLGE	GKLSPPLDSL	FFGPSASQVL	YLTEVVYALL	MPAGVPLTDG	SSDFQVHFLK
1130	1140	1150	1160	1170	1180	1190	1200
SGGLPLVLSM	LIRNNFLPNT	DMETRRGAYL	NALKIAKLLL	TAIGYGHVRA	VAEACQPVVD	GTDPITQINQ	VTHDQAVVLQ
1210	1220	1230	1240	1250	1260	1270	1280
SALQSIPNPS	SECVLRNESI	LLAQEISNEA	SRYMPDICVI	RAIQKIIWAS	ACGALGLVFS	PNEEITKIYQ	MTTNGSNKLE
1290	1300	1310	1320	1330	1340	1350	1360
VEDEQVCCEA	LEVMTLCFAL	LPTALDALSK	EKAWQTFIID	LLLHCPSKTV	RQLAQEQFFL	MCTRCCMGHR	PLLFFITLLF
1370	1380	1390	1400	1410	1420	1430	1440
TILGSTAREK	GKYSGDYFTL	LRHLLNYAYN	GNINIPNAEV	LLVSEIDWLK	RIRDNVKNTG	ETGVEEPILE	GHLGVTKELL
1450	1460	1470	1480	1490	1500	1510	1520
AFQTSEKKYH	FGCEKGGANL	IKELIDDFIF	PASKVYLQYL	RSGELPAEQA	IPVCSSPVTI	NAGFELLVAL	AIGCVRNLKQ
1530	1540	1550	1560	1570	1580	1590	1600
IVDCLTEMYY	MGTAITTCEA	LTEWEYLPPV	GPRPPKGFVG	LKNAGATCYM	NSVIQQLYMI	PSIRNSILAI	EGTGSDLHDD
1610	1620	1630	1640	1650	1660	1670	1680
MFGDEKQDSE	SNVDPRDDVF	GYPHQFEDKP	ALSKTEDRKE	YNIGVLRHLQ	VIFGHLAASQ	LQYYVPRGFW	KQFRLWGEPV
1690	1700	1710	1720	1730	1740	1750	1760
NLREQHDALE	FFNSLVDSLD	EALKALGHPA	ILSKVLGGSF	ADQKICQGCP	HRYECEESFT	TLNVDIRNHQ	NLLDSLEQYI
1770	1780	1790	1800	1810	1820	1830	1840
KGDLLEGANA	YHCEKCDKKV	DTVKRLLIKK	LPRVLAIQLK	RFDYDWEREC	AIKFNDYFEF	PRELDMGPYT	VAGVANLERD
1850	1860	1870	1880	1890	1900	1910	1920
NVNSENELIE	QKEQSDNETA	GGTKYRLVGV	LVHSGQASGG	HYYSYIIQRN	GKDDQTDHWY	KFDDGDVTEC	KMDDDEEMKN
1930	1940	1950	1960	1970	1980	1990	2000
QCFGGEYMGE	VFDHMMKRMS	YRRQKRWWNA	YILFYEQMDM	IDEDDEMIRY	ISELTIARPH	QIIMSPAIER	SVRKQNVKFM
2010	2020	2030	2040	2050	2060	2070	2080
HNRLQYSLEY	FQFVKKLLTC	NGVYLNPAPG	QDYLLPEAEE	ITMISIQLAA	RFLFTTGFHT	KKIVRGPASD	WYDALCVLLR
2090	2100	2110	2120	2130	2140	2150	2160
HSKNVRFWFT	HNVLFNVSNR	FSEYLLECPS	AEVRGAFAKL	IVFIAHFSLQ	DGSCPSPFAS	PGPSSQACDN	LSLSDHLLRA
2170	2180	2190	2200	2210	2220	2230	2240
TLNLLRREVS	EHGHHLQQYF	NLFVMYANLG	VAEKTQLLKL	NVPATFMLVS	LDEGPGPPIK	YQYAELGKLY	SVVSQLIRCC
2250	2260	2270	2280	2290	2300	2310	2320
NVSSTMQSSI	NGNPPLPNPF	GDLNLSQPIM	PIQQNVLDIL	FVRTSYVKKI	IEDCSNSEDT	IKLLRFCSWE	NPQFSSTVLS
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	-51.53	2	34.8	12.0	0	2391-2413	K.CMVALFSSCPVAYQILQGNGDLK.R	Carbamidomethyl: 1, 9; Oxidation: 2

Detailed Protein Report

Protein 444: **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

Protein 445: 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 446: PREDICTED: metabotropic glutamate receptor 4 isoform X1 [Homo sapiens]

Accession:	gi|578811622	**Score:**	23.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.9
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	6.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTSDRERIGQ	DSAYEQEGKV	QFVIDAVYAM	GHALHAMHRD	LCPGRVGLCP	RMDPVDGTQL	LKYIRNVNFS	GIAGNPVTFN
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
ENGDAPGRYD	IYQYQLRNDS	AEYKVIGSWT	DHLHLRIERM	HWPGSGQQLP	RSICSLPCQP	GERKKTVKGM	PCCWHCEPCT
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
GYQYQVDRYT	CKTCPYDMRP	TENRTGCRPI	PIIKLEWGSP	WAVLPLFLAV	VGIAATLFVV	ITFVRYNDTP	IVKASGRELS
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
YVLLAGIFLC	YATTFLMIAE	PDLGTCSLRR	IFLGLGMSIS	YAALLTKTNR	IYRIFEQGKR	SVSAPRFISP	ASQLAITFSL
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
ISLQLLGICV	WFVVDPSHSV	VDFQDQRTLD	PRFARGVLKC	DISDLSLICL	LGYSMLLMVT	CTVYAIKTRG	VPETFNEAKP
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
IGFTMYTTCI	VWLAFIPIFF	GTSQSADKLY	IQTTTLTVSV	SLSASVSLGM	LYMPKVYIIL	FHPEQNVPKR	KRSLKAVVTA
490	**500**	**510**	**520**	**530**			
ATMSNKFTQK	GNFRPNGEAK	SELCENLEAP	ALATKQTYVT	YTNHAI			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1390	1	977.5200	-44.32	2	47.5	12.4	1	270-287	R.RIFLGLGMSISYAALLTK.T	

Detailed Protein Report

Protein 447: deoxyribonuclease-2-beta isoform 1 precursor [Homo sapiens]

Accession:	gi|194473657	**Score:**	23.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.7
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	9.1
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MKQKMMARLL	RTSFALLFLG	LFGVLGAATI	SCRNEEGKAV	DWFTFYKLPK	RQNKESGETG	LEYLYLDSTT	RSWRKSEQLM
90	100	110	120	130	140	150	160
NDTKSVLGRT	LQQLYEAYAS	KSNNTAYLIY	NDGVPKPVNY	SRKYGHTKGL	LLWNRVQGFW	LIHSIPQFPP	IPEEGYDYPP
170	180	190	200	210	220	230	240
TGRRNGQSGI	CITFKYNQYE	AIDSQLLVCN	PNVYSCSIPA	TFHQELIHMP	QLCTRASSSE	IPGRLLTTLQ	SAQGQKFLHF
250	260	270	280	290	300	310	320
AKSDSFLDDI	FAAWMAQRLK	THLLTETWQR	KRQELPSNCS	LPYHVYNIKA	IKLSRHSYFS	SYQDHAKWCI	SQKGTKNRWT
330	340	350	360	370			
CIGDLNRSPH	QAFRSGGFIC	TQNWQIYQAF	QGLVLYYESC	K			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2252	1	569.2585	-75.58	3	56.8	10.9	2	75-89	R.KSEQLMNDTKSVLGR.T	
2758	1	1086.0280	-8.69	2	65.6	12.6	2	317-334	K.NRWTCIGDLNRSPHQAFR.S	

Detailed Protein Report

Protein 448: dual specificity protein kinase TTK isoform 2 [Homo sapiens]

Accession:	gi|262399361	**Score:**	23.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.9
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MESEDLSGRE	LTIDSIMNKV	RDIKNKFKNE	DLTDELSLNK	ISADTTDNSG	TVNQIMMMAN	NPEDWLSLLL	KLEKNSVPLS
90	100	110	120	130	140	150	160
DALLNKLIGR	YSQAIEALPP	DKYGQNESFA	RIQVRFAELK	AIQEPDDARD	YFQMARANCK	KFAFVHISFA	QFELSQGNVK
170	180	190	200	210	220	230	240
KSKQLLQKAV	ERGAVPLEML	EIALRNLNLQ	KKQLLSEEEK	KNLSASTVLT	AQESFSGSLG	HLQNRNNSCD	SRGQTTKARF
250	260	270	280	290	300	310	320
LYGENMPPQD	AEIGYRNSLR	QTNKTKQSCP	FGRVPVNLLN	SPDCDVKTDD	SVVPCFMKRQ	TSRSECRDLV	VPGSKPSGND
330	340	350	360	370	380	390	400
SCELRNLKSV	QNSHFKEPLV	SDEKSSELII	TDSITLKNKT	ESSLLAKLEE	TKEYQEPEVP	ESNQKQWQSK	RKSECINQNP
410	420	430	440	450	460	470	480
AASSNHWQIP	ELARKVNTEK	HTTFEQPVFS	VSKQSPPIST	SKWFDPKSIC	KTPSSNTLDD	YMSCFRTPVV	KNDFPPACQL
490	500	510	520	530	540	550	560
STPYGQPACF	QQQQHQILAT	PLQNLQVLAS	SSANECISVK	GRIYSILKQI	GSGGSSKVFQ	VLNEKKQIYA	IKYVNLEEAD
570	580	590	600	610	620	630	640
NQTLDSYRNE	IAYLNKLQQH	SDKIIRLYDY	EITDQYIYMV	MECGNIDLNS	WLKKKKSIDP	WERKSYWKNM	LEAVHTIHQH
650	660	670	680	690	700	710	720
GIVHSDLKPA	NFLIVDGMLK	LIDFGIANQM	QPDTTSVVKD	SQVGTVNYMP	PEAIKDMSSS	RENGKSKSKI	SPKSDVWSLG
730	740	750	760	770	780	790	800
CILYYMTYGK	TPFQQIINQI	SKLHAIIDPN	HEIEFPDIPE	KDLQDVLKCC	LKRDPKQRIS	IPELLAHPYV	QIQTHPVNQM
810	820	830	840	850	860		
AKGTTEEMKY	VLGQLVGLNS	PNSILKAAKT	LYEHYSGGES	HNSSSSKTFE	KKRGKK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
309	1	936.1804	52.20	3	32.6	11.1	2	391-414	K.RKSECINQNPAASSNHWQIPELAR.K	Carbamidomethyl: 5

Detailed Protein Report

Protein 449: 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

Quantitation

QD:QU **Median:** 0.78 **CV:** 0.00 % **No. of Peptides:** 1

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	Ratios
333	1	734.3935	-67.03	2	34.1	13.3	0	1033-1045	R.VPVLDTLIELVTR.G		QD:QU 0.78
1877	1	1059.3256	-215.69	1	53.8	10.2	1	1400-1408	K.RDGINSLER.K		

Detailed Protein Report

Protein 450: protein phosphatase 1 regulatory subunit 29 precursor [Homo sapiens]

Accession:	gi|116268101	**Score:**	23.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.6
Database Date:	2015-11-30	**pI:**	8.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578836905	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein phosphatase 1 regulatory subunit 29 isoform X3 [Homo sapiens]
gi|578836903	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein phosphatase 1 regulatory subunit 29 isoform X2 [Homo sapiens]
gi|530419503	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein phosphatase 1 regulatory subunit 29 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MLRLGLCAAA	LLCVCRPGAV	RADCWLIEGD	KGYVWLAICS	QNQPPYETIP	QHINSTVHDL	RLNENKLKAV	LYSSLNRFGN
90	100	110	120	130	140	150	160
LTDLNLTKNE	ISYIEDGAFL	GQSSLQVLQL	GYNKLSNLTE	GMLRGMSRLQ	FLFVQHNLIE	VVTPTAFSEC	PSLISIDLSS
170	180	190	200	210	220	230	240
NRLSRLDGAT	FASLASLMVC	ELAGNPFNCE	CDLFGFLAWL	VVFNNVTKNY	DRLQCESPRE	FAGYPLLVPR	PYHSLNAITV
250	260	270	280	290	300	310	320
LQAKCRNGSL	PARPVSHPTP	YSTDAQREPD	ENSGFNPDEI	LSVEPPASST	TDASAGPAIK	LHHVTFTSAT	LVVIIPHPYS
330	340	350	360	370	380	390	400
KMYILVQYNN	SYFSDVMTLK	NKKEIVTLDK	LRAHTEYTFC	VTSLRNSRRF	NHTCLTFTTR	DPVPGDLAPS	TSTTTHYIMT
410	420	430	440	450	460	470	480
ILGCLFGMVI	VLGAVYYCLR	KRRMQEEKQK	SVNVKKTILE	MRYGADVDAG	SIVHAAQKLG	EPPVLPVSRM	ASIPSMIGEK
490	500	510	520	530	540	550	560
LPTAKGLEAG	LDTPKVATKG	NYIEVRTGAG	GDGLARPEDD	LPDLENGQGS	AAEISTIAKE	VDKVNQIINN	CIDALKLDSA
570	580	590	600	610	620	630	640
SFLGGGSSSG	DPELAFECQS	LPAAAAASSA	TGPGALERPS	FLSPPYKESS	HHPLQRQLSA	DAAVTRKTCS	VSSSGSIKSA
650	660	670	680	690	700	710	720
KVFSLDVPDH	PAATGLAKGD	SKYIEKGSPL	NSPLDRLPLV	PAGSGGGSGG	GGGIHHLEVK	PAYHCSEHRH	SFPALYYEEG
730	740	750	760	770	780	790	800
ADSLSQRVSF	LKPLTRSKRD	STYSQLSPRH	YYSGYSSSPE	YSSESTHKIW	ERFRPYKKHH	REEVYMAAGH	ALRKKVQFAK
810	820	830					
DEDLHDILDY	WKGVSAQQKL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1279	1	955.9599	-14.52	2	46.1	12.2	2	366-380	R.NSRRFNHTCLTFTTR.D	Carbamidomethyl: 9

Detailed Protein Report

Protein 451: 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

Protein 452: **PREDICTED: zinc finger and BTB domain-containing protein 38 isoform X2 [Homo sapiens]**

Accession:	gi|530374206	**Score:**	23.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	134.3
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMTVMSLSRD	LKDDFHSDTV	LSILNEQRIR	GILCDVTIIV	EDTKFKAHSN	VLAASSLYFK	NIFWSHTICI	SSHVLELDDL
90	100	110	120	130	140	150	160
KAEVFTEILN	YIYSSTVVVK	RQETVTDLAA	AGKKLGISFL	EDLTDRNFSN	SPGPYVFCIT	EKGVVKEEKN	EKRHEEPAIT
170	180	190	200	210	220	230	240
NGPRITNAFS	IIETENSNNM	FSPLDLRASF	KKVSDSMRTA	SLCLERTDVC	HEAEPVRTLA	EHSYAVSSVA	EAYRSQPVRE
250	260	270	280	290	300	310	320
HDGSSPGNTG	KENCEALAAK	PKTCRKPKTF	SIPQDSDSAT	ENIPPPPVSN	LEVNQERSPQ	PAAVLTRSKS	PNNEGDVHFS
330	340	350	360	370	380	390	400
REDENQSSDV	PGPPAAEVPP	LVYNCSCCSK	AFDSSTLLSA	HMQLHKPTQE	PLVCKYCNKQ	FTTLNRLDRH	EQICMRSSHM
410	420	430	440	450	460	470	480
PIPGGNQRFL	ENYPTIGQNG	GSFTGPEPLL	SENRIGEFSS	TGSTLPDTDH	MVKFVNGQML	YSCVVCKRSY	VTLSSLRRHA
490	500	510	520	530	540	550	560
NVHSWRRTYP	CHYCNKVFAL	AEYRTRHEIW	HTGERRYQCI	FCLETFMTYY	ILKNHQKSFH	AIDHRLSISK	KTANGGLKPS
570	580	590	600	610	620	630	640
VYPYKLYRLL	PMKCKRAPYK	SYRNSSYENA	RENSQMNESA	PGTYVVQNPH	SSELPTLNFQ	DTVNTLTNSP	AIPLETSACQ
650	660	670	680	690	700	710	720
DIPTSANVQN	AEGTKWGEEA	LKMDLDNNFY	STEVSVSSTE	NAVSSDLRAG	DVPVLSLSNS	SENAASVISY	SGSAPSVIVH
730	740	750	760	770	780	790	800
SSQFSSVIMH	SNAIAAMTSS	NHRAFSDPAV	SQSLKDDSKP	EPDKVGRFAS	RPKSIKEKKK	TTSHTRGEIP	EESNYVADPG
810	820	830	840	850	860	870	880
GSLSKTTNIA	EETSKIETYI	AKPALPGTST	NSNVAPLCQI	TVKIGNEAIV	KRHILGSKLF	YKRGRRPKYQ	MQEEPLPQGN
890	900	910	920	930	940	950	960
DPEPSGDSPL	GLCQSECMEM	SEVFDDASDQ	DSTDKPWRPY	YNYKPKKKSR	QLKKMRKVNW	RKEHGNRSPS	HKCKYPAELD
970	980	990	1000	1010	1020	1030	1040
CAVGKAPQDK	PFEEEETKEM	PKLQCELCDG	DKAVGAGNQG	RPHRHLTSRP	YACELCAKQF	QSPSTLKMHM	RCHTGEKPYQ
1050	1060	1070	1080	1090	1100	1110	1120
CKTCGRCFSV	QGNLQKHERI	HLGLKEFVCQ	YCNKAFTLNE	TLKIHERIHT	GEKRYHCQFC	FQRFLYLSTK	RNHEQRHIRE
1130	1140	1150	1160	1170	1180	1190	1200
HNGKGYACFQ	CPKICKTAAA	LGMHQKKHLF	KSPSQQEKIG	DVCHENSNPL	ENQHFIGSED	NDQKDNIQTG	VENVVL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2863	1	922.9727	-41.66	2	65.0	11.0	1	29-44	R.IRGILCDVTIIVEDTK.F	Carbamidomethyl: 6

Detailed Protein Report

Protein 453: PREDICTED: interferon regulatory factor 2 isoform X2 [Homo sapiens]

Accession:	gi|530377663	**Score:**	23.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.1
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPVERMRMRP	WLEEQINSNT	IPGLKWLNKE	KKIFQIPWMH	AARHGWDVEK	DAPLFRNWAI	HTGKHQPGVD	KPDPKTWKAN
90	100	110	120	130	140	150	160
FRCAMNSLPD	IEEVKDKSIK	KGNNAFRVYR	MLPLSERPSK	KGKKPKTEKE	DKVKHIKQEP	VESSLGLSNG	VSDLSPEYAV
170	180	190	200	210	220	230	240
LTSTIKNEVD	STVNIIGQSH	LDSNIENQEI	VTNPPDICQV	VEVTTESDEQ	PVSMSELYPL	QISPVSSYAE	SETTDSVPSD
250	260	270	280	290	300	310	320
EESAEGRPHW	RKRNIEGKQY	LSNMGTRGSY	LLPGMASFVT	SNKPDLQVTI	KEESNPVPYN	SSWPPFQDLP	LSSSMTPASS
330	340	350					
SSRPDRETRA	SVIKKTSDIT	QARVKSC					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
513	1	587.1711	-250.83	2	35.0	11.4	0	111-120	R.MLPLSERPSK.K	Oxidation: 1

Detailed Protein Report

Protein 454: protocadherin Fat 1 precursor [Homo sapiens]

Accession:	gi|66346693	**Score:**	23.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	506.0
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578808907	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protocadherin Fat 1 isoform X3 [Homo sapiens]

Detailed Protein Report

10	20	30	40	50	60	70	80
MGRHLALLLL	LLLLFQHFGD	SDGSQRLEQT	PLQFTHLEYN	VTVQENSAAK	TYVGHPVKMG	VYITHPAWEV	RYKIVSGDSE
90	100	110	120	130	140	150	160
NLFKAEEYIL	GDFCFLRIRT	KGGNTAILNR	EVKDHYTLIV	KALEKNTNVE	ARTKVRVQVL	DTNDLRPLFS	PTSYSVSLPE
170	180	190	200	210	220	230	240
NTAIRTSIAR	VSATDADIGT	NGEFYYSFKD	RTDMFAIHPT	SGVIVLTGRL	DYLETKLYEM	EILAADRGMK	LYGSSGISSM
250	260	270	280	290	300	310	320
AKLTVHIEQA	NECAPVITAV	TLSPSELDRD	PAYAIVTVDD	CDQGANGDIA	SLSIVAGDLL	QQFRTVRSFP	GSKEYKVKAI
330	340	350	360	370	380	390	400
GGIDWDSHPF	GYNLTLQAKD	KGTPPQFSSV	KVIHVTSPQF	KAGPVKFEKD	VYRAEISEFA	PPNTPVVMVK	AIPAYSHLRY
410	420	430	440	450	460	470	480
VFKSTPGKAK	FSLNYNTGLI	SILEPVKRQQ	AAHFELEVTT	SDRKASTKVL	VKVLGANSNP	PEFTQTAYKA	AFDENVPIGT
490	500	510	520	530	540	550	560
TVMSLSAVDP	DEGENGYVTY	SIANLNHVPF	AIDHFTGAVS	TSENLDYELM	PRVYTLRIRA	SDWGLPYRRE	VEVLATITLN
570	580	590	600	610	620	630	640
NLNDNTPLFE	KINCEGTIPR	DLGVGEQITT	VSAIDADELQ	LVQYQIEAGN	ELDFFSLNPN	SGVLSLKRSL	MDGLGAKVSF
650	660	670	680	690	700	710	720
HSLRITATDG	ENFATPLYIN	ITVAASHKLV	NLQCEETGVA	KMLAEKLLQA	NKLHNQGEVE	DIFFDSHSVN	AHIPQFRSTL
730	740	750	760	770	780	790	800
PTGIQVKENQ	PVGSSVIFMN	STDLDTGFNG	KLVYAVSGGN	EDSCFMIDME	TGMLKILSPL	DRETTDKYTL	NITVYDLGIP
810	820	830	840	850	860	870	880
QKAAWRLLHV	VVVDANDNPP	EFLQESYFVE	VSEDKEVHSE	IIQVEATDKD	LGPNGHVTYS	IVTDTDTFSI	DSVTGVVNIA
890	900	910	920	930	940	950	960
RPLDRELQHE	HSLKIEARDQ	AREEPQLFST	VVVKVSLEDV	NDNPPTFIPP	NYRVKVREDL	PEGTVIMWLE	AHDPDLGQSG
970	980	990	1000	1010	1020	1030	1040
QVRYSLLDHG	EGNFDVDKLS	GAVRIVQQLD	FEKKQVYNLT	VRAKDKGKPV	SLSSTCYVEV	EVVDVNENLH	PPVFSSFVEK
1050	1060	1070	1080	1090	1100	1110	1120
GTVKEDAPVG	SLVMTVSAHD	EDARRDGEIR	YSIRDGSGVG	VFKIGEETGV	IETSDRLDRE	STSHYWLTVF	ATDQGVVPLS
1130	1140	1150	1160	1170	1180	1190	1200
SFIEIYIEVE	DVNDNAPQTS	EPVYYPEIME	NSPKDVSVVQ	IEAFDPDSSS	NDKLMYKITS	GNPQGFFSIH	PKTGLITTTS
1210	1220	1230	1240	1250	1260	1270	1280
RKLDREQQDE	HILEVTVTDN	GSPPKSTIAR	VIVKILDEND	NKPQFLQKFY	KIRLPEREKP	DRERNARREP	LYHVIATDKD
1290	1300	1310	1320	1330	1340	1350	1360
EGPNAEISYS	IEDGNEHGKF	FIEPKTGVVS	SKRFSAAGEY	DILSIKAVDN	GRPQKSSTTR	LHIEWISKPK	PSLEPISFEE
1370	1380	1390	1400	1410	1420	1430	1440
SFFTFTVMES	DPVAHMIGVI	SVEPPGIPLW	FDITGGNYDS	HFDVDKGTGT	IIVAKPLDAE	QKSNYNLTVE	ATDGTTTILT
1450	1460	1470	1480	1490	1500	1510	1520
QVFIKVIDTN	DHRPQFSTSK	YEVVIPEDTA	PETEILQISA	VDQDEKNKLI	YTLQSSRDPL	SLKKFRLDPA	TGSLYTSEKL
1530	1540	1550	1560	1570	1580	1590	1600
DHEAVHQHTL	TVMVRDQDVP	VKRNFARIVV	NVSDTNDHAP	WFTASSYKGR	VYESAAVGSV	VLQVTALDKD	KGKNAEVLYS
1610	1620	1630	1640	1650	1660	1670	1680
IESGNIGNSF	MIDPVLGSIK	TAKELDRSNQ	AEYDLMVKAT	DKGSPPMSEI	TSVRIFVTIA	DNASPKFTSK	EYSVELSETV
1690	1700	1710	1720	1730	1740	1750	1760
SIGSFVGMVT	AHSQSSVVYE	IKDGNTGDAF	DINPHSGTII	TQKALDFETL	PIYTLIIQGT	NMAGLSTNTT	VLVHLQDEND
1770	1780	1790	1800	1810	1820	1830	1840
NAPVFMQAEY	TGLISESASI	NSVVLTDRNV	PLVIRAADAD	KDSNALLVYH	IVEPSVHTYF	AIDSSTGAIH	TVLSLDYEET
1850	1860	1870	1880	1890	1900	1910	1920
SIFHFTVQVH	DMGTPRLFAE	YAANVTVHVI	DINDCPPVFA	KPLYEASLLL	PTYKGVKVIT	VNATDADSSA	FSQLIYSITE
1930	1940	1950	1960	1970	1980	1990	2000
GNIGEKFSMD	YKTGALTVQN	TTQLRSRYEL	TVRASDGRFA	GLTSVKINVK	ESKESHLKFT	QDVYSAVVKE	NSTEAETLAV
2010	2020	2030	2040	2050	2060	2070	2080
ITAIGNPINE	PLFYHILNPD	RRFKISRTSG	VLSTTGTPFD	REQQEAFDVV	VEVTEEHKPS	AVAHVVVKVI	VEDQNDNAPV
2090	2100	2110	2120	2130	2140	2150	2160
FVNLPYYAVV	KVDTEVGHVI	RYVTAVDRDS	GRNGEVHYYL	KEHHEHFQIG	PLGEISLKKQ	FELDTLNKEY	LVTVVAKDGG
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
2147	1	719.8600	-56.51	2	55.4	10.9	1	1300-1312	K.FFIEPKTGVVSSK.R	

Detailed Protein Report

Protein 455: PREDICTED: autophagy-related protein 2 homolog B isoform X1 [Homo sapiens]

Accession:	gi|578825925	**Score:**	23.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	232.5
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

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	NYRSRKKKKL
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
1611	1	621.3254	12.46	2	50.4	11.2	2	1590-1601	R.HGRNTVCGGKGR.N	

Detailed Protein Report

Protein 456: low-density lipoprotein receptor-related protein 1B precursor [Homo sapiens]

Accession:	gi|93102379	**Score:**	23.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	515.2
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSEFLLALLT	LSGLLPIARV	LTVGADRDQQ	LCDPGEFLCH	DHVTCVSQSW	LCDGDPDCPD	DSDESLDTCP	EEVEIKCPLN
90	100	110	120	130	140	150	160
HIACLGTNKC	VHLSQLCNGV	LDCPDGYDEG	VHCQELLSNC	QQLNCQYKCT	MVRNSTRCYC	EDGFEITEDG	RSCKDQDECA
170	180	190	200	210	220	230	240
VYGTCSQTCR	NTHGSYTCSC	VEGYLMQPDN	RSCKAKIEPT	DRPPILLIAN	FETIEVFYLN	GSKMATLSSV	NGNEIHTLDF
250	260	270	280	290	300	310	320
IYNEDMICWI	ESRESSNQLK	CIQITKAGGL	TDEWTINILQ	SFHNVQQMAI	DWLTRNLYFV	DHVGDRIFVC	NSNGSVCVTL
330	340	350	360	370	380	390	400
IDLELHNPKA	IAVDPIAGKL	FFTDYGNVAK	VERCDMDGMN	RTRIIDSKTE	QPAALALDLV	NKLVYWVDLY	LDYVGVVDYQ
410	420	430	440	450	460	470	480
GKNRHTVIQG	RQVRHLYGIT	VFEDYLYATN	SDNYNIVRIN	RFNGTDIHSL	IKIENAWGIR	IYQKRTQPTV	RSHACEVDPY
490	500	510	520	530	540	550	560
GMPGGCSHIC	LLSSSYKTRT	CRCRTGFNLG	SDGRSCKRPK	NELFLFYGKG	RPGIVRGMDL	NTKIADEYMI	PIENLVNPRA
570	580	590	600	610	620	630	640
LDFHAETNYI	YFADTTSFLI	GRQKIDGTER	ETILKDDLDN	VEGIAVDWIG	NNLYWTNDGH	RKTINVARLE	KASQSRKTLL
650	660	670	680	690	700	710	720
EGEMSHPRGI	VVDPVNGWMY	WTDWEEDEID	DSVGRIEKAW	MDGFNRQIFV	TSKMLWPNGL	TLDFHTNTLY	WCDAYYDHIE
730	740	750	760	770	780	790	800
KVFLNGTHRK	IVYSGRELNH	PFGLSHHGNY	VFWTDYMNGS	IFQLDLITSE	VTLLRHERPP	LFGLQIYDPR	KQQGDNMCRV
810	820	830	840	850	860	870	880
NNGGCSTLCL	AIPGGRVCAC	ADNQLLDENG	TTCTFNPGEA	LPHICKAGEF	RCKNRHCIQA	RWKCDGDDDC	LDGSDEDSVN
890	900	910	920	930	940	950	960
CFNHSCPDDQ	FKCQNNRCIP	KRWLCDGAND	CGSNEDESNQ	TCTARTCQVD	QFSCGNGRCI	PRAWLCDRED	DCGDQTDEMA
970	980	990	1000	1010	1020	1030	1040
SCEFPTCEPL	TQFVCKSGRC	ISSKWHCDSD	DDCGDGSDEV	GCVHSCFDNQ	FRCSSGRCIP	GHWACDGDND	CGDFSDEAQI
1050	1060	1070	1080	1090	1100	1110	1120
NCTKEEIHSP	AGCNGNEFQC	HPDGNCVPDL	WRCDGEKDCE	DGSDEKGCNG	TIRLCDHKTK	FSCWSTGRCI	NKAWVCDGDI
1130	1140	1150	1160	1170	1180	1190	1200
DCEDQSDEDD	CDSFLCGPPK	HPCANDTSVC	LQPEKLCNGK	KDCPDGSDEG	YLCDECSLNN	GGCSNHCSVV	PGRGIVCSCP
1210	1220	1230	1240	1250	1260	1270	1280
EGLQLNKDNK	TCEIVDYCSN	HLKCSQVCEQ	HKHTVKCSCY	EGWKLDVDGE	SCTSVDPFEA	FIIFSIRHEI	RRIDLHKRDY
1290	1300	1310	1320	1330	1340	1350	1360
SLLVPGLRNT	IALDFHFNQS	LLYWTDVVED	RIYRGKLSES	GGVSAIEVVV	EHGLATPEGL	TVDWIAGNIY	WIDSNLDQIE
1370	1380	1390	1400	1410	1420	1430	1440
VAKLDGSLRT	TLIAGAMEHP	RAIALDPRYG	ILFWTDWDAN	FPRIESASMS	GAGRKTIYKD	MKTGAWPNGL	TVDHFEKRIV
1450	1460	1470	1480	1490	1500	1510	1520
WTDARSDAIY	SALYDGTNMI	EIIRGHEYLS	HPFAVSLYGS	EVYWTDWRTN	TLSKANKWTG	QNVSVIQKTS	AQPFDLQIYH
1530	1540	1550	1560	1570	1580	1590	1600
PSRQPQAPNP	CAANDGKGPC	SHMCLINHNR	SAACACPHLM	KLSSDKKTCY	EMKKFLLYAR	RSEIRGVDID	NPYFNFITAF
1610	1620	1630	1640	1650	1660	1670	1680
TVPDIDDVTV	IDFDASEERL	YWTDIKTQTI	KRAFINGTGL	ETVISRDIQS	IRGLAVDWVS	RNLYWISSEF	DETQINVARL
1690	1700	1710	1720	1730	1740	1750	1760
DGSLKTSIIH	GIDKPQCLAA	HPVRGKLYWT	DGNTINMANM	DGSNSKILFQ	NQKEPVGLSI	DYVENKLYWI	SSGNGTINRC
1770	1780	1790	1800	1810	1820	1830	1840
NLDGGNLEVI	ESMKEELTKA	TALTIMDKKL	WWADQNLAQL	GTCSKRDGRN	PTILRNKTSG	VVHMKVYDKE	AQQGSNSCQL
1850	1860	1870	1880	1890	1900	1910	1920
NNGGCSQLCL	PTSETTRTCM	CTVGYYLQKN	RMSCQGIESF	LMYSVHEGIR	GIPLEPSDKM	DALMPISGTS	FAVGIDFHAE
1930	1940	1950	1960	1970	1980	1990	2000
NDTIYWTDMG	FNKISRAKRD	QTWKEDIITN	GLGRVEGIAV	DWIAGNIYWT	DHGFNLIEVA	RLNGSFRYVI	ISQGLDQPRS
2010	2020	2030	2040	2050	2060	2070	2080
IAVHPEKGLL	FWTEWGQMPC	IGKARLDGSE	KVVLVSMGIA	WPNGISIDYE	ENKLYWCDAR	TDKIERIDLE	TGGNREMVLS
2090	2100	2110	2120	2130	2140	2150	2160
GSNVDMFSVA	VFGAYIYWSD	RAHANGSVRR	GHKNDATETI	TMRTGLGVNL	KEVKIFNRVR	EKGTNVCARD	NGGCKQLCLY
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
2037	2	977.3860	-129.29	2	54.0	11.5	1	1364-1381	K.LDGSLRTTLIAGAMEHPR.A	Oxidation: 14

Detailed Protein Report

Protein 457: ectoderm-neural cortex protein 1 isoform 2 [Homo sapiens]

Accession:	gi|375268727	**Score:**	23.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.8
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.6
		No. of unique 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
1958	2	948.3829	-82.11	2	53.0	13.0	0	220-236	K.TGHALFLLGGQTFMCDK.L	Carbamidomethyl: 15

Detailed Protein Report

Protein 458: tripartite motif-containing protein 5 isoform alpha [Homo sapiens]

Accession:	gi|283046694	**Score:**	23.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.3
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.9
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|530395903	refseq_human (refseq_human_20140103.fasta)	PREDICTED: tripartite motif-containing protein 5 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MASGILVNVK	EEVTCPICLE	LLTQPLSLDC	GHSFCQACLT	ANHKKSMLDK	GESSCPVCRI	SYQPENIRPN	RHVANIVEKL
90	100	110	120	130	140	150	160
REVKLSPEGQ	KVDHCARHGE	KLLLFCQEDG	KVICWLCERS	QEHRGHHTFL	TEEVAREYQV	KLQAALEMLR	QKQQEAEELE
170	180	190	200	210	220	230	240
ADIREEKASW	KTQIQYDKTN	VLADFEQLRD	ILDWEESNEL	QNLEKEEEDI	LKSLTNSETE	MVQQTQSLRE	LISDLEHRLQ
250	260	270	280	290	300	310	320
GSVMELLQGV	DGVIKRTENV	TLKKPETFPK	NQRRVFRAPD	LKGMLEVFRE	LTDVRRYWVD	VTVAPNNISC	AVISEDKRQV
330	340	350	360	370	380	390	400
SSPKPQIIYG	ARGTRYQTFV	NFNYCTGILG	SQSITSGKHY	WEVDVSKKTA	WILGVCAGFQ	PDAMCNIEKN	ENYQPKYGYW
410	420	430	440	450	460	470	480
VIGLEEGVKC	SAFQDSSFHT	PSVPFIVPLS	VIICPDRVGV	FLDYEACTVS	FFNITNHGFL	IYKFSHCSFS	QPVFPYLNPR
490	500						
KCGVPMTLCS	PSS						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1780	1	945.9067	-62.20	2	50.8	10.3	2	85-101	K.LSPEGQKVDHCARHGEK.L	
1800	1	599.2749	39.82	2	52.8	12.9	0	482-493	K.CGVPMTLCSPSS.-	Oxidation: 5

Detailed Protein Report

Protein 459: 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

QD:QU **Median:** 0.67 **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		QD:QU	0.67

Detailed Protein Report

Protein 460: **PREDICTED: arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3 isoform X2 [Homo sapiens]**

Accession:	gi|530386889	**Score:**	23.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.7
Database Date:	2015-11-30	**pI:**	11.8
		Sequence Coverage [%]:	5.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MERGWPQGDS CPGERPAACR RAHSVCDSLD LHGASAGRAA AALQAALCAA SEQPARPRSV CSGGPEPPPT GARGLLLGLL

        90        100        110        120        130        140        150        160
RPRLGRRGLA PSGPPVSPAP SPASSPAPTR RSRTRGEPTP RPRPASMTFL EVNRLELAAA EAPGAGLGRA GSAGFLRGAA

       170        180        190        200        210        220        230        240
LWSSQRWPVL RGGRGPEGPR RGLAALRKSF SFRLRRGQEV RRSESGLLAR PPRARTRSDG DAGSLGAFPS RRDLLGSDAP

       250        260        270        280        290        300        310        320
RAAPEPGRPR TAAGLWRLLT SRFRRREPAP AAPLWGRRAA AAPELLRAPS DSFVNSQEWT LSRSVPELKV GIVGNLSSGK

       330        340        350        360        370        380        390        400
SALVHRYLTG TYVQEESPEG GRFKKEIVVD GQSYLLLIRD EGGPPELQFA AWVDAVVFVF SLEDEISFQT VYNYFLRLCS

       410        420        430        440        450        460        470        480
FRNASEVPMV LVGTQDAISA ANPRVIDDSR ARKLSTDLKR CTYYETCATY GLNVERVFQD VAQKVVALRK KQQLAIGPCK

       490        500        510        520        530        540        550        560
SLPNSPSHSA VSAASIPAVH INQATNGGGS AFSDYSSSVP STPSISQREL RIETIAASST PTPIRKQSKR RSNIFTICAT

       570        580
VSNFSSTKRP FQLLPN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1530	1	873.6409	147.98	2	47.7	10.1	1	345-359	K.KEIVVDGQSYLLLIR.D	

Detailed Protein Report

Protein 461: PREDICTED: serine/arginine-rich splicing factor 4 isoform X1 [Homo sapiens]

Accession:	gi|578799577	**Score:**	23.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.4
Database Date:	2015-11-30	**pI:**	12.5
		Sequence Coverage [%]:	6.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578799579	refseq_human (refseq_human_20140103.fasta)	PREDICTED: serine/arginine-rich splicing factor 4 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MRQAGEVTYA	DAHKGRKNEG	VIEFVSYSDM	KRALEKLDGT	EVNGRKIRLV	EDKPGSRRRR	SYSRSRSHSR	SRSRSRHSRK
90	100	110	120	130	140	150	160
SRSRSGSSKS	SHSKSRSRSR	SGSRSRSKSR	SRSQSRSRSK	KEKSRSPSKE	KSRSRSHSAG	KSRSKSKDQA	EEKIQNNDNV
170	180	190	200	210	220	230	240
GKPKSRSPSR	HKSKSKSRSR	SQERRVEEEK	RGSVSRGRSQ	EKSLRQSRSR	SRSKGGSRSR	SRSRSKSKDK	RKGRKRSREE
250	260	270	280	290	300	310	320
SRSRSRSRSK	SERSRKRGSK	RDSKAGSSKK	KKKEDTDRSQ	SRSPSRSVSK	EREHAKSESS	QREGRGESEN	AGTNQETRSR
330	340	350	360	370	380		
SRSNSKSKPN	LPSESRSRSK	SASKTRSRSK	SRSRSASRSP	SRSRSRSHSR	S		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2024	1	788.7867	-118.83	2	53.8	11.0	1	1-14	-.MRQAGEVTYADAHK.G	

Detailed Protein Report

Protein 462: transcriptional protein SWT1 [Homo sapiens]

Accession:	gi|157502207	**Score:**	23.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	103.2
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|157502209	refseq_human (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	
69	1	665.8831	-34.85	2	29.6	12.5	2	515-527	R.NKGLISGVKSLSK.E	

Detailed Protein Report

Protein 463: nuclear receptor corepressor 2 isoform 2 [Homo sapiens]

Accession:	gi|331284176	**Score:**	23.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	267.9
Database Date:	2015-11-30	**pI:**	8.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:**	0.07	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MSGSTQPVAQ	TWRATEPRYP	PHSLSYPVQI	ARTHTDVGLL	EYQHHSRDYA	SHLSPGSIIQ	PQRRRPSLLS	EFQPGNERSQ
90	100	110	120	130	140	150	160
ELHLRPESHS	YLPELGKSEM	EFIESKRPRL	ELLPDPLLRP	SPLLATGQPA	GSEDLTKDRS	LTGKLEPVSP	PSPPHTDPEL
170	180	190	200	210	220	230	240
ELVPPRLSKE	ELIQNMDRVD	REITMVEQQI	SKLKKKQQQL	EEEAAKPPEP	EKPVSPPPIE	SKHRSLVQII	YDENRKKAEA
250	260	270	280	290	300	310	320
AHRILEGLGP	QVELPLYNQP	SDTRQYHENI	KINQAMRKKL	ILYFKRRNHA	RKQWEQKFCQ	RYDQLMEAWE	KKVERIENNP
330	340	350	360	370	380	390	400
RRRAKESKVR	EYYEKQFPEI	RKQRELQERM	QRVGQRGSGL	SMSAARSEHE	VSEIIDGLSE	QENLEKQMRQ	LAVIPPMLYD
410	420	430	440	450	460	470	480
ADQQRIKFIN	MNGLMADPMK	VYKDRQVMNM	WSEQEKETFR	EKFMQHPKNF	GLIASFLERK	TVAECVLYYY	LTKKNENYKS
490	500	510	520	530	540	550	560
LVRRSYRRRG	KSQQQQQQQQ	QQQQQQQQQP	MPRSSQEEKD	EKEKEKEAEK	EEEKPEVEND	KEDLLKEKTD	DTSGEDNDEK
570	580	590	600	610	620	630	640
EAVASKGRKT	ANSQGRRKGR	ITRSMANEAN	SEEAITPQQS	AELASMELNE	SSRWTEEEME	TAKKGLLEHG	RNWSAIARMV
650	660	670	680	690	700	710	720
GSKTVSQCKN	FYFNYKKRQN	LDEILQQHKL	KMEKERNARR	KKKKAPAAAS	EEAAFPPVVE	DEEMEASGVS	GNEEEMVEEA
730	740	750	760	770	780	790	800
EATVNNSSDT	ESIPSPHTEA	AKDTGQNGPK	PPATLGADGP	PPGPPTPPPE	DIPAPTEPTP	ASEATGAPTP	PPAPPSPSAP
810	820	830	840	850	860	870	880
PPVVPKEEKE	EETAAAPPVE	EGEEQKPPAA	EELAVDTGKA	EEPVKSECTE	EAEEGPAKGK	DAEAAEATAE	GALKAEKKEG
890	900	910	920	930	940	950	960
GSGRATTAKS	SGAPQDSDSS	ATCSADEVDE	AEGGDKNRLL	SPRPSLLTPT	GDPRANASPQ	KPLDLKQLKQ	RAAAIPPIQV
970	980	990	1000	1010	1020	1030	1040
TKVHEPPRED	AAPTKPAPPA	PPPPQNLQPE	SDAPQQPGSS	PRGKSRSPAP	PADKEAEKPV	FFPAFAAEAQ	KLPGDPPCWT
1050	1060	1070	1080	1090	1100	1110	1120
SGLPFPVPPR	EVIKASPHAP	DPSAFSYAPP	GHPLPLGLHD	TARPVLPRPP	TISNPPPLIS	SAKHPSVLER	QIGAISQGMS
1130	1140	1150	1160	1170	1180	1190	1200
VQLHVPYSEH	AKAPVGPVTM	GLPLPMDPKK	LAPFSGVKQE	QLSPRGQAGP	PESLGVPTAQ	EASVLRGTAL	GSVPGGSITK
1210	1220	1230	1240	1250	1260	1270	1280
GIPSTRVPSD	SAITYRGSIT	HGTPADVLYK	GTITRIIGED	SPSRLDRGRE	DSLPKGHVIY	EGKKGHVLSY	EGGMSVTQCS
1290	1300	1310	1320	1330	1340	1350	1360
KEDGRSSSGP	PHETAAPKRT	YDMMEGRVGR	AISSASIEGL	MGRAIPPERH	SPHHLKEQHH	IRGSITQGIP	RSYVEAQEDY
1370	1380	1390	1400	1410	1420	1430	1440
LRREAKLLKR	EGTPPPPPPS	RDLTEAYKTQ	ALGPLKLKPA	HEGLVATVKE	AGRSIHEIPR	EELRHTPELP	LAPRPLKEGS
1450	1460	1470	1480	1490	1500	1510	1520
ITQGTPLKYD	TGASTTGSKK	HDVRSLIGSP	GRTFPPVHPL	DVMADARALE	RACYEESLKS	RPGTASSSGG	SIARGAPVIV
1530	1540	1550	1560	1570	1580	1590	1600
PELGKPRQSP	LTYEDHGAPF	AGHLPRGSPV	TTREPTPRLQ	EGSLSSSKAS	QDRKLTSTPR	EIAKSPHSTV	PEHHPHPISP
1610	1620	1630	1640	1650	1660	1670	1680
YEHLLRGVSG	VDLYRSHIPL	AFDPTSIPRG	IPLDAAAAYY	LPRHLAPNPT	YPHLYPPYLI	RGYPDTAALE	NRQTIINDYI
1690	1700	1710	1720	1730	1740	1750	1760
TSQQMHHNAA	TAMAQRADML	RGLSPRESSL	ALNYAAGPRG	IIDLSQVPHL	PVLVPPTPGT	PATAMDRLAY	LPTAPQPFSS
1770	1780	1790	1800	1810	1820	1830	1840
RHSSSPLSPG	GPTHLTKPTT	TSSSERERDR	DRERDRDRER	EKSILTSTTT	VEHAPIWRPG	TEQSSGSSGG	GGGSSSRPAS
1850	1860	1870	1880	1890	1900	1910	1920
HSHAHQHSPI	SPRTQDALQQ	RPSVLHNTGM	KGIITAVEPS	TPTVLRSTST	SSPVRPAATF	PPATHCPLGG	TLDGVYPTLM
1930	1940	1950	1960	1970	1980	1990	2000
EPVLLPKEAP	RVARPERPRA	DTGHAFLAKP	PARSGLEPAS	SPSKGSEPRP	LVPPVSGHAT	IARTPAKNLA	PHHASPDPPA
2010	2020	2030	2040	2050	2060	2070	2080
PPASASDPHR	EKTQSKPFSI	QELELRSLGY	HGSSYSPEGV	EPVSPVSSPS	LTHDKGLPKH	LEELDKSHLE	GELRPKQPGP
2090	2100	2110	2120	2130	2140	2150	2160
VKLGGEAAHL	PHLRPLPESQ	PSSSPLLQTA	PGVKGHQRVV	TLAQHISEVI	TQDYTRHHPQ	QLSAPLPAPL	YSFPGASCPV
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	
1282	1	530.6426	-232.27	2	44.5	10.1	1	441-448	R.EKFMQHPK.N	Oxidation: 4	QD:QU	0.07

Detailed Protein Report

Protein 464: **PREDICTED: immunoglobulin-like and fibronectin type III domain-containing protein 1 isoform X3 [Homo sapiens]**

Accession:	gi|578801693	**Score:**	23.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	355.2
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	2

Quantitation

QD:QU	**Median:**	1.75	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MAGKLRKSHI	PGVSIWQLVE	EIPEGCSTPD	FEQKPVTSAL	PEGKNAVFRA	VVCGEPRPEV	RWQNSKGDLS	DSSKYKISSS
90	100	110	120	130	140	150	160
PGSKEHVLQI	NKLTGEDTDL	YRCTAVNAYG	EAACSVRLTV	IEVGFRKNRK	RHREPQEDLR	KELMDFRKLL	KKRAPPAPKK
170	180	190	200	210	220	230	240
KMDLEQIWQL	LMTADRKDYE	KICLKYGIVD	YRGMLRRLQE	MKKEQEDKMA	QYINTISSLR	HIRVTKDGNA	KFDLELDLKD
250	260	270	280	290	300	310	320
SQSKIYLYKD	GEMIPYGFNN	QTKHCLRRLG	KRYEFQIQDL	RPEDSGIYQV	KVEDAVVFST	ELEASAIPPR	VVVPLAETHC
330	340	350	360	370	380	390	400
EEQGDAVFEC	TLSSPCPSAA	WHFRHRLLHP	SDKYEVYVSP	DGLTHRLVVR	GARFSDMGPY	SLGTGLYTSS	AWLVVEAGKD
410	420	430	440	450	460	470	480
KDLQSTSADH	KLQRQGAQAS	GAEESGSIES	QGEKSREQGP	RGGSLEGAGP	ASGLQHIASP	DRDGLGRHGY	SLMGDKGTAD
490	500	510	520	530	540	550	560
SAWGPGQEGE	GFPVAEGSRA	TLPRENQSHR	EGGWARSLAE	RPHLQGESSE	SGLGLPEKQQ	QDRGRDSNSD	ECWRKAGGWE
570	580	590	600	610	620	630	640
AGSSRLQAGG	LGSSREGKEH	RGDSGRQLDR	HAPEQLWDAR	LGPGRGKSDL	QGCQSDPVGS	WPRGKQIEIS	QDDSLAEMDR
650	660	670	680	690	700	710	720
GDAPSRERGR	GIVVWGGGTG	LGEAGDSNGA	GGPGTLELTG	GRGSGSKVGM	APESWGSQGG	RDADYGEARG	YWGSGELLEQ
730	740	750	760	770	780	790	800
IPGGKDFQEP	SISGGRKFLL	GDGSPEIKAE	DSLQEADGIC	RGESVVTGSA	YKTGPGGPGD	PRGCEGVLQE	LRGRDGQETA
810	820	830	840	850	860	870	880
WASGEVEYDP	RSFQSSQGWT	AGHRAAGGIG	RIESKGTSPW	DDTPSSLRKT	GAHHGPGVLG	PSGGQEGMGG	IWVAGLTESG
890	900	910	920	930	940	950	960
QGVDARSHWL	SRAPGLGAQG	SGGTLGDKKG	LRGPGSIGSE	PDFWNGSGSS	RVKGPRGETG	YKDGLEGPGR	MESRYEGGLG
970	980	990	1000	1010	1020	1030	1040
YSREISSKSG	AGYSYGSGVP	GEMGSGHGAG	CRVSPRAPAG	VESEEGGGYR	HGSGAPGGVW	SGNEDSGPAG	GGSGRVASLK
1050	1060	1070	1080	1090	1100	1110	1120
NGSGGPDGAP	MNDTRNWASA	CQAGMDPRGG	HHSDGGLGSP	GVTGSAGRGG	LKAPGVVETV	GMGCVEAEPE	SSGRIRPWGQ
1130	1140	1150	1160	1170	1180	1190	1200
TGNYGGFRAS	EALGAFGEGG	YEDGSGGPGA	MGPGSLRAGS	KVGEGDGTRC	PGAKASGAGA	GYRDDTRHPE	SLAPHNGAAS
1210	1220	1230	1240	1250	1260	1270	1280
GSQWAYGAGN	VLGYEDGSEL	PGPQGTGVRT	AYGERSRGLG	PRSTGPGGEA	GFRDGSGGLQ	GMGSADGPGC	RKGIGSSGEM
1290	1300	1310	1320	1330	1340	1350	1360
GSVDKEGYKK	DLGAPENMGS	GSKADYRDGV	GGSGAMGSMD	EAGYRKDLGA	PEGISSGSKA	DYRGGLQDSR	EAGSGSKADY
1370	1380	1390	1400	1410	1420	1430	1440
SGGLKGSREI	GSMDETDNRK	DLGVPEGMGA	GYRAGLRGPG	EMGSLDESGH	RNGIGGYGEM	GSGYREDLGA	PEGMGTGSKA
1450	1460	1470	1480	1490	1500	1510	1520
GYRDGLRGSG	EMRSMDEAGY	RKNLGAPERM	DSGSKAGYRG	GLRGSGEMGL	IEAGYRKDLG	VSEGGGSGSK	AGYRGGLGSG
1530	1540	1550	1560	1570	1580	1590	1600
EMGSVDKAGY	RKDLGASEAI	GSGSKAGFTD	GLGGSEEMGS	VNKAGYRKDL	GAPKGMGSGS	KASFRDGLGG	SGEMGSVNEA
1610	1620	1630	1640	1650	1660	1670	1680
GYRKDLGVPE	GIGSGSKAGF	RDGLGGSEEM	GSVNKAGYRK	DLGAPKGIGS	GSKAGFRDGL	GSSGEMGSMD	EAGYRKNLGA
1690	1700	1710	1720	1730	1740	1750	1760
PEGIGSGSKA	GFRDGLGSSV	EMGSVNEAGY	RKDLGAPEGM	GSGSKAGFRD	GLGGSGEMGS	VNEAGYRKDL	GAPKGIGSGS
1770	1780	1790	1800	1810	1820	1830	1840
KADFRDALGS	SGEMGSMDEA	GYRKDLWAPE	GIGSGSKAGF	RDGLGSSVEM	GSVNEAGYRK	DLGAPEGMGS	GSKAGFRDGL
1850	1860	1870	1880	1890	1900	1910	1920
GGSGEMGSVN	EAGYRKDLGA	PKGIGSGSKA	DFRDALGSSG	EMGSMDEAGY	RKDLWAPEGI	GSGSKAGFRD	GLGSSVEMGS
1930	1940	1950	1960	1970	1980	1990	2000
VNEAGYRKDL	GAPEGMGSGS	KEGFRDGLGG	SEEMGSVNKA	GYRKDLGAPK	GMGSGSKEGF	RDGLGGSEEM	GSMDEAGYRK
2010	2020	2030	2040	2050	2060	2070	2080
DLGAPEGIGS	GSKAGFRDGL	GGSEEMRSMD	EAGYRKDLGA	PERIGSGSKA	GFRDGLGSSV	EMGSVNEAGY	RKDLGAPKGM
2090	2100	2110	2120	2130	2140	2150	2160
GSGSKTGFRD	GLGGSEEMES	MDEAGYRKDL	GAPEGIGSGS	KAGFRDGLGS	STEMGSVNEA	GYRKDLGAPK	GMGSESKAGF
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
548	1	512.1851	-91.29	2	35.5	10.1	0	468-476	R.HGYSLMGDK.G	Oxidation: 6	QD:QU 1.75
765	1	937.7156	-58.56	3	38.1	12.9	1	2411-2439	R. ETRLVDGAGPGVEPGMAGMPGT D	Oxidation: 16, 19	

Detailed Protein Report

Protein 465: 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

Protein 466: **PREDICTED: thyroid receptor-interacting protein 11 isoform X2 [Homo sapiens]**

Accession: gi|530404931
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 22.9
MW [kDa]: 177.3
pI: 5.1
Sequence Coverage [%]: 2.2
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSLLKLNNEY	EVIKSTATRD	ISLDSELHDL	RLNLEAKEQE	LNQSISEKET	LIAEIEELDR	QNQEATKHMI	LIKDQLSKQQ
90	100	110	120	130	140	150	160
NEGDSIISKL	KQDLNDEKKR	VHQLEDDKMD	ITKELDVQKE	KLIQSEVALN	DLHLTKQKLE	DKVENLVDQL	NKSQESNVSI
170	180	190	200	210	220	230	240
QKENLELKEH	IRQNEEELSR	IRNELMQSLN	QDSNSNFKDT	LLKEREAEVR	NLKQNLSELE	QLNENLKKVA	FDVKMENEKL
250	260	270	280	290	300	310	320
VLACEDVRHQ	LEECLAGNNQ	LSLEKNTIVE	TLKMEKGEIE	AELCWAKKRL	LEEANKYEKT	IEELSNARNL	NTSALQLEHE
330	340	350	360	370	380	390	400
HLIKLNQKKD	MEIAELKKNI	EQMDTDHKET	KDVLSSSLEE	QKQLTQLINK	KEIFIEKLKE	RSSKLQEELD	KYSQALRKNE
410	420	430	440	450	460	470	480
ILRQTIEEKD	RSLGSMKEEN	NHLQEELERL	REEQSRTAPV	ADPKTLDSVT	ELASEVSQLN	TIKEHLEEEI	KHHQKIIEDQ
490	500	510	520	530	540	550	560
NQSKMQLLQS	LQEQKKEMDE	FRYQHEQMNA	THTQLFLEKD	EEIKSLQKTI	EQIKTQLHEE	RQDIQTDNSD	IFQETKVQSL
570	580	590	600	610	620	630	640
NIENGSEKHD	LSKAETERLV	KGIKERELEI	KLLNEKNISL	TKQIDQLSKD	EVGKLTQIIQ	QKDLEIQALH	ARISSTSHTQ
650	660	670	680	690	700	710	720
DVVYLQQQLQ	AYAMEREKVF	AVLNEKTREN	SHLKTEYHKM	MDIVAAKEAA	LIKLQDENKK	LSTRFESSGQ	DMFRETIQNL
730	740	750	760	770	780	790	800
SRIIREKDIE	IDALSQKCQT	LLAVLQTSST	GNEAGGVNSN	QFEELLQERD	KLKQQVKKME	EWKQQVMTTV	QNMQHESAQL
810	820	830	840	850	860	870	880
QEELHQLQAQ	VLVDSDNNSK	LQVDYTGLIQ	SYEQNETKLK	NFGQELAQVQ	HSIGQLCNTK	DLLLGKLDII	SPQLSSASLL
890	900	910	920	930	940	950	960
TPQSAECLRA	SKSEVLSESS	ELLQQELEEL	RKSLQEKDAT	IRTLQENNHR	LSDSIAATSE	LERKEHEQTD	SEIKQLKEKQ
970	980	990	1000	1010	1020	1030	1040
DVLQKLLKEK	DLLIKAKSDQ	LLSSNENFTN	KVNENELLRQ	AVTNLKERIL	ILEMDIGKLK	GENEKIVETY	RGKETEYQAL
1050	1060	1070	1080	1090	1100	1110	1120
QETNMKFSMM	LREKEFECHS	MKEKALAFEQ	LLKEKEQGKT	GELNQLLNAV	KSMQEKTVVF	QQERDQVMLA	LKQKQMENTA
1130	1140	1150	1160	1170	1180	1190	1200
LQNEVQRLRD	KEFRSNQELE	RLRNHLLESE	DSYTREALAA	EDREAKLRKK	VTVLEEKLVS	SSNAMENASH	QASVQVESLQ
1210	1220	1230	1240	1250	1260	1270	1280
EQLNVVSKQR	DETALQLSVS	QEQVKQYALS	LANLQMVLEH	FQQEEKAMYS	AELEKQKQLI	AEWKKNAENL	EGKVISLQEC
1290	1300	1310	1320	1330	1340	1350	1360
LDEANAALDS	ASRLTEQLDV	KEEQIEELKR	QNELRQEMLD	DVQKKLMSLA	NSSEGKVDKV	LMRNLFIGHF	HTPKNQRHEV
1370	1380	1390	1400	1410	1420	1430	1440
LRLMGSILGV	RREEMEQLFH	DDQGGVTRWM	TGWLGGGSKS	VPNTPLRPNQ	QSVVNSSFSE	LFVKFLETES	HPSIPPPKLS
1450	1460	1470	1480	1490	1500	1510	1520
VHDMKPLDSP	GRRKRDTNAP	ESFKDTAESR	SGRRTDVNPF	LAPRSAAVPL	INPAGLGPGG	PGHLLLKPIS	DVLPTFTPLP
1530	1540						
ALPDNSAGVV	LKDLLKQ						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2902	1	836.7384	-37.57	3	65.4	10.0	2	1092- 1112	K.SMQEKTVVFQQERDQVMLALK.Q	

Detailed Protein Report

Protein 467: cadherin-6 preproprotein [Homo sapiens]

Accession:	gi|4826673	**Score:**	22.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	88.3
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRTYRYFLLL	FWVGQPYPTL	STPLSKRTSG	FPAKKRALEL	SGNSKNELNR	SKRSWMWNQF	FLLEEYTGSD	YQYVGKLHSD
90	100	110	120	130	140	150	160
QDRGDGSLKY	ILSGDGAGDL	FIINENTGDI	QATKRLDREE	KPVYILRAQA	INRRTGRPVE	PESEFIIKIH	DINDNEPIFT
170	180	190	200	210	220	230	240
KEVYTATVPE	MSDVGTFVVQ	VTATDADDPT	YGNSAKVVYS	ILQGQPYFSV	ESETGIIKTA	LLNMDRENRE	QYQVVIQAKD
250	260	270	280	290	300	310	320
MGGQMGGLSG	TTTVNITLTD	VNDNPPRFPQ	STYQFKTPES	SPPGTPIGRI	KASDADVGEN	AEIEYSITDG	EGLDMFDVIT
330	340	350	360	370	380	390	400
DQETQEGIIT	VKKLLDFEKK	KVYTLKVEAS	NPYVEPRFLY	LGPFKDSATV	RIVVEDVDEP	PVFSKLAYIL	QIREDAQINT
410	420	430	440	450	460	470	480
TIGSVTAQDP	DAARNPVKYS	VDRHTDMDRI	FNIDSGNGSI	FTSKLLDRET	LLWHNITVIA	TEINNPKQSS	RVPLYIKVLD
490	500	510	520	530	540	550	560
VNDNAPEFAE	FYETFVCEKA	KADQLIQTLH	AVDKDDPYSG	HQFSFSLAPE	AASGSNFTIQ	DNKDNTAGIL	TRKNGYNRHE
570	580	590	600	610	620	630	640
MSTYLLPVVI	SDNDYPVQSS	TGTVTVRVCA	CDHHGNMQSC	HAEALIHPTG	LSTGALVAIL	LCIVILLVTV	VLFAALRRQR
650	660	670	680	690	700	710	720
KKEPLIISKE	DIRDNIVSYN	DEGGGEEDTQ	AFDIGTLRNP	EAIEDNKLRR	DIVPEALFLP	RRTPTARDNT	DVRDFINQRL
730	740	750	760	770	780	790	800
KENDTDPTAP	PYDSLATYAY	EGTGSVADSL	SSLESVTTDA	DQDYDYLSDW	GPRFKKLADM	YGGVDSDKDS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2713	2	701.4134	71.40	2	65.0	11.3	2	702-713	R.RTPTARDNTDVR.D	

Detailed Protein Report

Protein 468: **PREDICTED: ubiquilin-4 isoform X3 [Homo sapiens]**

Accession:	gi|530365094	**Score:**	22.9
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:	2

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
2774	2	937.4636	35.15	2	63.8	12.4	0	217-231	R.HMIMANPQMQQLMER.N	Oxidation: 13
1812	1	916.3298	-105.96	2	53.0	10.4	1	284-298	R.RMYTDIQEPMFSAAR.E	Oxidation: 2

Detailed Protein Report

Protein 469: septin-7 isoform 3 [Homo sapiens]

Accession: gi|339639597
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 22.9
MW [kDa]: 46.5
pI: 9.1
Sequence Coverage [%]: 5.7
No. of unique Peptides: 2

Quantitation

QD:QU **Median:** 1.22 **CV:** 0.00 % **No. of Peptides:** 1

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		
150	1	894.4204	-71.26	2	31.8	11.9	2	381-395	R.ILEQQNSSRTLEKNK.K		QD:QU 1.22

Detailed Protein Report

Protein 470: **PREDICTED: histone-lysine N-methyltransferase EHMT1 isoform X7 [Homo sapiens]**

Accession:	gi|530426806	**Score:**	22.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	99.7
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAADAEAVP	ARGEPQQDCC	VKTELLGEET	PMAADEGSAE	KQAGEAHMAA	DGETNGSCEN	SDASSHANAA	KHTQDSARVN
90	100	110	120	130	140	150	160
PQDGTNTLTR	IAENGVSERD	SEAAKQNHVT	ADDFVQTSVI	GSNGYILNKP	ALQAQPLRTT	STLASSLPGH	AAKTLPGGAG
170	180	190	200	210	220	230	240
KGRTPSAFPQ	TPAAPPATLG	EGSADTEDRK	LPAPGADVKV	HRARKTMPKS	VVGLHAASKD	PREVREARDH	KEPKEEINKN
250	260	270	280	290	300	310	320
ISDFGRQQLL	PPFPSLHQSL	PQNQCYMATT	KSQTACLPFV	LAAAVSRKKK	RRMGTYSLVP	KKKTKVLKQR	TVIEMFKSIT
330	340	350	360	370	380	390	400
HSTVGSKGEK	DLGASSLHVN	GESLEMDSDE	DDSEELEEDD	GHGAEQAAAF	PTEDSRTSKE	SMSEADRAQK	MDGESEEEQE
410	420	430	440	450	460	470	480
SVDTGEEEEG	GDESDLSSES	SIKKKFLKRK	GKTDSPWIKP	ARKRRRRSRK	KPSGALGSES	YKSSAGSAEQ	TAPGDSTGYM
490	500	510	520	530	540	550	560
EVSLDSLDLR	VKGILSSQAE	GLANGPDVLE	TDGLQEVPLC	SCRMETPKSR	EITTLANNQC	MATESVDHEL	GRCTNSVVKY
570	580	590	600	610	620	630	640
ELMRPSNKAP	LLVLCEDHRG	RMVKHQCCPG	CGYFCTAGNF	MECQPESSIS	HRFHKDCASR	VNNASYCPHC	GEESSKAKEV
650	660	670	680	690	700	710	720
TIAKADTTST	VTPVPGQEKG	SALEGRADTT	TGSAAGPPLS	EDDKLQGAAS	HVPEGFDPTG	PAGLGRPTPG	LSQGPGKETL
730	740	750	760	770	780	790	800
ESALIALDSE	KPKKLRFHPK	QLYFSARQGE	LQKVLLMLVD	GIDPNFKMEH	QNKRSPLHAA	AEAGHVDICH	MLVQAGANID
810	820	830	840	850	860	870	880
TCSEDQRTPL	MEAAENNHLE	AVKYLIKAGA	LVDPKDAEGS	TCLHLAAKKG	HYEVVQYLLS	NGQMDVNCQD	DGGWTPMIWA
890	900	910	920	930			
TEYKHVDLVK	LLLSKGSDIN	IRDNDDGTMK	RGALSRQKEE	KREAEEP			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1764	1	990.9536	23.24	2	50.6	10.5	1	621-638	R.VNNASYCPHCGEESSKAK.E	Carbamidomethyl: 7

Detailed Protein Report

Protein 471: otogelin precursor [Homo sapiens]

Accession:	gi|471270262	**Score:**	22.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	314.6
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MGVLASALCW	LLCVWLPWGE	QAAESLRVQR	LGERVVDSGR	SGARGMRNVK	GMRNGPAQTR	VSSSSSHQEA	TLAMGDKATV
90	100	110	120	130	140	150	160
VGGQQAEAPD	SVAMSSWERR	LHRAKCAPSY	LFSCFNGGEC	VHPAFCDCRR	FNATGPRCQM	VYNAGPERDS	ICRAWGQHHV
170	180	190	200	210	220	230	240
ETFDGLYYYL	SGKGSYTLVG	RHEPEGQSFS	IQVHNDPQCG	SSPYTCSRAV	SLFFVGEQEI	HLAKEVTHGG	MRVQLPHVMG
250	260	270	280	290	300	310	320
SARLQQLAGY	VIVRHQSAFT	LAWDGASAVY	IKMSPELLGW	THGLCGNNNA	DPKDDLVTSS	GKLTDDVVEF	VHSWQEQAPN
330	340	350	360	370	380	390	400
QPPGPTTSSL	PRPPCLQQNP	GTMQGVYEQC	EALLRPPFDA	CHAYVSPLPF	TASCTSDLCQ	SMGDVATWCR	ALAEYARACA
410	420	430	440	450	460	470	480
QAGRPLQGWR	TQLRQCTVHC	KEKAFTYNEC	IACCPASCHP	RASCVDSEIA	CVDGCYCPNG	LIFEDGGCVA	PAECPCEFHG
490	500	510	520	530	540	550	560
TLYPPGSVVK	EDCNTCTCTS	GKWECSTAVC	PAECSVTGDI	HFTTFDGRRY	TFPATCQYIL	AKSRSSGTFT	VTLQNAPCGL
570	580	590	600	610	620	630	640
NQDGACVQSV	SVILHQDPRR	QVTLTQAGDV	LLFDQYKIIP	PYTDDAFEIR	RLSSVFLRVR	TNVGVRVLYD	REGLRLYLQV
650	660	670	680	690	700	710	720
DQRWVEDTVG	LCGTFNGNTQ	DDFLSPVGVP	ESTPQLFGNS	WKTLSACSPL	VSGSPLDPCD	VHLQAASYSV	QACSVLTGEM
730	740	750	760	770	780	790	800
FAPCSAFLSP	VPYFEQCRRD	ACRCGQPCLC	ATLAHYAHLC	RRHGLPVDFR	ARLPACALSC	EASKEYSPCV	APCGRTCQDL
810	820	830	840	850	860	870	880
ASPEACGVDG	GDDLSRDECV	EGCACPPDTY	LDTQADLCVP	RNQCSCHFQG	VDYPPGDSDI	PSLGHCHCKD	GVMSCDSRAP
890	900	910	920	930	940	950	960
AAACPAGQVF	VNCSDLHTDL	ELSRERTCEQ	QLLNLSVSAR	GPCLSGCACP	QGLLRHGDAC	FLPEECPCTW	KGKEYFPGDQ
970	980	990	1000	1010	1020	1030	1040
VMSPCHTCVC	QRGSFQCTLH	PCASTCTAYG	DRHYRTFDGL	PFDFVGACKV	HLVKSTSDVS	FSVIVENVNC	YSSGMICRKF
1050	1060	1070	1080	1090	1100	1110	1120
ISINVGNSLI	VFDDDSGNPS	PESFLDDKQE	VHTWRVGFFT	LVHFPQEHIT	LLWDQRTTVH	VQAGPQWQGQ	LAGLCGNFDL
1130	1140	1150	1160	1170	1180	1190	1200
KTINEMRTPE	NLELTNPQEF	GSSWAAVECP	DTLDPRDMCV	LNPLREPFAK	KECSILLSEV	FEICHPVVDV	TWFYSNCLTD
1210	1220	1230	1240	1250	1260	1270	1280
TCGCSQGGDC	ECFCASVSAY	AHQCCQHGVA	VDWRTPRLCP	YDCDFFNKVL	GKGPYQLSSL	AAGGALVGMK	AVGDDIVLVR
1290	1300	1310	1320	1330	1340	1350	1360
TEDVAPADIV	SFLLTAALYK	AKAHDPDVVS	LEAADRPNFF	LHVTANGSLE	LAKWQGRDTF	QQHASFLLHR	GTRQAGLVAL
1370	1380	1390	1400	1410	1420	1430	1440
ESLAKPSSFL	YVSGAVLALR	LYEHTEVFRR	GTLFRLLDAK	PSGAAYPICE	WRYDACASPC	FQTCRDPRAA	SCRDVPRVEG
1450	1460	1470	1480	1490	1500	1510	1520
CVPVCPTPQV	LDEVTQRCVY	LEDCVEPAVW	VPTEALGNET	LPPSQGLPTP	SDEEPQLSQE	SPRTPTHRPA	LTPAAPLTTA
1530	1540	1550	1560	1570	1580	1590	1600
LNPPVTATEE	PVVSPGPTQT	TLQQPLELTA	SQLPAGPTES	PASKGVTASL	LAIPHTPESS	SLPVALQTPT	PGMVSGAMET
1610	1620	1630	1640	1650	1660	1670	1680
TRVTVIFAGS	PNITVSSRSP	PAPRFPLMTK	AVTVRGHGSL	PVRTTPPQPS	LTASPSSRPV	ASPGAISRSP	TSSGSHKAVL
1690	1700	1710	1720	1730	1740	1750	1760
TPAVTKVISR	TGVPQPTQAQ	SASSPSTPLT	VAGTAAEQVP	VSPLATRSLE	IVLSTEKGEA	GHSQPMGSPA	SPQPHPLPSA
1770	1780	1790	1800	1810	1820	1830	1840
PPRPAQHTTM	ATRSPALPPE	TPAAASLSTA	TDGLAATPFM	SLESTRPSQL	LSGLPPDTSL	PLAKVGTSAP	VATPGPKASV
1850	1860	1870	1880	1890	1900	1910	1920
ITTPLQPQAT	TLPAQTLSPV	LPFTPAAMTQ	AHPPTHIAPP	AAGTAPGLLL	GATLPTSGVL	PVAEGTASMV	SVVPRKSTTG
1930	1940	1950	1960	1970	1980	1990	2000
KVAILSKQVS	LPTSMYGSAE	GGPTELTPAT	SHPLTPLVAE	PEGAQAGTAL	PVPTSYALSR	VSARTAPQDS	MLVLLPQLAE
2010	2020	2030	2040	2050	2060	2070	2080
AHGTSAGPHL	AAEPVDEATT	EPSGRSAPAL	SIVEGLAEAL	ATTTEANTST	TCVPIAEQDC	VRHICLEGQL	IRVNQSQHCP
2090	2100	2110	2120	2130	2140	2150	2160
QGAAPPRCGI	LGLAVRVGGD	RCCPLWECAC	RCSIFPDLSF	VTFDGSHVAL	FKEAIYILSQ	SPDEMLTVHV	LDCKSANLGH
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
2044	1	1135.9200	78.97	3	54.1	22.8	1	921-951	R.GPCLSGCACPQGLLRHGDACFLPEECPCTWK.G	Carbamidomethyl: 7, 9

Detailed Protein Report

Protein 472: round spermatid basic protein 1-like protein [Homo sapiens]

Accession:	gi|158534055	**Score:**	22.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	94.8
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAEPPSPVHC	VAAAAPTATV	SEKEPFGKLQ	LSSRDPPGSL	SAKKVRTEEK	KAPRRVNGEG	GSGGNSRQLQ	PPAAPSPQSY
90	100	110	120	130	140	150	160
GSPASWSFAP	LSAAPSPSSS	RSSFSFSAGT	AVPSSASASL	SQPVPRKLLV	PPTLLHAQPH	HLLLPAAAAA	ASANAKSRRP
170	180	190	200	210	220	230	240
KEKREKERRR	HGLGGAREAG	GASREENGEV	KPLPRDKIKD	KIKERDKEKE	REKKKHKVMN	EIKKENGEVK	ILLKSGKEKP
250	260	270	280	290	300	310	320
KTNIEDLQIK	KVKKKKKKKH	KENEKRKRPK	MYSKSIQTIC	SGLLTDVEDQ	AAKGILNDNI	KDYVGKNLDT	KNYDSKIPEN
330	340	350	360	370	380	390	400
SEFPFVSLKE	PRVQNNLKRL	DTLEFKQLIH	IEHQPNGGAS	VIHAYSNELS	HLSPMEMERF	AEEFVGLVFS	ENENSAAFYV
410	420	430	440	450	460	470	480
MGIVHGAATY	LPDFLDYFSF	NFPNSPVKME	ILGKKDIETT	TMSNFHAQVK	RTYSHGTYRA	GPMRQISLVG	AVDEEVGDYF
490	500	510	520	530	540	550	560
PEFLDMLEES	PFLKCTLPWG	TLSSLKLQSR	KDSDDGPIMW	VRPGEQMIPV	ADMPKSPFKR	KRTTNEIKNL	QYLPRTSEPR
570	580	590	600	610	620	630	640
EMLFEDRTRA	HADHIGQGFE	RQTTAAVGVL	KAVHCGEWPD	QPRITKDVIC	FHAEDFLEVV	QRMQLDLHEP	PLSQCVQWVD
650	660	670	680	690	700	710	720
DAKLNQLRRE	GIRYARIQLY	DNDIYFIPRN	VVHQFKTVSA	VCSLAWHIRL	KLYHSEEDTS	QNTATHETGT	SSDSTSSVLG
730	740	750	760	770	780	790	800
PHTDNMICAV	SKASLDSVFS	DKLHSKYELQ	QIKHEPIASV	RIKEEPVNVN	IPEKTTALNN	MDGKNVKAKL	DHVQFAEFKI
810	820	830	840	850			
DMDSKFENSN	KDLKEELCPG	NLSLVDTRQH	SSAHSNQDKK	DDDILC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1767	4	627.2880	-110.44	2	50.6	22.8	2	330-339	K.EPRVQNNLKR.L	

Detailed Protein Report

Protein 473: **PREDICTED: arf-GAP with GTPase, ANK repeat and PH domain-containing protein 1 isoform X8 [Homo sapiens]**

Accession:	gi|578803598	**Score:**	22.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.9
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDAGGRFKKE	IVVDGQSYLL	LIRDEGGPPE	AQFAMWVDAV	IFVFSLEDEI	SFQTVYHYYS	RMANYRNTSE	IPLVLVGTQD
90	100	110	120	130	140	150	160
AISSANPRVI	DDARARKLSN	DLKRCTYYET	CATYGLNVER	VFQDVAQKIV	ATRKKQQLSI	GPCKSLPNSP	SHSSVCSAQV
170	180	190	200	210	220	230	240
SAVHISQTSN	GGGSLSDYSS	SVPSTPSTSQ	KELRIDVPPT	ANTPTPVRKQ	SKRRSNLFTS	RKGSDPDKEK	KGLESRADSI
250	260	270	280	290	300	310	320
GSGRAIPIKQ	GMLLKRSGKS	LNKEWKKKYV	TLCDNGVLTY	HPSLHDYMQN	VHGKEIDLLR	TTVKVPGKRP	PRATSACAPI
330	340	350	360	370	380	390	400
SSPKTNGLSK	DMSSLHISPN	SGNVTSASGS	QMASGISLVS	FNSRPDGMHQ	RSYSVSSADQ	WSEATVIANS	AISSDTGLGD
410	420	430	440	450	460	470	480
SVCSSPSISS	TTSPKLDPPP	SPHANRKKHR	RKKSTSNFKA	DGLSGTAEAK	RKAWKLNRVG	SLRNIYSSST	NTEEQEENFE
490	500	510	520	530	540	550	560
FIIVSLTGQT	WHFEATTYEE	RDAWVQAIES	QILASLQSCE	SSKNKSRLTS	QSEAMALQSI	RNMRGNSHCV	DCETQNPNWA
570	580	590	600	610	620	630	640
SLNLGALMCI	ECSGIHRNLG	THLSRVRSLD	LDDWPVELIK	VMSSIGNELA	NSVWEESSQG	RTKPSVDSTR	EEKERWIRAK
650	660	670	680	690	700	710	720
YEQKLFLAPL	PCTELSLGQH	LLRATADEDL	RTAILLLAHG	SRDEVNETCG	EGDGRTALHL	ACRKGNVVLA	QLLIWYGVDV
730	740	750	760	770	780	790	
TARDAHGNTA	LAYARQASSQ	ECIDVLLQYG	CPDERFVLMA	TPNLSRRNNN	RNNSSGRVPT	II	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
139	1	768.0380	181.88	2	30.5	12.7	0	528-541	R.LTSQSEAMALQSIR.N	

Detailed Protein Report

Protein 474: PREDICTED: LOW QUALITY PROTEIN: hemicentin-2 [Homo sapiens]

Accession:	gi|578818143	**Score:**	22.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	546.0
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMPGAPLLRL	LTAVSAAVAV	AVAGAPGTVM	PPTTGDATLA	FVFDVTGSMW	DELMQVIDGA	SRILERSLSR	RSQAIANYAL
90	100	110	120	130	140	150	160
VPFHDPDIGP	VTLTADPTVF	QRELRELYVQ	GGGDCPEMSV	GAIKAAVEVA	NPGSFIYVFS	DARAKDYHKK	EELLRLLQLK
170	180	190	200	210	220	230	240
QSQVVFVLTG	DCGDRTHPGY	LAYEEIAATS	SGQVFHLDKQ	QVTEVLKWVE	SAIQASKVHL	LSTDHEEEGE	HTWRLPFDPS
250	260	270	280	290	300	310	320
LKEVTISLSG	PGPEIEVQDP	LGRILQEDEG	LNVLLNIPDS	AKVVAFKPEH	PGLWSIKVYS	SGRHSVRITG	VSNIDFRAGF
330	340	350	360	370	380	390	400
STQPLLDLNH	TLEWPLQGVP	ISLVINSTGL	KAPGRLDSVE	LAQSSGKPLL	TLPTKPLSNG	STHQLWGGPP	FHTPKERFYL
410	420	430	440	450	460	470	480
KVKGKDHEGN	PLLRVSGVSY	SGVAPGAPLV	SMAPRIHGYL	HQPLLVSCSV	HSALPFRLQL	RRGEARLGEE	RHFQESGNSS
490	500	510	520	530	540	550	560
WEILRASKAE	EGTYECTAVS	RAGTGRAKAQ	IVVTDPPPQL	VPAPNVTVSP	GETAVLSCRV	LGEAPYNLTW	VRDWRVLPAS
570	580	590	600	610	620	630	640
TGRVAQLADL	SLEISGIIPT	DGGRYQCVAS	NANGVTRASV	WLLVREAPQV	SIHTSSQHFS	QGVEVKVSCS	ASGYPTPHIS
650	660	670	680	690	700	710	720
WSRESQALQE	DSRIHVDAQG	TLIIQGVAPE	DAGNYSCQAT	NEVGTDQETV	TLYYTDPPSV	SAVNAVVLVA	VGEEAVLVCE
730	740	750	760	770	780	790	800
ASGVPPPRVI	WYRGGLEMIL	APEGSSSGKL	RIPAAQERDA	GTYTCRAVNE	LGDASAEIQL	AVGHAPQLTE	LPRDVTVELG
810	820	830	840	850	860	870	880
RSALLACRAT	GRPPPTVTWR	RGDGQPLGLR	LGAGRGSRSR	QPDSGVLFFE	SVAPEDQAPY	VCEARNVFGK	VQAEARLIVT
890	900	910	920	930	940	950	960
GHAPPQIASS	APTVRVLEGQ	PVSLPCIVLA	GRPLPERHWL	KDGRPLPPGS	RHSIRADGSL	HLDRALQEHA	GRYSCVATNT
970	980	990	1000	1010	1020	1030	1040
AGSQHRDVEL	VVQVPPRIHP	TATHHITNEG	VAASLPCVAS	GVPAPTITWT	KETNALTSRG	PHYNVSKEGT	LLIAQPSAQD
1050	1060	1070	1080	1090	1100	1110	1120
AGAYVCTATN	TVGFSSQEMR	LSVNTKPRIH	MNGSRNADVP	LQVTAKAGEE	VTLDCEAKGS	PPPLVTWTKD	SRPVPPITNR
1130	1140	1150	1160	1170	1180	1190	1200
YGLLPSGSLR	LAQVQVGDSG	HYECTASNPA	GSASHRYVLG	VQVPPQVQPG	PRVLKVLVGE	ALDLNCVAEG	NPEPQLSWSK
1210	1220	1230	1240	1250	1260	1270	1280
DGVVLQGRGP	QGSVHFAAIR	TSDAGRYRCE	ASNSAGVDAW	EVELRVLEPP	HWGADETSGL	LERVAGENAS	LPCPARGTPK
1290	1300	1310	1320	1330	1340	1350	1360
PQVTWRKGPS	SEPLHGQPGV	AVLEEGSLFL	ASVSPADSGD	YECQATNEVG	STSRRAKLVV	YVPPSIREDG	RKANVSGMAG
1370	1380	1390	1400	1410	1420	1430	1440
QSLTLECDAN	GFPVPEIVWL	KDAQLIPKVG	GHRLLDEGQS	LHFPRIQEGD	SGLYSCRAEN	QAGTAQRDFH	LLVLTPPSVL
1450	1460	1470	1480	1490	1500	1510	1520
GAGAAQEVLG	LAGADVELQC	WTSGVPTPQV	EWTKDRQPVL	PGGPHLQVQE	DGQVLRITGS	HVGDEGRYQC	VAFSPAGQQA
1530	1540	1550	1560	1570	1580	1590	1600
RDFQLRVHAP	PTIWGSNETG	EVAVMEDHLV	QLLCEARGVP	TPNITWFKDG	ALLPTSTKVV	YTRGGRQLQL	GRAQSSDAGV
1610	1620	1630	1640	1650	1660	1670	1680
YTCKASNAVG	AAEKATRLDV	YVPPTIEGAG	GRPYVVKAVA	GRPVALECVA	RGHPSPTLSW	HHEGLPVAES	NESRLETDGS
1690	1700	1710	1720	1730	1740	1750	1760
VLRLESPGEA	SSGLYSCVAS	SPAGEAVLQY	SVEVQVPPQL	LVAEGLGQVT	TIVGQPLELP	CQASGSPVPT	IQWLQNGRPA
1770	1780	1790	1800	1810	1820	1830	1840
EELAGVQVAS	QGTTLHIDHV	ELDHSGLFAC	QATNEAGTAG	AEVEVSVHGE	WAPGVLEVPI	GQYHWGXEHH	SSFPAACDPP
1850	1860	1870	1880	1890	1900	1910	1920
VHRGWGAHPK	PPLVEGWCSP	GSLWGEPTGI	PVAYSLPPPL	QIEKVDLRDE	GIYTCAATNL	AGESKREVAL	KVLVPPNIEP
1930	1940	1950	1960	1970	1980	1990	2000
GPVNKAVLEN	ASVTLECLAS	GVPPPDVSWF	KGHQPVSSWM	GVTVSVDGRV	LRIEQAQLSD	AGSYRCVASN	VAGSTELRYG
2010	2020	2030	2040	2050	2060	2070	2080
LRVNVPPRIT	LPPSLPGPVL	VNTPVRLTCN	ATGAPSPTLM	WLKDGNPVSP	AGTPGLQVFP	GGRVLTLASA	RASDSGRYSC
2090	2100	2110	2120	2130	2140	2150	2160
VAVSAVGEDR	QDVVLQVHMP	PSILGEELNV	SVVANESVAL	ECQSHAMPPP	VLSWWKDGRP	LEPRPGVHLS	ADKALLQVDR
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
61	1	623.8088	95.46	5	29.5	12.6	2	866-895	R.NVFGKVQAEARLIVTGHAPPQIASSAPTVR.V	

Detailed Protein Report

Protein 475: rap1 GTPase-activating protein 1 isoform c [Homo sapiens]

Accession:	gi|224809582	**Score:**	22.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.3
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	1

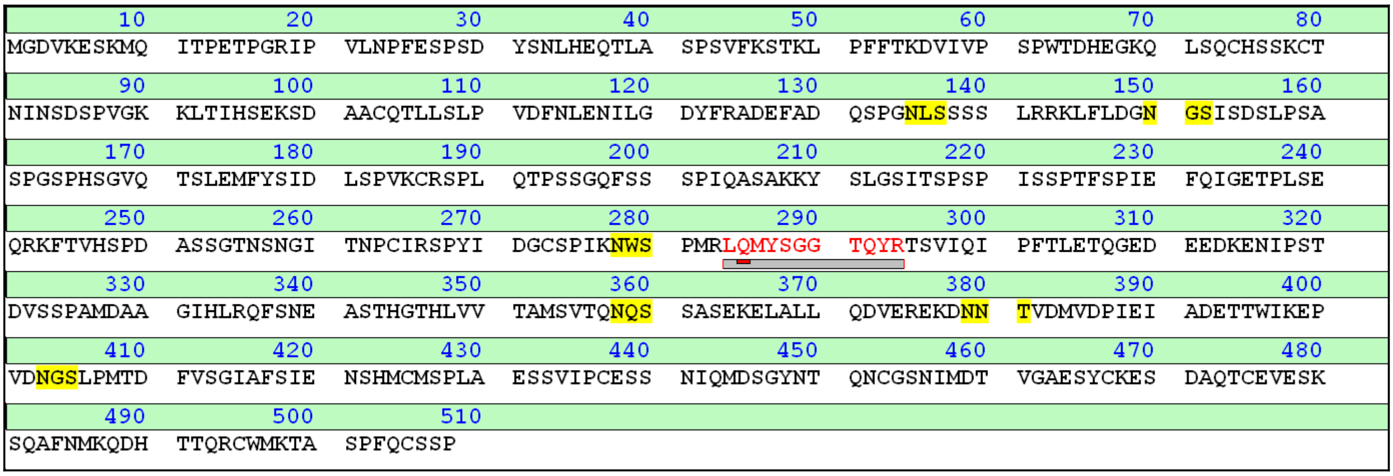
10	20	30	40	50	60	70	80
MIEKMQGSRM	DEQRCSFPPP	LKTEEDYIPY	PSVHEVLGRE	GPFPLILLPQ	FGGYWIEGTN	HEITSIPETE	PLQSPTTKVK
90	100	110	120	130	140	150	160
LECNPTARIY	RKHFLGKEHF	NYYSLDAALG	HLVFSLKYDV	IGDQEHLRLL	LRTKCRTYHD	VIPISCLTEF	PNVVQMAKLV
170	180	190	200	210	220	230	240
CEDVNVDRFY	PVLYPKASRL	IVTFDEHVIS	NNFKFGVIYQ	KLGQTSEEEL	FSTNEESPAF	VEFLEFLGQK	VKLQDFKGFR
250	260	270	280	290	300	310	320
GGLDVTHGQT	GTESVYCNFR	NKEIMFHVST	KLPYTEGDAQ	QLQRKRHIGN	DIVAVVFQDE	NTPFVPDMIA	SNFLHAYVVV
330	340	350	360	370	380	390	400
QAEGGGPDGP	LYKVSVTARD	DVPFFGPPLP	DPAVFRKGPE	FQEFLLTKLI	NAEYACYKAE	KFAKLEERTR	AALLETLYEE
410	420	430	440	450	460	470	480
LHIHSQSMMG	LGGDEDKMEN	GSGGGGFFES	FKRVIRSRSQ	SMDAMGLSNK	KPNTVSTSHS	GSFAPNNPDL	AKAAGISLIV
490	500	510	520	530	540	550	560
PGKSPTRKKS	GPFGSRRSSA	IGIENIQEVQ	EKRESPPAGQ	KTPDSGHVSQ	EPKSENSSTQ	SSPEMPTTKN	RAETAAQRAE
570	580	590	600	610	620	630	640
ALKDFSRSSS	SASSFASVVE	ETEGVDGEDT	GLESVSSSGT	PHKRDSFIYS	TWLEDSVSTT	SGGSSPGPSR	SPHPDAGKLG
650	660	670					
DPACPEIKIQ	LEASEQHMPQ	LGC					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2007	1	660.8874	-123.62	3	53.6	11.5	1	534-551	K.SENSSTQSSPEMPTTKNR.A	

Detailed Protein Report

Protein 476: PREDICTED: protein aurora borealis isoform X1 [Homo sapiens]

Accession:	gi|578825016	**Score:**	22.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.2
Database Date:	2015-11-30	**pI:**	4.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.5
		No. of unique Peptides:	1



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        10          20          30          40          50          60          70          80
MGDVKESKMQ  ITPETPGRIP  VLNPFESPSD  YSNLHEQTLA  SPSVFKSTKL  PFFTKDVIVP  SPWTDHEGKQ  LSQCHSSKCT
        90         100         110         120         130         140         150         160
NINSDSPVGK  KLTIHSEKSD  AACQTLLSLP  VDFNLENILG  DYFRADEFAD  QSPGNLSSSS  LRRKLFLDGN  GSISDSLPSA
       170         180         190         200         210         220         230         240
SPGSPHSGVQ  TSLEMFYSID  LSPVKCRSPL  QTPSSGQFSS  SPIQASAKKY  SLGSITSPSP  ISSPTFSPIE  FQIGETPLSE
       250         260         270         280         290         300         310         320
QRKFTVHSPD  ASSGTNSNGI  TNPCIRSPYI  DGCSPIKNWS  PMRLQMYSGG  TQYRTSVIQI  PFTLETQGED  EEDKENIPST
       330         340         350         360         370         380         390         400
DVSSPAMDAA  GIHLRQFSNE  ASTHGTHLVV  TAMSVTQNQS  SASEKELALL  QDVEREKDNN  TVDMVDPIEI  ADETTWIKEP
       410         420         430         440         450         460         470         480
VDNGSLPMTD  FVSGIAFSIE  NSHMCMSPLA  ESSVIPCESS  NIQMDSGYNT  QNCGSNIMDT  VGAESYCKES  DAQTCEVESK
       490         500         510
SQAFNMKQDH  TTQRCWMKTA  SPFQCSSP
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Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1061	1	660.1801	-190.79	2	41.8	10.0	0	284-294	R.LQMYSGGTQYR.T	Oxidation: 3

Detailed Protein Report

Protein 477: E3 ubiquitin-protein ligase listerin [Homo sapiens]

Accession:	gi|231573214	**Score:**	22.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	205.0
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
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 Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
48	1	1097.0025	-131.66	2	30.5	11.6	2	1127-1145	R.SREHGTLWSLIIAKLILSR.S	

Detailed Protein Report

Protein 478: coiled-coil domain-containing protein 171 [Homo sapiens]

Accession:	gi|38348729	**Score:**	22.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	152.7
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
MNLNTSSNTG	DTQRLKIASL	DVKQILKNET	ELDITDNLRK	KLHWAKKEKL	EITTKHNAEL	ASYESQIAKL	RSEVEKGEAL
90	100	110	120	130	140	150	160
RQSLEYDLAV	ARKEAGLGRR	AAEERLAEAH	RIQEKLCAQN	SELQAKTNET	EKAFQTSQQK	WKEECRRFEH	DLEERDNMIQ
170	180	190	200	210	220	230	240
NCNREYDLLM	KEKSRLEKTL	QEALEKHQRE	KNEMESHIRE	TALEEFRLQE	EQWEAERREL	QFIVQEQDTA	VQNMHKKVEK
250	260	270	280	290	300	310	320
LETEHMDCSD	LLRRQTSELE	FSTQREERLR	KEFEATTLRV	RKLEENIEAE	RAAHLESKFN	SEIIQLRIRD	LEGALQVEKA
330	340	350	360	370	380	390	400
SQAEAVADLE	IIKNEFKEVE	SAYEREKHNA	QESFAKLNLL	EKEYFSKNKK	LNEDIEEQKK	VIIDLSKRLQ	YNEKSCSELQ
410	420	430	440	450	460	470	480
EELVMAKKHQ	AFLVETCENN	VKELESILDS	FTVSGQWTSG	IHKDKDKPPS	FSVVLERLRR	TLTDYQNKLE	DASNEEKACN
490	500	510	520	530	540	550	560
ELDSTKQKID	SHTKNIKELQ	DKLADVNKEL	SHLHTKCADR	EALISTLKVE	LQNVLHCWEK	EKAQAAQSES	ELQKLSQAFH
570	580	590	600	610	620	630	640
KDAEEKLTFL	HTLYQHLVAG	CVLIKQPEGM	LDKFSWSELC	AVLQENVDAL	IADLNRANEK	IRHLEYICKN	KSDTMRELQQ
650	660	670	680	690	700	710	720
TQEDTFTKVA	EQIKAQESCW	HRQKKELELQ	YSELFLEVQK	RAQKFQEIAE	KNMEKLNHIE	KSHEQLVLEN	SHFKKLLSQT
730	740	750	760	770	780	790	800
QREQMSLLAA	CALMAGALYP	LYSRSCALST	QRDFLQEQVN	TFELFKLEIR	TLAQALSTVE	EKKQEEAKMK	KKTFKGLIRI
810	820	830	840	850	860	870	880
FRKGVIAVLA	ANRLKILGQS	CASLFTWMES	FKEGIGMLVC	TGEPQDKHKF	PKHQKEQLRC	LQALSWLTSS	DLLAAIISSM
890	900	910	920	930	940	950	960
AELQDVIGKA	DPNSRICGHL	LIGAAKNSFA	KLMDKISLVM	ECIPLHSSRS	ITYVEKDSLV	QRLAHGLHKV	NTLALKYGLR
970	980	990	1000	1010	1020	1030	1040
GHVPITKSTA	SLQKQILGFT	QRLHAAEVER	RSLRLEVTEF	KRSVNEMKKE	LDKAQGLQMQ	LNEFKQSKLI	THEKFESACE
1050	1060	1070	1080	1090	1100	1110	1120
ELNNALLREE	QAQMLLNEQA	QQLQELNYKL	ELHSSEEADK	NQTLGEAVKS	LSEAKMELRR	KDQSLRQLNR	HLTQLEQDKR
1130	1140	1150	1160	1170	1180	1190	1200
RLEENIHDAE	SALRMAAKDK	ECVANHMRAV	ENTLHKVRDQ	ISLSWSAASR	NDFTLQLPKL	HLETFAMEGL	KGGPEVVACQ
1210	1220	1230	1240	1250	1260	1270	1280
AMIKSFMDVY	QLASTRIMTL	EKEMTSHRSH	IAALKSELHT	ACLRENASLQ	SIGSRDHSNL	SIPSRAPLPA	DTTGIGDFLP
1290	1300	1310	1320	1330			
LKAELDTTYT	FLKETFINTV	PHALTSSHSS	PVTMSANANR	PTQIGL			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
151	1	773.9066	22.69	2	31.9	12.1	1	541-554	K.EKAQAAQSESELQK.L	

Detailed Protein Report

Protein 479: CUB and sushi domain-containing protein 3 isoform 3 [Homo sapiens]

Accession:	gi|205277354	**Score:**	22.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	387.1
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.5
		No. of unique Peptides:	1

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
1304	1	661.3930	144.57	1	46.4	11.2	0	2937-2941	R.QPECK.A	Carbamidomethyl: 4

Detailed Protein Report

Protein 480: PREDICTED: fatty-acid amide hydrolase 2 isoform X4 [Homo sapiens]

Accession:	gi|530426388	**Score:**	22.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.2
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	1

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	

Detailed Protein Report

Protein 481: **PREDICTED: NAD-dependent protein deacylase sirtuin-5, mitochondrial isoform X3 [Homo sapiens]**

Accession:	gi|530381706	**Score:**	22.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.7
Database Date:	2015-11-30	**pI:**	11.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.9
		No. of unique Peptides:	1

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
605	1	730.9957	75.86	2	36.2	11.8	1	255-266	R.LFLKPLPVMKMK.L	Oxidation: 9

Detailed Protein Report

Protein 482: **multiple epidermal growth factor-like domains protein 8 isoform 2 precursor [Homo sapiens]**

Accession:	gi|145701025	**Score:**	22.7
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 [%]:**	1.6
		No. of unique Peptides:	2

Detailed Protein Report

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        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
2125	1	1023.8906	-13.46	3	57.0	12.4	2	1-31	-.MALGKVLAMALVLALAVLGSLSPGARAGDCK.G	Carbamidomethyl: 30; Oxidation: 1
1779	1	820.8211	-36.25	2	50.8	10.3	1	1000-1012	R.WAYARCPDVDECR.L	Carbamidomethyl: 12

Detailed Protein Report

Protein 483: staphylococcal nuclease domain-containing protein 1 [Homo sapiens]

Accession:	gi|77404397	**Score:**	22.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.9
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

```
        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
349	1	626.3170	35.99	3	34.4	11.5	1	733-747	R.GEFCIAKFVDGEWYR.A	Carbamidomethyl: 4

Detailed Protein Report

Protein 484: azurocidin preproprotein [Homo sapiens]

Accession:	gi|11342670	**Score:**	22.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.9
Database Date:	2015-11-30	**pI:**	11.9
		Sequence Coverage [%]:	5.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTRLTVLALL	AGLLASSRAG	SSPLLDIVGG	RKARPRQFPF	LASIQNQGRH	FCGGALIHAR	FVMTAASCFQ	SQNPGVSTVV
90	100	110	120	130	140	150	160
LGAYDLRRRE	RQSRQTFSIS	SMSENGYDPQ	QNLNDLMLLQ	LDREANLTSS	VTILPLPLQN	ATVEAGTRCQ	VAGWGSQRSG
170	180	190	200	210	220	230	240
GRLSRFPRFV	NVTVTPEDQC	RPNNVCTGVL	TRRGGICNGD	GGTPLVCEGL	AHGVASFSLG	PCGRGPDFFT	RVALFRDWID
250	260						
GVLNNPGPGP	A						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2226	3	753.2849	-148.34	2	56.5	22.6	0	37-49	R.QFPFLASIQNQGR.H	

Detailed Protein Report

Protein 485: **PREDICTED: tyrosine-protein phosphatase non-receptor type 11 isoform X2 [Homo sapiens]**

Accession:	gi|578824047	**Score:**	22.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	64.0
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.4
		No. of unique 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	QLKQTLQQQE	CKLLYSRKEG	QRQENKNKNR
250	260	270	280	290	300	310	320
YKNILPFDHT	RVVLHDGDPN	EPVSDYINAN	IIMPEFETKC	NNSKPKKSYI	ATQGCLQNTV	NDFWRMVFQE	NSRVIVMTTK
330	340	350	360	370	380	390	400
EVERGKSKCV	KYWPDEYALK	EYGVMRVRNV	KESAAHDYTL	RELKLSKVGQ	ALLQGNTERT	VWQYHFRTWP	DHGVPSDPGG
410	420	430	440	450	460	470	480
VLDFLEEVHH	KQESIMDAGP	VVVHCSAGIG	RTGTFIVIDI	LIDIIREKGV	DCDIDVPKTI	QMVRSQRSGM	VQTEAQYRFI
490	500	510	520	530	540	550	560
YMAVQHYIET	LQRRIEEEQK	SKRKGHEYTN	IKYSLADQTS	GDQSPLPPCT	PTPPCAEMRE	DSARVYENVG	LMQQQKSFR

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
360	1	559.1189	-258.27	2	33.2	10.9	0	449-458	K.GVDCDIDVPK.T	Carbamidomethyl: 4

Detailed Protein Report

Protein 486: zinc finger and SCAN domain-containing protein 29 [Homo sapiens]

Accession:	gi|109715825	**Score:**	22.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.7
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:**	0.45	**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		QD:QU	0.45

Detailed Protein Report

Protein 487: 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 488: **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
Modification(s):	Oxidation	**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
1973	1	902.8715	-0.36	2	55.1	10.4	0	861-876	R.TPVSDDAESTSMFDMR.C	Oxidation: 12

Detailed Protein Report

Protein 489: dynein heavy chain 6, axonemal [Homo sapiens]

Accession:	gi|194353966	**Score:**	22.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	475.7
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	0.6
		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
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2662	1	698.0710	213.61	2	62.1	10.4	0	1359-1372	R.LNALAAIVQGSLPK.L	

Detailed Protein Report

Protein 490: 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 491: **PAS domain-containing protein 1 [Homo sapiens]**

Accession:	gi|157785548	**Score:**	22.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.4
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

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	1	557.6353	40.20	3	65.8	22.5	1	451-465	K.DVKCFCGLSLSNSLK.N	Carbamidomethyl: 4

Detailed Protein Report

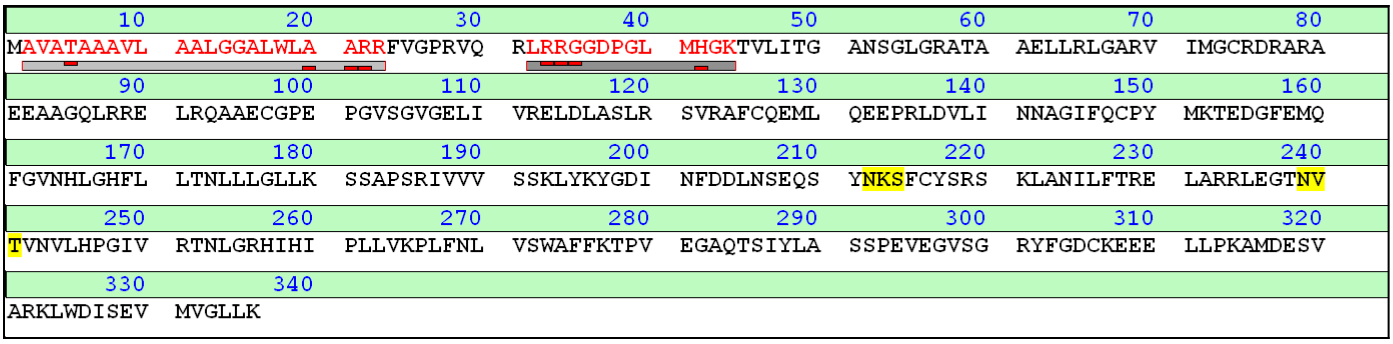
Protein 492: **retinol dehydrogenase 14 [Homo sapiens]**

Accession: gi|10190746
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 22.4
MW [kDa]: 36.8
pI: 9.9
Sequence Coverage [%]: 10.4
No. of unique Peptides: 2

Quantitation

QD:QU **Median:** 0.73 **CV:** 0.00 % **No. of 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	Ratios
1653	1	698.3330	-119.22	3	50.9	11.2	1	2-23	M. AVATAAAVLAALGGALWLAARR. F		
865	1	705.2586	-165.25	2	40.9	11.2	2	32-44	R.LRRGGDPGLMHGK.T	Oxidation: 10	QD:QU 0.73

Detailed Protein Report

Protein 493: 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

Protein 494: neuropathy target esterase isoform c [Homo sapiens]

Accession:	gi|260656039	**Score:**	22.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	143.3
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
MEAPLQTGMV	LGVMIGAGVA	VVVTAVLILL	VVRRLRVPKT	PAPDGPRYRF	RKRDKVLFYG	RKIMRKVSQS	TSSLVDTSVS
90	100	110	120	130	140	150	160
ATSRPRMRKK	LKMLNIAKKI	LRIQKETPTL	QRKEPPPAVL	EADLTEGDLA	NSHLPSEVLY	MLKNVRVLGH	FEKPLFLELC
170	180	190	200	210	220	230	240
RHMVFQRLGQ	GDYVFRPGQP	DASIYVVQDG	LLELCLPGPD	GKECVVKEVV	PGDSVNSLLS	ILDVITGHQH	PQRTVSARAA
250	260	270	280	290	300	310	320
RDSTVLRLPV	EAFSAVFTKY	PESLVRVVQI	IMVRLQRVTF	LALHNYLGLT	NELFSHEIQP	LRLFPSPGLP	TRTSPVRGSK
330	340	350	360	370	380	390	400
RMVSTSATDE	PRETPGRPPD	PTGAPLPGPT	GDPVKPTSLE	TPSAPLLSRC	VSMPGDISGL	QGGPRSDFDM	AYERGRISVS
410	420	430	440	450	460	470	480
LQEEASGGSL	AAPARTPTQE	PREQPAGACE	YSYCEDESAT	GGCPFGPYQG	RQTSSIFEAA	KQELAKLMRI	EDVSLHFVLW
490	500	510	520	530	540	550	560
GCLHVYQRMI	DKAEDVCLFV	AQPGELVGQL	AVLTGEPLIF	TLRAQRDCTF	LRISKSDFYE	IMRAQPSVVL	SAAHTVAARM
570	580	590	600	610	620	630	640
SPFVRQMDFA	IDWTAVEAGR	ALYRQGDRSD	CTYIVLNGRL	RSVIQRGSGK	KELVGEYGRG	DLIGVVEALT	RQPRATTVHA
650	660	670	680	690	700	710	720
VRDTELAKLP	EGTLGHIKRR	YPQVVTRLIH	LLSQKILGNL	QQLQGPFPGS	GLGVPPHSEL	TNPASNLATV	AILPVCAEVP
730	740	750	760	770	780	790	800
MVAFTLELQH	ALQAIGPTLL	LNSDIIRARL	GASALDSIQE	FRLSGWLAQQ	EDAHRIVLYQ	TDASLTPWTV	RCLRQADCIL
810	820	830	840	850	860	870	880
IVGLGDQEPT	LGQLEQMLEN	TAVRALKQLV	LLHREEGAGP	TRTVEWLNMR	SWCSGHLHLR	CPRRLFSRRS	PAKLHELYEK
890	900	910	920	930	940	950	960
VFSRRADRHS	DFSRLARVLT	GNTIALVLGG	GGARGCSHIG	VLKALEEAGV	PVDLVGGTSI	GSFIGALYAE	ERSASRTKQR
970	980	990	1000	1010	1020	1030	1040
AREWAKSMTS	VLEPVLDLTY	PVTSMFTGSA	FNRSIHRVFQ	DKQIEDLWLP	YFNVTTDITA	SAMRVHKDGS	LWRYVRASMT
1050	1060	1070	1080	1090	1100	1110	1120
LSGYLPPLCD	PKDGHLLMDG	GYINNLPADI	ARSMGAKTVI	AIDVGSQDET	DLSTYGDSLS	GWWLLWKRLN	PWADKVKVPD
1130	1140	1150	1160	1170	1180	1190	1200
MAEIQSRLAY	VSCVRQLEVV	KSSSYCEYLR	PPIDCFKTMD	FGKFDQIYDV	GYQYGKAVFG	GWSRGNVIEK	MLTDRRSTDL
1210	1220	1230	1240	1250	1260	1270	1280
NESRRADVLA	FPSSGFTDLA	EIVSRIEPPT	SYVSDGCADG	EESDCLTEYE	EDAGPDCSRD	EGGSPEGASP	STASEMEEEK
1290	1300	1310					
SILRQRRCLP	QEPPGSATDA						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
55	1	699.0697	59.10	3	29.4	10.8	0	1206-1225	R.ADVLAFPSSGFTDLAEIVSR.I	

BRUKER

Detailed Protein Report

Protein 495: coiled-coil domain-containing protein 78 [Homo sapiens]

Accession:	gi|199559954	**Score:**	22.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.5
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEHAATTGPR	PGPPSRRVEN	VVLRAKDWLP	GAPGGTAVWA	TSLEAEVPPD	LALNKEQQLQ	ISKELVDIQI	TTHHLHEQHE
90	100	110	120	130	140	150	160
AEIFQLKSEI	LRLESRVLEL	ELRGDGTSQG	CAVPVESDPR	HPRAAAQELR	HKAQVPGHSD	DHRFQVQPKN	TMNPENEQHR
170	180	190	200	210	220	230	240
LGSGLQGEVK	WALEHQEARQ	QALVTRVATL	GRQLQGAREE	ARAAGQRLAT	QAVVLCSCQG	QLRQAEAENA	RLQLQLKKLK
250	260	270	280	290	300	310	320
DEYVLRLQHC	AWQAVEHADG	AGQAPATTAL	RTFLEATLED	IRAAHRSREQ	QLARAARSYH	KRLVDLSRRH	EELLVAYRAP
330	340	350	360	370	380	390	400
GNPQAIFDIA	SLDLEPLPVP	LVTDFSHRED	QHGGPGALLS	SPKKRPGGAS	QGGTSEPQGL	DAASWAQIHQ	KLRDFSRSTQ
410	420	430	440				
SWNGSGHSCW	SGPRWLKSNF	LSYRSTWTST	WAGTSTKS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1714	1	917.4108	-54.09	2	50.0	11.5	1	1-17	-.MEHAATTGPRPGPPSRR.V	Oxidation: 1

Detailed Protein Report

Protein 496: 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:	1

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		

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1490	1	719.8392	-53.72	2	48.8	11.2	1	1445-1456	R.HRAACLIQAHYR.G	

Detailed Protein Report

Protein 497: janus kinase and microtubule-interacting protein 3 [Homo sapiens]

Accession:	gi|157502225	**Score:**	22.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	98.5
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578819295	refseq_human (refseq_human_20140103.fasta)	PREDICTED: janus kinase and microtubule-interacting protein 3 isoform X7 [Homo sapiens]

10	20	30	40	50	60	70	80
MSKRGMSSRA	KGDKAEALAA	LQAANEDLRA	KLTDIQIELQ	QEKSKVSKVE	REKNQELRQV	REHEQHKTAV	LLTELKTKLH
90	100	110	120	130	140	150	160
EEKMKELQAV	RETLLRQHEA	ELLRVIKIKD	NENQRLQALL	SALRDGGPEK	VKTVLLSEAK	EEAKKGFEVE	KVKMQQEISE
170	180	190	200	210	220	230	240
LKGAKRQVEE	ALTLVIQADK	IKAAEIRSVY	HLHQEEITRI	KKECEREIRR	LMEEIKFKDR	AVFVLERELG	VQAGHAQRLQ
250	260	270	280	290	300	310	320
LQKEALDEQL	SQVREADRHP	GSPRRELPHA	AGAGDASDHS	GSPEQQLDEK	DARRFQLKIA	ELSAIIRKLE	DRNALLSEER
330	340	350	360	370	380	390	400
NELLKRVREA	ESQYKPLLDK	NKRLSRKNED	LSHALRRMEN	KLKFVTQENI	EMRQRAGIIR	RPSSLNDLDQ	SQDEREVDFL
410	420	430	440	450	460	470	480
KLQIVEQQNL	IDELSKTLET	AGYVKSVLER	DKLLRFRKQR	KKMAKLPKPV	VVETFFGYDE	EASLESDGSS	VSYQTDRTDQ
490	500	510	520	530	540	550	560
TPCTPDDDLE	EGMAKEETEL	RFRQLTMEYQ	ALQRAYALLQ	EQVGGTLDAE	REVKTREQLQ	AEVQRAQARI	EDLEKALAEQ
570	580	590	600	610	620	630	640
GQDMKWIEEK	QALYRRNQEL	VEKIKQMETE	EARLRHEVQD	ARDQNELLEF	RILELEERER	KSPAISFHHT	PFVDGKSPLQ
650	660	670	680	690	700	710	720
VYCEAEGVTD	IVVAELMKKL	DILGDNANLT	NEEQVVVIQA	RTVLTLAEKW	LQQIEETEAA	LQRKMVDLES	EKELFSKQKG
730	740	750	760	770	780	790	800
YLDEELDYRK	QALDQANKHI	LELEAMLYDA	LQQEAGAKVA	ELLSEEEREK	LKVAVEQWKR	QVMSELRERD	AQILRERMEL
810	820	830	840	850			
LQLAQQRIKE	LEERIEAQKR	QIKELEEKFL	FLFLFFSLAF	ILWS			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2340	1	899.3808	-154.38	2	59.7	11.2	1	167-182	R.QVEEALTLVIQADKIK.A	

Detailed Protein Report

Protein 498: PREDICTED: sickle tail protein homolog isoform X17 [Homo sapiens]

Accession:	gi|530392291	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	162.3
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 6.19 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MQRELVYARG	DGPGAPRPGS	TAHPPHAIPN	SPPSTPVPHS	MPPSPSRIPY	GGTRSMVVPG	NATIPRDRIS	SLPVSRPISP
90	100	110	120	130	140	150	160
SPSAILERRD	VKPDEDMSGK	NIAMYRNEGF	YADPYLYHEG	RMSIASSHGG	HPLDVPDHII	AYHRTAIRSA	SAYCNPSMQA
170	180	190	200	210	220	230	240
EMHMEQSLYR	QKSRKYPDSH	LPTLGSKTPP	ASPHRVSDLR	MIDMHAHYNA	HGPPHTMQPD	RASPSRQAFK	KEPGTLVYIE
250	260	270	280	290	300	310	320
KPRSAAGLSS	LVDLGPPLME	KQVFAYSTAT	IPKDRETSEK	MMKTTANRNH	TDSAGTPHVS	GGKMLSALES	TVPPSQPPPV
330	340	350	360	370	380	390	400
GTSAIHMSLL	EMRRSVAELR	LQLQQMRQLQ	LQNQELLRAM	MKKAELEISG	KVMETMKRLE	DPVQRQRVLV	EQERQKYLHE
410	420	430	440	450	460	470	480
EEKIVKKLCE	LEDFVEDLKK	DSTAASRLVT	LKDVEDGAFL	LRQVGEAVAT	LKGEFPTLQN	KMRAILRIEV	EAVRFLKEEP
490	500	510	520	530	540	550	560
HKLDSLLKRV	RSMTDVLTML	RRHVTDGLLK	GTDAAQAAQY	MAMEKATAAE	VLKSQEEAAH	TSGQPFHSTG	APGDAKSEVV
570	580	590	600	610	620	630	640
PLSGMMVRHA	QSSPVVIQPS	QHSVALLNPA	QNLPHVASSP	AVPQEATSTL	QMSQAPQSPQ	IPMNGSAMQS	LFIEEIHSVS
650	660	670	680	690	700	710	720
AKNRAVSIEK	AEKKWEEKRQ	NLDHYNGKEF	EKLLEEAQAN	IMKSIPNLEM	PPATGPLPRG	DAPVDKVELS	EDSPNSEQDL
730	740	750	760	770	780	790	800
EKLGGKSPPP	PPPPPRRSYL	PGSGLTTTRS	GDVVYTGRKE	NITAKASSED	AGPSPQTRAT	KYPAEEPASA	WTPSPPPVTT
810	820	830	840	850	860	870	880
SSSKDEEEEE	EEGDKIMAEL	QAFQKCSFMD	VNSNSHAEPS	RADSHVKDTR	SGATVPPKEK	KNLEFFHEDV	RKSDVEYENG
890	900	910	920	930	940	950	960
PQMEFQKVTT	GAVRPSDPPK	WERGMENSIS	DASRTSEYKT	EIIMKENSIS	NMSLLRDSRN	YSQETVPKAS	FGFSGISPLE
970	980	990	1000	1010	1020	1030	1040
DEINKGSKIS	GLQYSIPDTE	NQTLNYGKTK	EMEKQNTDKC	HVSSHTRLTE	SSVHDFKTED	QEVITTDFGQ	VVLRPKEARH
1050	1060	1070	1080	1090	1100	1110	1120
ANVNPNEDGE	SSSSSPTEEN	AATDNIAFMI	TETTVQVLSS	GEVHDIVSQK	GEDIQTVNID	ARKEMTPRQE	GTDNEDPVVC
1130	1140	1150	1160	1170	1180	1190	1200
LDKKPVIIIF	DEPMDIRSAY	KRLSTIFEEC	DEELERMMME	EKIEEEEEEE	NGDSVVQNNN	TSQMSHKKVA	PGNLRTGQQV
1210	1220	1230	1240	1250	1260	1270	1280
ETKSQPHSLA	TETRNPGGQE	MNRTELNKFS	HVDSPNSECK	GEDATDDQFE	SPKKKFKFKF	PKKQLAALTQ	AIRTGTKTGK
1290	1300	1310	1320	1330	1340	1350	1360
KTLQVVVYEE	EEEDGTLKQH	KEAKRFEIAR	SQPEDTPENT	VRRQEQPSIE	STSPISRTDE	IRKNTYRTLD	SLEQTIKQLE
1370	1380	1390	1400	1410	1420	1430	1440
NTISEMSPKA	LVDTSCSSNR	DSVASSSHIA	QEASPRPLLV	PDEGPTALEP	PTSIPSASRK	GSSGAPQTSR	MPVPMSAKNR
1450	1460	1470					
PGTLDKPGKQ	SKLQDPRQYR	QVVLP					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
588	1	581.7946	6.95	2	35.9	10.0	0	1008-1017	R.LTESSVHDFK.T		QD:QU 6.19

Detailed Protein Report

Protein 499: PREDICTED: cyclin-dependent kinase 7 isoform X1 [Homo sapiens]

Accession:	gi|530379082	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.7
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	8.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530430719	refseq_human (refseq_human_20140103.fasta)	PREDICTED: cyclin-dependent kinase 7 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MRSWTSLGRD	SLPPFTRPEI	RTPTKLSPLR	KSNLDIDQKL	KMVIIKDNSL	VLTPSHIKAY	MLMTLQGLEY	LHQHWILHRD
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LKPNNLLLDE	NGVLKLADFG	LAKSFGSPNR	AYTHQVVTRW	YRAPELLFGA	RMYGVGVDMW	AVGCILAELL	LRVPFLPGDS
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
DLDQLTRIFE	TLGTPTEEQW	PDMCSLPDYV	TFKSFPGIPL	HHIFSAAGDD	LLDLIQGLFL	FNPCARITAT	QALKMKYFSN
250	**260**	**270**	**280**	**290**			
RPGPTPGCQL	PRPNCPVETL	KEQSNPALAI	KRKRTEALEQ	GGLPKKLIF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
50	1	662.2443	-185.28	2	29.3	10.8	0	47-58	K.DNSLVLTPSHIK.A	

Detailed Protein Report

Protein 500: **PREDICTED: nascent polypeptide-associated complex subunit alpha isoform X6 [Homo sapiens]**

Accession:	gi|578823772	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	201.3
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

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
52	1	717.7555	-144.48	2	30.5	11.1	0	1531- 1544	K.EASSPPAVTPSTYK.G	

Detailed Protein Report

Protein 501: PREDICTED: FERM domain-containing protein 4A isoform X7 [Homo sapiens]

Accession:	gi|530392249	**Score:**	22.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.9
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MFIASGSSLQ RFPNAPENDF LTWRSQESDS SQSAKKDMLA ALKSRQEALE ETLRQRLEEL KKLCLREAEL TGKLPVEYPL
        90        100        110        120        130        140        150        160
DPGEEPPIVR RRIGTAFKLD EQKILPKGEE AELERLEREF AIQSQITEAA RRLASDPNVS KKLKKQRKTS YLNALKKLQE
       170        180        190        200        210        220        230        240
IENAINENRI KSGKKPTQRA SLIIDDGNIA SEDSSLSDAL VLEDEDSQVT STISPLHSPH KGLPPRPPSH NRPPPPQSLE
       250        260        270        280        290        300        310        320
GLRQMHYHRN DYDKSPIKPK MWSESSLDEP YEKVKKRSSH SHSSSHKRFP STGSCAEAGG GSNSLQNSPI RGLPHWNSQS
       330        340        350        360        370        380        390        400
SMPSTPDLRV RSPHYVHSTR SVDISPTRLH SLALHFRHRS SSLESQGKLL GSENDTGSPD FYTPRTRSSN GSDPMDDCSS
       410        420        430        440        450        460        470        480
CTSHSSSEHY YPAQMNANYS TLAEDSPSKA RQRQRQRQRA AGALGSASSG SMPNLAARGG AGGAGGAGGG VYLHSQSQPS
       490        500        510        520        530        540        550        560
SQYRIKEYPL YIEGGATPVV VRSLESDQEG HYSVKAQFKT SNSYTAGGLF KESWRGGGGD EGDTGRLTPS RSQILRTPSL
       570        580        590        600        610        620        630        640
GREGAHDKGA GRAAVSDELR QWYQRSTASH KEHSRLSHTS STSSDSGSQY STSSQSTFVA HSRVTRMPQM CKATSAALPQ
       650        660        670        680        690        700        710
SQRSSTPSSE IGATPPSSPH HILTWQTGSY NDSCFLDSSL YPELADVQWY GQEKAKPGTL V
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2251	1	952.9306	-31.49	2	56.8	10.2	1	627-643	R.MPQMCKATSAALPQSQR.S	Carbamidomethyl: 5

Detailed Protein Report

Protein 502: 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

Protein 503: 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

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
2052	1	840.8203	-18.08	2	56.0	10.4	0	168-182	K.YMGQMCGLCGNFDGK.V	Carbamidomethyl: 6

Protein 504: metallothionein-4 [Homo sapiens]

Accession: gi|14269578

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 22.0

MW [kDa]: 6.4

pI: 10.8

Sequence Coverage [%]: 25.8

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

Protein 505: PREDICTED: splicing factor, suppressor of white-apricot homolog isoform X1 [Homo sapiens]

Accession: gi|578824119
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 22.0
MW [kDa]: 96.4
pI: 9.4
Sequence Coverage [%]: 2.9
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MYGASGGRAK PERKSGAKEE AGPGGAGGGG SRVELLVFGY ACKLFRDDER ALAQEQGQHL IPWMGDHKIL IDRYDGRGHL
        90        100        110        120        130        140        150        160
HDLSEYDAEY STWNRDYQLS EEEARIEALC DEERYLALHT DLLEEEARQE EEYKRLSEAL AEDGSYNAVG FTYGSDYYDP
       170        180        190        200        210        220        230        240
SEPTEEEEPS KQREKNEAEN LEENEEPFVA PLGLSVPSDV ELPPTAKMHA IIERTASFVC RQGAQFEIML KAKQARNSQF
       250        260        270        280        290        300        310        320
DFLRFDHYLN PYYKFIQKAM KEGRYTVLAE NKSDEKKKSG VSSDNEDDDD EEDGNYLHPS LFASKKCNRL EELMKPLKVV
       330        340        350        360        370        380        390        400
DPDHPLAALV RKAQADSSTP TPHNADGAPV QPSQVEYTAD STVAAMYYSY YMLPDGTYCL APPPPGIDVT TYYSTLPAGV
       410        420        430        440        450        460        470        480
TVSNSPGVTT TAPPPPGTTP LPPPTTAETS SGATSTTTTT SALAPVAAII PPPPDVQPVI DKLAEYVARN GLKFETSVRA
       490        500        510        520        530        540        550        560
KNDQRFEFLQ PWHQYNAYYE FKKQFFLQKE GGDSMQAVSA PEEAPTDSAP EKPSDAGEDG APEDAAEVGA RAGSGGKKEA
       570        580        590        600        610        620        630        640
SSSKTVPDGK LVKAKQKLED RLAAAAREKL AQASKESKEK QLQAERKRKA ALFLQTLKNP LPEAEAGKIE ESPFSVEESS
       650        660        670        680        690        700        710        720
TTPCPLLTGG RPLPTLEVKP PDRPSSKSKD PPREEEKEKK KKKHKKRSRT RSRSPKYHSS SKSRSRSHSK AKHSLPSAYR
       730        740        750        760        770        780        790        800
TVRRSRSRSR SPRRRAHSPE RRREERSVPT AYRVSRSPGA SRKRTRSRSP HEKKKKRRSR SRTKSKARSQ SVSPSKQAAP
       810        820        830        840        850        860        870        880
RPAAPAAHSA HSASVSPVES RGSSQERSRG VSQEKEAQIS SAIVSSVQSK ITQDLMAKVR AMLAASKNLQ TSAS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2815	1	698.3601	23.69	2	64.3	10.1	1	1-13	-.MYGASGGRAKPER.K	Oxidation: 1

Detailed Protein Report

Protein 506: cullin-4A isoform 2 [Homo sapiens]

Accession:	gi|11140811	**Score:**	22.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.8
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	2

Alias proteins:

Accession	Name	Description
gi|511772961	refseq_human (refseq_human_20140103.fasta)	cullin-4A isoform 2 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MLYKQLRQAC EDHVQAQILP FREDSLDSVL FLKKINTCWQ DHCRQMIMIR SIFLFLDRTY VLQNSTLPSI WDMGLELFRT
        90        100        110        120        130        140        150        160
HIISDKMVQS KTIDGILLLI ERERSGEAVD RSLLRSLLGM LSDLQVYKDS FELKFLEETN CLYAAEGQRL MQEREVPEYL
       170        180        190        200        210        220        230        240
NHVSKRLEEE GDRVITYLDH STQKPLIACV EKQLLGEHLT AILQKGLDHL LDENRVPDLA QMYQLFSRVR GGQQALLQHW
       250        260        270        280        290        300        310        320
SEYIKTFGTA IVINPEKDKD MVQDLLDFKD KVDHVIEVCF QKNERFVNLM KESFETFINK RPNKPAELIA KHVDSKLRAG
       330        340        350        360        370        380        390        400
NKEATDEELE RTLDKIMILF RFIHGKDVFE AFYKKDLAKR LLVGKSASVD AEKSMLSKLK HECGAAFTSK LEGMFKDMEL
       410        420        430        440        450        460        470        480
SKDIMVHFKQ HMQNQSDSGP IDLTVNILTM GYWPTYTPME VHLTPEMIKL QEVFKAFYLG KHSGRKLQWQ TTLGHAVLKA
       490        500        510        520        530        540        550        560
EFKEGKKEFQ VSLFQTLVLL MFNEGDGFSF EEIKMATGIE DSELRRTLQS LACGKARVLI KSPKGKEVED GDKFIFNGEF
       570        580        590        600        610        620        630        640
KHKLFRIKIN QIQMKETVEE QVSTTERVFQ DRQYQIDAAI VRIMKMRKTL GHNLLVSELY NQLKFPVKPG DLKKRIESLI
       650        660
DRDYMERDKD NPNQYHYVA
```

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	332-341	R.TLDKIMILFR.F	
2723	1	774.4242	-43.85	2	63.0	11.3	2	564-575	K.LFRIKINQIQMK.E	Oxidation: 11

Detailed Protein Report

Protein 507: 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:	2

Quantitation

QD:QU	**Median:** 1.36	**CV:** 0.00 %	**No. of 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	Ratios
1190	3	644.3159	-45.97	2	45.0	10.9	1	64-74	K.CITIPRSLDGR.L	Carbamidomethyl: 1	QD:QU 1.36
2171	1	862.9449	30.12	2	57.5	11.0	1	410-425	K.VLTQMGSPSIRCSSVS.-	Carbamidomethyl: 12; Oxidation: 5	

Detailed Protein Report

Protein 508: **rho guanine nucleotide exchange factor 19 [Homo sapiens]**

Accession:	gi|40255149	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.1
Database Date:	2015-11-30	**pI:**	8.0
		Sequence Coverage [%]:	4.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDCGPPATLQ	PHLTGPPGTA	HHPVAVCQQE	SLSFAELPAL	KPPSPVCLDL	FPVAPEELRA	PGSRWSLGTP	APLQGLLWPL
90	100	110	120	130	140	150	160
SPGGSDTEIT	SGGMRPSRAG	SWPHCPGAQP	PALEGPWSPR	HTQPQRRASH	GSEKKSAWRK	MRVYQREEVP	GCPEAHAVFL
170	180	190	200	210	220	230	240
EPGQVVQEQA	LSTEEPRVEL	SGSTRVSLEG	PERRRFSASE	LMTRLHSSLR	LGRNSAARAL	ISGSGTGAAR	EGKASGMEAR
250	260	270	280	290	300	310	320
SVEMSGDRVS	RPAPGDSREG	DWSEPRLDTQ	EEPPLGSRST	NERRQSRFLL	NSVLYQEYSD	VASARELRRQ	QREEEGPGDE
330	340	350	360	370	380	390	400
AEGAEEGPGP	PRANLSPSSS	FRAQRSARGS	TFSLWQDIPD	VRGSGVLATL	SLRDCKLQEA	KFELITSEAS	YIHSLSVAVG
410	420	430	440	450	460	470	480
HFLGSAELSE	CLGAQDKQWL	FSKLPEVKST	SERFLQDLEQ	RLEADVLRFS	VCDVVLDHCP	AFRRVYLPYV	TNQAYQERTY
490	500	510	520	530	540	550	560
QRLLLENPRF	PGILARLEES	PVCQRLPLTS	FLILPFQRIT	RLKMLVENIL	KRTAQGSEDE	DMATKAFNAL	KELVQECNAS
570	580	590	600	610	620	630	640
VQSMKRTEEL	IHLSKKIHFE	GKIFPLISQA	RWLVRHGELV	ELAPLPAAPP	AKLKLSSKAV	YLHLFNDCLL	LSRRKELGKF
650	660	670	680	690	700	710	720
AVFVHAKMAE	LQVRDLSLKL	QGIPGHVFLL	QLLHGQHMKH	QFLLRARTES	EKQRWISALC	PSSPQEDKEV	ISEGEDCPQV
730	740	750	760	770	780	790	800
QCVRTYKALH	PDELTLEKTD	ILSVRTWTSD	GWLEGVRLAD	GEKGWVPQAY	VEEISSLSAR	LRNLRENKRV	TSATSKLGEA
810							
PV							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2498	1	673.3379	-69.90	2	61.8	10.5	1	636-647	K.ELGKFAVFVHAK.M	

Detailed Protein Report

Protein 509: PREDICTED: zinc finger protein basonuclin-1 isoform X2 [Homo sapiens]

Accession:	gi|578827289	**Score:**	21.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	110.6
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCYCIGPQSR	CSNNFFKNIF	FSSKRQDFGL	TAISCTLNCS	CQSFKPGKIN	HRQCDQCKHG	WVAHALSKLR	IPPMYPTSQV
90	100	110	120	130	140	150	160
EIVQSNVVFD	ISSLMLYGTQ	AIPVRLKILL	DRLFSVLKQD	EVLQILHALD	WTLQDYIRGY	VLQDASGKVL	DHWSIMTSEE
170	180	190	200	210	220	230	240
EVATLQQFLR	FGETKSIVEL	MAIQEKEEQS	IIIPPSTANV	DIRAFIESCS	HRSSSLPTPV	DKGNPSSIHP	FENLISNMTF
250	260	270	280	290	300	310	320
MLPFQFFNPL	PPALIGSLPE	QYMLEQGHDQ	SQDPKQEVHG	PFPDSSFLTS	SSTPFQVEKD	QCLNCPDAIT	KKEDSTHLSD
330	340	350	360	370	380	390	400
SSSYNIVTKF	ERTQLSPEAK	VKPERNSLGT	KKGRVFCTAC	EKTFYDKGTL	KIHYNAVHLK	IKHKCTIEGC	NMVFSSLRSR
410	420	430	440	450	460	470	480
NRHSANPNPR	LHMPMNRNNR	DKDLRNSLNL	ASSENYKCPG	FTVTSPDCRP	PPSYPGSGED	SKGQPAFPNI	GQNGVLFPNL
490	500	510	520	530	540	550	560
KTVQPVLPFY	RSPATPAEVA	NTPGILPSLP	LLSSSIPEQL	ISNEMPFDAL	PKKKSRKSSM	PIKIEKEAVE	IANEKRHNLS
570	580	590	600	610	620	630	640
SDEDMPLQVV	SEDEQEACSP	QSHRVSEEQH	VQSGGLGKPF	PEGERPCHRE	SVIESSGAIS	QTPEQATHNS	ERETEQTPAL
650	660	670	680	690	700	710	720
IMVPREVEDG	GHEHYFTPGM	EPQVPFSDYM	ELQQRLLAGG	LFSALSNRGM	AFPCLEDSKE	LEHVGQHALA	RQIEENRFQC
730	740	750	760	770	780	790	800
DICKKTFKNA	CSVKIHHKNM	HVKEMHTCTV	EGCNATFPSR	RSRDRHSSNL	NLHQKALSQE	ALESSEDHFR	AAYLLKDVAK
810	820	830	840	850	860	870	880
EAYQDVAFTQ	QASQTSVIFK	GTSRMGSLVY	PITQVHSASL	ESYNSGPLSE	GTILDLSTTS	SMKSESSSHS	SWDSDGVSEE
890	900	910	920	930	940	950	960
GTVLMEDSDG	NCEGSSLVPG	EDEYPICVLM	EKADQSLASL	PSGLPITCHL	CQKTYSNKGT	FRAHYKTVHL	RQLHKCKVPG
970	980	990	1000				
CNTMFSSVRS	RNRHSQNPNL	HKSLASSPSH	LQ				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1802	1	990.7899	-140.63	2	51.0	10.5	1	2-17	M.CYCIGPQSRCSNNFFK.N	Carbamidomethyl: 1, 10

Detailed Protein Report

Protein 510: rho-associated protein kinase 2 [Homo sapiens]

Accession:	gi|41872583	**Score:**	21.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	160.8
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MSRPPPTGKM PGAPETAPGD GAGASRQRKL EALIRDPRSP INVESLLDGL NSLVLDLDFP ALRKNKNIDN FLNRYEKIVK

        90        100        110        120        130        140        150        160
KIRGLQMKAE DYDVVKVIGR GAFGEVQLVR HKASQKVYAM KLLSKFEMIK RSDSAFFWEE RDIMAFANSP WVVQLFYAFQ

       170        180        190        200        210        220        230        240
DDRYLYMVME YMPGGDLVNL MSNYDVPEKW AKFYTAEVVL ALDAIHSMGL IHRDVKPDNM LLDKHGHLKL ADFGTCMKMD

       250        260        270        280        290        300        310        320
ETGMVHCDTA VGTPDYISPE VLKSQGGDGF YGRECDWWSV GVFLYEMLVG DTPFYADSLV GTYSKIMDHK NSLCFPEDAE

       330        340        350        360        370        380        390        400
ISKHAKNLIC AFLTDREVRL GRNGVEEIRQ HPFFKNDQWH WDNIRETAAP VVPELSSDID SSNFDDIEDD KGDVETFPIP

       410        420        430        440        450        460        470        480
KAFVGNQLPF IGFTYYRENL LLSDSPSCRE TDSIQSRKNE ESQEIQKKLY TLEEHLSNEM QAKEELEQKC KSVNTRLEKT

       490        500        510        520        530        540        550        560
AKELEEEITL RKSVESALRQ LEREKALLQH KNAEYQRKAD HEADKKRNLE NDVNSLKDQL EDLKKRNQNS QISTEKVNQL

       570        580        590        600        610        620        630        640
QRQLDETNAL LRTESDTAAR LRKTQAESSK QIQQLESNNR DLQDKNCLLE TAKLKLEKEF INLQSALESE RRDRTHGSEI

       650        660        670        680        690        700        710        720
INDLQGRICG LEEDLKNGKI LLAKVELEKR QLQERFTDLE KEKSNMEIDM TYQLKVIQQS LEQEEAEHKA TKARLADKNK

       730        740        750        760        770        780        790        800
IYESIEEAKS EAMKEMEKKL LEERTLKQKV ENLLLEAEKR CSLLDCDLKQ SQQKINELLK QKDVLNEDVR NLTLKIEQET

       810        820        830        840        850        860        870        880
QKRCLTQNDL KMQTQQVNTL KMSEKQLKQE NNHLMEMKMN LEKQNAELRK ERQDADGQMK ELQDQLEAEQ YFSTLYKTQV

       890        900        910        920        930        940        950        960
RELKEECEEK TKLGKELQQK KQELQDERDS LAAQLEITLT KADSEQLARS IAEEQYSDLE KEKIMKELEI KEMMARHKQE

       970        980        990       1000       1010       1020       1030       1040
LTEKDATIAS LEETNRTLTS DVANLANEKE ELNNKLKDVQ EQLSRLKDEE ISAAAIKAQF EKQLLTERTL KTQAVNKLAE

      1050       1060       1070       1080       1090       1100       1110       1120
IMNRKEPVKR GNDTDVRRKE KENRKLHMEL KSEREKLTQQ MIKYQKELNE MQAQIAEESQ IRIELQMTLD SKDSDIEQLR

      1130       1140       1150       1160       1170       1180       1190       1200
SQLQALHIGL DSSSIGSGPG DAEADDGFPE SRLEGWLSLP VRNNTKKFGW VKKYVIVSSK KILFYDSEQD KEQSNPYMVL

      1210       1220       1230       1240       1250       1260       1270       1280
DIDKLFHVRP VTQTDVYRAD AKEIPRIFQI LYANEGESKK EQEFPVEPVG EKSNYICHKG HEFIPTLYHF PTNCEACMKP

      1290       1300       1310       1320       1330       1340       1350       1360
LWHMFKPPPA LECRRCHIKC HKDHMDKKEE IIAPCKVYYD ISTAKNLLLL ANSTEEQQKW VSRLVKKIPK KPPAPDPFAR

      1370       1380       1390
SSPRTSMKIQ QNQSIRRPSR QLAPNKPS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2066	1	1044.9156	-114.45	2	56.2	11.5	2	583-600	R.KTQAESSKQIQQLESNNR.D	
302	1	409.4394	-221.40	3	32.5	10.3	2	730-739	K.SEAMKEMEKK.L	Oxidation: 7

Detailed Protein Report

Protein 511: transcription factor SOX-6 isoform 3 [Homo sapiens]

Accession: gi|224967050
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 21.8
MW [kDa]: 88.9
pI: 6.9
Sequence Coverage [%]: 3.5
No. of unique Peptides: 2

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
1137	4	500.6373	-249.35	2	42.7	11.7	0	232-239	R.QQQEQIAR.Q	
1327	1	660.9680	-58.76	3	46.7	10.1	0	344-363	K.MPSTPQPPNTAGTVSPTGIK.N	

Detailed Protein Report

Protein 512: 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

QD:QU	**Median:**	0.82	**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	QD:QU 0.82
1859	1	682.2687	-75.42	3	53.6	10.7	1	1808-1825	K.KLDVEEPDSANSSFYSTR.S		

Detailed Protein Report

Protein 513: 2-oxoglutarate dehydrogenase-like, mitochondrial isoform c [Homo sapiens]

Accession:	gi|221316669	**Score:**	21.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	91.2
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 1.31 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MFINDVEQCQ	WIRQKFETPG	VMQFSSEEKR	TLLARLVRSM	RFEDFLARKW	SSEKRFGLEG	CEVMIPALKT	IIDKSSEMGI
90	100	110	120	130	140	150	160
ENVILGMPHR	GRLNVLANVI	RKDLEQIFCQ	FDPKLEAADE	GSGDVKYHLG	MYHERINRVT	NRNITLSLVA	NPSHLEAVDP
170	180	190	200	210	220	230	240
VVQGKTKAEQ	FYRGDAQGKK	VMSILVHGDA	AFAGQGVVYE	TFHLSDLPSY	TTNGTVHVVV	NNQIGFTTDP	RMARSSPYPT
250	260	270	280	290	300	310	320
DVARVVNAPI	FHVNADDPEA	VIYVCSVAAE	WRNTFNKDVV	VDLVCYRRRG	HNEMDEPMFT	QPLMYKQIHR	QVPVLKKYAD
330	340	350	360	370	380	390	400
KLIAEGTVTL	QEFEEEIAKY	DRICEEAYGR	SKDKKILHIK	HWLDSPWPGF	FNVDGEPKSM	TCPATGIPED	MLTHIGSVAS
410	420	430	440	450	460	470	480
SVPLEDFKIH	TGLSRILRGR	ADMTKNRTVD	WALAEYMAFG	SLLKEGIHVR	LSGQDVERGT	FSHRHHVLHD	QEVDRRTCVP
490	500	510	520	530	540	550	560
MNHLWPDQAP	YTVCNSSLSE	YGVLGFELGY	AMASPNALVL	WEAQFGDFHN	TAQCIIDQFI	STGQAKWVRH	NGIVLLLPHG
570	580	590	600	610	620	630	640
MEGMGPEHSS	ARPERFLQMS	NDDSDAYPAF	TKDFEVSQLY	DCNWIVVNCS	TPANYFHVLR	RQILLPFRKP	LIIFTPKSLL
650	660	670	680	690	700	710	720
RHPEAKSSFD	QMVSGTSFQR	VIPEDGAAAR	APEQVQRLIF	CTGKVYYDLV	KERSSQDLEE	KVAITRLEQI	SPFPFDLIKQ
730	740	750	760	770	780	790	800
EAEKYPGAEL	AWCQEEHKNM	GYYDYISPRF	MTILRRARPI	WYVGRDPAAA	PATGNRNTHL	VSLKKFLDTA	FNLQAFEGKT
810							
F							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
865	1	676.8710	-83.95	2	39.3	10.8	2	91-102	R.GRLNVLANVIRK.D		QD:QU	1.31

Detailed Protein Report

Protein 514: protein MRVI1 isoform b [Homo sapiens]

Accession:	gi|154091332	**Score:**	21.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.7
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	3.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTGDATSPEG	ETDKNLANRV	HSPHKRLSHR	HLKVSTASLT	SVDPAGHIID	LVNDQLPDIS	ISEEDKKKNL	ALLEEAKLVS
90	100	110	120	130	140	150	160
ERFLTRRGRK	SRSSPGDSPS	AVSPNLSPSA	SPTSSRSNSL	TVPTPPGLDV	CSGPPSPLPG	APPQKGDEAD	VSSPHPGEPN
170	180	190	200	210	220	230	240
VPKGLADRKQ	NDQRKVSQGR	LAPRPPPVEK	SKEIAIEQKE	NFDPLQYPET	TPKGLAPVTN	SSGKMALNSP	QPGPVESELG
250	260	270	280	290	300	310	320
KQLLKTGWEG	SPLPRSPTQD	AAGVGPPASQ	GRGPAGEPMG	PEAGSKAELP	PTVSRPPLLR	GLSWDSGPEE	PGPRLQKVLA
330	340	350	360	370	380	390	400
KLPLAEEEKR	FAGKAGGKLA	KAPGLKDFQI	QVQPVRMQKL	TKLREEHILM	RNQNLVGLKL	PDLSEAAEQE	KGLPSELSPA
410	420	430	440	450	460	470	480
IEEEESKSGL	DVMPNISDVL	LRKLRVHRSL	PGSAPPLTEK	EVENVFVQLS	LAFRNDSYTL	ESRINQAERE	RNLTEENTEK
490	500	510	520	530	540	550	560
ELENFKASIT	SSASLWHHCE	HRETYQKLLE	DIAVLHRLAA	RLSSRAEVVG	AVRQEKRMSK	ATEVMMQYVE	NLKRTYEKDH
570	580	590	600	610	620	630	640
AELMEFKKLA	NQNSSRSCGP	SEDGVPRTAR	SMSLTLGKNM	PRRRVSVAVV	PKFNALNLPG	QTPSSSSIPS	LPALSESPNG
650	660	670	680	690	700	710	720
KGSLPVTSAL	PALLENGKTN	GDPDCEASAP	ALTLSCLEEL	SQETKARMEE	EAYSKGFQEG	LKKTKELQDL	KEEEEEQKSE
730	740	750	760	770	780	790	800
SPEEPEEVEE	TEEEEKGPRS	SKLEELVHFL	QVMYPKLCQH	WQVIWMMAAV	MLVLTVVLGL	YNSYNSCAEQ	ADGPLGRSTC
810	820	830					
SAAQRDSWWS	SGLQHEQPTE	Q					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2109	1	1065.5116	-99.60	2	54.9	11.2	2	181-199	R.LAPRPPPVEKSKEIAIEQK.E	

Detailed Protein Report

Protein 515: nischarin isoform 1 [Homo sapiens]

Accession:	gi|66472382	**Score:**	21.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	166.5
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATARTFGPE	REAEPAKEAR	VVGSELVDTY	TVYIIQVTDG	SHEWTVKHRY	SDFHDLHEKL	VAERKIDKNL	LPPKKIIGKN
90	100	110	120	130	140	150	160
SRSLVEKREK	DLEVYLQKLL	AAFPGVTPRV	LAHFLHFHFY	EINGITAALA	EELFEKGEQL	LGAGEVFAIG	PLQLYAVTEQ
170	180	190	200	210	220	230	240
LQQGKPTCAS	GDAKTDLGHI	LDFTCRLKYL	KVSGTEGPFG	TSNIQEQLLP	FDLSIFKSLH	QVEISHCDAK	HIRGLVASKP
250	260	270	280	290	300	310	320
TLATLSVRFS	ATSMKEVLVP	EASEFDEWEP	EGTTLEGPVT	AVIPTWQALT	TLDLSHNSIS	EIDESVKLIP	KIEFLDLSHN
330	340	350	360	370	380	390	400
GLLVVDNLQH	LYNLVHLDLS	YNKLSSLEGL	HTKLGNIKTL	NLAGNLLESL	SGLHKLYSLV	NLDLRDNRIE	QMEEVRSIGS
410	420	430	440	450	460	470	480
LPCLEHVSLL	NNPLSIIPDY	RTKVLAQFGE	RASEVCLDDT	VTTEKELDTV	EVLKAIQKAK	EVKSKLSNPE	KKGGEDSRLS
490	500	510	520	530	540	550	560
AAPCIRPSSS	PPTVAPASAS	LPQPILSNQG	IMFVQEEALA	SSLSSTDSLT	PEHQPIAQGC	SDSLESIPAG	QAASDDLRDV
570	580	590	600	610	620	630	640
PGAVGGASPE	HAEPEVQVVP	GSGQIIFLPF	TCIGYTATNQ	DFIQRLSTLI	RQAIERQLPA	WIEAANQREE	GQGEQGEEED
650	660	670	680	690	700	710	720
EEEEEEEDVA	ENRYFEMGPP	DVEEEEGGGQ	GEEEEEEEED	EEAEEERLAL	EWALGADEDF	LLEHIRILKV	LWCFLIHVQG
730	740	750	760	770	780	790	800
SIRQFAACLV	LTDFGIAVFE	IPHQESRGSS	QHILSSLRFV	FCFPHGDLTE	FGFLMPELCL	VLKVRHSENT	LFIISDAANL
810	820	830	840	850	860	870	880
HEFHADLRSC	FAPQHMAMLC	SPILYGSHTS	LQEFLRQLLT	FYKVAGGCQE	RSQGCFPVYL	VYSDKRMVQT	AAGDYSGNIE
890	900	910	920	930	940	950	960
WASCTLCSAV	RRSCCAPSEA	VKSAAIPYWL	LLTPQHLNVI	KADFNPMPNR	GTHNCRNRNS	FKLSRVPLST	VLLDPTRSCT
970	980	990	1000	1010	1020	1030	1040
QPRGAFADGH	VLELLVGYRF	VTAIFVLPHE	KFHFLRVYNQ	LRASLQDLKT	VVIAKTPGTG	GSPQGSFADG	QPAERRASND
1050	1060	1070	1080	1090	1100	1110	1120
QRPQEVPAEA	LAPAPAEVPA	PAPAAASASG	PAKTPAPAEA	STSALVPEET	PVEAPAPPPA	EAPAQYPSEH	LIQATSEENQ
1130	1140	1150	1160	1170	1180	1190	1200
IPSHLPACPS	LRHVASLRGS	AIIELFHSSI	AEVENEELRH	LMWSSVVFYQ	TPGLEVTACV	LLSTKAVYFV	LHDGLRRYFS
1210	1220	1230	1240	1250	1260	1270	1280
EPLQDFWHQK	NTDYNNSPFH	ISQCFVLKLS	DLQSVNVGLF	DQHFRLTGST	PMQVVTCLTR	DSYLTHCFLQ	HLMVVLSSLE
1290	1300	1310	1320	1330	1340	1350	1360
RTPSPEPVDK	DFYSEFGNKT	TGKMENYELI	HSSRVKFTYP	SEEEIGDLTF	TVAQKMAEPE	KAPALSILLY	VQAFQVGMPP
1370	1380	1390	1400	1410	1420	1430	1440
PGCCRGPLRP	KTLLLTSSEI	FLLDEDCVHY	PLPEFAKEPP	QRDRYRLDDG	RRVRDLDRVL	MGYQTYPQAL	TLVFDDVQGH
1450	1460	1470	1480	1490	1500	1510	
DLMGSVTLDH	FGEVPGGPAR	ASQGREVQWQ	VFVPSAESRE	KLISLLARQW	EALCGRELPV	ELTG	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2021	1	890.3901	-125.48	2	55.7	10.8	0	359-375	K.TLNLAGNLLESLSGLHK.L	

Detailed Protein Report

Protein 516: **phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 isoform b [Homo sapiens]**

Accession:	gi|40254823	**Score:**	21.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	133.1
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.90 **CV:** 0.00 % **No. of 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	Ratios
623	1	584.8181	3.43	2	36.4	21.6	0	79-87	K.LDQLIEFYK.K		QD:QU 0.90

Detailed Protein Report

Protein 517: 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 [%]:	7.7
		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
1765	1	917.4139	-26.15	2	50.6	11.4	2	242-257	K.NARNNKSEEAIDTESR.L	

Detailed Protein Report

Protein 518: apprataxin and PNK-like factor [Homo sapiens]

Accession:	gi|27734905	**Score:**	21.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.9
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Carbamidomethyl, Oxidation	**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; Oxidation: 5

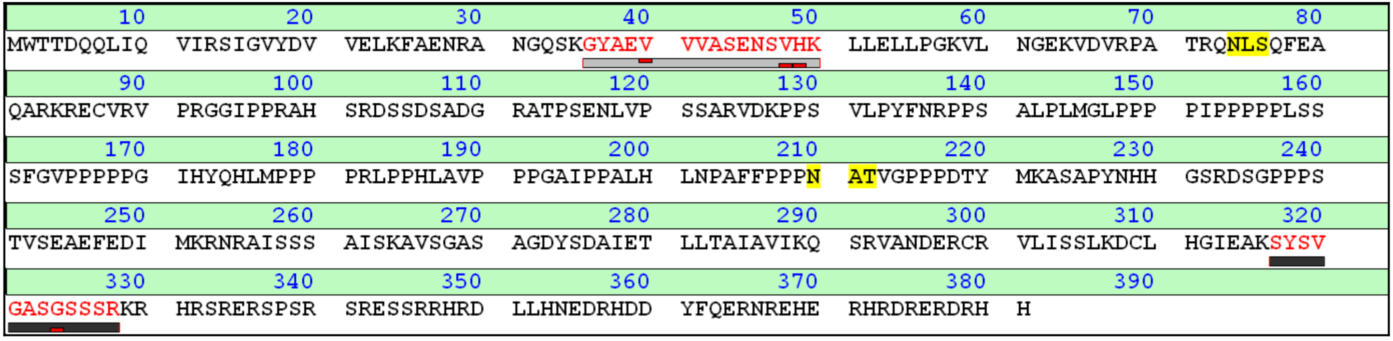
Detailed Protein Report

Protein 519: **PREDICTED: cleavage and polyadenylation specificity factor subunit 7 isoform X5 [Homo sapiens]**

Accession:	gi|530397403	**Score:**	21.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.9
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	7.1
		No. of unique Peptides:	2

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
1937	1	794.7610	-177.32	2	54.6	10.1	0	36-50	K.GYAEVVVASENSVHK.L	
2417	1	572.6438	-211.80	2	58.9	11.5	0	317-328	K.SYSVGASGSSSR.K	

Detailed Protein Report

Protein 520: protein FAM83F [Homo sapiens]

Accession: gi|156564372
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 21.6
MW [kDa]: 55.5
pI: 9.2
Sequence Coverage [%]: 7.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAESQLNCLD	EAHVNEKVTE	AQAAFYYCER	RRAALEALLG	GGEQAYRERL	KEEQLRDFLS	SPERQALRAA	WSPYEDAVPA
90	100	110	120	130	140	150	160
ANARGKSKAK	AKAPAPAPAE	SGESLAYWPD	RSDTEVPPLD	LGWTDTGFYR	GVSRVTLFTH	PPKDEKAPHL	KQVVRQMIQQ
170	180	190	200	210	220	230	240
AQKVIAVVMD	LFTDGDIFQD	IVDAACKRRV	PVYIILDEAG	VKYFLEMCQD	LQLTDFRIRN	IRVRSVTGVG	FYMPMGRIKG
250	260	270	280	290	300	310	320
TLSSRFLMVD	GDKVATGSYR	FTWSSSHVDR	NLLLLLTGQN	VEPFDTEFRE	LYAISEEVDL	YRQLSLAGRV	GLHYSSTVAR
330	340	350	360	370	380	390	400
KLINPKYALV	SGCRHPPGEM	MRWAARQQRE	AGGNPEGQEE	GASGGESAWR	LESFLKDLVT	VEQVLPPVEP	IPLGELSQKD
410	420	430	440	450	460	470	480
GRMVSHMHRD	LKPKSREAPS	RNGMGEAARG	EAAPARRFSS	RLFSRRAKRP	AAPNGMASSV	STETSEVEFL	TGKRPNENSS
490	500	510					
ADISGKTSPS	SAKPSNCVIS						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1194	1	628.4650	156.14	3	43.4	11.0	2	310-326	R.VGLHYSSTVARKLINPK.Y	

Detailed Protein Report

Protein 521: inhibitor of nuclear factor kappa-B kinase subunit alpha [Homo sapiens]

Accession:	gi|62241001	**Score:**	21.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	84.6
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.6
		No. of unique 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
2406	1	665.3146	-54.38	2	60.5	21.5	0	366-377	R.KPASQCVLDGVR.G	Carbamidomethyl: 6

Detailed Protein Report

Protein 522: transcription initiation factor TFIID subunit 4B [Homo sapiens]

Accession:	gi|148792970	**Score:**	21.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	91.0
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPAGLTEPAG	AAPPAAVSAS	GTVTMAPAGA	LPVRVESTPV	ALGAVTKAPV	SVCVEPTASQ	PLRSPVGTLV	TKVAPVSAPP
90	100	110	120	130	140	150	160
KVSSGPRLPA	PQIVAVKAPN	TTTIQFPANL	QLPPGTVLIK	SNSGPLMLVS	PQQTVTRAET	TSNITSRPAV	PANPQTVKIC
170	180	190	200	210	220	230	240
TVPNSSSQLI	KKVAVTPVKK	LAQIGTTVVT	TVPKPSSVQS	VAVPTSVVTV	TPGKPLNTVT	TLKPSSLGAS	STPSNEPNLK
250	260	270	280	290	300	310	320
AENSAAVQIN	LSPTMLENVK	KCKNFLAMLI	KLACSGSQSP	EMGQNVKKLV	EQLLDAKIEA	EEFTRKLYVE	LKSSPQPHLV
330	340	350	360	370	380	390	400
PFLKKSVVAL	RQLLPNSQSF	IQQCVQQTSS	DMVIATCTTT	VTTSPVVTTT	VSSSQSEKSI	IVSGATAPRT	VSVQTLNPLA
410	420	430	440	450	460	470	480
GPVGAKAGVV	TLHSVGPTAA	TGGTTAGTGL	LQTSKPLVTS	VANTVTTVSL	QPEKPVVSGT	AVTLSLPAVT	FGETSGAAIC
490	500	510	520	530	540	550	560
LPSVKPVVSS	AGTTSDKPVI	GTPVQIKLAQ	PGPVLSQPAG	IPQAVQVKQL	VVQQPSGGNE	KQVTTISHSS	TLTIQKCGQK
570	580	590	600	610	620	630	640
TMPVNTIIPT	SQFPPASILK	QITLPGNKIL	SLQASPTQKN	RIKENVTSCF	RDEDDINDVT	SMAGVNLNEE	NACILATNSE
650	660	670	680	690	700	710	720
LVGTLIQSCK	DEPFLFIGAL	QKRILDIGKK	HDITELNSDA	VNLISQATQE	RLRGLLEKLT	AIAQHRMTTY	KASENYILCS
730	740	750	760	770	780	790	800
DTRSQLKFLE	KLDQLEKQRK	DLEEREMLLK	AAKSRSNKED	PEQLRLKQKA	KELQQLELAQ	IQHRDANLTA	LAAIGPRKKR
810	820	830	840	850	860	870	
PLESGIEGLK	DNLLASGTSS	LTATKQLHRP	RITRICLRDL	IFCMEQEREM	KYSRALYLAL	LK	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2538	3	913.4572	17.18	2	62.4	21.4	1	835-848	R.ICLRDLIFCMEQER.E	Carbamidomethyl: 2

Detailed Protein Report

Protein 523: PREDICTED: uncharacterized protein LOC102725205, partial [Homo sapiens]

Accession:	gi|578845222	**Score:**	21.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	95.5
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	2

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
1138	1	983.4246	-85.91	2	44.4	11.1	1	82-103	R.TAVVGRIPGAGMPAGAGGPACR.C	
992	1	647.6724	-181.96	2	40.9	10.3	0	614-625	K.VEYADGGMPEAR.L	

Detailed Protein Report

Protein 524: ubiquitin-associated and SH3 domain-containing protein A isoform 3 [Homo sapiens]

Accession:	gi|343478263	**Score:**	21.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.1
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.6
		No. of unique Peptides:	2

10	20	30	40	50	60	70	80
MAAGETQLYA	KVSNKLKSRS	SPSLLEPLLA	MGFPVHTALK	ALAATGRKTA	EEALAWLHDH	CNDPSLDDPI	PQEYALFLCP
90	100	110	120	130	140	150	160
TGPLLEKLQE	FWRESKRQCA	KNRAHEVFPH	VTLCDFFTCE	DQKVECLYEA	LKRAGDRLLG	SFPTAVPLAL	HSSISYLGFF
170	180	190	200	210	220	230	240
VSGSPADVIR	EFAMTFATEA	SLLADCSVKP	CTKQLHLTLA	HKFYPHHQRT	LEQLARAIPL	GHSCQWTAAL	YSRDMRFVHY
250	260	270	280	290	300	310	320
QTLRALFQYK	PQNVDELTLS	PGDYIFVDPT	QQDEASEGWV	IGISQRTGCR	GFLPENYTDR	ASESDTWVKH	RMYTFSLATD
330	340	350	360	370	380	390	400
LNSRKDGEAS	SRCSGEFLPQ	TARSLSSLQA	LQATVARKSV	LVVRHGERVD	QIFGKAWLQQ	CSTPDGKYYR	PDLNFPCSLP
410	420	430	440	450	460	470	480
RRSRGIKDFE	NDPPLSSCGI	FQSRIAGDAL	LDSGIRISSV	FASPALRCVQ	TAKLILEELK	LEKKIKIRVE	PGIFEWTKWE
490	500	510	520	530			
AGKTTPTLMS	LEELKEANFN	IDTDYRSLPW	ACASVKKIKR	KENGSW			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
869	1	955.4602	-71.25	3	39.3	10.1	1	20-47	R.SSPSLLEPLLAMGFPVHTALKALAATGR.K	Oxidation: 12
2807	1	937.4543	-19.47	2	64.2	11.3	0	217-233	R.AIPLGHSCQWTAALYSR.D	

Detailed Protein Report

Protein 525: 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

Quantitation

QD:QU **Median:** 0.82 **CV:** 0.00 % **No. of 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	Ratios	
88	1	877.8653	-84.40	2	31.0	21.3	2	193-208	K.IMHPSSRSPQNSGGRK.S	Oxidation: 2	QD:QU	0.82

Detailed Protein Report

Protein 526: PREDICTED: CAS1 domain-containing protein 1 isoform X2 [Homo sapiens]

Accession:	gi|578814529	**Score:**	21.3
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:	1

Quantitation

QD:QU	**Median:**	1.91	**CV:**	0.00 %	**No. of Peptides:**	1

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
175	2	793.8315	-49.90	2	32.2	21.3	1	160-173	R.RQPQCCPCAAPLSR.S	Carbamidomethyl: 8	QD:QU 1.91

Detailed Protein Report

Protein 527: 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 528: PREDICTED: zinc finger protein 451 isoform X2 [Homo sapiens]

Accession:	gi|530381758	**Score:**	21.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	111.8
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.71 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MGDPGSEIIE	SVPPAGPEAS	ESTTDENEDD	IQFVSEGPLR	PVLEYIDLVS	SDDEEPSTSY	TDENIKRKDH	IDYQKDKVAL
90	100	110	120	130	140	150	160
TLARLARHVE	VEKQQKEEKN	RAFREKIDFQ	HAHGLQELEF	IRGHSDTEAA	RLCVDQWLKM	PGLKTGTINC	GTKSSFRRGG
170	180	190	200	210	220	230	240
HTWVSGKPIL	CPIMHCNKEF	DNGHLLLGHL	KRFDHSPCDP	TITLHGPFFS	SFACVVCYKK	FVTQQQYRDH	LFDKEATDDG
250	260	270	280	290	300	310	320
HNNNLLPQII	QCFACPNCFL	LFSRKEECSK	HMSGKNHFHQ	SFKLGDNKGI	AHPISFPSFA	KKLLISLCKD	VPFQVKCVAC
330	340	350	360	370	380	390	400
HKTLRSHMEL	TAHFRVHCRN	AGPVAVAEKS	ITQVAEKFIL	RGYCPDCNQV	FVDETSTQNH	KQNSGHKVRV	INSVEESVLL
410	420	430	440	450	460	470	480
YCHSSEGNKD	PSSDLHLLLD	QSKFSSLKRT	MSIKESSSLE	CIAIPKKKMN	LKDKSHEGVA	CVQKEKSVVK	TWFCECNQRF
490	500	510	520	530	540	550	560
PSEDAVEKHV	FSANTMGYKC	VVCGKVCDDS	GVIRLHMSRI	HGGAHLNNFL	FWCRTCKKEL	TRKDTIMAHV	TEFHNGHRYF
570	580	590	600	610	620	630	640
YEMDEVEGET	LPSSSTTLDN	LTANKPSSAI	TVIDHSPANS	SPRGKWQCRI	CEDMFDSQEY	VKQHCMSLAS	HKFHRYSCAH
650	660	670	680	690	700	710	720
CRKPFHKIET	LYRHCQDEHD	NEIKIKYFCG	LCDLIFNVEE	AFLSHYEEHH	SIDYVFVSEK	TETSIKTEDD	FPVIETSNQL
730	740	750	760	770	780	790	800
TCGCRESYIC	KVNRKEDYSR	CLQIMLDKGK	LWFRCSLCSA	TAQNLTDMNT	HIHQVHKEKS	DEEEQQYVIK	CGTCTKAFHD
810	820	830	840	850	860	870	880
PESAQQHFHR	KHCFLQKPSV	AHFGSEKSNL	YKFTASASHT	ERKLKQAINY	SKSLDMEKGV	ENDLSYQNIE	EEIVELPDLD
890	900	910	920	930	940	950	960
YLRTMTHIVF	VDFDNWSNFF	GHLPGHLNQG	TFIWGFQGGN	TNWKPPLNCK	IYNYLNRIGC	FFLHPRCSKR	KDAADFAICM
970	980						
HNVTVMITWV	PKILQ						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2396	1	832.2427	-131.97	2	58.6	10.3	0	610-622	R.ICEDMFDSQEYVK.Q	Carbamidomethyl: 2	QD:QU 0.71

Detailed Protein Report

Protein 529: PDZ domain-containing RING finger protein 4 isoform 2 [Homo sapiens]

Accession:	gi|142976783	**Score:**	21.3
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

QD:QU **Median:** 0.46 **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
1046	1	639.3055	-106.40	2	41.6	11.1	2	369-378	R.FRQLLELKCK.I		QD:QU 0.46

Detailed Protein Report

Protein 530: PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform X6 [Homo sapiens]

Accession: gi|530427511
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 21.3
MW [kDa]: 60.5
pI: 9.8
Sequence Coverage [%]: 6.5
No. of unique 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
814	1	737.3793	37.51	3	40.2	10.9	0	164-186	K.GIGMGNIGPAGMGMEGIGFGINK.M	Oxidation: 4, 12

Detailed Protein Report

Protein 531: **noelin isoform 2 precursor [Homo sapiens]**

Accession:	gi|5453547	**Score:**	21.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.9
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	20.7
		No. of unique Peptides:	2

```
        10         20         30         40         50         60         70         80
MPGRWRWQRD MHPARKLLSL LFLILMGTEL TQVLPTNPEE SWQVYSSAQD SEGRCICTVV APQQTMCSRD ARTKQLRQLL
        90        100        110        120        130        140
EKVQNMSQSI EVLDRRTQRD LQYVEKMENQ MKGLESKFKQ VEESHKQHLA RQFKG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2540	1	856.9279	52.38	2	62.4	10.2	0	55-69	R.CICTVVAPQQTMCSR.D	Carbamidomethyl: 1; Oxidation: 12
1127	1	759.8346	-63.26	2	44.2	11.0	0	83-95	K.VQNMSQSIEVLDR.R	

Detailed Protein Report

Protein 532: 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

Quantitation

QD:QU **Median:** 0.87 **CV:** 0.00 % **No. of 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	Ratios
1179	1	941.4167	-103.81	2	44.9	10.9	1	193-208	R.MRVDIEVDPLQLLGQR.A		QD:QU 0.87

Detailed Protein Report

Protein 533: 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 534: **X-linked retinitis pigmentosa GTPase regulator-interacting protein 1 [Homo sapiens]**

Accession:	gi|112734867	**Score:**	21.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	146.6
Database Date:	2015-11-30	**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 535: PREDICTED: apolipophorins-like [Homo sapiens]

Accession:	gi|578797156	**Score:**	21.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.4
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578828430	refseq_human (refseq_human_20140103.fasta)	PREDICTED: apolipophorins-like [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MDADASSRPL DTDLSFSLRM CAKKEIKQPL LDALPSCGTE HCVGLMKELI ASAAVEADEV EAWLSSLAFL PQPTDAMVHM

        90        100        110        120        130        140        150        160
LLPLLQTPRA SPGAFLGISA LVHNLCASLD GPCGQLPGVG SLVRILGDAL GENCTIQEPS DDDKVRTSSV LSTGFSAPSG

       170        180        190        200        210        220        230        240
AEANQLQLVL KAVGNAGLAA MALTPTLSAC ASLRSSTPEI RLGAIQAFRR VPCSADRSVL SRLYQSLEED AEIRINAYLA

       250        260        270        280        290        300        310        320
LMRCPSEEVF AQVRRTQAGE LSTQVGSFVW SHILQLLETH DPLKRALRDT LPEDILSQEF HPEMWKHSSY SDVTFRSVSG

       330        340        350        360        370        380        390        400
SLGANLEGTL LFSPASFLPR SATVNLTIHT MGRAFNLLEL GLRLENAEEI AHRLFGRKSF WGQEDGREPE PEEPPGPEPG

       410        420        430        440        450        460        470        480
PAPQPASPEC PGDRDRRMRY LQQKVTRRRG ARQALRCELS VKLLGQELSF VNCGATGSHV NHWPLNLAEL AIKLMKGQEV

       490        500        510        520        530        540        550        560
QMNRRLSLAA QELVFPTVSG LPARLTLNAS AAISIRVRGT TDFQQRSDFS VNGYVKPRYL APGSWRRLGG GIPSLQRAAE

       570        580        590        600        610        620        630        640
AWVTSVWGPR DAAGTCLSLS ALLQISAQMG TAGILGQAGL RWVTSVRSAA SLDGGIQVQK GRVLKVHLNT PEEAVELLSF

       650        660        670        680        690
SSQLYLITRD GVRSLRHVPG PSEVQSCTGE EGRQQGLHDI VPRWASQG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2604	1	913.4894	86.61	2	63.2	21.0	0	657-673	R.HVPGPSEVQSCTGEEGR.Q	Carbamidomethyl: 11

Detailed Protein Report

Protein 536: kinesin-like protein KIF20B isoform 2 [Homo sapiens]

Accession: gi|46049114
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 21.0
MW [kDa]: 206.0
pI: 5.5
Sequence Coverage [%]: 2.0
No. of unique Peptides: 1

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]					
1683	1	954.5011	22.43	3	51.3	10.8	1	448-471	K.GKICMIVNISQCYLAYDETLNVLK.F	Carbamidomethyl: 4, 12; Oxidation: 5

Detailed Protein Report

Protein 537: **2'-5'-oligoadenylate synthase 2 isoform 1 [Homo sapiens]**

Accession:	gi|74229019	**Score:**	21.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.4
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	2

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
2142	2	596.7577	-225.65	2	57.2	10.2	2	556-566	R.KLKPKGSLPPK.Y	
1541	1	669.8176	-79.84	2	49.5	10.7	2	707-717	R.SHRILNNNSKR.N	

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Detailed Protein Report

Protein 538: 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 539: **PREDICTED: membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2 isoform X1 [Homo sapiens]**

Accession:	gi|530386693	**Score:**	20.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	157.1
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSKSLKKKSH	WTSKVHESVI	GRNPEGQLGF	ELKGGAENGQ	FPYLGEVKPG	KVAYESGSKL	VSEELLLEVN	ETPVAGLTIR
90	100	110	120	130	140	150	160
DVLAVIKHCK	DPLRLKCVKQ	GGIVDKDLRH	YLNLRFQKGS	VDHELQQIIR	DNLYLRTVPC	TTRPHKEGEV	PGVDYIFITV
170	180	190	200	210	220	230	240
EDFMELEKSG	ALLESGTYED	NYYGTPKPPA	EPAPLLLNVT	DQILPGATPS	AEGKRKRNKS	VSNMEKASIE	PPEEEEEERP
250	260	270	280	290	300	310	320
VVNGNGVVVT	PESSEHEDKS	AGASGEMPSQ	PYPAPVYSQP	EELKEQMDDT	KPTKPEDNEE	PDPLPDNWEM	AYTEKGEVYF
330	340	350	360	370	380	390	400
IDHNTKTTSW	LDPRLAKKAK	PPEECKENEL	PYGWEKIDDP	IYGTYYVDHI	NRRTQFENPV	LEAKRKLQQH	NMPHTELGTK
410	420	430	440	450	460	470	480
PLQAPGFREK	PLFTRDASQL	KGTFLSTTLK	KSNMGFGFTI	IGGDEPDEFL	QVKSVIPDGP	AAQDGKMETG	DVIVYINEVC
490	500	510	520	530	540	550	560
VLGHTHADVV	KLFQSVPIGQ	SVNLVLCRGY	PLPFDPEDPA	NSMVPPLAIM	ERPPPVMVNG	RHNYETYLEY	ISRTSQSVPD
570	580	590	600	610	620	630	640
ITDRPPHSLH	SMPTDGQLDG	TYPPPVHDDN	VSMASSGATQ	AELMTLTIVK	GAQGFGFTIA	DSPTGQRVKQ	ILDIQGCPGL
650	660	670	680	690	700	710	720
CEGDLIVEIN	QQNVQNLSHT	EVVDILKDCP	IGSETSLIIH	RGGFFSPWKT	PKPIMDRWEN	QGSPQTSLSA	PAIPQNLPFP
730	740	750	760	770	780	790	800
PALHRSSFPD	STEAFDPRKP	DPYELYEKSR	AIYESRRPDY	KELDVHLRRM	ESGFGFRILG	GDEPGQPILI	GAVIAMGSAD
810	820	830	840	850	860	870	880
RDGRLHPGDE	LVYVDGIPVA	GKTHRYVIDL	MHHAARNGQV	NLTVRRKVLC	GGEPCPENGR	SPGSVSTHHS	SPRSDYATYT
890	900	910	920	930	940	950	960
NSNHAAPSSN	ASPPEGFASH	SLQTSDVVIH	RKENEGFGFV	IISSLNRPES	GSTITVPHKI	GRIIDGSPAD	RCAKLKVGDR
970	980	990	1000	1010	1020	1030	1040
ILAVNGQSII	NMPHADIVKL	IKDAGLSVTL	RIIPQEELNS	PTSAPSSEKQ	SPMAQQSPLA	QQSPLAQPSP	ATPNSPIAQP
1050	1060	1070	1080	1090	1100	1110	1120
APPQPLQLQG	HENSYRSEVK	ARQDVKPDIR	QPPFTDYRQP	PLDYRQPPGG	DYQQPPPLDY	RQPPLLDYRQ	HSPDTRQYPL
1130	1140	1150	1160	1170	1180	1190	1200
SDYRQPQDFD	YFTVDMEKGA	KGFGFSIRGG	REYKMDLYVL	RLAEDGPAIR	NGRMRVGDQI	IEINGESTRD	MTHARAIELI
1210	1220	1230	1240	1250	1260	1270	1280
KSGGRRVRLL	LKRGTGQVPE	YDEPAPWSSP	AAAAPGLPEV	GVSLDDGLAP	FSPSHPAPPS	DPSHQISPGP	TWDIKREHDV
1290	1300	1310	1320	1330	1340	1350	1360
RKPKELSACG	QKKQRLGEQR	ERSASPQRAA	RPRLEEAPGG	QGRPEAGRPA	SEARAPGLAA	ADAADAARAG	GKEAPRAAAG
1370	1380	1390	1400	1410	1420	1430	1440
SELCRREGPG	AAPAFAGPGG	GGSGALEAEG	RAGARAGPRP	GPRPPGGAPA	RKAAVAPGPW	KVPGSDKLPS	VLKPGASAAS
1450							
R							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
301	1	638.3361	5.51	2	33.8	10.3	0	374-384	R.TQFENPVLEAK.R	

Detailed Protein Report

Protein 540: PREDICTED: ataxin-7-like protein 1 isoform X1 [Homo sapiens]

Accession: gi|530385637
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 20.9
MW [kDa]: 92.6
pI: 10.5
Sequence Coverage [%]: 3.8
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MTSERSRIPC	LSAAAAEGTG	KKQQEGRAMA	TLDRKVPSPE	AFLGKPWSSW	IDAAKLHCSD	NVDLEEAGKE	GGKSREVMRL
90	100	110	120	130	140	150	160
NKEDMHLFGH	YPAHDDFYLV	VCSACNQVVK	PQVFQSHCER	RHGSMCRPSP	SPVSPASNPR	TSLVQVKTKA	CLSGHHSASS
170	180	190	200	210	220	230	240
TSKPFKTPKD	NLLTSSSKQH	TVFPAKGSRD	KPCVPVPVVS	LEKIPNLVKA	DGANVKMNST	TTTAVSASST	SSSAVSTPPL
250	260	270	280	290	300	310	320
IKPVLMSKSV	PPSPEKILNG	KGILPTTIDK	KHQNGTKNSN	KPYRRLSERE	FDPNKHCGVL	DPETKKPCTR	SLTCKTHSLS
330	340	350	360	370	380	390	400
HRRAVPGRKK	QFDLLLAEHK	AKSREKEVKD	KEHLLTSTRE	ILPSQSGPAQ	DSLLGSSGSS	GPEPKVASPA	KSRPPNSVLP
410	420	430	440	450	460	470	480
RPSSANSISS	STSSNHSGHT	PEPPLPPVGG	DLASRLSSDE	GEMDGADESE	KLDCQFSTHH	PRPLAFCSFG	SRLMGRGYYV
490	500	510	520	530	540	550	560
FDRRWDRFRF	ALNSMVEKHL	NSQMWKKIPP	AADSPLPSPA	AHITTPVPAS	VLQPFSNPSA	VYLPSAPISS	RLTSSYIMTS
570	580	590	600	610	620	630	640
AMLSNAAFVT	SPDPSALMSH	TTAFPHVAAT	LSIMDSTFKA	PSAVSPIPAV	IPSPSHKPSK	TKTSKSSKVK	DLSTRSDESP
650	660	670	680	690	700	710	720
SNKKRKPQSS	TSSSSSSSSS	SLQTSLSSPL	SGPHKKNCVL	NASSALNSYQ	AAPPYNSLSV	HNSNNGVSPL	SAKLEPSGRT
730	740	750	760	770	780	790	800
SLPGGPADIV	RQVGAVGGSS	DSCPLSVPSL	ALHAGDLSLA	SHNAVSSLPL	SFDKSEGKKR	KNSSSSSKAC	KITKMPGMNS
810	820	830	840	850	860	870	880
VHKKNPPSLL	APVPDPVNST	SSRQVRDLLA	PPSPALGGRG	SWAAPLLSRA	APTGNTSLIP	VLVFPEGSFH	PLL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
92	1	726.3490	-5.83	3	31.1	10.2	1	121-140	R.RHGSMCRPSPSPVSPASNPR.T	Carbamidomethyl: 6

Detailed Protein Report

Protein 541: glycolipid transfer protein domain-containing protein 2 precursor [Homo sapiens]

Accession:	gi|304571945	**Score:**	20.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.6
Database Date:	2015-11-30	**pI:**	11.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.7
		No. of unique Peptides:	2

Quantitation

QD:QU **Median:** 1.44 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MGVAARPPAL RHWFSHSIPL AIFALLLLYL SVRSLGARSG CGPRAQPCVP GETAPFQVRQ ESGTLEAPER KQPPCLGPRG
        90        100        110        120        130        140        150        160
MLGRMMRRFH ASLKPEGDVG LSPYLAGWRA LVEFLTPLGS VFAFATREAF TKVTDLEARV HGPDAEHYWS LVAMAAWERR
       170        180        190        200        210        220        230        240
AGLLEQPGAA PRDPTRSSGS RTLLLLHRAL RWSQLCLHRV ATGALGGPEA GVQCSDAYRA ALGPHHPWLV RQTARLAFLA
       250        260        270        280        290        300
FPGRRRLLEL ACPGATEAEA RAALLRAAGT LEDVYNRTQS LLAERGLLQL A
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2172	1	900.3349	-132.49	2	55.8	10.4	2	72-87	K.QPPCLGPRGMLGRMMR.R		
366	1	800.8792	-30.48	2	34.5	10.5	0	247-261	R.LLELACPGATEAEAR.A	Carbamidomethyl: 6	QD:QU 1.44

Detailed Protein Report

Protein 542: 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 543: PREDICTED: centrosomal protein of 290 kDa isoform X4 [Homo sapiens]

Accession:	gi|530400856	**Score:**	20.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	234.7
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:** 0.77	**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
1299	1	500.8071	-19.25	2	46.4	10.4	2	2-9	M.QKLSLRQK.S		QD:QU 0.77

Detailed Protein Report

Protein 544: PREDICTED: ribosomal protein S6 kinase-like 1 isoform X5 [Homo sapiens]

Accession:	gi|530404733	**Score:**	20.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.3
Database Date:	2015-11-30	**pI:**	7.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.8
		No. of unique 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
2112	1	1072.4083	-80.50	2	56.8	10.0	0	2-21	M.SLVACECLPSPGLEPEPCSR.A	Carbamidomethyl: 18

Detailed Protein Report

Protein 545: NF-X1-type zinc finger protein NFXL1 [Homo sapiens]

Accession:	gi|89363020	**Score:**	20.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.3
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.3
		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 546: **cytoskeleton-associated protein 2 isoform 3 [Homo sapiens]**

Accession:	gi|557878731	**Score:**	20.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.2
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
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 547: Fanconi anemia group J protein [Homo sapiens]

Accession: gi|301897118
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 20.6
MW [kDa]: 140.8
pI: 6.5
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 548: **PREDICTED: transmembrane and coiled-coil domains protein 2 isoform X7 [Homo sapiens]**

Accession:	gi|530365798	**Score:**	20.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.6
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	7.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MKSKEEETAV DKGDLVALSL PAGHGDTDGP ISLDVPDGAP DPQRTKAAID HLHQKILKIT EQIKIEQEAR DDNVAEYLKL
        90        100        110        120        130        140        150        160
ANNADKQQVS RIKQVFEKKN QKSAQTIAQL HKKLEHYRRR LKEIEQNGPS RQPKDVLRDM QQGLKDVGAN VRAGISGFGG
       170        180        190        200        210        220        230        240
GVVEGVKGSL SGLSQATHTA VVSKPREFAS LIRNKFGSAD NIAHLKDPLE DGPPEEAARA LSGSATLVSS PKYGSDDECS
       250        260        270        280        290        300        310        320
SASASSAGAG SNSGAGPGGA LGSPKSNALY GAPGNLDALL EELREIKEGQ SHLEDSMEDL KTQLQRDYTY MTQCLQEERY
       330        340        350        360        370        380        390        400
RYERLEEQLN DLTELHQNEM TNLKQELASM EEKVAYQSYE RARDIQEAVE SCLTRVTKLE LQQQQQQVVQ LEGVENANAR
       410        420        430        440        450        460        470
ALLGKFINVI LALMAVLLVF VSTIANFITP LMKTRLRITS TTLLVLVLFL LWKHWDSLTY LLEHVLLPS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1834	1	682.2742	-131.55	3	53.3	10.2	1	146-167	K.DVGANVRAGISGFGGGVVEGVK.G	

Detailed Protein Report

Protein 549: PREDICTED: monocarboxylate transporter 8 isoform X1 [Homo sapiens]

Accession:	gi|530421807	**Score:**	20.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.8
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
MALQSQASEE AKGPWQEADQ EQQEPVGSPE PESEPEPEPE PEPVPVPPPE PQPEPQPLPD PAPLPELEFE SERVHEPEPT
        90        100        110        120        130        140        150        160
PTVETRGTAR GFQPPEGGFG WVVVFAATWC NGSIFGIHNS VGILYSMLLE EEKEKNRQVE FQAAWVGALA MGMIFFCSPI
       170        180        190        200        210        220        230        240
VSIFTDRLGC RITATAGAAV AFIGLHTSSF TSSLSLRYFT YGILFGCGCS FAFQPSLVIL GHYFQRRLGL ANGVVSAGSS
       250        260        270        280        290        300        310        320
IFSMSFPFLI RMLGDKIKLA QTFQVLSTFM FVLMLLSLTY RPLLPSSQDT PSKRGVRTLH QRFLAQLRKY FNMRVFRQRT
       330        340        350        360        370        380        390        400
YRIWAFGIAA AALGYFVPYV HLMKYVEEEF SEIKETWVLL VCIGATSGLG RLVSGHISDS IPGLKKIYLQ AYSATVLGTT
       410        420
MWPSTLPVCP PSSGL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2201	1	916.4855	-5.38	2	56.1	20.5	0	355-371	K.ETWVLLVCIGATSGLGR.L	Carbamidomethyl: 8

Detailed Protein Report

Protein 550: 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:	2

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
114	1	1234.5408	-47.71	2	31.4	10.3	1	9-30	R.LGHCHPLRIMGSVDQEEPNAHK.V	
644	1	852.1620	38.48	3	38.0	10.0	2	478-500	K.VLEIPLEPKNNMRATIDCAGILK.L	Oxidation: 12

Detailed Protein Report

Protein 551: PREDICTED: zinc finger protein 717 isoform X8 [Homo sapiens]

Accession:	gi|578805503	**Score:**	20.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.9
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MFPVFSGCFQ ELQEKNKSLE LVSFEEVAVH FTWEEWQDLD DAQRTLYRDV MLETYSSLVS LGHYITKPEM IFKLEQGAEP

        90        100        110        120        130        140        150        160
WIVEETPNLR LSAVQIIDDL IERSHESHDR FFWQIVITNS NTSTQERVEL GKTFNLNSNH VLNLIINNGN SSGMKPGQFN

       170        180        190        200        210        220        230        240
DCQNMLFPIK PGETQSGEKP HVCDITRRSH RHHEHLTQHH KIQTLLQTFQ CNEQGKTFNT EAMFFIHKRV HIVQTFGKYN

       250        260        270        280        290        300        310        320
EYEKACNNSA VIVQVITQVG QPTCCRKSDF TKHQQTHTGE KPYECVECEK PSISKSDLML QCKMPTEEKP YACNWCEKLF

       330        340        350        360        370        380        390        400
SYKSSLIIHQ RIHTGEKPYG CNECGKTFRR KSFLTLHERT HTGDKPYKCI ECGKTFHCKS LLTLHHRTHS GEKPYQCSEC

       410        420        430        440        450        460        470        480
GKTFSQKSYL TIHHRTHTGE KPYACDHCEE AFSHKSRLTV HQRTHTGEKP YECNECGKPF INKSNLRLHQ RTHTGEKPYE

       490        500        510        520        530        540        550        560
CNECGKTFHR KSFLTIHQWT HTGEKPYECN ECGKTFRCKS FLTVHQRTHA GEKPYACNEC GKTYSHKSYL TVHHRTHTGE

       570        580        590        600        610        620        630        640
KPFRCNECRK TFSQKSGLSI HQRTHTGEKP YECKECGKTF CQKSHLSRHQ QTHIGEKSDV AEAGYVFPQN HSFFP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2173	1	1273.4977	-108.18	2	55.8	10.1	1	245-267	K.ACNNSAVIVQVITQVGQPTCCRK.S	Carbamidomethyl: 2, 21

Detailed Protein Report

Protein 552: **PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform X5 [Homo sapiens]**

Accession:	gi|578822285	**Score:**	20.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	70.9
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	2

```
        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 CPDVRLNIIS NLDCVNEVIG IRQLSQSLLP AIVELAEDAK WRVRLAIIEY
       490        500        510        520        530        540        550        560
MPLLAGQLGV EFFDEKLNSL CMAWLVDHVY AIREAATNNL MKLVQKFGTE WAQNTIVPKV LVMANDPNYL HRMTTLFCIN
       570        580        590        600        610        620        630        640
ALSEACGQEI TTKQMLPIVL KMAGDQVANV RFNVAKSLQK IGPILDTNAL QGEVKPVLQK LGQDEDMDVK YFAQEAISVL
       650
ALA
```

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	
2800	1	942.9802	-36.08	2	64.1	10.2	0	436-452	R.LNIISNLDCVNEVIGIR.Q	

Detailed Protein Report

Protein 553: **PREDICTED: lipopolysaccharide-responsive and beige-like anchor protein isoform X6 [Homo sapiens]**

Accession:	gi|530378481	**Score:**	20.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	173.9
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	2

```
        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
RDITKKSLHM NLQNIIDFVR SRITNMSKNC IKWICSN
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1142	1	555.2290	-64.32	2	44.4	10.2	0	803-812	K.QHPDPDSSVK.I	
1642	1	698.8555	-54.14	2	50.8	10.1	0	1488-1501	K.SPVDIVTGGISPVR.D	

Detailed Protein Report

Protein 554: Down syndrome cell adhesion molecule-like protein 1 [Homo sapiens]

Accession:	gi|21359935	**Score:**	20.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	230.5
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MTGAGEPRRE	EPPPQPSAGL	RSRESGAPSA	GGWERAERGR	GAAARPATGP	PPRRIGPLYG	MWLVTFLLLL	DSLHKARPED
90	100	110	120	130	140	150	160
VGTSLYFVND	SLQQVTFSSS	VGVVVPCPAA	GSPSAALRWY	LATGDDIYDV	PHIRHVHANG	TLQLYPFSPS	AFNSFIHDND
170	180	190	200	210	220	230	240
YFCTAENAAG	KIRSPNIRVK	AVFREPYTVR	VEDQRSMRGN	VAVFKCLIPS	SVQEYVSVVS	WEKDTVSIIP	EHRFFITYHG
250	260	270	280	290	300	310	320
GLYISDVQKE	DALSTYRCIT	KHKYSGETRQ	SNGARLSVTD	PAESIPTILD	GFHSQEVWAG	HTVELPCTAS	GYPIPAIRWL
330	340	350	360	370	380	390	400
KDGRPLPADS	RWTKRITGLT	ISDLRTEDSG	TYICEVTNTF	GSAEATGILM	VIDPLHVTLT	PKKLKTGIGS	TVILSCALTG
410	420	430	440	450	460	470	480
SPEFTIRWYR	NTELVLPDEA	ISIRGLSNET	LLITSAQKSH	SGAYQCFATR	KAQTAQDFAI	IALEDGTPRI	VSSFSEKVVN
490	500	510	520	530	540	550	560
PGEQFSLMCA	AKGAPPPTVT	WALDDEPIVR	DGSHRTNQYT	MSDGTTISHM	NVTGPQIRDG	GVYRCTARNL	VGSAEYQARI
570	580	590	600	610	620	630	640
NVRGPPSIRA	MRNITAVAGR	DTLINCRVIG	YPYYSIKWYK	DALLLPDNHR	QVVFENGTLK	LTDVQKGMDE	GEYLCSVLIQ
650	660	670	680	690	700	710	720
PQLSISQSVH	VAVKVPPLIQ	PFEFPPASIG	QLLYIPCVVS	SGDMPIRITW	RKDGQVIISG	SGVTIESKEF	MSSLQISSVS
730	740	750	760	770	780	790	800
LKHNGNYTCI	ASNAAATVSR	ERQLIVRVPP	RFVVQPNNQD	GIYGKAGVLN	CSVDGYPPPK	VMWKHAKGSG	NPQQYHPVPL
810	820	830	840	850	860	870	880
TGRIQILPNS	SLLIRHVLEE	DIGYYLCQAS	NGVGTDISKS	MFLTVKIPAM	ITSHPNTTIA	IKGHAKELNC	TARGERPIII
890	900	910	920	930	940	950	960
RWEKGDTVID	PDRVMRYAIA	TKDNGDEVVS	TLKLKPADRG	DSVFFSCHAI	NSYGEDRGLI	QLTVQEPPDP	PELEIREVKA
970	980	990	1000	1010	1020	1030	1040
RSMNLRWTQR	FDGNSIITGF	DIEYKNKSDS	WDFKQSTRNI	SPTINQANIV	DLHPASVYSI	RMYSFNKIGR	SEPSKELTIS
1050	1060	1070	1080	1090	1100	1110	1120
TEEAAPDGPP	MDVTLQPVTS	QSIQVTWKAP	KKELQNGVIR	GYQIGYRENS	PGSNGQYSIV	EMKATGDSEV	YTLDNLKKFA
1130	1140	1150	1160	1170	1180	1190	1200
QYGVVVQAFN	RAGTGPSSSE	INATTLEDVP	SQPPENVRAL	SITSDVAVIS	WSEPPRSTLN	GVLKGYRVIF	WSLYVDGEWG
1210	1220	1230	1240	1250	1260	1270	1280
EMQNITTTRE	RVELRGMEKF	TNYSVQVLAY	TQAGDGVRSS	VLYIQTKEDV	PGPPAGIKAV	PSSASSVVVS	WLPPTKPNGV
1290	1300	1310	1320	1330	1340	1350	1360
IRKYTIFCSS	PGSGQPAPSE	YETSPEQLFY	RIAHLNRGQQ	YLLWVAAVTS	AGRGNSSEKV	TIEPAGKAPA	KIISFGGTVT
1370	1380	1390	1400	1410	1420	1430	1440
TPWMKDVRLP	CNSVGDPAPA	VKWTKDSEDS	AIPVSMDGHR	LIHTNGTLLL	RAVKAEDSGY	YTCTATNTGG	FDTIIVNLLV
1450	1460	1470	1480	1490	1500	1510	1520
QVPPDQPRLT	VSKTSASSIT	LTWIPGDNGG	SSIRGFVLQY	SVDNSEEWKD	VFISSSERSF	KLDSLKCGTW	YKVKLAAKNS
1530	1540	1550	1560	1570	1580	1590	1600
VGSGRISEII	EAKTHGREPS	FSKDQHLFTH	INSTHARLNL	QGWNNGGCPI	TAIVLEYRPK	GTWAWQGLRA	NSSGEVFLTE
1610	1620	1630	1640	1650	1660	1670	1680
LREATWYELR	MRACNSAGCG	NETAQFATLD	YDGSTIPPIK	SAQGEGDDVK	KLFTIGCPVI	LATLGVALLF	IVRKKRKEKR
1690	1700	1710	1720	1730	1740	1750	1760
LKRLRDAKSL	AEMLISKNNR	SFDTPVKGPP	QGPRLHIDIP	RVQLLIEDKE	GIKQLGDDKA	TIPVTDAEFS	QAVNPQSFCT
1770	1780	1790	1800	1810	1820	1830	1840
GVSLHHPTLI	QSTGPLIDMS	DIRPGTNPVS	RKNVKSAHST	RNRYSSQWTL	TKCQASTPAR	TLTSDWRTVG	SQHGVTVTES
1850	1860	1870	1880	1890	1900	1910	1920
DSYSASLSQD	TDKGRNSMVS	TESASSTYEE	LARAYEHAKL	EEQLQHAKFE	ITECFISDSS	SDQMTTGTNE	NADSMTSMST
1930	1940	1950	1960	1970	1980	1990	2000
PSEPGICRFT	ASPPKPQDAD	RGKNVAVPIP	HRANKSDYCN	LPLYAKSEAF	FRKADGREPC	PVVPPREASI	RNLARTYHTQ
2010	2020	2030	2040	2050	2060	2070	2080
ARHLTLDPAS	KSLGLPHPGA	PAAASTATLP	QRTLAMPAPP	AGTAPPAPGP	TPAEPPTAPS	AAPPAPSTEP	PRAGGPHTKM
2090	2100	2110	2120				
GGSRDSLLEM	STSGVGRSQK	QGAGAYSKSY	TLV				

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2598	1	728.7090	-26.65	3	61.1	20.2	2	867-884	K.ELNCTARGERPIIIRWEK.G	

Detailed Protein Report

Protein 555: **PREDICTED: uncharacterized protein C4orf50 [Homo sapiens]**

Accession:	gi|530358255	**Score:**	20.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.6
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
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
1707	5	1273.8380	122.41	1	51.6	20.2	0	449-459	K.DIVLGIEDMIR.A	

Detailed Protein Report

Protein 556: 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 557: uromodulin-like 1 isoform 4 [Homo sapiens]

Accession:	gi|338753361	**Score:**	20.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	136.4
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl, Oxidation	**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; Oxidation: 10, 14

Detailed Protein Report

Protein 558: replication factor C subunit 4 [Homo sapiens]

Accession:	gi|4506491	**Score:**	19.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.7
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|31881687	refseq_human (refseq_human_20140103.fasta)	replication factor C subunit 4 [Homo sapiens]

10	20	30	40	50	60	70	80
MQAFLKGTSI	STKPPLTKDR	GVAASAGSSG	ENKKAKPVPW	VEKYRPKCVD	EVAFQEEVVA	VLKKSLEGAD	LPNLLFYGPP
90	100	110	120	130	140	150	160
GTGKTSTILA	AARELFGPEL	FRLRVLELNA	SDERGIQVVR	EKVKNFAQLT	VSGSRSDGKP	CPPFKIVILD	EADSMTSAAQ
170	180	190	200	210	220	230	240
AALRRTMEKE	SKTTRFCLIC	NYVSRIIEPL	TSRCSKFRFK	PLSDKIQQQR	LLDIAKKENV	KISDEGIAYL	VKVSEGDLRK
250	260	270	280	290	300	310	320
AITFLQSATR	LTGGKEITEK	VITDIAGVIP	AEKIDGVFAA	CQSGSFDKLE	AVVKDLIDEG	HAATQLVNQL	HDVVVENNLS
330	340	350	360	370			
DKQKSIITEK	LAEVDKCLAD	GADEHLQLIS	LCATVMQQLS	QNC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1817	2	727.2971	-204.84	2	51.2	19.9	2	206-217	K.IQQQRLLDIAKK.E	

Detailed Protein Report

Protein 559: 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	

Detailed Protein Report

Protein 560: 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	

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Detailed Protein Report

Protein 561: PREDICTED: myotubularin-related protein 12 isoform X5 [Homo sapiens]

Accession:	gi|530378841	**Score:**	19.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.8
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	1

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		
FLSLQEIQTA	YSKFKQLFLI	GFPSPPPYCG	SDHTATLLFS	PSSAYHLPSG	EHFGFFL		

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

Detailed Protein Report

Protein 562: 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 563: integrin beta-like protein 1 isoform 3 [Homo sapiens]

Accession:	gi|418203907	**Score:**	19.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.9
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.96 **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		QD:QU 0.96

Detailed Protein Report

Protein 564: PREDICTED: alpha-(1,3)-fucosyltransferase 11 isoform X4 [Homo sapiens]

Accession:	gi|578819000	**Score:**	19.5
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

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
508	2	464.6701	-41.63	2	35.0	19.5	0	343-349	K.NDEEYMK.Y	

Detailed Protein Report

Protein 565: **calcium/calmodulin-dependent protein kinase type II subunit delta isoform 2 [Homo sapiens]**

Accession:	gi|26667189	**Score:**	19.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.40 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MASTTTCTRF	TDEYQLFEEL	GKGAFSVVRR	CMKIPTGQEY	AAKIINTKKL	SARDHQKLER	EARICRLLKH	PNIVRLHDSI
90	100	110	120	130	140	150	160
SEEGFHYLVF	DLVTGGELFE	DIVAREYYSE	ADASHCIQQI	LESVNHCHLN	GIVHRDLKPE	NLLLASKSKG	AAVKLADFGL
170	180	190	200	210	220	230	240
AIEVQGDQQA	WFGFAGTPGY	LSPEVLRKDP	YGKPVDMWAC	GVILYILLVG	YPPFWDEDQH	RLYQQIKAGA	YDFPSPEWDT
250	260	270	280	290	300	310	320
VTPEAKDLIN	KMLTINPAKR	ITASEALKHP	WICQRSTVAS	MMHRQETVDC	LKKFNARRKL	KGAILTTMLA	TRNFSAAKSL
330	340	350	360	370	380	390	400
LKKPDGVKES	TESSNTTIED	EDVKARKQEI	IKVTEQLIEA	INNGDFEAYT	KICDPGLTAF	EPEALGNLVE	GMDFHRFYFE
410	420	430	440	450	460	470	480
NALSKSNKPI	HTIILNPHVH	LVGDDAACIA	YIRLTQYMDG	SGMPKTMQSE	ETRVWHRRDG	KWQNVHFHRS	GSPTVPIN

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
681	1	625.0022	-34.99	3	38.5	19.4	2	252-268	K.MLTINPAKRITASEALK.H	Oxidation: 1	QD:QU	0.40

Detailed Protein Report

Protein 566: 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

Quantitation

QD:QU **Median:** 11.07 **CV:** 0.00 % **No. of 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	Ratios
217	2	728.3427	-30.59	2	32.7	19.4	0	26-38	K.LGHPDTLNQGEFK.E		QD:QU 11.07

Detailed Protein Report

Protein 567: **PREDICTED: zinc finger transcription factor Trps1 isoform X4 [Homo sapiens]**

Accession:	gi|530389293	**Score:**	19.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	141.4
Database Date:	2015-11-30	**pI:**	8.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVRKKNPPLR	NVASEGEGQI	LEPIGTESKV	SGKNKEFSAD	QMSENTDQSD	AAELNHKEEH	SLHVQDPSSS	SKKDLKSAVL
90	100	110	120	130	140	150	160
SEKAGFNYES	PSKGGNFPSF	PHDEVTDRNM	LAFSSPAAGG	VCEPLKSPQR	AEADDPQDMA	CTPSGDSLET	KEDQKMSPKA
170	180	190	200	210	220	230	240
TEETGQAQSG	QANCQGLSPV	SVASKNPQVP	SDGGVRLNKS	KTDLLVNDNP	DPAPLSPELQ	DFKCNICGYG	YYGNDPTDLI
250	260	270	280	290	300	310	320
KHFRKYHLGL	HNRTRQDAEL	DSKILALHNM	VQFSHSKDFQ	KVNRSVFSGV	LQDINSSRPV	LLNGTYDVQV	TSGGTFIGIG
330	340	350	360	370	380	390	400
RKTPDCQGNT	KYFRCKFCNF	TYMGNSSTEL	EQHFLQTHPN	KIKASLPSSE	VAKPSEKNSN	KSIPALQSSD	SGDLGKWQDK
410	420	430	440	450	460	470	480
ITVKAGDDTP	VGYSVPIKPL	DSSRQNGTEA	TSYYWCKFCS	FSCESSSSLK	LLEHYGKQHG	AVQSGGLNPE	LNDKLSRGSV
490	500	510	520	530	540	550	560
INQNDLAKSS	EGETMTKTDK	SSSGAKKKDF	SSKGAEDNMV	TSYNCQFCDF	RYSKSHGPDV	IVVGPLLRHY	QQLHNIHKCT
570	580	590	600	610	620	630	640
IKHCPFCPRG	LCSPEKHLGE	ITYPFACRKS	NCSHCALLLL	HLSPGAAGSS	RVKHQCHQCS	FTTPDVDVLL	FHYESVHESQ
650	660	670	680	690	700	710	720
ASDVKQEANH	LQGSDGQQSV	KESKEHSCTK	CDFITQVEEE	ISRHYRRAHS	CYKCRQCSFT	AADTQSLLEH	FNTVHCQEQD
730	740	750	760	770	780	790	800
ITTANGEEDG	HAISTIKEEP	KIDFRVYNLL	TPDSKMGEPV	SESVVKREKL	EEKDGLKEKV	WTESSSDDLR	NVTWRGADIL
810	820	830	840	850	860	870	880
RGSPSYTQAS	LGLLTPVSGT	QEQTKTLRDS	PNVEAAHLAR	PIYGLAVETK	GFLQGAPAGG	EKSGALPQQY	PASGENKSKD
890	900	910	920	930	940	950	960
ESQSLLRRRR	GSGVFCANCL	TTKTSLWRKN	ANGGYVCNAC	GLYQKLHSTP	RPLNIIKQNN	GEQIIRRRTR	KRLNPEALQA
970	980	990	1000	1010	1020	1030	1040
EQLNKQQRGS	NEEQVNGSPL	ERRSEDHLTE	SHQREIPLPS	LSKYEAQGSL	TKSHSAQQPV	LVSQTLDIHK	RMQPLHIQIK
1050	1060	1070	1080	1090	1100	1110	1120
SPQESTGDPG	NSSSVSEGKG	SSERGSPIEK	YMRPAKHPNY	SPPGSPIEKY	QYPLFGLPFV	HNDFQSEADW	LRFWSKYKLS
1130	1140	1150	1160	1170	1180	1190	1200
VPGNPHYLSH	VPGLPNPCQN	YVPYPTFNLP	PHFSAVGSDN	DIPLDLAIKH	SRPGPTANGA	SKEKTKAPPN	VKNEGPLNVV
1210	1220	1230	1240	1250	1260	1270	1280
KTEKVDRSTQ	DELSTKCVHC	GIVFLDEVMY	ALHMSCHGDS	GPFQCSICQH	LCTDKYDFTT	HIQRGLHRNN	AQVEKNGKPK
1290							
E							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1488	1	955.7431	8.20	3	47.1	19.3	2	508-531	K.KDFSSKGAEDNMVTSYNCQFCDFR.Y	Carbamidomethyl: 21; Oxidation: 12

Detailed Protein Report

Protein 568: **zinc finger protein 19 [Homo sapiens]**

Accession:	gi|38045956	**Score:**	19.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.4
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAMPLKAQY	QEMVTFEDVA	VHFTKTEWTG	LSPAQRALYR	SVMLENFGNL	TALGYPVPKP	ALISLLERGD	MAWGLEAQDD
90	100	110	120	130	140	150	160
PPAERTKNVC	KDVETNIDSE	STLIQGISEE	RDGMMSHGQL	KSVPQRTDFP	ETRNVEKHQD	IPTVKNIQGK	VPRIPCARKP
170	180	190	200	210	220	230	240
FICEECGKSF	SYFSYYARHQ	RIHTGEKPFE	CSECGKAFNG	NSSLIRHQRI	HTGERPYQCE	ECGRAFNDNA	NLIRHQRIHS
250	260	270	280	290	300	310	320
GDRPYYCTEC	GNSFTSSSEF	VIHQRIHTGE	KPYECNECGK	AFVGNSPLLR	HQKIHTGEKP	YECNECGKSF	GRTSHLSQHQ
330	340	350	360	370	380	390	400
RIHTGEKPYS	CKVCGQAFNF	HTKLTRHQRI	HSEEKPFDCV	DCGKAFSAQE	QLKRHLRIHT	QESSYVCDEC	GKALTSKRNL
410	420	430	440	450	460		
HQHQRIHTGE	KPYECSKYEK	AFGTSSQLGH	LEHVYSGEKP	VLDICRFGLP	EFFTPFYW		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2142	1	882.4021	13.71	2	55.4	19.2	0	350-364	R.IHSEEKPFDCVDCGK.A	Carbamidomethyl: 13

Detailed Protein Report

Protein 569: uncharacterized protein KIAA1107 [Homo sapiens]

Accession:	gi|197245440	**Score:**	19.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	149.4
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSTADLLDT	ILKAIEENIT	TENSCSLLMA	LDTLLNSDST	KEMGFTCKIQ	ALRDKLWIFL	VQSFYAVRHT	ESWKLMSTDD
90	100	110	120	130	140	150	160
QQKIQAAAFD	KGDDRRLGKK	PIFSSSQQRK	QVSDSGDIKI	KSWRGNNKKE	CWSYLSTNKK	MKSDGLGASG	HSSSTNRNSI
170	180	190	200	210	220	230	240
NKTLKQDDVK	EKDGTKIASK	ITKELKTGGK	NVSGKPKTVT	KSKTENGDKA	RLENMSPRQV	VERSATAAAA	ATGQKNLLNG
250	260	270	280	290	300	310	320
KGVRNQEGQI	SGARPKVLTG	NLNVQAKAKP	LKKATGKDSP	CLSIAGPSSR	STDSSMEFSI	STECLDEPKE	NGSTEEEKPS
330	340	350	360	370	380	390	400
GHKLSFCDSP	GQMMKNSVDS	VKNSTVAIKS	RPVSRVTNGT	SNKKSIHEQD	TNVNNSVLKK	VSGKGCSEPV	PQAILKKRGT
410	420	430	440	450	460	470	480
SNGCTAAQQR	TKSTPSNLTK	TQGSQGESPN	SVKSSVSSRQ	SDENVAKLDH	NTTTEKQAPK	RKMVKQVHTA	LPKVNAKIVA
490	500	510	520	530	540	550	560
MPKNLNQSKK	GETLNNKDSK	QKMPPGQVIS	KTQPSSQRPL	KHETSTVQKS	MFHDVRDNNN	KDSVSEQKPH	KPLINLASEI
570	580	590	600	610	620	630	640
SDAEALQSSC	RPDPQKPLND	QEKEKLALEC	QNISKLDKSL	KHELESKQIC	LDKSETKFPN	HKETDDCDAA	NICCHSVGSD
650	660	670	680	690	700	710	720
NVNSKFYSTT	ALKYMVSNPN	ENSLNSNPVC	DLDSTSAGQI	HLISDRENQV	GRKDTNKQSS	IKCVEDVSLC	NPERTNGTLN
730	740	750	760	770	780	790	800
SAQEDKKSKV	PVEGLTIPSK	LSDESAMDED	KHATADSDVS	SKCFSGQLSE	KNSPKNMETS	ESPESHETPE	TPFVGHWNLS
810	820	830	840	850	860	870	880
TGVLHQRESP	ESDTGSATTS	SDDIKPRSED	YDAGGSQDDD	GSNDRGISKC	GTMLCHDFLG	RSSSDTSTPE	ELKIYDSNLR
890	900	910	920	930	940	950	960
IEVKMKKQSN	NDLFQVNSTS	DDEIPRKRPE	IWSRSAIVHS	RERENIPRGS	VQFAQEIDQV	SSSADETEDE	RSEAENVAEN
970	980	990	1000	1010	1020	1030	1040
FSISNPAPQQ	FQGIINLAFE	DATENECREF	SATKKFKRSV	LLSVDECEEL	GSDEGEVHTP	FQASVDSFSP	SDVFDGISHE
1050	1060	1070	1080	1090	1100	1110	1120
HHGRTCYSRF	SRESEDNILE	CKQNKGNSVC	KNESTVLDLS	SIDSSRKNKQ	SVSATEKKNT	IDVLSSRSRQ	LLREDKKVNN
1130	1140	1150	1160	1170	1180	1190	1200
GSNVENDIQQ	RSKFLDSDVK	SQERPCHLDL	HQREPNSDIP	KNSSTKSLDS	FRSQVLPQEG	PVKESHSTTT	EKANIALSAG
1210	1220	1230	1240	1250	1260	1270	1280
DIDDCDTLAQ	TRMYDHRPSK	TLSPIYEMDV	IEAFEQKVES	ETHVTDMDFE	DDQHFAKQDW	TLLKQLLSEQ	DSNLDVTNSV
1290	1300	1310	1320	1330	1340	1350	1360
PEDLSLAQYL	INQTLLLARD	SSKPQGITHI	DTLNRWSELT	SPLDSSASIT	MASFSSEDCS	PQGEWTILEL	ETQH

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2225	1	916.3247	-158.70	2	56.5	19.1	2	273-290	K.KATGKDSPCLSIAGPSSR.S	Carbamidomethyl: 9

Detailed Protein Report

Protein 570: putative sodium-coupled neutral amino acid transporter 10 isoform a [Homo sapiens]

Accession:	gi|83921602	**Score:**	19.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.7
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
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
203	1	1043.9225	-84.97	2	32.5	19.1	1	854-873	K.GPEQVPVPDPAREAGGPEER.L	

Detailed Protein Report

Protein 571: PREDICTED: nucleolar complex protein 3 homolog isoform X1 [Homo sapiens]

Accession:	gi|530394138	**Score:**	19.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.7
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	4.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKARRNKKQI	PSFRKLIKTS	KVKLENKLKN	KQFKQQSTLK	KYRKEQRKLR	QAVKDAVSKK	PIPLENPKEK	RPGKRIEREE
90	100	110	120	130	140	150	160
EEEEEALPLD	MMDEDDLQLM	KDLGQRVSFL	TRDLSSSEPV	HAKKRKHERI	IDKYEKIPRT	LQTAPEKELI	HLLPIKDKSG
170	180	190	200	210	220	230	240
IIPQTREKPV	TDSNKDEEDQ	EEERELEEEI	IEDPIQELTI	EEHLIERKKK	LQEKKMHIAA	LASAILSDPE	NNIKKLKELR
250	260	270	280	290	300	310	320
SMLMEQDPDV	AVTVRKLVIV	SLMELFKDIT	PSYKIRPLTE	AEKSTKTRKE	TQKLREFEEG	LVSQYKFYLE	NLEQMVKDWK
330	340	350	360	370	380	390	400
QRKLKKSNVV	SLKAYKGLAE	VAVKSLCELL	VALPHFNFHN	NIIVLIVPLM	NDMSKLISEM	CCEAVKKLFK	QDKLGQASLG
410	420	430	440	450	460	470	480
VIKVISGFVK	GRNYEVRPEM	LKTFLCLRIK	EVEVKKDTED	INKPKKFMTF	KEKRKSLSRM	QRKWKKAEEK	LERELREAEA
490	500	510					
SESTEKKLKL	VCSPYKCGIF						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2876	1	1132.6192	-5.27	2	65.1	19.1	2	215-235	K.KMHIAALASAILSDPENNIKK.L	

Detailed Protein Report

Protein 572: 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

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
1080	1	795.3895	26.37	3	43.6	18.6	1	208-227	R.IHTGEKPFQCNECGKAFFDR.S	Carbamidomethyl: 10

Detailed Protein Report

Protein 573: glycogenin-1 isoform 3 [Homo sapiens]

Accession: gi|296040507
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 18.6
MW [kDa]: 31.4
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 574: 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_human(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 575: PREDICTED: orofacial cleft 1 candidate gene 1 protein [Homo sapiens]

Accession:	gi|530358739	**Score:**	18.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.0
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530435542	refseq_human (refseq_human_20140103.fasta)	PREDICTED: orofacial cleft 1 candidate gene 1 protein [Homo sapiens]
gi|530382966	refseq_human (refseq_human_20140103.fasta)	PREDICTED: orofacial cleft 1 candidate gene 1 protein [Homo sapiens]

10	20	30	40	50	60	70	80
MRETGLKSVH	CQGQEAENME	REKFQQKALK	QTKQKKSKSA	EFLMVKEDRE	ATEGTGNPAF	NMSSPDLSAC	QTAEKKVIRH
90	100	110	120	130	140	150	160
DMPDRTLAAH	QQKFRLPASA	EPKGNEYGRN	YFDPLMDEEI	NPRQCATEVS	REGAPSKEKW	SIPKKIGPCS	MDYDPNLLEE
170	180	190	200	210	220	230	240
DDELHSQGDS	LTDHSVKGKS	TVWRIGEAED	YSQDISYLEE	LEEHRFSVCC	SSVADSRYGD	FFKHLHFVLV	SASSELQLSQ
250	260	270	280	290	300	310	320
WQSQGFWYII	LLMFFLWFLR	LYLHYLGQWL	FLQAISTPVT	KFHFSLHIVE	LCYPTSSLHI	GEELPVVVMG	PLMLNAILLL
330	340	350	360	370	380	390	400
LVLIRWGCQL	LFASCPDVLS	KLIITMGLWT	ILDPLAVFIL	DTLLGRLTDN	EETPVADAAK	LYWMFVRTVQ	PGILGVVITV
410	420	430					
LLYILLFVIS	SLILYLYCLR						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
48	1	630.8632	146.24	2	29.3	18.3	0	206-217	R.FSVCCSSVADSR.Y	

Detailed Protein Report

Protein 576: PREDICTED: period circadian protein homolog 1 isoform X2 [Homo sapiens]

Accession:	gi|530410420	**Score:**	18.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	130.2
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSGPLEGADG	GGDPRPGESF	CPGGVPSPGP	PQHRPCPGPS	LADDTDANSN	GSSGNESNGH	ESRGASQRSS	HSSSSGNGKD
90	100	110	120	130	140	150	160
SALLETTESS	KSTNSQSPSP	PSSSIAYSLL	SASSEQDNPS	TSGCSSEQSA	RARTQKELMT	ALRELKLRLP	PERRGKGRSG
170	180	190	200	210	220	230	240
TLATLQYALA	CVKQVQANQE	YYQQWSLEEG	EPCSMDMSTY	TLEELEHITS	EYTLQNQDTF	SVAVSFLTGR	IVYISEQAAV
250	260	270	280	290	300	310	320
LLRCKRDVFR	GTRFSELLAP	QDVGVFYGST	APSRLPTWGT	GASAGSGLRD	FTQEKSVFCR	IRGGPDRDPG	PRYQPFRLTP
330	340	350	360	370	380	390	400
YVTKIRVSDG	APAQPCCLLI	AERIHSGYEA	PRIPPDKRIF	TTRHTPSCLF	QDVDERAAPL	LGYLPQDLLG	APVLLFLHPE
410	420	430	440	450	460	470	480
DRPLMLAIHK	KILQLAGQPF	DHSPIRFCAR	NGEYVTMDTS	WAGFVHPWSR	KVAFVLGRHK	VRTAPLNEDV	FTPPAPSPAP
490	500	510	520	530	540	550	560
SLDTDIQELS	EQIHRLLLQP	VHSPSPTGLC	GVGAVTSPGP	LHSPGSSSDS	NGGDAEGPGP	PAPVTFQQIC	KDVHLVKHQG
570	580	590	600	610	620	630	640
QQLFIESRAR	PQSRPRLPAT	GTFKAKALPC	QSPDPELEAG	SAPVQAPLAL	VPEEAERKEA	SSCSYQQINC	LDSILRYLES
650	660	670	680	690	700	710	720
CNLPSTTKRK	CASSSSYTTS	SASDDDRQRT	GPVSVGTKKD	IIMMEDLPGL	APGPAPSPAP	SPTVAPDPAP	DAYRPVGLTK
730	740	750	760	770	780	790	800
AVLSLHTQKE	EQAFLSRFRD	LGRLRGLDSS	STAPSALGER	GCHHGPAPPS	RRHHCRSKAK	RSRHHQNPRA	EAPCYVSHPS
810	820	830	840	850	860	870	880
PVPPSTPWPT	PPATTPFPAV	VQPYPLPVFS	PRGGPQPLPP	APTSVPPAAF	PAPLVTPMVA	LVLPNYLFPT	PSSYPYGALQ
890	900	910	920	930	940	950	960
TPAEGPPTPA	SHSPSPSLPA	LAPSPPHRPD	SPLFNSRCSS	PLQLNLLQLE	ELPRAEGAAV	AGGPGSSAGP	PPPSAEAAEP
970	980	990	1000	1010	1020	1030	1040
EARLAEVTES	SNQDALSGSS	DLLELLLQED	SRSGTGSAAS	GSLGSGLGSG	SGSGSHEGGS	TSASITRSSQ	SSHTSKYFGS
1050	1060	1070	1080	1090	1100	1110	1120
IDSSEAEAGA	ARGGAEPGDQ	VIKYVLQDPI	WLLMANADQR	VMMTYQVPSR	DMTSVLKQDR	ERLRAMQKQQ	PRFSEDQRRE
1130	1140	1150	1160	1170	1180	1190	1200
LGAVHSWVRK	GQLPRALDVM	ACVDCGSSTQ	DPGHPDDPLF	SELDGLGLEP	MEEGGGEQGS	SGGGSGEGEG	CEEAQGGAKA
1210	1220	1230	1240				
SSSQDLAMEE	EEEGRSSSSP	ALPTAGNCTS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2488	1	673.3201	-14.80	3	61.7	18.2	1	1081-1097	R.VMMTYQVPSRDMTSVLK.Q	Oxidation: 2, 12

Detailed Protein Report

Protein 577: **macrophage mannose receptor 1 precursor [Homo sapiens]**

Accession:	gi|4505245	**Score:**	18.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	165.9
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
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
1638	1	1069.9824	-53.73	2	49.0	18.2	2	324-341	K.NAKWENLECVQKLGYICK.K	

Detailed Protein Report

Protein 578: protein phosphatase 1 regulatory subunit 26 [Homo sapiens]

Accession:	gi|45387958	**Score:**	18.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	127.3
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.9
		No. of unique 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							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1803	1	590.7798	-21.71	2	52.9	18.1	0	881-891	K.EPAPPPGVCTR.S	Carbamidomethyl: 9

Detailed Protein Report

Protein 579: PREDICTED: transmembrane 7 superfamily member 3 isoform X1 [Homo sapiens]

Accession:	gi|530399194	**Score:**	18.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	58.7
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGFLQLLVVA	VLASEHRVAG	AAEVFGNSSE	GLIEFSVGKF	RYFELNRPFP	EEAILHDISS	NVTFLIFQIH	SQYQNTTVSF
90	100	110	120	130	140	150	160
SPTLLSNSSE	TGTASGLVFI	LRPEQSTCTW	YLGTSGIQPV	QNMAILLSYS	ERDPVPGGCN	LEFDLDIDPN	IYLEYNFFET
170	180	190	200	210	220	230	240
TIKFAPANLG	YARGVDPPPC	DAGTDQDSRW	RLQYDVYQYF	LPENDLTEEM	LLKHLQRMVS	VPQVKASALK	VVTLTANDKT
250	260	270	280	290	300	310	320
SVSFSSLPGQ	GVIYNVIVWD	PFLNTSAAYI	PAHTYACSFE	AGEGSCASLG	RVSSKVFFTL	FALLGFFICF	FGHRFWKTEL
330	340	350	360	370	380	390	400
FFIGFIIMGF	FFYILITRLT	PIKYDGNLKI	FHDDGVFWVT	FSCIAILIPV	VFMGCLRILN	ILTCGVIGSY	SVVLAIDSYW
410	420	430	440	450	460	470	480
STSLSYITLN	VLKRALNKDF	HRAFTNVPFQ	TNDFIILAVW	GMLAVSGITL	QIRRERGRPF	FPPHPYKLWK	QERERRVTNI
490	500	510	520				
LDPSYHIPPL	RERLYGRLTQ	IKGLFQKEQP	AGERTPLLL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2409	1	954.4178	-134.28	2	58.8	18.1	2	214-230	K.HLQRMVSVPQVKASALK.V	Oxidation: 5

Detailed Protein Report

Protein 580: PREDICTED: putative L-type amino acid transporter 1-like protein MLAS-like [Homo sapiens]

Accession:	gi|578846041	**Score:**	18.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.1
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAGAGPKRRA LAAPVAEEKE EAREKMLASK RADGAAPAGE GEGVTLQRNI TLLNGVAIIV GAIIGSGIFV TPTGVLKEAG
        90        100        110        120        130        140        150        160
SPGLALVMWA ACGVFSIVGA LCYAELGTTI SKSGGDYAYM LDVYGSLPAF LKLWIELLVI RPSSQYIVAL VFATYLLKPL
       170        180        190        200        210        220        230
FPSCPVPEEA AKLMACHCVR EYGARAGGWE VVVPGSLHPC ITTPLAPTSL HFCVPGPSRQ F
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1084	1	705.1875	-311.96	1	42.0	18.1	1	26-31	K.MLASKR.A	

Detailed Protein Report

Protein 581: PREDICTED: protein DBF4 homolog B isoform X7 [Homo sapiens]

Accession:	gi|578831452	**Score:**	18.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.4
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.0
		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 582: 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 583: 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 584: PREDICTED: SCAN domain-containing protein 3 isoform X1 [Homo sapiens]

Accession:	gi|578840800	**Score:**	17.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	133.8
Database Date:	2015-11-30	**pI:**	7.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEEMIPLDSA	KESLGTQLQS	MEDRMECESP	EPHPLQDNGS	FLWFSMMSQS	MGGDNLSSLD	TNEAEIEPEN	MREKFFRSLA
90	100	110	120	130	140	150	160
RLLENKSNNT	KIFSKAKYCQ	LIKEVKEAKA	KAKKESVDYR	RLARFDVILV	QGNEKLIEAV	NGETDKIRYY	LHSEDLFDIL
170	180	190	200	210	220	230	240
HNTHLSIGHG	GRTRMEKELQ	AKYKNITKEV	IMLYLTLCKP	CQQKNSKLKK	VLTSKSIKEV	SSRCQVDLID	MQLNPDGEYR
250	260	270	280	290	300	310	320
FILHYQDLCT	KLTFLRSLKS	KRPTEVAHAL	LDIFTIIGAP	SVLQSDNGRE	FSSQVVSELS	NIWPELKIVH	GKSQTCQSQS
330	340	350	360	370	380	390	400
SAEQTEDIRK	RIFSWMQTNN	SSHWTEFLWF	IQMSQNQPYH	RSMQQTPCES	AFSSEAKLGL	SHSQLTEELV	ASLHTENELD
410	420	430	440	450	460	470	480
QADKELENTL	RAQYEENIET	GTDSSDIEEN	LSVTPKVAEK	SPPESRLRFL	SCVVCEKECT	GVNSCISCDG	NIHAICGVPS
490	500	510	520	530	540	550	560
QHGTEGCGRQ	ITCSLCYETS	TMKRKHDEIQ	RSLPVKPSKM	LKPSGTPFSP	DKVGDWMAKQ	ASLDFFVKKR	HAFSEHSSSN
570	580	590	600	610	620	630	640
KRNVNNRSYP	EEGKTKRVHA	SFTRKYDPSY	IEFGFVAVID	GEVLKPQCII	CGDVLANEAM	KPSKLKRHLY	SKHKEISSQP
650	660	670	680	690	700	710	720
KEFFERKSSE	LKSQPKQVFN	VSHINISALR	ASYKVALPVA	KSKTPYTIAE	TLVKDCIKEV	CLEMLGESAA	KKVAQVPLSN
730	740	750	760	770	780	790	800
DTIARRIQEL	ANDMEDQLIE	QIKLAKYFSL	QLDECRDIAN	MIILLVYVRF	EHDDDIKEEF	FFSASLPTNT	TSSELYEAVK
810	820	830	840	850	860	870	880
NYIVNKCGLE	FKFCVGVCSD	GAASMTGKHS	EVVTQIKELA	PECKTTHCFI	HRESLAMKKI	SAELNSVLND	IVKIVNYIKS
890	900	910	920	930	940	950	960
NSLNSRLFSL	LCDNMEADHK	QLLLHAEIRW	LSRGKVLSRM	FEIRNELLVF	LQGKKPMWSQ	LFKDVNWTAR	LAYLSDIFSI
970	980	990	1000	1010	1020	1030	1040
FNDLNASMQG	KNATYFSMAD	KVEGQKQKLE	AWKNRISTDC	YDMFHNLTTI	INEVGNDLDI	AHLRKVISEH	LTNLLECFEF
1050	1060	1070	1080	1090	1100	1110	1120
YFPSKEDPRI	GNLWIQNPFL	SSKDNLNLTV	TLQDKLLKLA	TDEGLKISFE	NTASLPSFWI	KAKNDYPELA	EIALKLLLLF
1130	1140	1150	1160	1170	1180		
PSTYLCETGF	STLSVIKTKH	RNSLNIHYPL	RVALSSIQPR	LDKLTSKKQA	HLSH		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1614	1	873.9372	77.88	2	48.7	17.9	0	362-377	R.SMQQTPCESAFSSEAK.L	Oxidation: 2

Detailed Protein Report

Protein 585: **nicotinate phosphoribosyltransferase isoform 2 [Homo sapiens]**

Accession:	gi|558472750	**Score:**	17.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.1
Database Date:	2015-11-30	**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 586: mesencephalic astrocyte-derived neurotrophic factor precursor [Homo sapiens]

Accession:	gi|299523086	**Score:**	17.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.7
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	10.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRRMWATQGL	AVALALSVLP	GSRALRPGDC	EVCISYLGRF	YQDLKDRDVT	FSPATIENEL	IKFCREARGK	ENRLCYYIGA
90	100	110	120	130	140	150	160
TDDAATKIIN	EVSKPLAHHI	PVEKICEKLK	KKDSQICELK	YDKQIDLSTV	DLKKLRVKEL	KKILDDWGET	CKGCAEKSDY
170	180	190					
IRKINELMPK	YAPKAASART	DL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2038	2	696.9685	-53.02	3	55.9	17.7	2	69-87	R.GKENRLCYYIGATDDAATK.I	

Detailed Protein Report

Protein 587: 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 588: 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; Oxidation: 1

Detailed Protein Report

Protein 589: aldo-keto reductase family 1 member C2 isoform 2 [Homo sapiens]

Accession:	gi|207028673	**Score:**	17.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.7
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	17.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MDSKYQCVKL NDGHFMPVLG FGTYAPAEVP KSKALEAVKL AIEAGFHHID SAHVYNNEEQ VGLAIRSKIA DGSVKREDIF
        90        100        110        120        130        140
YTSKLWSNSH RPELVRPALE RSLKNLQLDY VDLYLIHFPV SVKEDIGILT WKKSPKHNS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2935	1	859.1202	17.35	3	65.9	17.7	1	10-33	K.LNDGHFMPVLGFGTYAPAEVPKSK.A	

Detailed Protein Report

Protein 590: potassium channel subfamily K member 10 isoform 2 [Homo sapiens]

Accession:	gi|20143944	**Score:**	17.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.3
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
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
1557	2	494.2527	-64.89	2	49.7	17.6	1	3-10	K.FPIETPRK.Q	

Detailed Protein Report

Protein 591: PREDICTED: suppression of tumorigenicity 18 protein isoform X4 [Homo sapiens]

Accession:	gi|578815754	**Score:**	17.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.1
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDAEAEDKTL	RTRSKGTEVP	MDSLIQELSV	AYDCSMAKKR	TAEDQALGVP	VNKRKSLLMK	PRHYSPKADC	QEDRSDRTED
90	100	110	120	130	140	150	160
DGPLETHGHS	TAEEIMIKPM	DESLLSTAQE	NSSRKEDRYS	CYQELMVKSL	MHLGKFEKNV	SVQTVSENLN	DSGIQSLKAE
170	180	190	200	210	220	230	240
SDEADECFLI	HSDDGRDKID	DSQPPFCSSD	DNESNSESAE	NGWDSGSNFS	EETKPPRVPK	YVLTDHKKDL	LEVPEIKTEG
250	260	270	280	290	300	310	320
DKFIPCENRC	DSETERKDPQ	NALAEPLDGN	AQPSFPDVEE	EDSESLAVMT	EEGSDLEKAK	GNLSLLEQAI	ALQAERGCVF
330	340	350	360	370	380	390	400
HNTYKELDRF	LLEHLAGERR	QTKVIDMGGR	QIFNNKHSPR	PEKRETKCPI	PGCDGTGHVT	GLYPHHRSLS	GCPHKVRVPL
410	420	430	440	450	460	470	480
EILAMHENVL	KCPTPGCTGR	GHVNSNRNTH	RSLSGCPIAA	AEKLAMSQDK	NQLDSPQTGQ	CPDQAHRTSL	VKQIEFNFPS
490	500	510	520	530	540	550	560
QAITSPRATV	SKEQEKFGKV	PFDYASFDAQ	VFGKRPLIQT	VQGRKTPPFP	ESKHFPNPVK	FPNRLPSAGA	HTQSPGRASS
570	580	590	600	610	620	630	640
YSYGQCSEDT	HIAAAAAILN	LSTRCREATD	ILSNKPQSLH	AKKDPVSSLE	NLEEKKFPGE	ASIPSPKPKL	HARDLKKELI
650	660	670	680	690	700	710	720
TCPTPGCDGS	GHVTGNYASH	RSVSGCPLAD	KTLKSLMAAN	SQELKCPTPG	CDGSGHVTGN	YASHRSLSGC	PRARKGGVKM
730	740	750	760	770	780	790	800
TPTKEEKEDP	ELKCPVIGCD	GQGHISGKYT	SHRTASGCPL	AAKRQKENPL	NGASLSWKLN	KQELPHCPLP	GCNGLGHVNN
810	820	830	840	850	860	870	880
VFVTHRSLSG	CPLNAQVIKK	GKVSEELMTI	KLKATGGIES	DEEIRHLDEE	IKELNESNLK	IEADMMKLQT	QITSMESNLK
890	900	910	920	930	940	950	960
TIEEENKLIE	QNNESLLKEL	AGLSQALISS	LADIQLPQMG	PISEQNFEAY	VNTLTDMYSN	LERDYSPECK	ALLESIKQAV
970							
KGIHV							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1743	1	560.7234	-123.45	2	52.1	17.6	1	341-350	R.QTKVIDMGGR.Q	Oxidation: 7

Detailed Protein Report

Protein 592: 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 593: uncharacterized protein KIAA0930 isoform b [Homo sapiens]

Accession:	gi|57863295	**Score:**	17.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.8
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	5.9
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 1.83 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MLRAIAEERG RLSLRREVCG LGCFKDDRIV FWTWMFSTYF MEKWAPRQDD MLFYVRRKLA YSGSESGADG RKAAEPEVEV

        90        100        110        120        130        140        150        160
EVYRRDSKKL PGLGDPDIDW EESVCLNLIL QKLDYMVTCA VCTRADGGDI HIHKKKSQQV FASPSKHPMD SKGEESKISY

       170        180        190        200        210        220        230        240
PNIFFMIDSF EEVFSDMTVG EGEMVCVELV ASDKTNTFQG VIFQGSIRYE ALKKVYDNRV SVAARMAQKM SFGFYKYSNM

       250        260        270        280        290        300        310        320
EFVRMKGPQG KGHAEMAVSR VSTGDTSPCG TEEDSSPASP MHERVTSFST PPTPERNNRP AFFSPSLKRK VPRNRIAEMK

       330        340        350        360        370        380        390        400
KSHSANDSEE FFREDDGGAD LHNATNLRSR SLSGTGRSLV GSWLKLNRAD GNFLLYAHLT YVTLPLHRIL TDILEVRQKP

       410
ILMT
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
169	1	826.3632	22.55	3	30.9	17.2	0	261-284	R. VSTGDTSPCGTEEDSSPASPMHE V		QD:QU	1.83

Detailed Protein Report

Protein 594: histone demethylase UTY isoform 1 [Homo sapiens]

Accession:	gi|33188429	**Score:**	17.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	118.0
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKSCAVSLTT	AAVAFGDEAK	KMAEGKASRE	SEEESVSLTV	EEREALGGMD	SRLFGFVRLH	EDGARTKTLL	GKAVRCYESL
90	100	110	120	130	140	150	160
ILKAEGKVES	DFFCQLGHFN	LLLEDYSKAL	SAYQRYYSLQ	ADYWKNAAFL	YGLGLVYFYY	NAFHWAIKAF	QDVLYVDPSF
170	180	190	200	210	220	230	240
CRAKEIHLRL	GLMFKVNTDY	KSSLKHFQLA	LIDCNPCTLS	NAEIQFHIAH	LYETQRKYHS	AKEAYEQLLQ	TENLPAQVKA
250	260	270	280	290	300	310	320
TVLQQLGWMH	HNMDLVGDKA	TKESYAIQYL	QKSLEADPNS	GQSWYFLGRC	YSSIGKVQDA	FISYRQSIDK	SEASADTWCS
330	340	350	360	370	380	390	400
IGVLYQQQNQ	PMDALQAYIC	AVQLDHGHAA	AWMDLGTLYE	SCNQPQDAIK	CYLNAARSKR	CSNTSTLAAR	IKFLQNGSDN
410	420	430	440	450	460	470	480
WNGGQSLSHH	PVQQVYSLCL	TPQKLQHLEQ	LRANRDNLNP	AQKHQLEQLE	SQFVLMQQMR	HKEVAQVRTT	GIHNGAITDS
490	500	510	520	530	540	550	560
SLPTNSVSNR	QPHGALTRVS	SVSQPGVRPA	CVEKLLSSGA	FSAGCIPCGT	SKILGSTDTI	LLGSNCIAGS	ESNGNVPYLQ
570	580	590	600	610	620	630	640
QNTHTLPHNH	TDLNSSTEEP	WRKQLSNSAQ	GLHKSQSSCL	SGPNEEQPLF	STGSAQYHQA	TSTGIKKANE	HLTLPSNSVP
650	660	670	680	690	700	710	720
QGDADSHLSC	HTATSGGQQG	IMFTKESKPS	KNRSLVPETS	RHTGDTSNGC	ADVKGLSNHV	HQLIADAVSS	PNHGDSPNLL
730	740	750	760	770	780	790	800
IADNPQLSAL	LIGKANGNVG	TGTCDKVNNI	HPAVHTKTDH	SVASSPSSAI	STATPSPKST	EQRSINSVTS	LNSPHSGLHT
810	820	830	840	850	860	870	880
VNGEGLGKSQ	SSTKVDLPLA	SHRSTSQILP	SMSVSICPSS	TEVLKACRNP	GKNGLSNSCI	LLDKCPPPRP	PTSPYPPLPK
890	900	910	920	930	940	950	960
DKLNPPTPSI	YLENKRDAFF	PPLHQFCTNP	KNPVTVIRGL	AGALKLDLGL	FSTKTLVEAN	NEHMVEVRTQ	LLQPADENWD
970	980	990	1000	1010	1020	1030	1040
PTGTKKIWRC	ESNRSHTTIA	KYAQYQASSF	QESLRAGMQW	CDLSSLQPPP	PGFKRFSHLS	LPNSWNYRHL	PSCPTNFCIF
1050	1060	1070	1080				
VETGFHHVGQ	ACLELLTSGG	LLASASQSAG	ITGVSHHAR				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1890	1	1036.8846	-114.40	2	54.0	17.2	1	1-20	-.MKSCAVSLTTAAVAFGDEAK.K	Carbamidomethyl: 4; Oxidation: 1

Detailed Protein Report

Protein 595: **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

Quantitation

QD:QU **Median:** 0.43 **CV:** 0.00 % **No. of 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	Ratios
1	1	819.8504	-66.08	2	29.4	17.2	2	94-105	K.EMMKETFKYFLR.E	Oxidation: 2	QD:QU 0.43

Detailed Protein Report

Protein 596: probable RNA-binding protein 46 isoform 3 [Homo sapiens]

Accession:	gi|461496493	**Score:**	17.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.2
Database Date:	2015-11-30	**pI:**	6.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578808850	refseq_human (refseq_human_20140103.fasta)	PREDICTED: probable RNA-binding protein 46 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MNEENIDGTN	GCSKVRTGIQ	NEAALLALME	KTGYNMVQEN	GQRKFGGPPP	GWEGPPPPRG	CEVFVGKIPR	DMYEDELVPV
90	100	110	120	130	140	150	160
FERAGKIYEF	RLMMEFSGEN	RGYAFVMYTT	KEEAQLAIRI	LNNYEIRPGK	FIGVCVSLDN	CRLFIGAIPK	EKKKEEILDE
170	180	190	200	210	220	230	240
MKKVTEGVVD	VIVYPSATDK	TKNRGFAFVE	YESHRAAAMA	RRKLIPGTFQ	LWGHTIQVDW	ADPEKEVDEE	TMQRVKVLYV
250	260	270	280	290	300	310	320
RNLMISTTEE	TIKAEFNKFK	PGAVERVKKL	RDYAFVHFFN	REDAVAAMSV	MNGKCIDGAS	IEVTLAKPVN	KENTWRQHLN
330	340	350	360	370	380	390	400
GQISPNSENL	IVFANKEESH	PKTLGKLPTL	PARLNGQHSP	SPPEVERCTY	PFYPGTKLTP	ISMYSLKSNH	FNSAVMHLDY
410	420	430	440	450	460	470	480
YCNKNNWAPP	EYYLYSTTSQ	DGKVLLVYKI	VIPAIANGSQ	SYFMPDKLCT	TLEDAKELAA	QFTLLHGPF	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2007	2	719.2958	-4.73	2	55.5	17.2	0	2-14	M.NEENIDGTNGCSK.V	Carbamidomethyl: 11

Detailed Protein Report

Protein 597: probable G-protein coupled receptor 179 precursor [Homo sapiens]

Accession:	gi|93352554	**Score:**	17.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	257.2
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	0.4
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:**	0.42	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

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

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
881	4	509.2453	-102.22	2	41.1	17.2	1	1195-1204	R.AGKTGLAMLR.Q		QD:QU 0.42

Detailed Protein Report

Protein 598: **ankyrin repeat domain-containing protein SOWAHB [Homo sapiens]**

Accession:	gi|71274172	**Score:**	17.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.7
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
MARELSQEAL	LDFLCQAGGR	VTNAALLSHF	KSFLRDPDAS	PSQHQHRREL	FKGFVNSVAA	VRQDPDGTKY	VVLKRRYRDL
90	100	110	120	130	140	150	160
LGEEGLQRPR	EPPAAAPSAG	GAAPCSPRGA	RRGEPPQQQP	RRRRREKEPE	EEPAGAAARA	ADAACNGLPG	SDSRRAPGKG
170	180	190	200	210	220	230	240
GGSKGSPGQR	PPVPAAAAAG	AQARASCAAA	KTQGRCCWEC	LQNNLAVLPG	ELGALPHSAT	AEEKPARALP	AQDDRGASRE
250	260	270	280	290	300	310	320
REEGALAEPA	PVPAVAHSPP	ATVEAATSRA	SPPALLPGPA	PRGDRPELLT	PSSLHYSTLQ	QQQQRTREWV	ARHPQVPEAR
330	340	350	360	370	380	390	400
DQGPIRAWSV	LPDNFLQLPL	EPGSTEPNSE	PPDPCLSSHS	LFPVVPDESW	ESWAGNPSLT	VFRSIRCQLS	LQDLDDFVDQ
410	420	430	440	450	460	470	480
ESDGSEESSS	GPKDSPGASE	EGLQVVLGTP	DRGKLRNPAG	GLSVSRKEGS	PSRSPQGLRN	RGDGHISQQV	PAGANGLAGH
490	500	510	520	530	540	550	560
PLKPLPWPVP	KLRRSLRRSS	LAGRAKLSSS	DEEYLDEGLL	KRSRRPPRSR	KPSKAGTAPS	PRVDAGLSLK	LAEVKAVVAE
570	580	590	600	610	620	630	640
RGWRHSLWVP	SGEGSAALAP	HRTSEHKSSL	VPLDAREHEW	IVKLASGSWI	QVWTLFWEDP	QLALHKDFLT	GYTALHWIAK
650	660	670	680	690	700	710	720
HGDLRALQDL	VSGAKKAGIV	LDVNVRSSCG	YTPLHLAAIH	GHQGVIKLLV	QRLASRVNVR	DSSGKKPWQY	LTSNTSGEIW
730	740	750	760	770	780	790	800
QLLGAPRGKP	IFPVYPLVGS	SSPTRKAKSK	EISRSVTRKT	SFAALLKSQH	NKWKLANQYE	KFHSPREREE	YSD

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1748	1	945.9280	-39.73	2	50.4	17.1	1	91-111	R.EPPAAAPSAGGAAPCSPRGAR.R	

Detailed Protein Report

Protein 599: PREDICTED: SH3 domain-containing RING finger protein 3 isoform X2 [Homo sapiens]

Accession:	gi|578804249	**Score:**	17.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.9
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.35 **CV:** 0.00 % **No. of 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	Ratios
738	1	705.1981	-212.15	2	37.8	17.1	1	493-503	R.VLEKCQDGWFK.G	Carbamidomethyl: 5	QD:QU 0.35

Protein 600: centromere protein X isoform 3 [Homo sapiens]

Accession: gi|401871068
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 17.0
MW [kDa]: 6.5
pI: 6.1
Sequence Coverage [%]: 17.2
No. of unique Peptides: 1

Quantitation

QD:QU **Median:** 0.49 **CV:** 0.00 % **No. of Peptides:** 1

```
         10         20         30         40         50         60
MEGAGAGSGF RKELVSRLLH LHFKDDKTKE AAVRGVRQAQ AEDALRVDVD QLEKLLDF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
685	1	566.7912	-18.08	2	37.1	17.0	2	25-34	K.DDKTKEAAVR.G		QD:QU 0.49

Detailed Protein Report

Protein 601: zinc finger protein 586 isoform b [Homo sapiens]

Accession:	gi|116812602	**Score:**	17.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.8
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAAAALRAP	AQVVGMEGKM	RQHLLSRARV	YIYTKTREVI	VEKGLMSVGN	IGNYLRTSPA	SLNPEEITNT	GMFALEKGLM
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
SAANMGNYFT	KSLHSIFMRD	FILGKRPMSA	VSVENHFTKA	LHSCSVRHFT	LEKGLMSVLN	VGKPLLKSPV	SLTTGKFTLE
170	**180**	**190**	**200**	**210**	**220**		
QSVMNAMNVG	SPLLIHLVSL	NTGGFTLERG	LMSAVNVGDP	LLKTPVLLNT			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2516	1	715.3738	-22.06	2	62.0	17.0	0	190-203	R.GLMSAVNVGDPLLK.T	Oxidation: 3

Detailed Protein Report

Protein 602: conserved oligomeric Golgi complex subunit 1 [Homo sapiens]

Accession:	gi|21237783	**Score:**	16.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	108.9
Database Date:	2015-11-30	**pI:**	7.1
		Sequence Coverage [%]:	1.8
		No. of unique 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
2511	1	941.9690	8.39	2	62.0	16.9	1	72-89	R.CAVGLVDAVKATDQYCAR.L	

Detailed Protein Report

Protein 603: probable G-protein coupled receptor 116 precursor [Homo sapiens]

Accession: gi|148719671
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 16.9
MW [kDa]: 149.4
pI: 6.2
Sequence Coverage [%]: 0.7
No. of unique Peptides: 1

Alias proteins:

Accession	**Name**	**Description**
gi|148719673	refseq_human (refseq_human_20140103.fasta)	probable G-protein coupled receptor 116 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MKSPRRTTLC	LMFIVIYSSK	AALNWNYEST	IHPLSLHEHE	PAGEEALRQK	RAVATKSPTA	EEYTVNIEIS	FENASFLDPI
90	100	110	120	130	140	150	160
KAYLNSLSFP	IHGNNTDQIT	DILSINVTTV	CRPAGNEIWC	SCETGYGWPR	ERCLHNLICQ	ERDVFLPGHH	CSCLKELPPN
170	180	190	200	210	220	230	240
GPFCLLQEDV	TLNMRVRLNV	GFQEDLMNTS	SALYRSYKTD	LETAFRKGYG	ILPGFKGVTV	TGFKSGSVVV	TYEVKTTPPS
250	260	270	280	290	300	310	320
LELIHKANEQ	VVQSLNQTYK	MDYNSFQAVT	INESNFFVTP	EIIFEGDTVS	LVCEKEVLSS	NVSWRYEEQQ	LEIQNSSRFS
330	340	350	360	370	380	390	400
IYTALFNNMT	SVSKLTIHNI	TPGDAGEYVC	KLILDIFEYE	CKKKIDVMPI	QILANEEMKV	MCDNNPVSLN	CCSQGNVNWS
410	420	430	440	450	460	470	480
KVEWKQEGKI	NIPGTPETDI	DSSCSRYTLK	ADGTQCPSGS	SGTTVIYTCE	FISAYGARGS	ANIKVTFISV	ANLTITPDPI
490	500	510	520	530	540	550	560
SVSEGQNFSI	KCISDVSNYD	EVYWNTSAGI	KIYQRFYTTR	RYLDGAESVL	TVKTSTREWN	GTYHCIFRYK	NSYSIATKDV
570	580	590	600	610	620	630	640
IVHPLPLKLN	IMVDPLEATV	SCSGSHHIKC	CIEEDGDYKV	TFHTGSSSLP	AAKEVNKKQV	CYKHNFNASS	VSWCSKTVDV
650	660	670	680	690	700	710	720
CCHFTNAANN	SVWSPSMKLN	LVPGENITCQ	DPVIGVGEPG	KVIQKLCRFS	NVPSSPESPI	GGTITYKCVG	SQWEEKRNDC
730	740	750	760	770	780	790	800
ISAPINSLLQ	MAKALIKSPS	QDEMLPTYLK	DLSISIDKAE	HEISSSPGSL	GAIINILDLL	STVPTQVNSE	MMTHVLSTVN
810	820	830	840	850	860	870	880
VILGKPVLNT	WKVLQQQWTN	QSSQLLHSVE	RFSQALQSGD	SPPLSFSQTN	VQMSSMVIKS	SHPETYQQRF	VFPYFDLWGN
890	900	910	920	930	940	950	960
VVIDKSYLEN	LQSDSSIVTM	AFPTLQAILA	QDIQENNFAE	SLVMTTTVSH	NTTMPFRISM	TFKNNSPSGG	ETKCVFWNFR
970	980	990	1000	1010	1020	1030	1040
LANNTGGWDS	SGCYVEEGDG	DNVTCICDHL	TSFSILMSPD	SPDPSSLLGI	LLDIISYVGV	GFSILSLAAC	LVVEAVVWKS
1050	1060	1070	1080	1090	1100	1110	1120
VTKNRTSYMR	HTCIVNIAAS	LLVANTWFIV	VAAIQDNRYI	LCKTACVAAT	FFIHFFYLSV	FFWMLTLGLM	LFYRLVFILH
1130	1140	1150	1160	1170	1180	1190	1200
ETSRSTQKAI	AFCLGYGCPL	AISVITLGAT	QPREVYTRKN	VCWLNWEDTK	ALLAFAIPAL	IIVVVNITIT	IVVITKILRP
1210	1220	1230	1240	1250	1260	1270	1280
SIGDKPCKQE	KSSLFQISKS	IGVLTPLLGL	TWGFGLTTVF	PGTNLVFHII	FAILNVFQGL	FILLFGCLWD	LKVQEALLNK
1290	1300	1310	1320	1330	1340	1350	
FSLSRWSSQH	SKSTSLGSST	PVFSMSSPIS	RRFNNLFGKT	GTYNVSTPEA	TSSSLENSSS	ASSLLN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2911	1	671.8322	16.14	2	65.6	16.9	0	133-142	R.CLHNLICQER.D	Carbamidomethyl: 1, 7

Detailed Protein Report

Protein 604: 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

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
2170	1	682.3011	-106.73	3	57.5	16.9	2	81-97	K.YLTSLKNLHLSGNRICR.F	Carbamidomethyl: 16

Detailed Protein Report

Protein 605: **PREDICTED: iron-sulfur cluster assembly enzyme ISCU, mitochondrial isoform X1 [Homo sapiens]**

Accession:	gi|530400013	**Score:**	16.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.9
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	10.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAAGAFRLR	RAASALLLRS	PRLPARELSA	PARLYHKKVV	DHYENPRNVG	SLDKTSKNVG	TGLVGAPACG	DVMKLQIQVD
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
EKGKIVDARF	KTFGCGSAIA	SSSLATEWVK	GKTVEEALTI	KNTDIAKELC	LPPVKLHCSR	KEGMRNISLN	ASMEVY

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2964	1	619.9693	5.46	3	66.2	16.9	2	141-156	R.KEGMRNISLNASMEVY.-	Oxidation: 4

Detailed Protein Report

Protein 606: **dynein heavy chain 12, axonemal isoform 1 [Homo sapiens]**

Accession:	gi|194440727	**Score:**	16.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	356.7
Database Date:	2015-11-30	**pI:**	5.8
		Sequence Coverage [%]:	0.4
		No. of unique 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
1721	1	646.7566	-109.88	2	51.8	16.9	1	1602-1612	R.EFALSETPDRK.W	

Detailed Protein Report

Protein 607: **protein GNAS isoform GNASS [Homo sapiens]**

Accession:	gi|18426900	**Score:**	16.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.2
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Oxidation	**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 608: 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 609: 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 610: tubby-related protein 4 isoform 1 [Homo sapiens]

Accession:	gi|55953100	**Score:**	16.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	168.9
Database Date:	2015-11-30	**pI:**	8.3
		Sequence Coverage [%]:	1.2
		No. of unique 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					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2366	1	649.2906	-70.12	3	60.0	16.8	2	1340-1357	K.RLDSRAEEGSVQAITEGK.V	

Detailed Protein Report

Protein 611: 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

Protein 612: E3 ubiquitin-protein ligase RNF128 isoform 2 precursor [Homo sapiens]

Accession:	gi|37588871	**Score:**	16.8
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
1366	2	1207.8238	107.80	2	45.6	16.8	2	150-171	K.GTKILQSIQRGIQVTMVIEVGK.K	Oxidation: 16

Detailed Protein Report

Protein 613: von Willebrand factor D and EGF domain-containing protein precursor [Homo sapiens]

Accession:	gi|209571555	**Score:**	16.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	176.7
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPGGACVLVI	ALMFLAWGEA	QECSPGGHQF	LRSPYRSVRF	DSWHLQQSAV	QDLICDHSLS	PGWYRFLILD	RPAEMPTKCV
90	100	110	120	130	140	150	160
EMNHCGTQAP	IWLSLRDSET	LPSPGEIKQL	TACATWQFLF	STTKDCCLFQ	IPVSVRNCGN	FSVYLLQPTQ	GCMGYCAEAI
170	180	190	200	210	220	230	240
SDARLHPCGS	DETETGGDCV	RQLAASLPPP	PAGRPEVLVE	LIESRLFCRC	SFDVPATKNS	VGFHIAWSRL	SSQEVKEELT
250	260	270	280	290	300	310	320
QETTVQAFSL	LELDGINLRL	GDRIFCSASV	FFLENPHVQS	VAIESQEFFA	GFKLQPELST	ISEDGKEYYL	RIESTVPIIC
330	340	350	360	370	380	390	400
SEFSELDQEC	KISLKLKTIG	QGREHLGLNL	ALSSCHVDLL	QTSSCANGTC	SHTFVYYTAV	TDFSRDGDRV	SNIVVQPIVN
410	420	430	440	450	460	470	480
EDFLWNNYIP	DSIQIKVKDV	PTAYCYTFTD	PHIITFDGRV	YDNFKTGTFV	LYKSMSRDFE	VHVRQWDCRS	LHYPVSCNCG
490	500	510	520	530	540	550	560
FVAQEGGDIV	TFDMCNGQLR	ESQPYLFIKS	QDVTRNIKIS	ESYLGRKVTI	WFSSGAFIRA	DLGEWGMSLT	IRAPSVDYRN
570	580	590	600	610	620	630	640
TLGLCGTFDE	NPENDFHDKN	GMQIDQNFNN	YVAFINEWRI	LPGKSMSDTL	PVSMTSPGKP	SYCSCSLDTA	AYPSSEDLDS
650	660	670	680	690	700	710	720
VSRSEIALGC	KDLNHVSLSS	LIPELDVTSE	YINSDTLVRE	INKHTSPEEY	NLNLFLQEKK	HINLTKLGLN	VQKHPGNEKE
730	740	750	760	770	780	790	800
DSLQYLANKK	YTQGRGSHSQ	EMRYNRQNRW	KRQNFHEFPP	LFAFPSLSQT	DLEELTYFFP	EDHAEDVQQE	FFPSWPTPSG
810	820	830	840	850	860	870	880
LTEYSTLTLC	QETLANSSIG	RLCLAFLGKR	LDSVIEMCVK	DVLLKDDLSW	AEAGVALLEN	ECEKRIVEEG	KYNTEEYGTS
890	900	910	920	930	940	950	960
IEDILSVLKC	PNLCSGNGQC	MEWGCACSPS	FSSYDCSDSY	DKAPEITELG	NAGFCDVQKY	NCMMVRVFGK	GFKELPSIKC
970	980	990	1000	1010	1020	1030	1040
EVTKLQYNSS	EWMPGEPIYT	QTVFHNSRAV	DCQLPTDVQQ	FDTMDLVGGK	PTGKWQLKVS	NDGYKFSNPK	ITVIYDGACQ
1050	1060	1070	1080	1090	1100	1110	1120
VCGLYKNDSC	TIKENVCIID	GLCYVEGDKN	PTSPCLICRP	KISRFTWSFL	ENNQPPVIQA	LQDKLQTFYG	ENFEYQFVAF
1130	1140	1150	1160	1170	1180	1190	1200
DPEGSDIHFT	LDSGPEGASV	SSAGLFMWKT	DLLTTQQITV	RLNDDCDAET	RVTIEVTVKS	CDCLNGGSCV	SDRNFSPGSG
1210	1220	1230	1240	1250	1260	1270	1280
VYLCVCLPGF	HGSLCEVDIS	GCQSNPCGLG	SYISGFHSYS	CDCPPELKVE	TQFVNQFTTQ	TVVLTRSDKS	VNKEEDDKNA
1290	1300	1310	1320	1330	1340	1350	1360
QGRKRHVKPT	SGNAFTICKY	PCGKSRECVA	PNICKCKPGY	IGSNCQTALC	DPDCKNHGKC	IKPNICQCLP	GHGGATCDEE
1370	1380	1390	1400	1410	1420	1430	1440
HCNPPCQHGG	TCLAGNLCTC	PYGFVGPRCE	TMVCNRHCEN	GGQCLTPDIC	QCKPGWYGPT	CSTALCDPVC	LNGGSCNKPN
1450	1460	1470	1480	1490	1500	1510	1520
TCLCPNGFFG	EHCQNAFCHP	PCKNGGHCMR	NNVCVCREGY	TGRRFQKSIC	DPTCMNGGKC	VGPSTCSCPS	GWSGKRCNTP
1530	1540	1550	1560	1570	1580	1590	1600
ICLQKCKNGG	ECIAPSICHC	PSSWEGVRCQ	IPICNPKCLY	GGRCIFPNVC	SCRTEYSGVK	CEKKIQIRRH	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2213	1	916.8887	8.94	2	56.3	16.8	0	165-181	R.LHPCGSDETETGGDCVR.Q	Carbamidomethyl: 15

Detailed Protein Report

Protein 614: 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	

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Detailed Protein Report

Protein 615: **PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein LOC100129528 [Homo sapiens]**

Accession:	gi|530401977	**Score:**	16.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.6
Database Date:	2015-11-30	**pI:**	12.2
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530437161	refseq_human (refseq_human_20140103.fasta)	PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein LOC100129528 [Homo sapiens]

```
        10          20          30          40          50          60          70          80
MPALTEPVHV  HHELPTSSPG  RDPGPRAAHV  LSRKGPGSTS  CPRPLQEGTP  GSRAAHALSR  RGHRVHELPT  SSPGGDTGFM

        90         100         110         120         130         140         150         160
SCPRPFQEGT  PGSRAAHVLS  RRGHRGPRVH  ELPTSSPGRD  PGSTSCPRPL  QEGTRVTNCP  RPLQEGTPGS  RAAHVLSRRG

       170         180         190         200         210         220         230         240
HRVHELPTPS  PGRDPGFMSC  PRPLQEGTRV  TNCPRPLQEG  TRVTSCPRRL  QEGTRVTSCP  RPLQEGTRVT  NCPRALQEGT

       250         260         270         280         290         300         310         320
PGSRAAHALS  RKGPRVHELP  TSSPGGDTGF  TSCPRPLQEG  TPGSRAAHAL  SRRGHRVHEL  PTSSPGRDPG  HELPTSSPGG

       330         340         350         360
DTGFTSCPRT  FQEGTPGSGL  LPAHIVPLCK  SEER
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2039	1	942.3107	-153.18	2	54.0	16.7	0	35-53	K.GPGSTSCPRPLQEGTPGSR.A	

Detailed Protein Report

Protein 616: PREDICTED: E3 ubiquitin-protein ligase Hakai isoform X1 [Homo sapiens]

Accession:	gi|578814630	**Score:**	16.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.8
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIPCKHVFCY	DCAILHEKKG	DKMCPGCSDP	VQRIEQCTRG	SLFMCSIVQG	CKRTYLSQRD	LQAHINHRHM	RAGKPVTRAS
90	100	110	120	130	140	150	160
LENVHPPIAP	PPTEIPERFI	MPPDKHHMSH	IPPKQHIMMP	PPPLQHVPHE	HYNQPHEDIR	APPAELSMAP	PPPRSVSQET
170	180	190	200	210	220	230	240
FRISTRKHSN	LITVPIQDDS	NSGAREPPPP	APAPAHHHPE	YQGQPVVSHP	HHIMPPQQHY	APPPPPPPPI	SHPMPHPPQA
250	260	270	280	290	300	310	320
AGTPHLVYSQ	APPPPMTSAP	PPITPPPGHI	IAQMPPYMNH	PPPGPPPPQH	GGPPVTAPPP	HHYNPNSLPQ	FTEDQGTLSP
330	340	350	360	370	380		
PFTQPGGMSP	GIWPAPRGPP	PPPRLQGPPS	QTPLPGPHHP	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	34-53	R.IEQCTRGSLFMCSIVQGCKR.T	

Detailed Protein Report

Protein 617: **poly(A)-specific ribonuclease PARN-like domain-containing protein 1 isoform 2 precursor [Homo sapiens]**

Accession:	gi|27735155	**Score:**	16.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.1
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFCTRGLLFF	AFLAGLDIEF	TGLRSNLSGP	QQISLFDLPS	EWYLKTRQSV	QQFTVCQIGL	SVFSAIEGEA	NKYIAHSCNF
90	100	110	120	130	140	150	160
YLFPTTFGIL	DSEFSFQASS	VQFLNQYGFN	YNKFLKNGIP	YMNEEQEKKI	RHDILTGNWR	VRSSPDKDQI	KVVIDEVTRW
170	180	190	200	210	220	230	240
LELAKEGDWM	TLPGITGFQA	FEVQLVLRQA	LPNIWTVLKD	EGVVVKKVSK	QHRWYLQNTS	CDRESCWKEN	ILLSARGFSV
250	260	270	280	290	300	310	320
FFQMLVKAQK	PLVGHNMMMD	LLHLHEKFFR	PLPESYDQFK	QNIHSLFPVL	IDTKSVTKDI	WKEMNFPRVS	NLSEVYEVLN
330	340	350	360	370	380	390	400
SDLNPTKNSG	PEIVHASRCE	KYVETKCPHE	AAYDAFLCGS	VLLKVAHLLL	QKIYHIDPVP	ESSFPQYLDV	LAPYVNQVNL
410	420	430	440	450	460	470	480
IRAGVPKINF	SGPDYPSIRP	PILILSVKRW	PGVSEQQVYH	KFQNLCKFDV	RRLTRSQFLL	LTNKFKDARN	ILKEYRDHPT
490	500	510	520	530			
LCISLYRYWR	HSPNVNCLLQ	VCGIVTAWAL	LAFILGRSGT				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1449	1	405.2085	15.16	2	48.3	16.6	0	442-447	K.FQNLCK.F	Carbamidomethyl: 5

Detailed Protein Report

Protein 618: prolargin precursor [Homo sapiens]

Accession:	gi|4506041	**Score:**	16.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.8
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|41349454	refseq_human (refseq_human_20140103.fasta)	prolargin precursor [Homo sapiens]

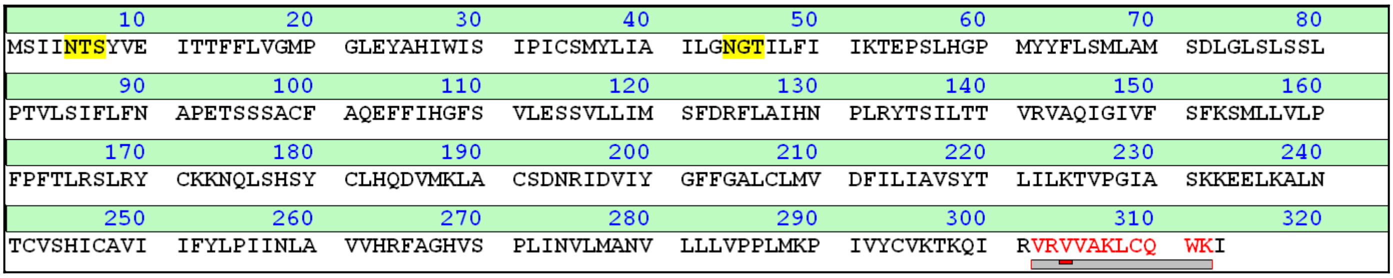
```
        10         20         30         40         50         60         70         80
MRSPLCWLLP LLILASVAQG QPTRRPRPGT GPGRRPRPRP RPTPSFPQPD EPAEPTDLPP PLPPGPPSIF PDCPRECYCP
        90        100        110        120        130        140        150        160
PDFPSALYCD SRNLRKVPVI PPRIHYLYLQ NNFITELPVE SFQNATGLRW INLDNNRIRK IDQRVLEKLP GLVFLYMEKN
       170        180        190        200        210        220        230        240
QLEEVPSALP RNLEQLRLSQ NHISRIPPGV FSKLENLLLL DLQHNRLSDG VFKPDTFHGL KNLMQLNLAH NILRKMPPRV
       250        260        270        280        290        300        310        320
PTAIHQLYLD SNKIETIPNG YFKSFPNLAF IRLNYNKLTD RGLPKNSFNI SNLLVLHLSH NRISSVPAIN NRLEHLYLNN
       330        340        350        360        370        380        390
NSIEKINGTQ ICPNDLVAFH DFSSDLENVP HLRYLRLDGN YLKPPIPLDL MMCFRLLQSV VI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1136	1	1207.6290	-47.21	3	44.3	16.6	2	2-34	M.RSPLCWLLPLLILASVAQGQPTRRPRPGTGPGR.R	Carbamidomethyl: 5

Detailed Protein Report

Protein 619: olfactory receptor 51A2 [Homo sapiens]

Accession:	gi|52317146	**Score:**	16.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.1
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	3.5
		No. of unique Peptides:	1



10	20	30	40	50	60	70	80
MSIINTSYVE	ITTFFLVGMP	GLEYAHIWIS	IPICSMYLIA	ILGNGTILFI	IKTEPSLHGP	MYYFLSMLAM	SDLGLSLSSL
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
PTVLSIFLFN	APETSSSACF	AQEFFIHGFS	VLESSVLLIM	SFDRFLAIHN	PLRYTSILTT	VRVAQIGIVF	SFKSMLLVLP
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
FPFTLRSLRY	CKKNQLSHSY	CLHQDVMKLA	CSDNRIDVIY	GFFGALCLMV	DFILIAVSYT	LILKTVPGIA	SKKEELKALN
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
TCVSHICAVI	IFYLPIINLA	VVHRFAGHVS	PLINVLMANV	LLLVPPLMKP	IVYCVKTKQI	RVRVVAKLCQ	WKI

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2802	1	665.3571	-56.63	2	64.1	16.5	2	302-312	R.VRVVAKLCQWK.I	

Protein 620: SLAM family member 7 isoform g [Homo sapiens]

Accession:	gi|543583727	**Score:**	16.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	16.5
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	12.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAGSPTCLTL	IYILWQLTEH	LSKPKVTMGL	QSNKNGTCVT	NLTCCMEHGE	EDVIYTWKAL	GQAANESHNG	SILPISWRWG
90	100	110	120	130	140	150	
ESDMTFICVA	RNPVSRNFSS	PILARKLCEE	NNPKGRSSKY	GLLHCGNTEK	DGKSPLTAHD	ARHTKAICL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1671	1	1058.9456	-92.93	2	51.2	16.5	2	97-114	R.NFSSPILARKLCEENNPK.G	Carbamidomethyl: 12

Detailed Protein Report

Protein 621: interferon-related developmental regulator 2 [Homo sapiens]

Accession:	gi|197333755	**Score:**	16.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.8
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAWNSPSRRP	VWQGGAPRED	GGARGVWLPS	SGQVSAQRTG	RRLVGLEPTP	TGSLTPRPPR	PVPGMPRARK	GNTLRKGGQR
90	100	110	120	130	140	150	160
RGGGARSSAQ	ADSGSSDDEA	ASEARSTASE	CPSLLSTTAE	DSLGGDVVDE	QGQQEDLEEK	LKEYVDCLTD	KSAKTRQGAL
170	180	190	200	210	220	230	240
ESLRLALASR	LLPDFLLERR	LTLADALEKC	LKKGKGEEQA	LAAAVLGLLC	VQLGPGPKGE	ELFHSLQPLL	VSVLSDSTAS
250	260	270	280	290	300	310	320
PAARLHCASA	LGLGCYVAAA	DIQDLVSCLA	CLESVFSRFY	GLGGSSTSPV	VPASLHGLLS	AALQAWALLL	TICPSTQISH
330	340	350	360	370	380	390	400
ILDRQLPRLP	QLLSSESVNL	RIAAGETIAL	LFELARDLEE	EFVYEDMEAL	CSVLRTLATD	SNKYRAKADR	RRQRSTFRAV
410	420	430	440	450	460	470	480
LHSVEGGECE	EEIVRFGFEV	LYMDSWARHR	IYAAFKEVLG	SGMHHHLQNN	ELLRDIFGLG	PVLLLDATAL	KACKVPRFEK
490	500	510					
HLYNAAAFKA	RTKARSRVRD	KRADIL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1054	1	849.7307	-100.08	3	41.7	16.5	2	193-218	K.KGKGEEQALAAAVLGLLCVQLGPGPK.G	

Detailed Protein Report

Protein 622: 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 623: PREDICTED: zinc finger protein 646 isoform X3 [Homo sapiens]

Accession:	gi|530409439	**Score:**	16.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	198.5
Database Date:	2015-11-30	**pI:**	6.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.4
		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 624: PREDICTED: nuclear pore complex protein Nup214 isoform X4 [Homo sapiens]

Accession:	gi|530427224	**Score:**	16.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	209.0
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

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
1945	2	1023.3932	-98.93	2	54.7	16.5	2	670-687	R.TSKACFQVGTSEEMKMLR.T	

Detailed Protein Report

Protein 625: lipocalin-1 isoform 3 precursor [Homo sapiens]

Accession:	gi|357933621	**Score:**	16.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.1
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	5.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKPLLLAVSL	GLIAALQAHH	LLASDEEIQD	VSGTWYLKAM	TVDREFPEMN	LESVTPMTLT	TLEGGNLEAK	VTMLISGRCQ
90	100	110	120	130	140	150	160
EVKAVLEKTD	EPGKYTADGG	KHVAYIIRSH	VKDHYIFYCE	GELHGKPVRG	AETPRTTWKP	WRTLRKPQEP	ADSARRASSS
170	180	190	200	210	220	230	240
PGRAKPALQG	AIRGRGHLGS	SAAQGRHHPA	PPSFTGTWKK	LPTPAERGWL	HPFLPPPAFP	LPCAPSPGSP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
362	1	529.2876	15.71	3	34.5	16.5	1	130-142	R.GAETPRTTWKPWR.T	

Detailed Protein Report

Protein 626: 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

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
719	1	690.8999	-31.62	2	39.0	16.5	2	402-413	R.TFLRAVTKLGFK.I	

Detailed Protein Report

Protein 627: 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 628: 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; Oxidation: 29

Detailed Protein Report

Protein 629: **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

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
1924	1	768.8264	-78.40	2	54.4	16.4	0	43-57	K.CVFVGEMAAQVGAVR.V	

Detailed Protein Report

Protein 630: zinc finger and SCAN domain-containing protein 30 isoform 2 [Homo sapiens]

Accession:	gi|569026709	**Score:**	16.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.5
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	5.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVAGKVLMAK	QEIVECVASA	AMISPGKLPG	ETHSQRIAEE	ALGGLDNSKK	QKGNAAGNKI	SQLPSQDRHF	SLATFNRRIP
90	100	110	120	130	140	150	160
TEHSVLESHE	SEGSFSMNSN	DITQQSVDTR	EKLYECFDCG	KAFCQSSKLI	RHQRIHTGER	PYACKECGKA	FSLSSDLVRH
170	180	190	200	210	220	230	240
QRIHSGEKPY	ECCECGKAFR	GSSELIRHRR	IHTGEKPYEC	GECGKAFSRS	SALIQHKKIH	TGDKSYECIA	CGKAFGRSSI
250	260	270	280	290	300	310	
LIEHQRIHTG	EKPYECNECG	KSFNQSSALT	QHQRIHTGEK	PYECSECRKT	FRHRSGLMQH	QRTHTRV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1677	1	956.4573	-48.17	2	49.5	16.4	2	51-68	K.QKGNAAGNKISQLPSQDR.H	

Detailed Protein Report

Protein 631: **bone morphogenetic protein 1 isoform 1 precursor [Homo sapiens]**

Accession:	gi|4502421	**Score:**	16.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.8
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPGVARLPLL	LGLLLLPRPG	RPLDLADYTY	DLAEEDDSEP	LNYKDPCKAA	AFLGDIALDE	EDLRAFQVQQ	AVDLRRHTAR
90	100	110	120	130	140	150	160
KSSIKAAVPG	NTSTPSCQST	NGQPQRGACG	RWRGRSRSRR	AATSRPERVW	PDGVIPFVIG	GNFTGSQRAV	FRQAMRHWEK
170	180	190	200	210	220	230	240
HTCVTFLERT	DEDSYIVFTY	RPCGCCSYVG	RRGGGPQAIS	IGKNCDKFGI	VVHELGHVVG	FWHEHTRPDR	DRHVSIVREN
250	260	270	280	290	300	310	320
IQPGQEYNFL	KMEPQEVESL	GETYDFDSIM	HYARNTFSRG	IFLDTIVPKY	EVNGVKPPIG	QRTRLSKGDI	AQARKLYKCP
330	340	350	360	370	380	390	400
ACGETLQDST	GNFSSPEYPN	GYSAHMHCVW	RISVTPGEKI	ILNFTSLDLY	RSRLCWYDYV	EVRDGFWRKA	PLRGRFCGSK
410	420	430	440	450	460	470	480
LPEPIVSTDS	RLWVEFRSSS	NWVGKGFFAV	YEAICGGDVK	KDYGHIQSPN	YPDDYRPSKV	CIWRIQVSEG	FHVGLTFQSF
490	500	510	520	530	540	550	560
EIERHDSCAY	DYLEVRDGHS	ESSTLIGRYC	GYEKPDDIKS	TSSRLWLKFV	SDGSINKAGF	AVNFFKEVDE	CSRPNRGGCE
570	580	590	600	610	620	630	640
QRCLNTLGSY	KCSCDPGYEL	APDKRRCEAA	CGGFLTKLNG	SITSPGWPKE	YPPNKNCIWQ	LVAPTQYRIS	LQFDFFETEG
650	660	670	680	690	700	710	720
NDVCKYDFVE	VRSGLTADSK	LHGKFCGSEK	PEVITSQYNN	MRVEFKSDNT	VSKKGFKAHF	FSEKRPALQP	PRGRPHQLKF
730	740						
RVQKRNRTPQ							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2634	3	753.8426	-101.90	2	61.7	16.4	1	525-537	R.LWLKFVSDGSINK.A	

Detailed Protein Report

Protein 632: protein-glutamine gamma-glutamyltransferase 5 isoform 2 [Homo sapiens]

Accession:	gi|4759230	**Score:**	16.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.9
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQGLEVALT	DLQSSRNNVR	HHTEEITVDH	LLVRRGQAFN	LTLYFRNRSF	QPGLDNIIFV	VETEDAVYLD	SEPQRQEYVM
90	100	110	120	130	140	150	160
NDYGFIYQGS	KNWIRPCPWN	YGQFEDKIID	ICLKLLDKSL	HFQTDPATDC	ALRGSPVYVS	RVVCAMINSN	DDNGVLNGNW
170	180	190	200	210	220	230	240
SENYTDGANP	AEWTGSVAIL	KQWNATGCQP	VRYGQCWVFA	AVMCTVMRCL	GIPTRVITNF	DSGHDTDGNL	IIDEYYDNTG
250	260	270	280	290	300	310	320
RILGNKKKDT	IWNFHVWNEC	WMARKDLPPA	YGGWQVLDAT	PQEMSNGVYC	CGPASVRAIK	EGEVDLNYDT	PFVFSMVNAD
330	340	350	360	370	380	390	400
CMSWLVQGGK	EQKLHQDTSS	VGNFISTKSI	QSDERDDITE	NYKYEEGSLQ	ERQVFLKALQ	KLKARSFHGS	QRGAELQPSR
410	420	430	440	450	460	470	480
PTSLSQDSPR	SLHTPSLRPS	DVVQVSLKFK	LLDPPNMGQD	ICFVLLALNM	SSQFKDLKVN	LSAQSLLHDG	SPLSPFWQDT
490	500	510	520	530	540	550	560
AFITLSPKEA	KTYPCKISYS	QYSQYLSTDK	LIRISALGEE	KSSPEKILVN	KIITLSYPSI	TINVLGAAVV	NQPLSIQVIF
570	580	590	600	610	620	630	640
SNPLSEQVED	CVLTVEGSGL	FKKQQKVFLG	VLKPQHQASI	ILETVPFKSG	QRQIQANMRS	NKFKDIKGYR	NVYVDFAL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2196	1	961.3531	-82.76	2	56.1	16.4	0	193-208	R.YGQCWVFAAVMCTVMR.C	Carbamidomethyl: 4

Detailed Protein Report

Protein 633: **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 634: 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 635: PREDICTED: synaptojanin-2 isoform X3 [Homo sapiens]

Accession:	gi|530384175	**Score:**	16.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.5
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	1.1
		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 636: zinc finger C3H1 domain-containing protein [Homo sapiens]

Accession:	gi|87116683	**Score:**	16.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	226.2
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

Detailed Protein Report

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        10         20         30         40         50         60         70         80
MATADTPAPA SSGLSPKEEG ELEDGEISDD DNNSQIRSRS SSSSSGGGLL PYPRRRPPHS ARGGGSGGGG GSSSSSSSSQ
        90        100        110        120        130        140        150        160
QQLRNFSRSR HASERGHLRG PSSYRPKEPF RSHPPSVRMP SSSLSESSPR PSFWERSHLA LDRFRFRGRP YRGGSRWSRG
       170        180        190        200        210        220        230        240
RGVGERGGKP GCRPPLGGGA GSGFSSSQSW REPSPPRKSS KSFGRSPSRK QNYSSKNENC VEETFEDLLL KYKQIQLELE
       250        260        270        280        290        300        310        320
CINKDEKLAL SSKEENVQED PKTLNFEDQT STDNVSITKD SSKEVAPEEK TQVKTFQAFE LKPLRQKLTL PGDKNRLKKV
       330        340        350        360        370        380        390        400
KDGAKPLSLK SDTTDSSQGL QDKEQNLTRR ISTSDILSEK KLGEDEEELS ELQLRLLALQ SASKKWQQKE QQVMKESKEK
       410        420        430        440        450        460        470        480
LTKTKTVQQK VKTSTKTHSA KKVSTTAKQA LRKQQTKAWK KLQQQKEQER QKEEDQRKQA EEEERRKREE EIRKIRDLSN
       490        500        510        520        530        540        550        560
QEEQYNRFMK LVGGKRRSRS KSSDPDLRRS LDKQPTDSGG GIYQYDNYEE VAMDTDSETS SPAPSPVQPP FFSECSLGYF
       570        580        590        600        610        620        630        640
SPAPSLSLPP PPQVSSLPPL SQPYVEGLCV SLEPLPPLPP LPPLPPEDPE QPPKPPFADE EEEEEMLLRE ELLKSLANKR
       650        660        670        680        690        700        710        720
AFKPEETSSN SDPPSPPVLN NSHPVPRSNL SIVSINTVSQ PRIQNPKFHR GPRLPRTVIS LPKHKSVVVT LNDSDDSESD
       730        740        750        760        770        780        790        800
GEASKSTNSV FGGLESMIKE ARRTAEQASK PKVPPKSEKE NDPLRTPEAL PEEKKIEYRL LKEEIANREK QRLIKSDQLK
       810        820        830        840        850        860        870        880
TSSSSPANSD VEIDGIGRIA MVTKQVTDAE SKLKKHRILL MKDESVLKNL VQQEAKKKES VRNAEAKITK LTEQLQATEK
       890        900        910        920        930        940        950        960
ILNVNRMFLK KLQEQIHRVQ QRVTIKKALT LKYGEELARA KAVASKEIGK RKLEQDRFGP NKMMRLDSSP VSSPRKHSAE
       970        980        990       1000       1010       1020       1030       1040
LIAMEKRRLQ KLEYEYALKI QKLKEARALK AKEQQNISPV VEEEPEFSLP QPSLHDLTQD KLTLDTEEND VDDEILSGSS
      1050       1060       1070       1080       1090       1100       1110       1120
RERRRSFLES NYFTKPNLKH TDTANKECIN KLNKNTVEKP ELFLGLKIGE LQKLYSKADS LKQLILKTTT GITEKVLHGQ
      1130       1140       1150       1160       1170       1180       1190       1200
EISVDVDFVT AQSKTMEVKP CPFRPYHSPL LVFKSYRFSP YYRTKEKLPL SSVSYSNMIE PDQCFCRFDL TGTCNDDDCQ
      1210       1220       1230       1240       1250       1260       1270       1280
WQHIQDYTLS RKQLFQDILS YNLSLIGCAE TSTNEEITAS AEKYVEKLFG VNKDRMSMDQ MAVLLVSNIN ESKGHTPPFT
      1290       1300       1310       1320       1330       1340       1350       1360
TYKDKRKWKP KFWRKPISDN SFSSDEEQST GPIKYAFQPE NQINVPALDT VVTPDDVRYF TNETDDIANL EASVLENPSH
      1370       1380       1390       1400       1410       1420       1430       1440
VQLWLKLAYK YLNQNEGECS ESLDSALNVL ARALENNKDN PEIWCHYLRL FSKRGTKDEV QEMCETAVEY APDYQSFWTF
      1450       1460       1470       1480       1490       1500       1510       1520
LHLESTFEEK DYVCERMLEF LMGAAKQETS NILSFQLLEA LLFRVQLHIF TGRCQSALAI LQNALKSAND GIVAEYLKTS
      1530       1540       1550       1560       1570       1580       1590       1600
DRCLAWLAYI HLIEFNILPS KFYDPSNDNP SRIVNTESFV MPWQAVQDVK TNPDMLLAVF EDAVKACTDE SLAVEERIEA
      1610       1620       1630       1640       1650       1660       1670       1680
CLPLYTNMIA LHQLLERYEA AMELCKSLLE SCPINCQLLE ALVALYLQTN QHDKARAVWL TAFEKNPQNA EVFYHMCKFF
      1690       1700       1710       1720       1730       1740       1750       1760
ILQNRGDNLL PFLRKFIASF FKPGFEKYNN LDLFRYLLNI PGPIDIPSRL CKGNFDDDMF NHQVPYLWLI YCLCHPLQSS
      1770       1780       1790       1800       1810       1820       1830       1840
IKETVEAYEA ALGVAMRCDI VQKIWMDYLV FANNRAAGSR NKVQEFKFFT DLVNRCLVTV PARYPIPFSS ADYWSNYEFH
      1850       1860       1870       1880       1890       1900       1910       1920
NRVIFFYLSC VPKTQHSKTL ERFCSVMPAN SGLALRLLQH EWEESNVQIL KLQAKMFTYN IPTCLATWKI AIAAEIVLKG
      1930       1940       1950       1960       1970       1980       1990
QREVHRLYQR ALQKLPLCAS LWKDQLLFEA SEGGKTDNLR KLVSKCQEIG VSLNELLNLN SNKTESKNH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
750	1	937.7415	-84.31	3	37.9	16.3	1	1135-1157	K.TMEVKPCPFRPYHSPLLVFKSYR.F	Oxidation: 2

BRUKER

Detailed Protein Report

Protein 637: soluble lamin-associated protein of 75 kDa [Homo sapiens]

Accession:	gi|153792633	**Score:**	16.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.9
Database Date:	2015-11-30	**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 638: peptidyl-prolyl cis-trans isomerase D [Homo sapiens]

Accession:	gi|4826932	**Score:**	16.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.7
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSHPSPQAKP SNPSNPRVFF DVDIGGERVG RIVLELFADI VPKTAENFRA LCTGEKGIGH TTGKPLHFKG CPFHRIIKKF
        90        100        110        120        130        140        150        160
MIQGGDFSNQ NGTGGESIYG EKFEDENFHY KHDREGLLSM ANAGRNTNGS QFFITTVPTP HLDGKHVVFG QVIKGIGVAR
       170        180        190        200        210        220        230        240
ILENVEVKGE KPAKLCVIAE CGELKEGDDG GIFPKDGSGD SHPDFPEDAD IDLKDVDKIL LITEDLKNIG NTFFKSQNWE
       250        260        270        280        290        300        310        320
MAIKKYAEVL RYVDSSKAVI ETADRAKLQP IALSCVLNIG ACKLKMSNWQ GAIDSCLEAL ELDPSNTKAL YRRAQGWQGL
       330        340        350        360        370        380
KEYDQALADL KKAQGIAPED KAIQAELLKV KQKIKAQKDK EKAVYAKMFA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
920	1	678.9535	63.37	2	40.0	16.2	0	32-43	R.IVLELFADIVPK.T	

Detailed Protein Report

Protein 639: 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_human(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	

Protein 640: 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

Quantitation

QD:QU **Median:** 1.06 **CV:** 0.00 % **No. of 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	Ratios
463	1	717.8711	-17.46	2	35.8	16.2	1	23-35	K.ARDPHSGHFVALK.S		QD:QU 1.06

Detailed Protein Report

Protein 641: **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 642: PREDICTED: zinc finger protein 831 isoform X4 [Homo sapiens]

Accession:	gi|530417824	**Score:**	16.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	132.1
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

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		
KAASVYLAVH	FPGSSLRDEG	PNGPPGSNGG	WTWTSPGEGG	PAQMSKSENP	LEFSSS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1981	3	1023.8811	-103.16	2	55.2	16.2	1	258-276	K.NLDVRTEAAPCPGSAFADR.E	Carbamidomethyl: 11

Detailed Protein Report

Protein 643: 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

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
1720	1	892.3075	-96.70	2	51.8	16.1	0	249-264	K.RPDEVPDDDEPAGPMK.T	Oxidation: 15

Detailed Protein Report

Protein 644: **cytoplasmic phosphatidylinositol transfer protein 1 isoform b [Homo sapiens]**

Accession:	gi|32307142	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.7
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	5.6
		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	MDDVREYEKN
250	260	270					
MHEQTNIKVC	NQHSSPVDDI	ESHAQTST					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
38	1	918.9134	2.10	2	29.2	16.1	1	171-185	R.EGWRDSHQPIMCSYK.L	

Detailed Protein Report

Protein 645: 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 646: PREDICTED: guanine nucleotide exchange factor VAV3 isoform X4 [Homo sapiens]

Accession:	gi|530361574	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	72.1
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 1.40 **CV:** 0.00 % **No. of Peptides:** 1

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	Ratios
877	1	705.9834	77.48	2	41.0	16.1	1	322-333	R.DLLVVPMQRVLK.Y		QD:QU 1.40

Detailed Protein Report

Protein 647: ras and Rab interactor 2 isoform 2 [Homo sapiens]

Accession:	gi|18466802	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.1
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578835435	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ras and Rab interactor 2 isoform X10 [Homo sapiens]
gi|578835433	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ras and Rab interactor 2 isoform X9 [Homo sapiens]
gi|578835431	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ras and Rab interactor 2 isoform X8 [Homo sapiens]
gi|578835429	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ras and Rab interactor 2 isoform X7 [Homo sapiens]
gi|530425753	refseq_human (refseq_human_20140103.fasta)	PREDICTED: ras and Rab interactor 2 isoform X3 [Homo sapiens]

10	20	30	40	50	60	70	80
MTAWTMGARG	LDKRGSFFKL	IDTIASEIGE	LKQEMVRTDV	NLENGLEPAE	THSMVRHKDG	GYSEEEDVKT	CARDSGYDSL
90	100	110	120	130	140	150	160
SNRLSILDRL	LHTHPIWLQL	SLSEEEAAEV	LQAQPPGIFL	VHKSTKMQKK	VLSLRLPCEF	GAPLKEFAIK	ESTYTFSLEG
170	180	190	200	210	220	230	240
SGISFADLFR	LIAFYCISRD	VLPFTLKLPY	AISTAKSEAQ	LEELAQMGLN	FWSSPADSKP	PNLPPPHRPL	SSDGVCPASL
250	260	270	280	290	300	310	320
RQLCLINGVH	SIKTRTPSEL	ECSQTNGALC	FINPLFLKVH	SQDLSGGLKR	PSTRTPNANG	TERTRSPPPR	PPPPAINSLH
330	340	350	360	370	380	390	400
TSPRLARTET	QTSMPETVNH	NKHGNVALPG	TKPTPIPPPR	LKKQASFLEA	EGGAKTLSGG	RPGAGPELEL	GTAGSPGGAP
410	420	430	440	450	460	470	480
PEAAPGDCTR	APPPSSESRP	PCHGGRQRLS	DMSISTSSSD	SLEFDRSMPL	FGYEADTNSS	LEDYEGESDQ	ETMAPPIKSK
490	500	510	520	530	540	550	560
KKRSSSFVLP	KLVKSQLQKV	SGVFSSFMTP	EKRMVRRIAE	LSRDKCTYFG	CLVQDYVSFL	QENKECHVSS	TDMLQTIRQF
570	580	590	600	610	620	630	640
MTQVKNYLSQ	SSELDPPIES	LIPEDQIDVV	LEKAMHKCIL	KPLKGHVEAM	LKDFHMADGS	WKQLKENLQL	VRQRNPQELG
650	660	670	680	690	700	710	720
VFAPTPDFVD	VEKIKVKFMT	MQKMYSPEKK	VMLLLRVCKL	IYTVMENNSG	RMYGADDFLP	VLTYVIAQCD	MLELDTEIEY
730	740	750	760	770	780	790	800
MMELLDPSLL	HGEGGYYLTS	AYGALSLIKN	FQEEQAARLL	SSETRDTLRQ	WHKRRTTNRT	IPSVDDFQNY	LRVAFQEVNS
810	820	830	840	850	860	870	880
GCTGKTLLVR	PYITTEDVCQ	ICAEKFKVGD	PEEYSLFLFV	DETWQQLAED	TYPQKIKAEL	HSRPQPHIFH	FVYKRIKNDP
890	900						
YGIIFQNGEE	DLTTS						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2319	1	719.3506	-2.64	2	57.7	16.1	1	1-13	-.MTAWTMGARGLDK.R	

Detailed Protein Report

Protein 648: **phosphatidylethanolamine N-methyltransferase isoform 4 [Homo sapiens]**

Accession:	gi|388890235	**Score:**	16.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.7
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.4
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.88 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MKRSGNPGAE	ADFCVMTRLL	GYVDPLDPSF	VAAVITITFN	PLYWNVVARW	EHKTRKLSRA	FGSPYLACYS	LSVTILLLNF
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LRSHCFTQAM	LSQPRMESLD	TPAAYSLGLA	LLGLGVVLVL	SSFFALGFAG	TFLGDYFGIL	KEARVTVFPF	NILDNPMYWG
170	**180**	**190**	**200**	**210**	**220**		
STANYLGWAI	MHASPTGLLL	TVLVALTYIV	ALLYEEPFTA	EIYRQKASGS	HKRS		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1867	3	993.3614	-92.34	2	51.9	16.1	2	1-18	-.MKRSGNPGAEADFCVMTR.L	Oxidation: 1	QD:QU	0.88

Detailed Protein Report

Protein 649: 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 650: **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 651: mucin-12 precursor [Homo sapiens]

Accession:	gi|256600257	**Score:**	16.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	542.4
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MLVIWILTLA LRLCASVTTV TPGSTVNTSI GGNTTSASTP SSSDPFTTFS DYGVSVTFIT GSTATKHFLD SSTNSGHSEE
        90        100        110        120        130        140        150        160
STVSHSGPGA TGTTLFPSHS ATSVFVGEPK TSPITSASME TTALPGSTTT AGLSEKSTTF YSSPRSPDRT LSPARTTSSG
       170        180        190        200        210        220        230        240
VSEKSTTSHS RPGPTHTIAF PDSTTMPGVS QESTASHSIP GSTDTTLSPG TTTPSSLGPE STTFHSSPGY TKTTRLPDNT
       250        260        270        280        290        300        310        320
TTSGLLEAST PVHSSTGSPH TTLSPSSSTT HEGEPTTFQS WPSSKDTSPA PSGTTSAFVK LSTTYHSSPS STPTTHFSAS
       330        340        350        360        370        380        390        400
STTLGHSEES TPVHSSPVAT ATTPPPARSA TSGHVEESTA YHRSPGSTQT MHFPESSTTS GHSEESATFH GSTTHTKSST
       410        420        430        440        450        460        470        480
PSTTAALAHT SYHSSLGSTE TTHFRDSSTI SGRSEESKAS HSSPDAMATT VLPAGSTPSV LVGDSTPSPI SSGSMETTAL
       490        500        510        520        530        540        550        560
PGSTTKPGLS EKSTTFYSSP RSPDTTHLPA SMTSSGVSEE STTSHSRPGS THTTAFPGST TMPGLSQEST ASHSSPGPTD
       570        580        590        600        610        620        630        640
TTLSPGSTTA SSLGPEYTTF HSRPGSTETT LLPDNTTASG LLEASMPVHS STRSPHTTLS PAGSTTRQGE STTFHSWPSS
       650        660        670        680        690        700        710        720
KDTRPAPPTT TSAFVEPSTT SHGSPSSIPT THISARSTTS GLVEESTTYH SSPGSTQTMH FPESDTTSGR GEESTTSHSS
       730        740        750        760        770        780        790        800
TTHTISSAPS TTSALVEEPT SYHSSPGSTA TTHFPDSSTT SGRSEESTAS HSSQDATGTI VLPARSTTSV LLGESTTSPI
       810        820        830        840        850        860        870        880
SSGSMETTAL PGSTTTPGLS ERSTTFHSSP RSPATTLSPA STTSSGVSEE STTSRSRPGS THTTAFPDST TTPGLSRHST
       890        900        910        920        930        940        950        960
TSHSSPGSTD TTLLPASTTT SGPSQESTTS HSSSGSTDTA LSPGSTTALS FGQESTTFHS NPGSTHTTLF PDSTTSSGIV
       970        980        990       1000       1010       1020       1030       1040
EASTRVHSST GSPRTTLSPA SSTSPGLQGE STAFQTHPAS THTTPSPPST ATAPVEESTT YHRSPGSTPT THFPASSTTS
      1050       1060       1070       1080       1090       1100       1110       1120
GHSEKSTIFH SSPDASGTTP SSAHSTTSGR GESTTSRISP GSTEITTLPG STTTPGLSEA STTFYSSPRS PTTTLSPASM
      1130       1140       1150       1160       1170       1180       1190       1200
TSLGVGEEST TSRSQPGSTH STVSPASTTT PGLSEESTTV YSSSRGSTET TVFPHSTTTS VHGEEPTTFH SRPASTHTTL
      1210       1220       1230       1240       1250       1260       1270       1280
FTEDSTTSGL TEESTAFPGS PASTQTGLPA TLTTADLGEE STTFPSSSGS TGTKLSPARS TTSGLVGEST PSRLSPSSTE
      1290       1300       1310       1320       1330       1340       1350       1360
TTTLPGSPTT PSLSEKSTTF YTSPRSPDAT LSPATTTSSG VSEESSTSHS QPGSTHTTAF PDSTTTSDLS QEPTTSHSSQ
      1370       1380       1390       1400       1410       1420       1430       1440
GSTEATLSPG STTASSLGQQ STTFHSSPGD TETTLLPDDT ITSGLVEAST PTHSSTGSLH TTLTPASSTS AGLQEESTTF
      1450       1460       1470       1480       1490       1500       1510       1520
QSWPSSSDTT PSPPGTTAAP VEVSTTYHSR PSSTPTTHFS ASSTTLGRSE ESTTVHSSPG ATGTALFPTR SATSVLVGEP
      1530       1540       1550       1560       1570       1580       1590       1600
TTSPISSGST ETTALPGSTT TAGLSEKSTT FYSSPRSPDT TLSPASTTSS GVSEESTTSH SRPGSTHTTA FPGSTTMPGV
      1610       1620       1630       1640       1650       1660       1670       1680
SQESTASHSS PGSTDTTLSP GSTTASSLGP ESTTFHSSPG STETTLLPDN TTASGLLEAS TPVHSSTGSP HTTLSPAGST
      1690       1700       1710       1720       1730       1740       1750       1760
TRQGESTTFQ SWPSSKDTMP APPTTTSAFV ELSTTSHGSP SSTPTTHFSA SSTTLGRSEE STTVHSSPVA TATTPSPARS
      1770       1780       1790       1800       1810       1820       1830       1840
TTSGLVEEST AYHSSPGSTQ TMHFPESSTA SGRSEESRTS HSSTTHTISS PPSTTSALVE EPTSYHSSPG STATTHFPDS
      1850       1860       1870       1880       1890       1900       1910       1920
STTSGRSEES TASHSSQDAT GTIVLPARST TSVLLGESTT SPISSGSMET TALPGSTTTP GLSEKSTTFH SSPRSPATTL
      1930       1940       1950       1960       1970       1980       1990       2000
SPASTTSSGV SEESTTSHSR PGSTHTTAFP DSTTTPGLSR HSTTSHSSPG STDTTLLPAS TTTSGPSQES TTSHSSPGST
      2010       2020       2030       2040       2050       2060       2070       2080
DTALSPGSTT ALSFGQESTT FHSSPGSTHT TLFPDSTTSS GIVEASTRVH SSTGSPRTTL SPASSTSPGL QGESTAFQTH
      2090       2100       2110       2120       2130       2140       2150       2160
PASTHTTPSP PSTATAPVEE STTYHRSPGS TPTTHFPASS TTSGHSEKST IFHSSPDASG TTPSSAHSTT SGRGESTTSR
      2170       2180       2190       2200       2210       2220       2230       2240
ISPGSTEITT LPGSTTTPGL SEASTTFYSS PRSPTTTLSP ASMTSLGVGE ESTTSRSQPG STHSTVSPAS TTTPGLSEES
      2250       2260       2270       2280       2290       2300       2310       2320
TTVYSSSPGS TETTVFPRTP TTSVRGEEPT TFHSRPASTH TTLFTEDSTT SGLTEESTAF PGSPASTQTG LPATLTTADL
      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
710	1	661.8474	-3.38	2	38.9	16.0	2	5182-5193	K.LACVNKCTKGTK.S	Carbamidomethyl: 7

Detailed Protein Report

Protein 652: intraflagellar transport protein 80 homolog isoform a [Homo sapiens]

Accession:	gi|46409657	**Score:**	16.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	88.0
Database Date:	2015-11-30	**pI:**	8.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 1.47 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MRLKISLLKE	PKHQELVSCV	GWTTAEELYS	CSDDHQIVKW	NLLTSETTQI	VKLPDDIYPI	DFHWFPKSLG	VKKQTQAESF
90	100	110	120	130	140	150	160
VLTSSDGKFH	LISKLGRVEK	SVEAHCGAVL	AGRWNYEGTA	LVTVGEDGQI	KIWSKTGMLR	STLAQQGTPV	YSVAWGPDSE
170	180	190	200	210	220	230	240
KVLYTAGKQL	IIKPLQPNAK	VLQWKAHDGI	ILKVDWNSVN	DLILSAGEDC	KYKVWDSYGR	PLYNSQPHEH	PITSVAWAPD
250	260	270	280	290	300	310	320
GELFAVGSFH	TLRLCDKTGW	SYALEKPNTG	SIFNIAWSID	GTQIAGACGN	GHVVFAHVVE	QHWEWKNFQV	TLTKRRAMQV
330	340	350	360	370	380	390	400
RNVLNDAVDL	LEFRDRVIKA	SLNYAHLVVS	TSLQCYVFST	KNWNTPIIFD	LKEGTVSLIL	QAERHFLLVD	GSSIYLYSYE
410	420	430	440	450	460	470	480
GRFISSPKFP	GMRTDILNAQ	TVSLSNDTIA	IRDKADEKII	FLFEASTGKP	LGDGKFLSHK	NEILEIALDQ	KGLTNDRKIA
490	500	510	520	530	540	550	560
FIDKNRDLCI	TSVKRFGKEE	QIIKLGTMVH	TLAWNDTCNI	LCGLQDTRFI	VWYYPNTVYV	DRDILPKTLY	ERDASEFSKN
570	580	590	600	610	620	630	640
PHIVSFVGNQ	VTIRRADGSL	VHISITPYPA	ILHEYVSSSK	WEDAVRLCRF	VKEQTMWACL	AAMAVANRDM	TTAEIAYAAI
650	660	670	680	690	700	710	720
GEIDKVQYIN	SIKNLPSKES	KMAHILLFSG	NIQEAEIVLL	QAGLVYQAIQ	ININLYNWER	ALELAVKYKT	HVDTVLAYRQ
730	740	750	760	770	780		
KFLETFGKQE	TNKRYLHYAE	GLQIDWEKIK	AKIEMEITKE	REQSSSSQSS	KSIGLKP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
870	1	663.6930	-210.56	2	40.9	16.0	0	101-113	K.SVEAHCGAVLAGR.W	Carbamidomethyl: 6	QD:QU 1.47

Detailed Protein Report

Protein 653: **transcription intermediary factor 1-alpha isoform b [Homo sapiens]**

Accession:	gi|47419909	**Score:**	16.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	112.9
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEVAVEKAVA	AAAAASAAAS	GGPSAAPSGE	NEAESRQGPD	SERGGEAARL	NLLDTCAVCH	QNIQSRAPKL	LPCLHSFCQR
90	100	110	120	130	140	150	160
CLPAPQRYLM	LPAPMLGSAE	TPPPVPAPGS	PVSGSSPFAT	QVGVIRCPVC	SQECAERHII	DNFFVKDTTE	VPSSTVEKSN
170	180	190	200	210	220	230	240
QVCTSCEDNA	EANGFCVECV	EWLCKTCIRA	HQRVKFTKDH	TVRQKEEVSP	EAVGVTSQRP	VFCPFHKKEQ	LKLYCETCDK
250	260	270	280	290	300	310	320
LTCRDCQLLE	HKEHRYQFIE	EAFQNQKVII	DTLITKLMEK	TKYIKFTGNQ	IQNRIIEVNQ	NQKQVEQDIK	VAIFTLMVEI
330	340	350	360	370	380	390	400
NKKGKALLHQ	LESLAKDHRM	KLMQQQQEVA	GLSKQLEHVM	HFSKWAVSSG	SSTALLYSKR	LITYRLRHLL	RARCDASPVT
410	420	430	440	450	460	470	480
NNTIQFHCDP	SFWAQNIINL	GSLVIEDKES	QPQMPKQNPV	VEQNSQPPSG	LSSNQLSKFP	TQISLAQLRL	QHMQQQQPPP
490	500	510	520	530	540	550	560
RLINFQNHSP	KPNGPVLPPH	PQQLRYPPNQ	NIPRQAIKPN	PLQMAFLAQQ	AIKQWQISSG	QGTPSTTNST	SSTPSSPTIT
570	580	590	600	610	620	630	640
SAAGYDGKAF	GSPMIDLSSP	VGGSYNLPSL	PDIDCSSTIM	LDNIVRKDTN	IDHGQPRPPS	NRTVQSPNSS	VPSPGLAGPV
650	660	670	680	690	700	710	720
TMTSVHPPIR	SPSASSVGSR	GSSGSSSKPA	GADSTHKVPV	VMLEPIRIKQ	ENSGPPENYD	FPVVIVKQES	DEESRPQNAN
730	740	750	760	770	780	790	800
YPRSILTSLL	LNSSQSSTSE	ETVLRSDAPD	STGDQPGLHQ	DNSSNGKSEW	LDPSQKSPLH	VGETRKEDDP	NEDWCAVCQN
810	820	830	840	850	860	870	880
GGELLCCEKC	PKVFHLSCHV	PTLTNFPSGE	WICTFCRDLS	KPEVEYDCDA	PSHNSEKKKT	EGLVKLTPID	KRKCERLLLF
890	900	910	920	930	940	950	960
LYCHEMSLAF	QDPVPLTVPD	YYKIIKNPMD	LSTIKKRLQE	DYSMYSKPED	FVADFRLIFQ	NCAEFNEPDS	EVANAGIKLE
970	980	990	1000	1010	1020		
NYFEELLKNL	YPEKRFPKPE	FRNESEDNKF	SDDSDDDFVQ	PRKKRLKSIE	ERQLLK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1407	1	637.4446	122.09	2	46.1	16.0	0	459-469	K.FPTQISLAQLR.L	

Detailed Protein Report

Protein 654: 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 655: AP-1 complex subunit mu-2 [Homo sapiens]

Accession:	gi|9506797	**Score:**	15.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.1
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSASAVFILD	VKGKPLISRN	YKGDVAMSKI	EHFMPLLVQR	EEEGALAPLL	SHGQVHFLWI	KHSNLYLVAT	TSKNANASLV
90	100	110	120	130	140	150	160
YSFLYKTIEV	FCEYFKELEE	ESIRDNFVIV	YELLDELMDF	GFPQTTDSKI	LQEYITQQSN	KLETGKSRVP	PTVTNAVSWR
170	180	190	200	210	220	230	240
SEGIKYKKNE	VFIDVIESVN	LLVNANGSVL	LSEIVGTIKL	KVFLSGMPEL	RLGLNDRVLF	ELTGRSKNKS	VELEDVKFHQ
250	260	270	280	290	300	310	320
CVRLSRFDND	RTISFIPPDG	DFELMSYRLS	TQVKPLIWIE	SVIEKFSHSR	VEIMVKAKGQ	FKKQSVANGV	EISVPVPSDA
330	340	350	360	370	380	390	400
DSPRFKTSVG	SAKYVPERNV	VIWSIKSFPG	GKEYLMRAHF	GLPSVEKEEV	EGRPPIGVKF	EIPYFTVSGI	QVRYMKIIEK
410	420	430					
SGYQALPWVR	YITQSGDYQL	RTS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1641	1	873.4079	-31.68	2	49.0	15.9	1	230-243	K.SVELEDVKFHQCVR.L	Carbamidomethyl: 12

Detailed Protein Report

Protein 656: **cadherin-related family member 4 precursor [Homo sapiens]**

Accession:	gi|203097724	**Score:**	15.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.8
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVLLRLLVFL	FAPVVSDLCS	LPCFINVSES	QGPGTVLQFL	SFNCSSYTPT	PTLELLNVQP	PTTFFNPPSL	ARWQGTYVGK
90	100	110	120	130	140	150	160
LTLSSSAQLD	ALMVNHYKVQ	LKFTCGNHVM	EGSLSVDVQR	DLSHIQCAGQ	FASPAGEMIQ	VPETVTPGAR	LYTLLLPGLE
170	180	190	200	210	220	230	240
LHGAQMSIIS	AQDLPHFPGP	FSINEQGWLQ	APSQGLLGQA	QKVFQLQISV	SFGQRQSCQG	MVIVKVLPVP	SSQVSFLEQA
250	260	270	280	290	300	310	320
QNITIPENLA	PGSEVVQVQA	RGVDLRYEIL	SPVPSPLFSI	GRADGVVRTT	TPLELARTSG	TAVSRLQVKA	FEQGQLWASA
330	340	350	360	370	380	390	400
KLNLTMNVQL	VNLWPPRCLP	ALLVSQIPET	APVGTVLNTL	TCEDPDSVGA	TLDYKLWFRS	SSNPASLCLY	DRVLEVNATL
410	420	430	440	450	460	470	480
DCDTPGACFQ	HAASILVLDG	GQPQMTTEVP	VLVMVTPINE	FSPACAPRTF	RVQEDAAPHT	LLGSVVGTDM	DYPHDNIEYY
490	500	510	520	530	540	550	560
TSGGPTTFAV	DRLSGEVHLL	GPLDYEQQRL	YRLTVLVIDH	GQDQNPNHHL	SGSCTITIEV	EDVNDHAPEC	EPPFQELTIY
570	580	590	600	610	620	630	640
APLGRSVEVT	KMSCQIPQEP	QRLIYSYSIV	GGNSQNRFIL	QGAILVHSDL	VLGPFWPEQP	RTYELLICVA	DAGPSTPHLS
650	660	670	680	690	700	710	720
TTATIIVHLV	PRRASTVATS	THRTTVPSTM	TPMLVTDTEA	FWQPQPWFVV	VLTATGALLL	LALGWLLGRL	LQGLAQLLQA
730	740	750	760	770	780	790	
PSKPAQALLL	NSIQGTEGSI	EGFLEAPKME	MSQAPSSVMS	LHFDGRAQDS	RTGRDYLFNT	HTGARRWL	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1960	1	1029.3192	-117.25	2	53.0	15.9	0	749-766	K.MEMSQAPSSVMSLHFDGR.A	Oxidation: 1, 3, 11

Detailed Protein Report

Protein 657: oxysterol-binding protein-related protein 10 isoform 2 [Homo sapiens]

Accession:	gi|291327480	**Score:**	15.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.2
Database Date:	2015-11-30	**pI:**	8.5
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MERAVQGTDG GGGSNSSSRS SSRATSAGSS PSCSLAGRGV SSRSAAAGLG GGGSRSSPGS VAASPSGGGG RRREPALEGV
        90        100        110        120        130        140        150        160
LSKYTNLLQG WQNRYFVLDF EAGILQYFVN EQSKHQKPRG VLSLSGAIVS LSDEAPHMLV VYSANGEMFK LRAADAKEKQ
       170        180        190        200        210        220        230        240
FWVTQLRACA KYHMEMNSKM MNQVEGQQKN LVHAIESLPG SGPLTALDQD LLLLKATSAA TLSCLGECLN LLQQSVHQAG
       250        260        270        280        290        300        310        320
QPSQKPGASE NILGWHGSKS HSTEQLKNGT LGSLPSASAN ITWAILPNSA EDEQTSQPEP EPNSGSELVL SEDEKSDNED
       330        340        350        360        370        380        390        400
KEETELGVME DQRSIILHLI SQLKLGMDLT KVVLPTFILE KRSLLEMYAD FMAHPDLLLA ITAGATPEER VICFVEYYLT
       410        420        430        440        450        460        470        480
AFHEGRKGAL AKKPYNPIIG ETFHCSWEVP KDRVKPKRTA SRSPASCHEH PMADDPSKSY KLRFVAEQVS HHPPISCFYC
       490        500        510        520        530        540        550        560
ECEEKRLCVN THVWTKSKFM GMSVGVSMIG EGVLRLLEHG EEYVFTLPSA YARSILTIPW VELGGKVSIN CAKTGYSATV
       570        580        590        600        610        620        630        640
IFHTKPFYGG KVHRVTAEVK HNPTNTIVCK AHGEWNGTLE FTYNNGETKV IDTTTLPVYP KKIRPLEKQG PMESRNLWRE
       650        660        670        680        690        700        710
VTRYLRLGDI DAATEQKRHL EEKQRVEERK RENLRTPWKP KYFIQEGDGW VYFNPLWKAH
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1650	1	1070.0254	31.14	2	49.1	15.9	2	2-23	M.ERAVQGTDGGGGSNSSSRSSSR.A	

Detailed Protein Report

Protein 658: beta-defensin 118 precursor [Homo sapiens]

Accession:	gi|16905373	**Score:**	15.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.6
Database Date:	2015-11-30	**pI:**	7.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.6
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MKLLLLALPM LVLLPQVIPA YSGEKKCWNR SGHCRKQCKD GEAVKDTCKN LRACCIPSNE DHRRVPATSP TPLSDSTPGI
        90        100        110        120        130
IDDILTVRFT TDYFEVSSKK DMVEESEAGR GTETSLPNVH HSS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2473	1	753.2385	-177.83	2	59.6	15.9	2	40-52	K.DGEAVKDTCKNLR.A	Carbamidomethyl: 9

Detailed Protein Report

Protein 659: 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_human (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 660: olfactory receptor 6Y1 [Homo sapiens]

Accession: gi|52353280
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 15.8
MW [kDa]: 36.6
pI: 9.4
Sequence Coverage [%]: 4.6
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MTTIILEVDN	HTVTTRFILL	GFPTRPAFQL	LFFSIFLATY	LLTLLENLLI	ILAIHSDGQL	HKPMYFFLSH	LSFLEMWYVT
90	100	110	120	130	140	150	160
VISPKMLVDF	LSHDKSISFN	GCMTQLYFFV	TFVCTEYILL	AIMAFDRYVA	ICNPLRYPVI	MTNQLCGTLA	GGCWFCGLMT
170	180	190	200	210	220	230	240
AMIKMVFIAQ	LHYCGMPQIN	HYFCDISPLL	NVSCEDASQA	EMVDFFLALM	VIAIPLCVVV	ASYAAILATI	LRIPSAQGRQ
250	260	270	280	290	300	310	320
KAFSTCASHL	TVVILFYSMT	LFTYARPKLM	YAYNSNKVVS	VLYTVIVPLL	NPIIYCLRNH	EVKAALRKTI	HCRGSGPQGN
330							
GAFSS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2724	1	856.9336	-33.77	2	65.2	15.8	0	2-16	M.TTIILEVDNHTVTTR.F	

Detailed Protein Report

Protein 661: **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 662: G-protein coupled receptor 55 [Homo sapiens]

Accession:	gi|33695107	**Score:**	15.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.6
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	6.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530371161	refseq_human (refseq_human_20140103.fasta)	PREDICTED: G-protein coupled receptor 55 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MSQQNTSGDC	LFDGVNELMK	TLQFAVHIPT	FVLGLLLNLL	AIHGFSTFLK	NRWPDYAATS	IYMINLAVFD	LLLVLSLPFK
90	100	110	120	130	140	150	160
MVLSQVQSPF	PSLCTLVECL	YFVSMYGSVF	TICFISMDRF	LAIRYPLLVS	HLRSPRKIFG	ICCTIWVLVW	TGSIPIYSFH
170	180	190	200	210	220	230	240
GKVEKYMCFH	NMSDDTWSAK	VFFPLEVFGF	LLPMGIMGFC	CSRSIHILLG	RRDHTQDWVQ	QKACIYSIAA	SLAVFVVSFL
250	260	270	280	290	300	310	320
PVHLGFFLQF	LVRNSFIVEC	RAKQSISFFL	QLSMCFSNVN	CCLDVFCYYF	VIKEFRMNIR	AHRPSRVQLV	LQDTTISRG

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2405	1	739.6886	40.20	3	58.8	15.8	0	1-20	-.MSQQNTSGDCLFDGVNELMK.T	

Detailed Protein Report

Protein 663: MAM domain-containing glycosylphosphatidylinositol anchor protein 2 isoform 2 [Homo sapiens]

Accession:	gi|38158013	**Score:**	15.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.3
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
MVSFRLSNKT	ASPSIKLLVD	DPIVVNPGEA	ITLVCVTTGG	EPAPSLTWVR	SFGTLPEKTV	LNGGTLTIPA	ITSDDAGTYS
90	100	110	120	130	140	150	160
CIANNNVGNP	AKKSTNIIVR	ALKKGRFWIT	PDPYHKDDNI	QIGREVKISC	QVEAVPSEEL	TFSWFKNGRP	LRSSERMVIT
170	180	190	200	210	220	230	240
QTDPDVSPGT	TNLDIIDLKF	TDFGTYTCVA	SLKGGGISDI	SIDVNISSST	VPPNLTVPQE	KSPLVTREGD	TIELQCQVTG
250	260	270	280	290	300	310	320
KPKPIILWSR	ADKEVAMPDG	SMQMESYDGT	LRIVNVSREM	SGMYRCQTSQ	YNGFNVKPRE	ALVQLIVQYP	PAVEPAFLEI
330	340	350	360	370	380	390	400
RQGQDRSVTM	SCRVLRAYPI	RVLTYEWRLG	NKLLRTGQFD	SQEYTEYAVK	SLSNENYGVY	NCSIINEAGA	GRCSFLVTGK
410	420	430	440	450	460	470	480
AYAPEFYYDT	YNPVWQNRHR	VYSYSLQWTQ	MNPDAVDRIV	AYRLGIRQAG	QQRWWEQEIK	INGNIQKGEL	ITYNLTELIK
490	500	510	520	530	540	550	560
PEAYEVRLTP	LTKFGEGDST	IRVIKYSAPV	NPHLREFHCG	FEDGNICLFT	QDDTDNFDWT	KQSTATRNTK	YTPNTGPNAD
570	580	590	600	610	620	630	640
RSGSKEGFYM	YIETSRPRLE	GEKARLLSPV	FSIAPKNPYG	PTNTAYCFSF	FYHMYGQHIG	VLNVYLRLKG	QTTIENPLWS
650	660	670	680	690	700	710	720
SSGNKGQRWN	EAHVNIYPIT	SFQLIFEGIR	GPGIEGDIAI	DDVSIAEGEC	AKQDLATKNS	VDGAVGILVH	IWLFPIIVLI
730							
SILSPRR							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
134	1	876.6061	150.69	2	30.4	15.8	2	327-341	R.SVTMSCRVLRAYPIR.V	

Detailed Protein Report

Protein 664: protein FAM154A isoform b [Homo sapiens]

Accession: gi|559098458
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 15.7
MW [kDa]: 46.8
pI: 9.4
Sequence Coverage [%]: 4.6
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MEGLTTSRRD FGPHKVAPVK VHQYDQFVPS EENMDLLTTY KKDYNPYPVC RVDPIKPRDS KYPCSDKMEC LPTYKADYLP
        90        100        110        120        130        140        150        160
WNQPRREPLR LEHKYQPASV RFDNRTTHQD DYPIKGLVKT ISCKPLAMPK LCNIPLEDVT NYKMSYVAHP VEKRFVHEAE
       170        180        190        200        210        220        230        240
KFRPCEIPFE SLTTQKQSYR GLMGEPAKSL KPLARPPGLD MPFCNTTEFR DKYQAWPMPR MFSKAPITYV PPEDRMDLLT
       250        260        270        280        290        300        310        320
TVQAHYTCPK GAPAQSCRPA LQIKKCGRFE GSSTTKDDYK QWSSMRTEPV KPVPQLDLPT EPLDCLTTTR AHYVPHLPIN
       330        340        350        360        370        380        390        400
TKSCKPHWSG PRGNVPVESQ TTYTISFTPK EMGRCLASYP EPPGYTFEEV DALGHRIYKP VSQAGSQQSS HLSVDDSENP
       410
NQRELEVLA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2413	1	1160.1933	96.65	2	58.9	15.7	2	43-61	K.DYNPYPVCRVDPIKPRDSK.Y	Carbamidomethyl: 8

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Detailed Protein Report

Protein 665: 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 666: olfactory receptor 9G9 [Homo sapiens]

Accession:	gi|513788269	**Score:**	15.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.0
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	3.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQRSNHTVTE	FILLGFTTDP	GMQLGLFVVF	LGVYSLTVVG	NSTLIVLICN	DSHLHTPMYF	VVGNLSFLDL	WYSSVYTPKI
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LVICISEDKS	ISFAGCLCQF	FFSAGLAYSE	CCLLAAMAYD	RYVAISKPLL	YAQAMSIKLC	ALLVAVSYCG	GFINSSIITK
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
KTFSFNFCCE	NIIDDFFCDL	LPLVKLACGE	KGGYKFLMYF	LLASNVICPA	VLILASYLFI	ITSVLRISSS	QGRLKAFSTC
250	**260**	**270**	**280**	**290**	**300**	**310**	
SSHLTSVTLY	YGSILYIYAL	PRSSYSFDMD	KIVSTFYTEV	LPMLNPMIYS	LRNKDVKEAL	KKLLP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2624	1	488.2210	-126.35	2	61.5	15.7	1	227-235	R.ISSSQGRLK.A	

Detailed Protein Report

Protein 667: **putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 [Homo sapiens]**

Accession:	gi|68509926	**Score:**	15.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	90.9
Database Date:	2015-11-30	**pI:**	7.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 1.41 **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	QD:QU 1.41

Detailed Protein Report

Protein 668: 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 669: vacuolar protein sorting-associated protein 33A [Homo sapiens]

Accession:	gi|18105056	**Score:**	15.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	67.6
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 7.65 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAAHLSYGRV	NLNVLREAVR	RELREFLDKC	AGSKAIVWDE	YLTGPFGLIA	QYSLLKEHEV	EKMFTLKGNR	LPAADVKNII
90	100	110	120	130	140	150	160
FFVRPRLELM	DIIAENVLSE	DRRGPTRDFH	ILFVPRRSLL	CEQRLKDLGV	LGSFIHREEY	SLDLIPFDGD	LLSMESEGAF
170	180	190	200	210	220	230	240
KECYLEGDQT	SLYHAAKGLM	TLQALYGTIP	QIFGKGECAR	QVANMMIRMK	REFTGSQNSI	FPVFDNLLLL	DRNVDLLTPL
250	260	270	280	290	300	310	320
ATQLTYEGLI	DEIYGIQNSY	VKLPPEKFAP	KKQGDGGKDL	PTEAKKLQLN	SAEELYAEIR	DKNFNAVGSV	LSKKAKIISA
330	340	350	360	370	380	390	400
AFEERHNAKT	VGEIKQFVSQ	LPHMQAARGS	LANHTSIAEL	IKDVTTSEDF	FDKLTVEQEF	MSGIDTDKVN	NYIEDCIAQK
410	420	430	440	450	460	470	480
HSLIKVLRLV	CLQSVCNSGL	KQKVLDYYKR	EILQTYGYEH	ILTLHNLEKA	GLLKPQTGGR	NNYPTIRKTL	RLWMDDVNEQ
490	500	510	520	530	540	550	560
NPTDISYVYS	GYAPLSVRLA	QLLSRPGWRS	IEEVLRILPG	PHFEERQPLP	TGLQKKRQPG	ENRVTLIFFL	GGVTFAEIAA
570	580	590	600				
LRFLSQLEDG	GTEYVIATTK	LMNGTSWIEA	LMEKPF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
770	1	689.8846	21.29	2	38.1	15.7	1	301-313	R.DKNFNAVGSVLSK.K		QD:QU	7.65

Detailed Protein Report

Protein 670: **pappalysin-2 isoform 2 precursor [Homo sapiens]**

Accession:	gi|116174734	**Score:**	15.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.1
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMCLKILRIS	LAILAGWALC	SANSELGWTR	KKSLVEREHL	NQVLLEGERC	WLGAKVRRPR	ASPQHHLFGV	YPSRAGNYLR
90	100	110	120	130	140	150	160
PYPVGEQEIH	HTGRSKPDTE	GNAVSLVPPD	LTENPAGLRG	AVEEPAAPWV	GDSPIGQSEL	LGDDDAYLGN	QRSKESLGEA
170	180	190	200	210	220	230	240
GIQKGSAMAA	TTTTAIFTTL	NEPKPETQRR	GWAKSRQRRQ	VWKRRAEDGQ	GDSGISSHFQ	PWPKHSLKHR	VKKSPPEESN
250	260	270	280	290	300	310	320
QNGGEGSYRE	AETFNSQVGL	PILYFSGRRE	RLLLRPEVLA	EIPREAFTVE	AWVKPEGGQN	NPAIIAGVFD	NCSHTVSDKG
330	340	350	360	370	380	390	400
WALGIRSGKD	KGKRDARFFF	SLCTDRVKKA	TILISHSRYQ	PGTWTHVAAT	YDGRHMALYV	DGTQVASSLD	QSGPLNSPFM
410	420	430	440	450	460	470	480
ASCRSLLLGG	DSSEDGHYFR	GHLGTLVFWS	TALPQSHFQH	SSQHSSGEEE	ATDLVLTASF	EPVNTEWVPF	RDEKYPRLEV
490	500	510	520	530	540	550	560
LQGFEPEPEI	LSPLQPPLCG	QTVCDNVELI	SQYNGYWPLR	GEKVIRYQVV	NICDDEGLNP	IVSEEQIRLQ	HEALNEAFSR
570	580	590	600	610	620	630	640
YNISWQLSVH	QVHNSTLRHR	VVLVNCEPSK	IGNDHCDPEC	EHPLTGYDGG	DCRLQGRCYS	WNRRDGLCHV	ECNNMLNDFD
650	660	670	680	690	700	710	720
DGDCCDPQVA	DVRKTCFDPD	SPKRAYMSVK	ELKEALQLNS	THFLNIYFAS	SVREDLAGAA	TWPWDKDAVT	HLGGIVLSPA
730	740	750	760	770	780	790	800
YYGMPGHTDT	MIHEVGHVLG	LYHVFKGVSE	RESCNDPCKE	TVPSMETGDL	CADTAPTPKS	ELCREPEPTS	DTCGFTRFPG
810	820	830					
APFTNYMSYT	GITTVLFCFL	LRIHGGL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
694	6	676.8503	-106.32	2	38.7	15.6	2	347-358	R.VKKATILISHSR.Y	

Detailed Protein Report

Protein 671: pre-mRNA-processing factor 17 [Homo sapiens]

Accession:	gi|7706657	**Score:**	15.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.5
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSAAIAALAA	SYGSGSGSES	DSDSESSRCP	LPAADSLMHL	TKSPSSKPSL	AVAVDSAPEV	AVKEDLETGV	HLDPAVKEVQ
90	100	110	120	130	140	150	160
YNPTYETMFA	PEFGPENPFR	TQQMAAPRNM	LSGYAEPAHI	NDFMFEQQRR	TFATYGYALD	PSLDNHQVSA	KYIGSVEEAE
170	180	190	200	210	220	230	240
KNQGLTVFET	GQKKTEKRKK	FKENDASNID	GFLGPWAKYV	DEKDVAKPSE	EEQKELDEIT	AKRQKKGKQE	EEKPGEEKTI
250	260	270	280	290	300	310	320
LHVKEMYDYQ	GRSYLHIPQD	VGVNLRSTMP	PEKCYLPKKQ	IHVWSGHTKG	VSAVRLFPLS	GHLLLSCSMD	CKIKLWEVYG
330	340	350	360	370	380	390	400
ERRCLRTFIG	HSKAVRDICF	NTAGTQFLSA	AYDRYLKLWD	TETGQCISRF	TNRKVPYCVK	FNPDEDKQNL	FVAGMSDKKI
410	420	430	440	450	460	470	480
VQWDIRSGEI	VQEYDRHLGA	VNTIVFVDEN	RRFVSTSDDK	SLRVWEWDIP	VDFKYIAEPS	MHSMPAVTLS	PNGKWLACQS
490	500	510	520	530	540	550	560
MDNQILIFGA	QNRFRLNKKK	IFKGHMVAGY	ACQVDFSPDM	SYVISGDGNG	KLNIWDWKTT	KLYSRFKAHD	KVCIGAVWHP
570	580						
HETSKVITCG	WDGLIKLWD						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1673	1	694.3984	86.12	2	51.2	15.6	1	227-238	K.GKQEEEKPGEEK.T	

Detailed Protein Report

Protein 672: **PREDICTED: mono [ADP-ribose] polymerase PARP16 isoform X3 [Homo sapiens]**

Accession:	gi|530406133	**Score:**	15.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.5
Database Date:	2015-11-30	**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 673: G protein-regulated inducer of neurite outgrowth 1 [Homo sapiens]

Accession:	gi|112821681	**Score:**	15.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	102.3
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530380833	refseq_human (refseq_human_20140103.fasta)	PREDICTED: G protein-regulated inducer of neurite outgrowth 1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MDTAEDPAWL	QLLQKDSSPP	GPRPTAFFCP	QDGSLGAGSS	AMRDYCPSQQ	KASPAPPRHT	PDQSPGMESR	HRSPSGAGEG
90	100	110	120	130	140	150	160
ASCSDGPRGS	LACPSPTCFS	PQESPSKETL	EAHGASISGT	PEATTSGKPE	PVSSVKTEPK	SSDDRNPMFL	EKMDFKSSKQ
170	180	190	200	210	220	230	240
ADSTSIGKED	PGSSRKADPM	FTGKAEPEIL	GKGDPVAPGR	MDPMTVRKED	LGSLGKVDPL	CSSKTYTVSP	RKEDPGSLRK
250	260	270	280	290	300	310	320
VDPVSSDKVD	PVFPRKEEPR	YSGKEHPVSS	EKVAPTSAEK	VDLVLSGKRD	PGPSGKADPM	PLESMDSAST	GKTEPGLLGK
330	340	350	360	370	380	390	400
LIPGSSGKNG	PVSSGTGAPG	SLGRLDPTCL	GMADPASVGN	VETVPATKED	SRFLGKMDPA	SSGEGRPVSG	HTDTTASAKT
410	420	430	440	450	460	470	480
DLTSLKNVDP	MSSGKVDPVS	LGKMDPMCSG	KPELLSPGQA	ERVSVGKAGT	VSPGKEDPVS	SRREDPISAG	SRKTSSEKVN
490	500	510	520	530	540	550	560
PESSGKTNPV	SSGPGDPRSL	GTAGPPSAVK	AEPATGGKGD	PLSSEKAGLV	ASGKAAPTAS	GKAEPLAVGK	EDPVSKGKAD
570	580	590	600	610	620	630	640
AGPSGQGDSV	SIGKVVSTPG	KTVPVPSGKV	DPVSLGKAEA	IPEGKVGSLP	LEKGSPVTTT	KADPRASGKA	QPQSGGKAET
650	660	670	680	690	700	710	720
KLPGQEGAAA	PGEAGAVCLK	KETPQASEKV	DPGSCRKAEP	LASGKGEPVS	LGKADSAPSR	KTESPSLGKV	VPLSLEKTKP
730	740	750	760	770	780	790	800
SSSSRQLDRK	ALGSARSPEG	ARGSEGRVEP	KAEPVSSTEA	SSLGQKDLEA	AGAERSPCPE	AAAPPPGPRT	RDNFTKAPSW
810	820	830	840	850	860	870	880
EASAPPPPRE	DAGTQAGAQA	CVSVAVSPMS	PQDGAGGSAF	SFQAAPRAPS	PPSRRDAGLQ	VSLGAAETRS	VATGPMTPQA
890	900	910	920	930	940	950	960
AAPPAFPEVR	VRPGSALAAA	VAPPEPAEPV	RDVSWDEKGM	TWEVYGAAME	VEVLGMAIQK	HLERQIEEHG	RQGAPAPPPA
970	980	990	1000	1010			
ARAGPGRSGS	VRTAPPDGAA	KRPPGLFRAL	LQSVRRPRCC	SRAGPTAE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2305	1	853.3930	-63.26	2	57.5	15.6	2	225-239	K.TYTVSPRKEDPGSLR.K	

Detailed Protein Report

Protein 674: 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 675: PREDICTED: kelch-like protein 18 isoform X4 [Homo sapiens]

Accession:	gi|578805908	**Score:**	15.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.4
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
MFTNDMMECK	QDEIVMQGMD	PSALEALINF	AYNGNLAIDQ	QNVQSLLMGA	SFLQLQSIKD	ACCTFLRERL	HPKNCLGVRQ
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
FAETMMCAVL	YDAANSFIHQ	HFVEVSMSEE	FLALPLEDVL	ELVSRDELNV	KSEEQVFEAA	LAWVRYDREQ	RGPYLPELLS
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
NIRLPLCRPQ	FLSDRVQQDD	LVRCCHKCRD	LVDEAKDYHL	MPERRPHLPA	FRTRPRCCTS	IAGLIYAVGG	LNSAANFYAG
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
DSLNVVEVFD	PIANCWERCR	PMTTARSRVG	VAVVNGLLYA	IGGYDGQLRL	STVEAYNPET	DTWTRVGSMN	SKRSSVCFSA
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
MGTVVLDGQI	YVCGGYDGNS	SLSSVETYSP	ETDKWTVVTS	MSSNRSAAGV	TVFEGRIYVS	GGHDGLQIFS	SVEHYNHHTA
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
TWHPAAGMLN	KRCRHGAASL	GSKMFVCGGY	DGSGFLSIAE	MYSSVADQWC	LIVPMHTRRS	RVSLVASCGR	LYAVGGYDGQ
490	**500**	**510**	**520**				
SNLSSVEMYD	PETDCWTFMA	PMACHEGGVG	VGCIPLLTI				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2688	1	645.8319	-38.25	2	64.7	15.6	2	459-470	R.RSRVSLVASCGR.L	

Detailed Protein Report

Protein 676: **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 677: 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 678: **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 679: **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 680: 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

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
453	1	669.3289	-79.98	2	35.6	15.5	0	36-47	K.SQVLFAVVFTAR.Y	

Detailed Protein Report

Protein 681: DNA-(apurinic or apyrimidinic site) lyase 2 isoform 1 [Homo sapiens]

Accession:	gi|18375507	**Score:**	15.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.4
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.83 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MLRVVSWNIN	GIRRPLQGVA	NQEPSNCAAV	AVGRILDELD	ADIVCLQETK	VTRDALTEPL	AIVEGYNSYF	SFSRNRSGYS
90	100	110	120	130	140	150	160
GVATFCKDNA	TPVAAEEGLS	GLFATQNGDV	GCYGNMDEFT	QEELRALDSE	GRALLTQHKI	RTWEGKEKTL	TLINVYCPHA
170	180	190	200	210	220	230	240
DPGRPERLVF	KMRFYRLLQI	RAEALLAAGS	HVIILGDLNT	AHRPIDHWDA	VNLECFEEDP	GRKWMDSLLS	NLGCQSASHV
250	260	270	280	290	300	310	320
GPFIDSYRCF	QPKQEGAFTC	WSAVTGARHL	NYGSRLDYVL	GDRTLVIDTF	QASFLLPEVM	GSDHCPVGAV	LSVSSVPAKQ
330	340	350	360	370	380	390	400
CPPLCTRFLP	EFAGTQLKIL	RFLVPLEQSP	VLEQSTLQHN	NQTRVQTCQN	KAQVRSTRPQ	PSQVGSSRGQ	KNLKSYFQPS
410	420	430	440	450	460	470	480
PSCPQASPDI	ELPSLPLMSA	LMTPKTPEEK	AVAKVVKGQA	KTSEAKDEKE	LRTSFWKSVL	AGPLRTPLCG	GHREPCVMRT
490	500	510	520				
VKKPGPNLGR	RFYMCARPRG	PPTDPSSRCN	FFLWSRPS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1941	1	695.2967	-51.70	2	54.6	15.5	1	75-87	R.NRSGYSGVATFCK.D		QD:QU 0.83

Detailed Protein Report

Protein 682: endothelial cell-specific molecule 1 isoform b precursor [Homo sapiens]

Accession:	gi|208022668	**Score:**	15.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.5
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	9.0
		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 683: **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	

Detailed Protein Report

Protein 684: 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	1	733.4795	128.10	3	38.6	15.5	1	643-661	K.DTGPDELRPMLAQNLMLKR.F	

Detailed Protein Report

Protein 685: PREDICTED: zinc finger protein 280C isoform X1 [Homo sapiens]

Accession:	gi|578838699	**Score:**	15.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.3
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDDDKPFQPK	NISKMAELFM	ECEEEELEPW	QKKVEETQDE	DDDELIFVGE	ISSSKPAISN	ILNRGHSSSS	SKGIKSEPHS
90	100	110	120	130	140	150	160
PGIPEIFRTA	SQRCRDPPSN	PVAASPRFHL	VSKSSQSSVT	VENASKPDFT	KNSQVGSDNS	SILLFDSTQE	SLPPSQDIPA
170	180	190	200	210	220	230	240
IFREGMKNTS	YVLKHPSTSK	VNSVTPKKPK	TSEDVPQINP	STSLPLIGSP	PVTSSQVMLS	KGTNTSSPYD	AGADYLRACP
250	260	270	280	290	300	310	320
KCNVQFNLLD	PLKYHMKHCC	PDMITKFLGV	IVKSERPCDE	DKTDSETGKL	IMLVNEFYYG	RHEGVTEKEP	KTYTTFKCFS
330	340	350	360	370	380	390	400
CSKVLKNNIR	FMNHMKHHLE	LEKQNNESWE	NHTTCQHCYR	QYPTPFQLQC	HIESTHTPHE	FSTICKICEL	SFETEHILLQ
410	420	430	440	450	460	470	480
HMKDTHKPGE	MPYVCQKKGV	HRCPKCRLQF	LTSKEKAEHK	AQHRTFIKPK	ELEGLPPGAK	VTIRASLGPL	QSKLPTAPFG
490	500	510	520	530	540	550	560
CAPGTSFLQV	TPPTSQNTTA	RNPRKSNASR	SKTSKLHATT	STASKVNTSK	PRGRIAKSKA	KPSYKQKRQR	NRKNKMSLAL
570	580	590	600	610	620	630	640
KNIRCRRGIH	KCIECHSKIK	DFASHFSIYI	HCSFCKYNTN	CNKAFVNHMM	SSHSNHPGKR	FCIFKKHSGT	LRGITLVCLK
650	660	670	680	690			
CDFLADSSGL	DRMAKHLSQR	KTHTCQVIIE	NVSKSTSTSE	PTTGCSLK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2524	1	1044.0930	71.27	2	62.2	15.4	0	387-403	K.ICELSFETEHILLQHMK.D	Oxidation: 16

Detailed Protein Report

Protein 686: PREDICTED: leucine-rich repeat-containing protein 16C isoform X1 [Homo sapiens]

Accession:	gi|530423607	**Score:**	15.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	148.1
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQTPDGISC	ELRGEITRFL	WPKEVELLLK	TWLPGEGAVQ	NHVLALLRWR	AYLLHTTCLP	LRVDCTFSYL	EVQAMALQET
90	100	110	120	130	140	150	160
PPQVTFELES	LRELVLEFPG	VAALEQLAQH	VAAAIKKVFP	RSTLGKLFRR	PTPASMLARL	ERSSPSESTD	PCSPCGGFLE
170	180	190	200	210	220	230	240
TYEALCDYNG	FPFREEIQWD	VDTIYHRQGC	RHFSLGDFSH	LGSRDLALSV	AALSYNLWFR	CLSCVDMKLS	LEVSEQILHM
250	260	270	280	290	300	310	320
MSQSSHLEEL	VLETCSLRGD	FVRRLAQALA	GHSSSGLREL	SLAGNLLDDR	GMTALSRHLE	RCPGALRRLS	LAQTGLTPRG
330	340	350	360	370	380	390	400
MRALGRALAT	NAAFDSTLTH	LDLSGNPGAL	GASEDSGGLY	SFLSRPNVLS	FLNLAGTDTA	LDTLFAAVSR	GCCTSLTHLD
410	420	430	440	450	460	470	480
ASRNVFSRTK	SRAAPAALQL	FLSRARTLRH	LGLAGCKLPP	DALRALLDGL	ALNTHLRDLH	LDLSACELRS	AGAQVIQDLV
490	500	510	520	530	540	550	560
CDAGAVSSLD	LADNGFGSDM	VTLVLAIGRS	RSLRHVALGR	NFNVRCKETL	DDVLHRIVQL	MQDDDCPLQS	LSVAESRLKL
570	580	590	600	610	620	630	640
GASVLLRALA	TNPNLTALDI	SGNAMGDAGA	KLLAKALRVN	SRLRSVVWDR	NHTSALGLLD	VAQALEQNHS	LKAMPLPLND
650	660	670	680	690	700	710	720
VAQAQRSRPE	LTARAVHQIQ	ACLLRNNRAD	PASSDHTTRL	QPLGLVSDPS	EQEVNELCQS	VQEHVELLGC	GAGPQGEAAV
730	740	750	760	770	780	790	800
RQAEDAIQNA	NFSLSILPIL	YEAGSSPSHH	WQLGQKLEGL	LRQVGEVCRQ	DIQDFTQATL	DTARSLCPQM	LQGSSWREQL
810	820	830	840	850	860	870	880
EGVLAGSRGL	PELLPEQLLQ	DAFTRLRDMR	LSITGTLAES	IVAQALAGLS	AARDQLVESL	AQQATVTMPP	ALPAPDGGEP
890	900	910	920	930	940	950	960
SLLEPGELEG	LFFPEEKEEE	KEKDDSPPQK	WPELSHGLHL	VPFIHSAAEE	AEPEPELAAP	GEDAEPQAGP	SARGSPSPAA
970	980	990	1000	1010	1020	1030	1040
PGPPAGPLPR	MDLPLAGQPL	RHPTRARPRP	RRQHHHRPPP	GGPQVPPALP	QEGNGLSARV	DEGVEEFFSK	RLIQQDRLWA
1050	1060	1070	1080	1090	1100	1110	1120
PEEDPATEGG	ATPVPRTLRK	KLGTLFAFKK	PRSTRGPRTD	LETSPGAAPR	TRKTTFGDLL	RPPTRPSRGE	ELGGAEGDTS
1130	1140	1150	1160	1170	1180	1190	1200
SPDPAGRSRP	RYTRDSKAYS	MILLPAEEEA	TLGARPDKRR	PLERGETELA	PSFEQRVQVM	LQRIGVSRGS	GGAEGKRKQS
1210	1220	1230	1240	1250	1260	1270	1280
KDGEIKKAGS	DGDIMDSSTE	APPISIKSRT	HSVSADPSCR	PGPGSQGPES	ATWKTLGQQL	NAELRSRGWG	QQDGPGPPSP
1290	1300	1310	1320	1330	1340	1350	1360
GQSPSPCRTS	PSPDSLGLPE	DPCLGPRNEE	RPLRLQRSPV	LKRRPKLEAP	PSPSLGSGLG	TEPLPPQPTE	PSSPERSPPS
1370	1380						
PATDQRGGGP	NP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2608	1	698.3486	-78.93	2	61.3	15.4	2	425-437	R.ARTLRHLGLAGCK.L	

Detailed Protein Report

Protein 687: interleukin-21 isoform 1 precursor [Homo sapiens]

Accession:	gi|11141875	**Score:**	15.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.6
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	9.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRSSPGNMER	IVICLMVIFL	GTLVHKSSSQ	GQDRHMIRMR	QLIDIVDQLK	NYVNDLVPEF	LPAPEDVETN	CEWSAFSCFQ
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
KAQLKSANTG	NNERIINVSI	KKLKRKPPST	NAGRRQKHRL	TCPSCDSYEK	KPPKEFLERF	KSLLQKMIHQ	HLSSRTHGSE
170							
DS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1445	1	977.1765	133.34	2	46.6	15.4	2	140-155	R.FKSLLQKMIHQHLSSR.T	

Detailed Protein Report

Protein 688: **PREDICTED: phosphorylase b kinase regulatory subunit alpha, liver isoform isoform X6 [Homo sapiens]**

Accession: gi|578837920
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 15.4
MW [kDa]: 118.7
pI: 5.8
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 689: myeloperoxidase precursor [Homo sapiens]

Accession:	gi|4557759	**Score:**	15.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.8
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	1.6
		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 690: zinc finger protein 559 isoform c [Homo sapiens]

Accession: gi|320202974

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 15.3

MW [kDa]: 57.3

pI: 10.2

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 691: uncharacterized protein C12orf45 [Homo sapiens]

Accession: gi|116256458
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 15.3
MW [kDa]: 20.1
pI: 5.0
Sequence Coverage [%]: 6.5
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MEVHGKPKAS PSCSSPTRDS SGVPVSKELL TAGSDGRGGI WDRLLINSQP KSRKTSTLQT VRIERSPLLD QVQTFLPQMA
        90        100        110        120        130        140        150        160
RANEKLRKEM AAAPPGRFNI ENIDGPHSKV IQMDVALFEM NQSDSKEVDS SEESSQDSSE NSSESEDEDD SIPSEVTIDN
       170        180        190
IKLPNSEGGK GKIEVLDSPA SKKKK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1974	1	648.7898	-114.18	2	53.2	15.3	2	86-97	K.LRKEMAAAPPGR.F	

Detailed Protein Report

Protein 692: 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 693: **serine protease 58 precursor [Homo sapiens]**

Accession:	gi|48255915	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.1
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	9.1
		No. of unique Peptides:	1

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
2776	1	862.7428	-25.62	3	65.9	15.2	2	167-188	R.DAYKTYNITENMLCVGIVPGRR.Q	Carbamidomethyl: 14; Oxidation: 12

Detailed Protein Report

Protein 694: bromodomain adjacent to zinc finger domain protein 1A isoform b [Homo sapiens]

Accession:	gi|32967605	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	175.3
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPLLHRKPFV	RQKPPADLRP	DEEVFYCKVT	NEIFRHYDDF	FERTILCNSL	VWSCAVTGRP	GLTYQEALES	EKKARQNLQS
90	100	110	120	130	140	150	160
FPEPLIIPVL	YLTSLTHRSR	LHEICDDIFA	YVKDRYFVEE	TVEVIRNNGA	RLQCRILEVL	PPSHQNGFAN	GHVNSVDGET
170	180	190	200	210	220	230	240
IIISDSDDSE	TQSCSFQNGK	KKDAIDPLLF	KYKVQPTKKE	LHESAIVKAT	QISRRKHLFS	RDKLKLFLKQ	HCEPQDGVIK
250	260	270	280	290	300	310	320
IKASSLSTYK	IAEQDFSYFF	PDDPPTFIFS	PANRRRGRPP	KRIHISQEDN	VANKQTLASY	RSKATKERDK	LLKQEEMKSL
330	340	350	360	370	380	390	400
AFEKAKLKRE	KADALEAKKK	EKEDKEKKRE	ELKKIVEEER	LKKKEEKERL	KVEREKEREK	LREEKRKYVE	YLKQWSKPRE
410	420	430	440	450	460	470	480
DMECDDLKEL	PEPTPVKTRL	PPEIFGDALM	VLEFLNAFGE	LFDLQDEFPD	GVTLEVLEEA	LVGNDSEGPL	CELLFFFLTA
490	500	510	520	530	540	550	560
IFQAIAEEEE	EVAKEQLTDA	DTKGCSLKSL	DLDSCTLSEI	LRLHILASGA	DVTSANAKYR	YQKRGGFDAT	DDACMELRLS
570	580	590	600	610	620	630	640
NPSLVKKLSS	TSVYDLTPGE	KMKILHALCG	KLLTLVSTRD	FIEDYVDILR	QAKQEFRELK	AEQHRKEREE	AAARIRKRKE
650	660	670	680	690	700	710	720
EKLKEQEQKM	KEKQEKLKED	EQRNSTADIS	IGEEEREDFD	TSIESKDTEQ	KELDQDMVTE	DEDDPGSHKR	GRRGKRGQNG
730	740	750	760	770	780	790	800
FKEFTRQEQI	NCVTREPLTA	DEEEALKQEH	QRKEKELLEK	IQSAIACTNI	FPLGRDRMYR	RYWIFPSIPG	LFIEEDYSGL
810	820	830	840	850	860	870	880
TEDMLLPRPS	SFQNNVQSQD	PQVSTKTGEP	LMSESTSNID	QGPRDHSVQL	PKPVHKPNRW	CFYSSCEQLD	QLIEALNSRG
890	900	910	920	930	940	950	960
HRESALKETL	LQEKSRICAQ	LARFSEEKFH	FSDKPQPDSK	PTYSRGRSSN	AYDPSQMCAE	KQLELRLRDF	LLDIEDRIYQ
970	980	990	1000	1010	1020	1030	1040
GTLGAIKVTD	RHIWRSALES	GRYELLSEEN	KENGIIKTVN	EDVEEMEIDE	QTKVIVKDRL	LGIKTETPST	VSTNASTPQS
1050	1060	1070	1080	1090	1100	1110	1120
VSSVVHYLAM	ALFQIEQGIE	RRFLKAPLDA	SDSGRSYKTV	LDRWRESLLS	SASLSQVFLH	LSTLDRSVIW	SKSILNARCK
1130	1140	1150	1160	1170	1180	1190	1200
ICRKKGDAEN	MVLCDGCDRG	HHTYCVRPKL	KTVPEGDWFC	PECRPKQRSR	RLSSRQRPSL	ESDEDVEDSM	GGEDDEVDGD
1210	1220	1230	1240	1250	1260	1270	1280
EEEGQSEEEE	YEVEQDEDDS	QEEEEVSLPK	RGRPQVRLPV	KTRGKLSSSF	SSRGQQQEPG	RYPSRSQQST	PKTTVSSKTG
1290	1300	1310	1320	1330	1340	1350	1360
RSLRKINSAP	PTETKSLRIA	SRSTRHSHGP	LQADVFVELL	SPRRKRRGRK	SANNTPENSP	NFPNFRVIAT	KSSEQSRSVN
1370	1380	1390	1400	1410	1420	1430	1440
IASKLSLQES	ESKRRCRKRQ	SPEPSPVTLG	RRSSGRQGGV	HELSAFEQLV	VELVRHDDSW	PFLKLVSKIQ	VPDYYDIIKK
1450	1460	1470	1480	1490	1500	1510	1520
PIALNIIREK	VNKCEYKLAS	EFIDDIELMF	SNCFEYNPRN	TSEAKAGTRL	QAFFHIQAQK	LGLHVTPSNV	DQVSTPPAAK
1530							
KSRI							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1095	1	877.2623	-142.07	2	42.2	15.2	2	1124-1139	R.KKGDAENMVLCDGCDR.G	

Detailed Protein Report

Protein 695: 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	

Protein 696: 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 697: small G protein signaling modulator 2 isoform 1 [Homo sapiens]

Accession:	gi|148612795	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	118.2
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique 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
527	1	501.2730	30.20	2	36.6	15.2	0	466-474	R.NLTAPNPMK.D	Oxidation: 8

Detailed Protein Report

Protein 698: AP-3 complex subunit delta-1 isoform 2 [Homo sapiens]

Accession:	gi|117553580	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	130.1
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.21 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MALKMVKGSI	DRMFDKNLQD	LVRGIRNHKE	DEAKYISQCI	DEIKQELKQD	NIAVKANAVC	KLTYLQMLGY	DISWAAFNII
90	100	110	120	130	140	150	160
EVMSASKFTF	KRIGYLAASQ	SFHEGTDVIM	LTTNQIRKDL	SSPSQYDTGV	ALTGLSCFVT	PDLARDLAND	IMTLMSHTKP
170	180	190	200	210	220	230	240
YIRKKAVLIM	YKVFLKYPES	LRPAFPRLKE	KLEDPDPGVQ	SAAVNVICEL	ARRNPKNYLS	LAPLFFKLMT	SSTNNWVLIK
250	260	270	280	290	300	310	320
IIKLFGALTP	LEPRLGKKLI	EPLTNLIHST	SAMSLLYECV	NTVIAVLISL	SSGMPNHSAS	IQLCVQKLRI	LIEDSDQNLK
330	340	350	360	370	380	390	400
YLGLLAMSKI	LKTHPKSVQS	HKDLILQCLD	DKDESIRLRA	LDLLYGMVSK	KNLMEIVKKL	MTHVDKAEGT	TYRDELLTKI
410	420	430	440	450	460	470	480
IDICSQSNYQ	YITNFEWYIS	ILVELTRLEG	TRHGHLIAAQ	MLDVAIRVKA	IRKFAVSQMS	ALLDSAHLLA	SSTQRNGICE
490	500	510	520	530	540	550	560
VLYAAAWICG	EFSEHLQEPH	HTLEAMLRPR	VTTLPGHIQA	VYVQNVVKLY	ASILQQKEQA	GEAEGAQAVT	QLMVDRLPQF
570	580	590	600	610	620	630	640
VQSADLEVQE	RASCILQLVK	HIQKLQAKDV	PVAEEVSALF	AGELNPVAPK	AQKKVPVPEG	LDLDAWINEP	LSDSESEDER
650	660	670	680	690	700	710	720
PRAVFHEEEQ	RRPKHRPSEA	DEEELARRRE	ARKQEQANNP	FYIKSSPSPQ	KRYQDTPGVE	HIPVVQIDLS	VPLKVPGLPM
730	740	750	760	770	780	790	800
SDQYVKLEEE	RRHRQKLEKD	KRRKKRKEKE	KKGKRRHSSL	PTESDEDIAP	AQQVDIVTEE	MPENALPSDE	DDKDPNDPYR
810	820	830	840	850	860	870	880
ALDIDLDKPL	ADSEKLPIQK	HRNTETSKSP	EKDVPMVEKK	SKKPKKKEKK	HKEKERDKEK	KKEKEKKKSP	KPKKKKHRKE
890	900	910	920	930	940	950	960
KEERTKGKKK	SKKQPPGSEE	AAGEPVQNGA	PEEEQLPPES	SYSLLAENSY	VKMTCDIRGS	LQEDSQVTVA	IVLENRSSSI
970	980	990	1000	1010	1020	1030	1040
LKGMELSVLD	SLNARMARPQ	GSSVHDGVPV	PFQLPPGVSN	EAQYVFTIQS	IVMAQKLKGT	LSFIAKNDEG	ATHEKLDFRL
1050	1060	1070	1080	1090	1100	1110	1120
HFSCSSYLIT	TPCYSDAFAK	LLESGDLSMS	SIKVDGIRMS	FQNLLAKICF	HHHFSVVERV	DSCASMYSRS	IQGHHVCLLV
1130	1140	1150	1160				
KKGENSVSVD	GKCSDSTLLS	NLLEEMKATL	AKC				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
545	1	592.3161	-55.37	2	35.4	15.2	1	17-26	K.NLQDLVRGIR.N		QD:QU 0.21

Detailed Protein Report

Protein 699: **CDK5 regulatory subunit-associated protein 2 isoform c [Homo sapiens]**

Accession:	gi|440309853	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	189.5
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	0.5
		No. of unique Peptides:	1

```
        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 SFSLYSDQTS YLSICLEENN
       650        660        670        680        690        700        710        720
RFQVEHFSQE ELKKKVSDLI QLVKELYTDN QHLKKTIFDL SCMGFQGNGF PDRLASTEQT EEAKKSRLPI LIKPSRSLGN
       730        740        750        760        770        780        790        800
MYRLPATQEV VTQLQSQILE LQGELKEFKT CNKQLHQKLI LAEAVMEGRP TPDKTLLNAQ PPVGAAYQDS PGEQKGIKTT
       810        820        830        840        850        860        870        880
SSVWRDKEMD SDQQRSYEID SEICPPDDLA SLPSCKENPE DVLSPTSVAT YLSSKSQPSA KVSVMGTDQS ESINTSNETE
       890        900        910        920        930        940        950        960
YLKQKIHDLE TELEGYQNFI FQLQKHSQCS EAIITVLCGT EGAQDGLSKP KNGSDGEEMT FSSLHQVRYV KHVKILGPLA
       970        980        990       1000       1010       1020       1030       1040
PEMIDSRVLE NLKQQLEEQE YKLQKEQNLN MQLFSEIHNL QNKFRDLSPP RYDSLVQSQA RELSLQRQQI KDGHGICVIS
      1050       1060       1070       1080       1090       1100       1110       1120
RQHMNTMIKA FEELLQASDV DYCVAEGFQE QLNQCAELLE KLEKLFLNGK SVGVEMNTQN ELMERIEEDN LTYQHLLPES
      1130       1140       1150       1160       1170       1180       1190       1200
PEPSASHALS DYETSEKSFF SRDQKQDNET EKTSVMVNSF SQDLLMEHIQ EIRTLRKRLE ESIKTNEKLR KQLERQGSEF
      1210       1220       1230       1240       1250       1260       1270       1280
VQGSTSIFAS GSELHSSLTS EIHFLRKQNQ ALNAMLIKGS RDKQKENDKL RESLSRKTVS LEHLQREYAS VKEENERLQK
      1290       1300       1310       1320       1330       1340       1350       1360
EGSEKERHNQ QLIQEVRCSG QELSRVQEEV KLRQQLLSQN DKLLQSLRVE LKAYEKLDEE HRRLREASGE GWKGQDPFRD
      1370       1380       1390       1400       1410       1420       1430       1440
LHSLLMEIQA LRLQLERSIE TSSTLQSRLK EQLARGAEKA QEGALTLAVQ AVSIPEVPLQ PDKHDGDKYP MESDNSFDLF
      1450       1460       1470       1480       1490       1500       1510       1520
DSSQAVTPKS VSETPPLSGN DTDSLSCDSG SSATSTPCVS RLVTGHHLWA SKNGRHVLGL IEDYEALLKQ ISQGQRLLAE
      1530       1540       1550       1560       1570       1580       1590       1600
MDIQTQEAPS STSQELGTKG PHPAPLSKFV SSVSTAKLTL EEAYRRLKLL WRVSLPEDGQ CPLHCEQIGE MKAEVTKLHK
      1610       1620       1630       1640       1650       1660       1670
KLFEQEKKLQ NTMKLLQLSK RQEKVIFDQL VVTHKILRKA RGNLELRPGG AHPGTCSPSR PGS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
667	1	575.7990	-26.64	2	38.3	15.2	1	1558-1566	K.LTLEEAYRR.L	

Detailed Protein Report

Protein 700: 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 701: **proline-, glutamic acid- and leucine-rich protein 1 isoform 2 [Homo sapiens]**

Accession:	gi|503774456	**Score:**	15.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	96.8
Database Date:	2015-11-30	**pI:**	4.1
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MELAVAVLRD	LLRYAAQLPA	LFRDISMNHL	PGLLTSLLGL	RPECEQSALE	GMKACMTYFP	RACGSLKGKL	ASFFLSRVDA
90	100	110	120	130	140	150	160
LSPQLQQLAC	ECYSRLPSLG	AGFSQGLKHT	ESWEQELHSL	LASLHTLLGA	LYEGAETAPV	QNEGPGVEML	LSSEDGDAHV
170	180	190	200	210	220	230	240
LLQLRQRFSG	LARCLGLMLS	SEFGAPVSVP	VQEILDFICR	TLSVSSKNIS	LHGDGPLRLL	LLPSIHLEAL	DLLSALILAC
250	260	270	280	290	300	310	320
GSRLLRFGIL	IGRLLPQVLN	SWSIGRDSLS	PGQERPYSTV	RTKVYAILEL	WVQVCGASAG	MLQGGASGEA	LLTHLLSDIS
330	340	350	360	370	380	390	400
PPADALKLRS	PRGSPDGSLQ	TGKPSAPKKL	KLDVGEAMAP	PSHRKGDSNA	NSDVCAAALR	GLSRTILMCG	PLIKEETHRR
410	420	430	440	450	460	470	480
LHDLVLPLVM	GVQQGEVLGS	SPYTSSRCRR	ELYCLLLALL	LAPSPRCPPP	LACALQAFSL	GQREDSLEVS	SFCSEALVTC
490	500	510	520	530	540	550	560
AALTHPRVPP	LQPMGPTCPT	PAPVPPPEAP	SPFRAPPFHP	PGPMPSVGSM	PSAGPMPSAG	PMPSAGPVPS	ARPGPPTTAN
570	580	590	600	610	620	630	640
HLGLSVPGLV	SVPPRLLPGP	ENHRAGSNED	PILAPSGTPP	PTIPPDETFG	GRVPRPAFVH	YDKEEASDVE	ISLESDSDDS
650	660	670	680	690	700	710	720
VVIVPEGLPP	LPPPPPSGAT	PPPIAPTGPP	TASPPVPAKE	EPEELPAAPG	PLPPPPPPPP	PVPGPVTLPP	PQLVPEGTPG
730	740	750	760	770	780	790	800
GGGPPALEED	LTVININSSD	EEEEEEEEEE	EEEEEEEEEE	EDFEEEEEDE	EEYFEEEEEE	EEEFEEEFEE	EEGELEEEEE
810	820	830	840	850	860	870	880
EEDEEEEEEL	EEVEREGESP	AAGPPPQELV	EEEPSAPPTL	LEEETEDGSD	KVQPPPETPA	EEEMETETEA	EALQEKEQDD
890	900	910					
TAAMLADFID	CPPDDEKPPP	PTEPDS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1945	1	948.3890	-149.84	2	52.8	15.2	2	333-351	R.GSPDGSLQTGKPSAPKKLK.L	

Detailed Protein Report

Protein 702: **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

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
189	1	652.8289	4.93	2	32.3	15.1	1	32-44	R.EGVSEELGGKGSR.R	

Detailed Protein Report

Protein 703: **membrane-associated phosphatidylinositol transfer protein 1 isoform b [Homo sapiens]**

Accession:	gi|195927017	**Score:**	15.1
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

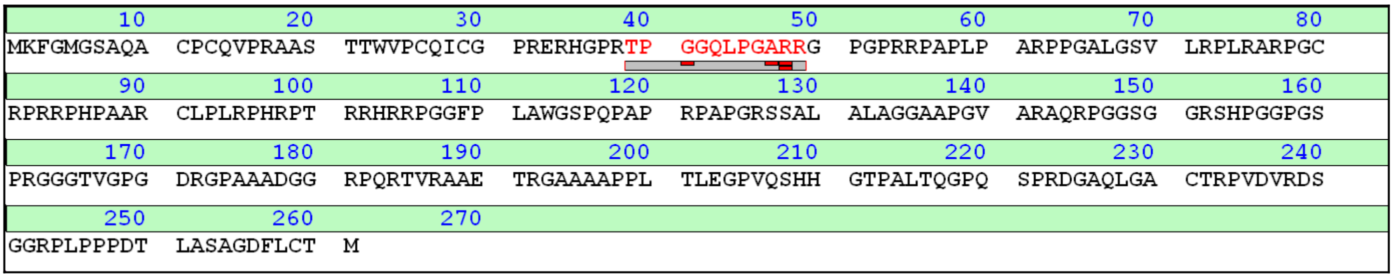
10	20	30	40	50	60	70	80
MLIKEYHILL	PMSLDEYQVA	QLYMIQKKSR	EESSGEGSGV	EILANRPYTD	GPGGSGQYTH	KVYHVGSHIP	GWFRALLPKA
90	100	110	120	130	140	150	160
ALQVEEESWN	AYPYTRTRYT	CPFVEKFSIE	IETYYLPDGG	QQPNVFNLSG	AERRQRILDT	IDIVRDAVAP	GEYKAEEDPR
170	180	190	200	210	220	230	240
LYHSVKTGRG	PLSDDWARTA	AQTGPLMCAY	KLCKVEFRYW	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
1596	2	598.6726	-241.40	2	48.5	15.1	0	1218-1229	R.EGPGTPPTTLAR.G	

Detailed Protein Report

Protein 704: bcl-2-binding component 3 isoform 1 [Homo sapiens]

Accession:	gi|187829730	**Score:**	15.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.5
Database Date:	2015-11-30	**pI:**	12.9
		Sequence Coverage [%]:	4.2
		No. of unique Peptides:	1



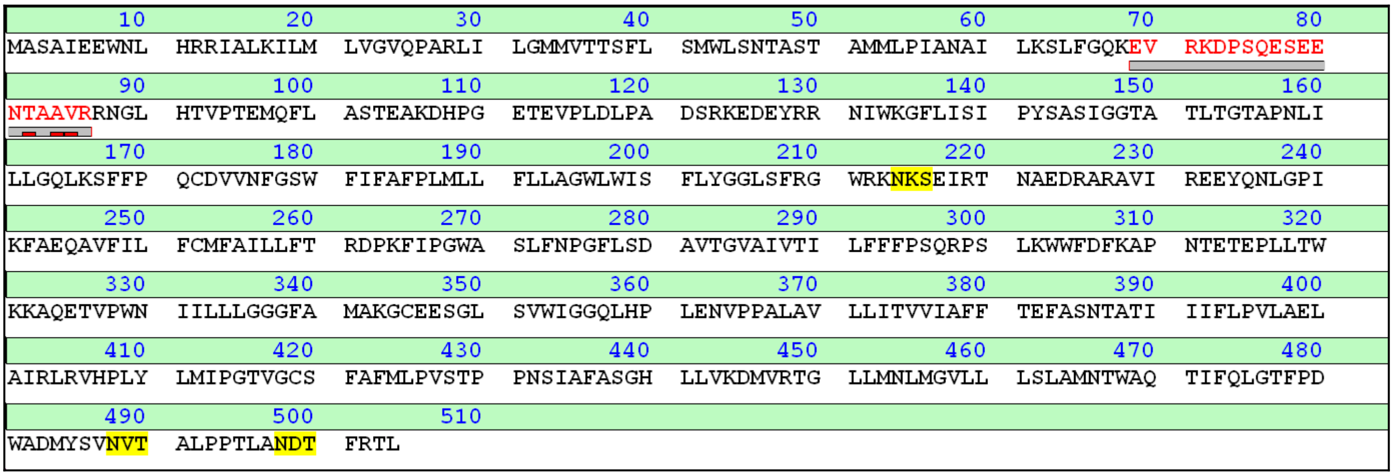
10	20	30	40	50	60	70	80
MKFGMGSAQA	CPCQVPRAAS	TTWVPCQICG	PRERHGPRTP	GGQLPGARRG	PGPRRPAPLP	ARPPGALGSV	LRPLRARPGC
90	100	110	120	130	140	150	160
RPRRPHPAAR	CLPLRPHRPT	RRHRRPGGFP	LAWGSPQPAP	RPAPGRSSAL	ALAGGAAPGV	ARAQRPGGSG	GRSHPGGPGS
170	180	190	200	210	220	230	240
PRGGGTVGPG	DRGPAAADGG	RPQRTVRAAE	TRGAAAAPPL	TLEGPVQSHH	GTPALTQGPQ	SPRDGAQLGA	CTRPVDVRDS
250	260	270					
GGRPLPPPDT	LASAGDFLCT	M					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1119	1	555.1856	-228.33	2	44.1	15.1	1	39-49	R.TPGGQLPGARR.G	

Detailed Protein Report

Protein 705: 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 706: **homeobox protein Hox-C10 [Homo sapiens]**

Accession:	gi|24497533	**Score:**	15.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.0
Database Date:	2015-11-30	**pI:**	9.3
		Sequence Coverage [%]:	5.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTCPRNVTPN	SYAEPLAAPG	GGERYSRSAG	MYMQSGSDFN	CGVMRGCGLA	PSLSKRDEGS	SPSLALNTYP	SYLSQLDSWG
90	100	110	120	130	140	150	160
DPKAAYRLEQ	PVGRPLSSCS	YPPSVKEENV	CCMYSAEKRA	KSGPEAALYS	HPLPESCLGE	HEVPVPSYYR	ASPSYSALDK
170	180	190	200	210	220	230	240
TPHCSGANDF	EAPFEQRASL	NPRAEHLESP	QLGGKVSFPE	TPKSDSQTPS	PNEIKTEQSL	AGPKGSPSES	EKERAKAADS
250	260	270	280	290	300	310	320
SPDTSDNEAK	EEIKAENTTG	NWLTAKSGRK	KRCPYTKHQT	LELEKEFLFN	MYLTRERRLE	ISKTINLTDR	QVKIWFQNRR
330	340	350					
MKLKKMNREN	RIRELTSNFN	FT					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1437	1	946.4677	34.49	2	46.5	15.1	2	233-250	K.ERAKAADSSPDTSDNEAK.E	

Detailed Protein Report

Protein 707: **protein sidekick-2 precursor [Homo sapiens]**

Accession:	gi|222352127	**Score:**	15.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	239.2
Database Date:	2015-11-30	**pI:**	6.6
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWGLLIWTLL	ALHQIRAARA	QDDVSPYFKT	EPVRTQVHLE	GNRLVLTCMA	EGSWPLEFKW	LHNNRELTKF	SLEYRYMITS
90	100	110	120	130	140	150	160
LDRTHAGFYR	CIVRNRMGAL	LQRQTEVQVA	YMGSFEEGEK	HQSVSHGEAA	VIRAPRIASF	PQPQVTWFRD	GRKIPPSSRI
170	180	190	200	210	220	230	240
AITLENTLVI	LSTVAPDAGR	YYVQAVNDKN	GDNKTSQPIT	LTVENVGGPA	DPIAPTIIIP	PKNTSVVAGT	SEVTLECVAN
250	260	270	280	290	300	310	320
ARPLIKLHII	WKKDGVLLSG	GISDHNRRLT	IPNPTGSDAG	YYECEAVLRS	SSVPSVVRGA	YLSVLEPPQF	VKEPERHITA
330	340	350	360	370	380	390	400
EMEKVVDIPC	QAKGVPPPSI	TWYKDAAVVE	VEKLTRFRQR	NDGGLQISGL	VPDDTGMFQC	FARNAAGEVQ	TSTYLAVTSI
410	420	430	440	450	460	470	480
APNITRGPLD	STVIDGMSVV	LACETSGAPR	PAITWQKGER	ILASGSVQLP	RFTPLESGSL	LISPTHISDA	GTYTCLATNS
490	500	510	520	530	540	550	560
RGVDEASADL	VVWARTRITK	PPQDQSVIKG	TQASMVCGVT	HDPRVTIRYI	WEKDGATLGT	ESHPRIRLDR	NGSLHISQTW
570	580	590	600	610	620	630	640
SGDIGTYTCR	VISAGGNDSR	SAHLRVRQLP	HAPEHPVATL	STVERRAINL	TWTKPFDGNS	PLIRYILEMS	ENNAPWTVLL
650	660	670	680	690	700	710	720
ASVDPKATSV	TVKGLVPARS	YQFRLCAVND	VGKGQFSKDT	ERVSLPEEPP	TAPPQNVIAS	GRTNQSIMIQ	WQPPPESHQN
730	740	750	760	770	780	790	800
GILKGYIIRY	CLAGLPVGYQ	FKNITDADVN	NLLLEDLIIW	TNYEIEVAAY	NSAGLGVYSS	KVTEWTLQGV	PTVPPGNVHA
810	820	830	840	850	860	870	880
EATNSTTIRF	TWNAPSPQFI	NGINQGYKLI	AWEPEQEEEV	TMVTARPNFQ	DSIHVGFVSG	LKKFTEYFTS	VLCFTTPGDG
890	900	910	920	930	940	950	960
PRSTPQLVRT	HEDVPGPVGH	LSFSEILDTS	LKVSWQEPGE	KNGILTGYRI	SWEEYNRTNT	RVTHYLPNVT	LEYRVTGLTA
970	980	990	1000	1010	1020	1030	1040
LTTYTIEVAA	MTSKGQGQVS	ASTISSGVPP	ELPGPPTNLG	ISNIGPRSVT	LQFRPGYDGK	TSISRWLVEA	QVGVVGEGEE
1050	1060	1070	1080	1090	1100	1110	1120
WLLIHQLSNE	PDARSMEVPD	LNPFTCYSFR	MRQVNIVGTS	PPSQPSRKIQ	TLQAPPDMAP	ANVSLRTASE	TSLWLRWMPL
1130	1140	1150	1160	1170	1180	1190	1200
PEMEYNGNPE	SVGYKIKYSR	SDGHGKTLSH	VVQDRVERDY	TIEDLEEWTE	YRVQVQAFNA	IGSGPWSQTV	VGRTRESVPS
1210	1220	1230	1240	1250	1260	1270	1280
SGPTNVSALA	TTSSSMLVRW	SEVPEADRNG	LVLGYKVMYK	EKDSDTQPRF	WLVEGNSSRS	AQLTGLGKYV	LYEVQVLAFT
1290	1300	1310	1320	1330	1340	1350	1360
RIGDGSPSHP	PILERTLDDV	PGPPMGILFP	EVRTTSVRLI	WQPPAAPNGI	ILAYQITHRL	NTTTANTATV	EVLAPSARQY
1370	1380	1390	1400	1410	1420	1430	1440
TATGLKPESV	YLFRITAQTR	KGWGEAAEAL	VVTTEKRDRP	QPPSRPMVQQ	EDVRARSVLL	SWEPGSDGLS	PVRYYTIQTR
1450	1460	1470	1480	1490	1500	1510	1520
ELPSGRWALH	SASVSHNASS	FIVDRLKPFT	SYKFRVKATN	DIGDSEFSEE	SESLTTLQAA	PDEAPTILSV	TPHTTTSVLI
1530	1540	1550	1560	1570	1580	1590	1600
RWQPPAEDKI	NGILLGFRIR	YRELLYEGLR	GFTLRGINNP	GATWAELTSM	YSMRNLSRPS	LTQYELDNLN	KHRRYEIRMS
1610	1620	1630	1640	1650	1660	1670	1680
VYNAVGEGPS	SPPQEVFVGE	AVPTAAPRNV	VVHGATATQL	DVTWEPPPLD	SQNGDIQGYK	IYFWEAQRGN	LTERVKTLFL
1690	1700	1710	1720	1730	1740	1750	1760
AENSVKLKNL	TGYTAYMVSV	AAFNAAGDGP	RSTPTQGQTQ	QAAPSAPSSV	KFSELTTTSV	NVSWEAPQFP	NGILEGYRLV
1770	1780	1790	1800	1810	1820	1830	1840
YEPCSPVDGV	SKIVTVDVKG	NSPLWLKVKD	LAEGVTYRFR	IRAKTFTYGP	EIEANVTTGP	GEGAPGPPGV	PIIVRYSSAI
1850	1860	1870	1880	1890	1900	1910	1920
AIHWSSGDPG	KGPITRYVIE	ARPSDEGLWD	ILIKDIPKEV	SSYTFSMDIL	KPGVSYDFRV	IAVNDYGFGT	PSSPSQSVPA
1930	1940	1950	1960	1970	1980	1990	2000
QKANPFYEEW	WFLVVIALVG	LIFILLLVFV	LIIRGQSKKY	AKKTDSGNSA	KSGALGHSEM	MSLDESSFPA	LELNNRRLSV
2010	2020	2030	2040	2050	2060	2070	2080
KNSFCRKNGL	YTRSPPRPSP	GSLHYSDEDV	TKYNDLIPAE	SSSLTEKPSE	ISDSQGSDSE	YEVDSNHQKA	HSFVNHYISD
2090	2100	2110	2120	2130	2140	2150	2160
PTYYNSWRRQ	QKGISRAQAY	SYTESDSGEP	DHTTVTNSTS	TQQGSLFRPK	ASRTPTPQNP	PNPPSQQSTL	YRPPSSLAPG
2170	2180						

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2022	1	1134.9008	-126.03	2	53.8	15.1	0	269-289	R.LTIPNPTGSDAGYYECEAVLR.S	

Detailed Protein Report

Protein 708: adenosylhomocysteinase isoform 2 [Homo sapiens]

Accession:	gi|239937451	**Score:**	15.1
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
1431	2	918.1671	157.08	2	46.4	15.1	2	361-377	K.KLDEAVAEAHLGKLNVK.L	

Detailed Protein Report

Protein 709: 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 710: PREDICTED: serine protease 44 [Homo sapiens]

Accession:	gi|530357996	**Score:**	15.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.4
Database Date:	2015-11-30	**pI:**	12.2
		Sequence Coverage [%]:	9.2
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.66 **CV:** 0.00 % **No. of 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	Ratios
1082	1	670.8357	-47.72	2	43.6	15.0	1	94-106	R.TSRITGGLPAPDR.K		QD:QU 0.66

Detailed Protein Report

Protein 711: E3 ubiquitin-protein ligase UHRF1 isoform 1 [Homo sapiens]

Accession:	gi|115430235	**Score:**	15.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	89.8
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

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
2699	1	973.4997	26.66	2	64.8	15.0	2	544-560	K.NSKYAPAEGNRYDGIYK.V	

Detailed Protein Report

Protein 712: **PREDICTED: transcription elongation factor A protein 3 isoform X4 [Homo sapiens]**

Accession:	gi|578799689	**Score:**	15.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.0
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSIQLLQTTR	IGVAVNGVRK	HCSDKEVVSL	AKVLIKNWKR	LLDSPGPPKG	EKGEEREKAK	KKEKGLECSD	WKPEAGLSPP
90	100	110	120	130	140	150	160
RKKREDPKTR	RDSVDSKSSA	SSSPKRPSVE	RSNSSKSKAE	SPKTPSSPLT	PTFASSMCLL	APCYLTGDSV	RDKCVEMLSA
170	180	190	200	210	220	230	240
ALKADDDYKD	YGVNCDKMAS	EIEDHIYQEL	KSTDMKYRNR	VRSRISNLKD	PRNPGLRRNV	LSGAISAGLI	AKMTAEEMAS
250	260	270	280	290	300	310	320
DELRELRNAM	TQEAIREHQM	AKTGGTTTDL	FQCSKCKKKN	CTYNQVQTRS	ADEPMTTFVL	CNECGNRWKM	ESAS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
291	1	657.3457	-71.91	2	32.4	15.0	0	219-232	R.NVLSGAISAGLIAK.M	

Detailed Protein Report

Protein 713: complement C1q subcomponent subunit C precursor [Homo sapiens]

Accession:	gi|56786155	**Score:**	15.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	25.8
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	5.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|166235903	refseq_human (refseq_human_20140103.fasta)	complement C1q subcomponent subunit C precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MDVGPSSLPH	LGLKLLLLLL	LLPLRGQANT	GCYGIPGMPG	LPGAPGKDGY	DGLPGPKGEP	GIPAIPGIRG	PKGQKGEPGL
90	100	110	120	130	140	150	160
PGHPGKNGPM	GPPGMPGVPG	PMGIPGEPGE	EGRYKQKFQS	VFTVTRQTHQ	PPAPNSLIRF	NAVLTNPQGD	YDTSTGKFTC
170	180	190	200	210	220	230	240
KVPGLYYFVY	HASHTANLCV	LLYRSGVKVV	TFCGHTSKTN	QVNSGGVLLR	LQVGEEVWLA	VNDYYDMVGI	QGSDSVFSGF
250							
LLFPD							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2715	1	725.3796	0.07	2	65.1	15.0	1	185-198	R.SGVKVVTFCGHTSK.T	

Detailed Protein Report

Protein 714: PREDICTED: RNA-binding protein EWS isoform X3 [Homo sapiens]

Accession:	gi|578837005	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.1
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASTDYSTYS	QAAAQQGYSA	YTAQPTQGYA	QTTQAYGQQS	YGTYGQPTDV	SYTQAQTTAT	YGQTAYATSY	GQPPTGYTTP
90	100	110	120	130	140	150	160
TAPQAYSQPV	QGYGTGAYDT	TTATVTTTQA	SYAAQSAYGT	QPAYPAYGQQ	PAATAPTRPQ	DGNKPTETSQ	PQSSTGGYNQ
170	180	190	200	210	220	230	240
PSLGYGQSNY	SYPQVPGSYP	MQPVTAPPSY	PPTSYSSTQP	TSYDQSSYSQ	QNTYGQPSSY	GQQSSYGQQS	SYGQQPPTSY
250	260	270	280	290	300	310	320
PPQTGSYSQA	PSQYSQQSSS	YGQQSSFRQD	HPSSMGVYGQ	ESGGFSGPGE	NRSMSGPDNR	GRGRGGFDRG	GMSRGGRGGG
330	340	350	360	370	380	390	400
RGGMGSAGER	GGFNKPGGPM	DEGPDLDLGP	PVDPDEDSDN	SAIYVQGLND	SVTLDDLADF	FKQCGVVKMN	KRTGQPMIHI
410	420	430	440	450	460	470	480
YLDKETGKPK	GDATVSYEDP	PTAKAAVEWF	DGKDFQGSKL	KVSLARKKPP	MNSMRGGLPP	REGRGMPPPL	RGGPGGPGGP
490	500	510	520	530	540	550	560
GGPMGRMGGR	GGDRGGFPPR	GPRGSRGNPS	GGGNVQHRAG	DWQCPNPSIG	DFCCDVIVCR	GCGNQNFAWR	TECNQCGDRG
570	580	590	600	610	620	630	640
RGGPGGMRGG	RGGLMDRGGP	GGMFRGGRGG	DRGGFRGGRG	MDRGGFGGGR	RGGPGGPPGP	LMEQMGGRRG	GRGGPGKMDK
650	660						
GEHRQERRDR	PY						

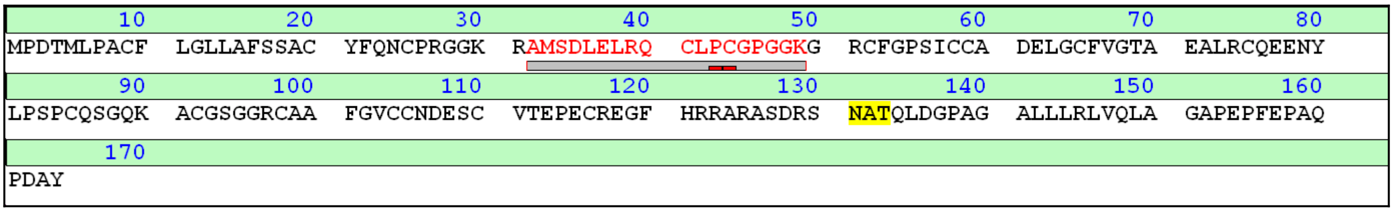
Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
6	1	1186.3900	-88.40	2	28.4	14.9	2	541-561	R.GCGNQNFAWRTECNQCGDRGR.G	

Detailed Protein Report

Protein 715: **vasopressin-neurophysin 2-copeptin preproprotein [Homo sapiens]**

Accession: gi|13259533
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 14.9
MW [kDa]: 17.3
pI: 5.1
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 716: RNA polymerase-associated protein RTF1 homolog [Homo sapiens]

Accession:	gi|195976782	**Score:**	14.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.3
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRGRLCVGRA	AAAAAAVAVP	LAGGQEGSPG	GGRRGSRGTT	MVKKRKGRVV	IDSDTEDSGS	DENLDQELLS	LAKRKRSDSE
90	100	110	120	130	140	150	160
EKEPPVSQPA	ASSDSETSDS	DDEWTFGSNK	NKKKGKARKI	EKKGTMKKQA	NKTASSGSSD	KDSSAESSAP	EEGEVSDSDS
170	180	190	200	210	220	230	240
NSSSSSSDSD	SSSEDEEFHD	GYGEDLMGDE	EDRARLEQMT	EKEREQELFN	RIEKREVLKR	RFEIKKKLKT	AKKKEKKEKK
250	260	270	280	290	300	310	320
KKQEEEQEKK	KLTQIQESQV	TSHNKERRSK	RDEKLDKKSQ	AMEELKAERE	KRKNRTAELL	AKKQPLKTSE	VYSDDEEEEE
330	340	350	360	370	380	390	400
DDKSSEKSDR	SSRTSSSDEE	EEKEEIPPKS	QPVSLPEELN	RVRLSRHKLE	RWCHMPFFAK	TVTGCFVRIG	IGNHNSKPVY
410	420	430	440	450	460	470	480
RVAEITGVVE	TAKVYQLGGT	RTNKGLQLRH	GNDQRVFRLE	FVSNQEFTES	EFMKWKEAMF	SAGMQLPTLD	EINKKELSIK
490	500	510	520	530	540	550	560
EALNYKFNDQ	DIEEIVKEKE	RFRKAPPNYA	MKKTQLLKEK	AMAEDLGDQD	KAKQIQDQLN	ELEERAEALD	RQRTKNISAI
570	580	590	600	610	620	630	640
SYINQRNREW	NIVESEKALV	AESHNMKNQQ	MDPFTRRQCK	PTIVSNSRDP	AVQAAILAQL	NAKYGSGVLP	DAPKEMSKGQ
650	660	670	680	690	700	710	720
GKDKDLNSKS	ASDLSEDLFK	VHDFDVKIDL	QVPSSESKAL	AITSKAPPAK	DGAPRRSLNL	EDYKKRRGLI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
90	1	650.3247	-10.31	3	29.8	14.9	2	624-642	K.YGSGVLPDAPKEMSKGQGK.D	

Detailed Protein Report

Protein 717: probable tRNA pseudouridine synthase 1 [Homo sapiens]

Accession:	gi|21040257	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.2
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAASEAAVVS	SPSLKTDTSP	VLETAGTVAA	MAATPSARAA	AAVVAAAART	GSEARVSKAA	LATKLLSLSG	VFAVHKPKGP
90	100	110	120	130	140	150	160
TSAELLNRLK	EKLLAEAGMP	SPEWTKRKKQ	TLKIGHGGTL	DSAARGVLVV	GIGSGTKMLT	SMLSGSKRYT	AIGELGKATD
170	180	190	200	210	220	230	240
TLDSTGRVTE	EKPYDKITQE	DIEGILQKFT	GNIMQVPPLY	SALKKDGQRL	STLMKRGEVV	EAKPARPVTV	YSISLQKFQP
250	260	270	280	290	300	310	320
PFFTLDVECG	GGFYIRSLVS	DIGKELSSCA	NVLELTRTKQ	GPFTLEEHAL	PEDKWTIDDI	AQSLEHCSSL	FPAELALKKS
330	340	350					
KPESNEQVLS	CEYITLNEPK	REDDVIKTC					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
36	1	660.7253	-198.17	2	29.1	14.8	2	206-216	K.DGQRLSTLMKR.G	Oxidation: 9

Detailed Protein Report

Protein 718: granulysin isoform 519 [Homo sapiens]

Accession: gi|157502222

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 14.8

MW [kDa]: 14.8

pI: 10.5

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

Detailed Protein Report

Protein 719: speckle-type POZ protein [Homo sapiens]

Accession:	gi|4507183	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.1
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530412967	refseq_human (refseq_human_20140103.fasta)	PREDICTED: speckle-type POZ protein isoform X3 [Homo sapiens]
gi|530412965	refseq_human (refseq_human_20140103.fasta)	PREDICTED: speckle-type POZ protein isoform X2 [Homo sapiens]
gi|56117836	refseq_human (refseq_human_20140103.fasta)	speckle-type POZ protein [Homo sapiens]
gi|56117834	refseq_human (refseq_human_20140103.fasta)	speckle-type POZ protein [Homo sapiens]
gi|56117832	refseq_human (refseq_human_20140103.fasta)	speckle-type POZ protein [Homo sapiens]
gi|56117830	refseq_human (refseq_human_20140103.fasta)	speckle-type POZ protein [Homo sapiens]
gi|56117828	refseq_human (refseq_human_20140103.fasta)	speckle-type POZ protein [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MSRVPSPPPP AEMSSGPVAE SWCYTQIKVV KFSYMWTINN FSFCREEMGE VIKSSTFSSG ANDKLKWCLR VNPKGLDEES
        90        100        110        120        130        140        150        160
KDYLSLYLLL VSCPKSEVRA KFKFSILNAK GEETKAMESQ RAYRFVQGKD WGFKKFIRRD FLLDEANGLL PDDKLTLFCE
       170        180        190        200        210        220        230        240
VSVVQDSVNI SGQNTMNMVK VPECRLADEL GGLWENSRFT DCCLCVAGQE FQAHKAILAA RSPVFSAMFE HEMEESKKNR
       250        260        270        280        290        300        310        320
VEINDVEPEV FKEMMCFIYT GKAPNLDKMA DDLLAAADKY ALERLKVMCE DALCSNLSVE NAAEILILAD LHSADQLKTQ
       330        340        350        360        370        380
AVDFINYHAS DVLETSGWKS MVVSHPHLVA EAYRSLASAQ CPFLGPPRKR LKQS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1325	1	508.1630	-228.12	2	45.1	14.8	1	67-74	K.WCLRVNPK.G	

Detailed Protein Report

Protein 720: PREDICTED: 39S ribosomal protein L20, mitochondrial isoform X2 [Homo sapiens]

Accession: gi|530360352

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 14.8

MW [kDa]: 12.1

pI: 12.4

Sequence Coverage [%]: 8.8

No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MVFLTAQLWL RNRVTDRYFR IQEVLKHARH FRGRKNRCYR LAVRTVIRAF VKCTKARYLK KKNMRTLWIN RITAASQEHG
        90        100        110
LKYPALIGNL VKALPGWLKG LP
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1869	2	604.2765	-84.36	2	53.7	14.8	2	36-44	K.NRCYRLAVR.T	Carbamidomethyl: 3

Detailed Protein Report

Protein 721: **PREDICTED: phosphorylase b kinase gamma catalytic chain, liver/testis isoform isoform X3 [Homo sapiens]**

Accession: gi|530408225
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 14.8
MW [kDa]: 34.4
pI: 6.4
Sequence Coverage [%]: 4.3
No. of unique Peptides: 1

Quantitation

QD:QU **Median:** 4.01 **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	QD:QU 4.01

Detailed Protein Report

Protein 722: long-chain-fatty-acid--CoA ligase 5 isoform b [Homo sapiens]

Accession: gi|42794758
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 14.8
MW [kDa]: 75.9
pI: 6.5
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 723: **inhibitor of growth protein 3 isoform 3 [Homo sapiens]**

Accession:	gi|38201659	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	11.3
Database Date:	2015-11-30	**pI:**	4.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	16.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLYLEDYLEM	IEQLPMDLRD	RFTEMREMDL	QVQNAMDQLE	QRVSEFFMNA	KKNKPEWREE	QMASIKKDYY	KALEDADEKV
90	**100**						
QLANQIYDLQ	HF						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
541	1	945.4099	-74.72	2	35.4	14.8	2	53-67	K.NKPEWREEQMASIKK.D	Oxidation: 10

Detailed Protein Report

Protein 724: **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 725: **formin-1 isoform c [Homo sapiens]**

Accession:	gi|472235321	**Score:**	14.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.8
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	4.4
		No. of unique 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
1018	1	920.4993	28.10	3	42.8	14.8	1	395-423	R.SSQSPAGETASISSVSASAEGAVNKVPLK.V	

Detailed Protein Report

Protein 726: PREDICTED: nardilysin isoform X1 [Homo sapiens]

Accession:	gi|530362704	**Score:**	14.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	105.5
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.0
		No. of unique Peptides:	1

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
923	1	512.2392	-109.51	2	41.6	14.7	0	816-824	R.LAHEIEALK.S	

Detailed Protein Report

Protein 727: 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 728: **epidermal growth factor receptor kinase substrate 8-like protein 3 isoform c [Homo sapiens]**

Accession:	gi|21071014	**Score:**	14.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.5
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSRPSSRAIY	LHRKEYSQNL	TSEPTLLQHR	VEHLMTCKQG	SQRVQGPEDA	LQKLFEMDAQ	GRVWSQDLIL	QVRDGWLQLL
90	100	110	120	130	140	150	160
DIETKEELDS	YRLDSIQAMN	VALNTCSYNS	ILSITVQEPG	LPGTSTLLFQ	CQEVGAERLK	TSLQKALEEE	LEQRPRLGGL
170	180	190	200	210	220	230	240
QPGQDRWRGP	AMERPLPMEQ	ARYLEPGIPP	EQPHQRTLEH	SLPPSPRPLP	RHTSAREPSA	FTLPPPRRSS	SPEDPERDEE
250	260	270	280	290	300	310	320
VLNHVLRDIE	LFMGKLEKAQ	AKTSRKKKFG	KKNKDQGGLT	QAQYIDCFQK	IKHSFNLLGR	LATWLKETSA	PELVHILFKS
330	340	350	360	370	380	390	400
LNFILARCPE	AGLAAQVISP	LLTPKAINLL	QSCLSPPESN	LWMGLGPAWT	TSRADWTGDE	PLPYQPTFSD	DWQLPEPSSQ
410	420	430	440	450	460	470	480
APLGYQDPVS	LRPSSPKPAQ	PALKMQVLYE	FEARNPRELT	VVQGEKLEVL	DHSKRWWLVK	NEAGRSGYIP	SNILEPLQPG
490	500	510	520	530	540	550	560
TPGTQGQSPS	RVPMLRLSSR	PEEVTDWLQA	ENFSTATVRT	LGSLTGSQLL	RIRPGELQML	CPQEAPRILS	RLEAVRRMLG
570							
ISP							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2785	1	711.3716	26.32	3	66.0	14.7	1	44-62	R.VQGPEDALQKLFEMDAQGR.V	

Detailed Protein Report

Protein 729: 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

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
2397	1	805.8341	-70.08	2	60.4	14.7	0	580-593	K.LCFVGLMSMIDPPR.A	Oxidation: 7, 9

Detailed Protein Report

Protein 730: inosine triphosphate pyrophosphatase isoform a [Homo sapiens]

Accession:	gi|15626999	**Score:**	14.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.4
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	10.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAASLVGKKI VFVTGNAKKL EEVVQILGDK FPCTLVAQKI DLPEYQGEPD EISIQKCQEA VRQVQGPVLV EDTCLCFNAL
        90        100        110        120        130        140        150        160
GGLPGPYIKW FLEKLKPEGL HQLLAGFEDK SAYALCTFAL STGDPSQPVR LFRGRTSGRI VAPRGCQDFG WDPCFQPDGY
       170        180        190        200
EQTYAEMPKA EKNAVSHRFR ALLELQEYFG SLAA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1227	1	786.7216	-67.73	3	43.9	14.6	2	19-39	K.KLEEVVQILGDKFPCTLVAQK.I	

Detailed Protein Report

Protein 731: **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 732: origin recognition complex subunit 6 [Homo sapiens]

Accession:	gi|7657427	**Score:**	14.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.1
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	7.5
		No. of unique 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
2162	1	701.2632	-88.04	3	57.4	14.6	0	42-60	R.TTETSSAVMCLDLAASWMK.C	Carbamidomethyl: 10

Detailed Protein Report

Protein 733: zinc finger and SCAN domain-containing protein 26 isoform b [Homo sapiens]

Accession: gi|161353483
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 14.6
MW [kDa]: 55.2
pI: 9.5
Sequence Coverage [%]: 4.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MATALVSAHS	LAPLNLKKEG	LRVVREDHYS	TWEQGFKLQG	NSKGLGQEPL	CKQFRQLRYE	ETTGPREALS	RLRELCQQWL
90	100	110	120	130	140	150	160
QPETHTKEQI	LELLVLEQFL	IILPKELQAR	VQEHHPESRE	DVVVVLEDLQ	LDLGETGQQD	PDQPKKQKIL	VEEMAPLKGV
170	180	190	200	210	220	230	240
QEQQVRHECE	VTKPEKEKGE	ETRIENGKLI	VVTDSCGRVE	SSGKISEPME	AHNEGSNLER	HQAKPKEKIE	YKCSEREQRF
250	260	270	280	290	300	310	320
IQHLDLIEHA	STHTGKKLCE	SDVCQSSSLT	GHKKVLSREK	GHQCHECGKA	FQRSSHLVRH	QKIHLGEKPY	QCNECGKVFS
330	340	350	360	370	380	390	400
QNAGLLEHLR	IHTGEKPYLC	IHCGKNFRRS	SHLNRHQRIH	SQEEPCECKE	CGKTFSQALL	LTHHQRIHSH	SKSHQCNECG
410	420	430	440	450	460	470	480
KAFSLTSDLI	RHHRIHTGEK	PFKCNICQKA	FRLNSHLAQH	VRIHNEEKPY	QCSECGEAFR	QRSGLFQHQR	YHHKDKLA

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2927	1	1254.6046	-9.85	2	65.7	14.6	2	23-43	R.VVREDHYSTWEQGFKLQGNSK.G	

Detailed Protein Report

Protein 734: rho-related GTP-binding protein RhoF precursor [Homo sapiens]

Accession:	gi|38016957	**Score:**	14.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.6
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	5.7
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MDAPGALAQT AAPGPGRKEL KIVIVGDGGC GKTSLLMVYS QGSFPEHYAP SVFEKYTASV TVGSKEVTLN LYDTAGQEDY
         90        100        110        120        130        140        150        160
DRLRPLSYQN THLVLICYDV MNPTSYDNVL IKWFPEVTHF CRGIPMVLIG CKTDLRKDKE QLRKLRAAQL EPITYMQGLS
        170        180        190        200        210        220
ACEQIRAALY LECSAKFREN VEDVFREAAK VALSALKKAQ RQKKRRLCLL L
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
171	1	614.7837	-164.46	2	30.9	14.6	2	187-198	R.EAAKVALSALKK.A	

Detailed Protein Report

Protein 735: Meckel syndrome type 1 protein isoform 2 [Homo sapiens]

Accession:	gi|260064077	**Score:**	14.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.3
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
MAVPVSSFAQ	RTRSRFRVHL	QRITSSNFLH	YQPAAELGKD	LIDLATFRPQ	PTASGHRPEE	DEEEEIVIGW	QEKLFSQFEV
90	100	110	120	130	140	150	160
DLYQNETACQ	SPLDYQYRQE	ILKLENSGGK	KNRRIFTYTD	SDRYTNLEEH	CQRMTTAASE	VPSFLVERMA	NVRRRRQDRR
170	180	190	200	210	220	230	240
GMEGGILKSR	IVTWEPSEEF	VRNNHVINTP	LQTMHIMADL	GPYKKLGYKK	YEHVLCTLKV	DSNGVITVKP	DFTGLKGPYR
250	260	270	280	290	300	310	320
IETEGEKQEL	WKYTIDNVSP	HAQPEEEERE	RRVFKDLYGR	HKEYLSSLVG	TDFEMTVPGA	LRLFVNGEVV	SAQGYEYDNL
330	340	350	360	370	380	390	400
YVHFFVELPT	AHWSSPAFQQ	LSGVTQTCTT	KSLAMDKVAH	FSYPFTFEAF	FLHEDESSDA	LPEWPVLYCE	VLSLDFWQRY
410	420	430	440	450	460	470	480
RVEGYGAVVL	PATPGSHTLT	VSTWRPVELG	TVAELRRFFI	GGSLELEDLS	YVRIPGSFKG	ERLSRFGLRT	ETTGTVTFRL
490	500	510	520	530	540	550	
HCLQQSRAFM	ESSSLQKRMR	SVLDRLEGFS	QQSSIHNVLE	AFRRARRRMQ	EARESLPQDL	VSPSGTLVS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2128	1	938.2619	96.17	3	57.0	14.6	2	16-39	R.FRVHLQRITSSNFLHYQPAAELGK.D	

Detailed Protein Report

Protein 736: ankyrin repeat and BTB/POZ domain-containing protein 2 [Homo sapiens]

Accession: gi|300796386
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 14.6
MW [kDa]: 113.6
pI: 5.8
Sequence Coverage [%]: 1.7
No. of unique Peptides: 1

Quantitation

QD:QU **Median:** 0.61 **CV:** 0.00 % **No. of 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	Ratios
1098	1	955.4548	-49.92	2	43.8	14.6	0	999-1015	K.VQGLDPLQDLQNTLAER.V		QD:QU 0.61

Detailed Protein Report

Protein 737: von Willebrand factor A domain-containing protein 3A precursor [Homo sapiens]

Accession:	gi|218505703	**Score:**	14.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	133.9
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKKYRKISIG	CFAMATQTSH	VFHGQENMFL	ENHCIRRNTG	RDSKKPLKQK	NMNGLGQNSD	NGLLVTHVNQ	TQDLLRLQGS
90	100	110	120	130	140	150	160
ETQSSDWEDS	EDWLSAHSLK	CQKLTLADLI	SQGTEVLEEG	TNVVQKICFS	TQIIRHFESK	LSDTIEVYQE	RIQWLTENSK
170	180	190	200	210	220	230	240
KAFGLIKGAR	VSILIDVSAI	SSGPQKEEFQ	KDLMSLIDEQ	LSHKEKLFVL	SFGTNAGSLW	PDPMEVSAST	LQELKLWVKT
250	260	270	280	290	300	310	320
LQPDGGSNLL	QALKKIFTLK	GLDSLVAIMR	SCPDQPSEIL	SDYIQQSTMG	RDLIIHFITY	RCDDQMPPAV	LKNLAEAVRG
330	340	350	360	370	380	390	400
YYHCYSPKME	HYTSRDMDEL	LAEIQKAQSL	LSHVQALQHS	SPCEALTCTM	EEISTEITNG	PLISLLPKPP	KHDAPLTIEF
410	420	430	440	450	460	470	480
PNLDKTSAEW	LKVNGLKAKK	LSLYQVLAPN	AFSPVEEFVP	ILQKTVSSTI	HEKAMIQFEW	HDGTVKNIHV	DPPFLYKYQQ
490	500	510	520	530	540	550	560
QLSRAMRMYE	RRIEWLSLAS	RRIWGTVCEK	RVVVLLDISA	TNSMYIIHIQ	HSLRLLLEEQ	LSNKDCFNLI	AFGSTIESWR
570	580	590	600	610	620	630	640
PEMVPVSHNN	LQSAWRWALN	LRCRGSRNVL	SALRKAVEVD	FKDKDKHQSQ	GIYLFTGGIP	DQDMPTLSAY	MAEACGGCDL
650	660	670	680	690	700	710	720
QLNVCLFYVG	EPKMDTTPPA	RYASHTDTAA	AYKEVTRAAG	GRFHWFGDTG	IYESDDINSI	MSEMEKALNY	SQKCAFLMAS
730	740	750	760	770	780	790	800
LKNHSGKVLG	SSALPKEKPK	TLQLRSQPKK	LCPPRPTVPL	GARMSIKDDP	DREKSPPLKS	LKWRPLSSRV	GISPAAAQPT
810	820	830	840	850	860	870	880
KEGMMELRRK	TKSREAETSL	LLFYTEKGND	VGSVYKKYPQ	GRGLRRTSSS	IDLPRKDTVC	SSQEWVAKYG	LKKLKLEISR
890	900	910	920	930	940	950	960
CMGPNCTHQK	SGQRSASAKH	CSIFPSVEIH	GVVRHIQWTP	REMEVYIRHL	EKVLRRYVQR	LQWLLSGSRR	LFGTVLESKV
970	980	990	1000	1010	1020	1030	1040
CILLDTSGSM	GPYLQQVKTE	LVLLIWEQLR	KCCDSFNLLS	FAESFQSWQD	TLVETTDAAC	HEAMQWVTHL	QAQGSTSILQ
1050	1060	1070	1080	1090	1100	1110	1120
ALLKAFSFHD	LEGLYLLTDG	KPDTSCSLVL	NEVQKLREKR	DVKVHTISLN	CSDRAAVEFL	RKLASFTGGR	YHCPVGEDTL
1130	1140	1150	1160	1170	1180	1190	
SKIHSLLTKG	FINEKDPTLP	PFEGDDLRIL	AQEITKARSF	LWQAQSFRSQ	LQKKNDAEPK	VTLS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2766	1	645.8375	-40.89	2	63.6	14.6	0	292-301	R.DLIIHFITYR.C	

Detailed Protein Report

Protein 738: 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

Detailed Protein Report

Protein 739: **PREDICTED: signal-induced proliferation-associated 1-like protein 3 isoform X3 [Homo sapiens]**

Accession: gi|578834186
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 14.6
MW [kDa]: 120.1
pI: 9.7
Sequence Coverage [%]: 1.1
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MYQDYEIMFH	VSTLLPYTPN	NRQQLLRKRH	IGNDIVTIIF	QEPGALPFTP	KNIRSHFQHV	FIIVRVHNPC	TDNVCYSMAV
90	100	110	120	130	140	150	160
TRSKDAPPFG	PPIPSGTTFR	KSDVFRDFLL	AKVINAENAA	HKSDKFHTMA	TRTRQEYLKD	LAENCVSNTP	IDSTGKFNLI
170	180	190	200	210	220	230	240
SLTSKKKEKT	KARAGAEQHS	AGAIAWRVVA	QDYAQGVEID	CILGISNEFV	VLLDLRTKEV	VFNCYCGDVI	GWTPDSSTLK
250	260	270	280	290	300	310	320
IFYGRGDHIF	LQATEGSVED	IREIVQRLKV	MTSGWETVDM	TLRRNGLGQL	GFHVKYDGTV	AEVEDYGFAW	QAGLRQGSRL
330	340	350	360	370	380	390	400
VEICKVAVVT	LTHDQMIDLL	RTSVTVKVVI	IPPFEDGTPR	RGWPETYDMN	TSEPKTEQES	ITPGGRPPYR	SNAPWQWSGP
410	420	430	440	450	460	470	480
ASHNSLPASK	WATPTTPGHA	QSLSRPLKQT	PIVPFRESQP	LHSKRPVSFP	ETPYTVSPAG	ADRVPPYRQP	SGSFSTPGSA
490	500	510	520	530	540	550	560
TYVRYKPSPE	RYTAAPHPLL	SLDPHFSHDG	TSSGDSSSGG	LTSQESTMER	QKPEPLWHVP	AQARLSAIAG	SSGNKHPSRQ
570	580	590	600	610	620	630	640
DAAGKDSPNR	HSKGEPQYSS	HSSSNTLSSN	ASSSHSDDRW	FDPLDPLEPE	QDPLSKGGSS	DSGIDTTLYT	SSPSCMSLAK
650	660	670	680	690	700	710	720
APRPAKPHKP	PGSMGLCGGG	REAAGRSHHA	DRRREVSPAP	AVAGQSKGYR	PKLYSSGSST	PTGLAGGSRD	PPRQPSDMGS
730	740	750	760	770	780	790	800
RVGYPAQVYK	TASAETPRPS	QLAQPSPFQL	SASVPKSFFS	KQPVRNKHPT	GWKRTEEPPP	RPLPFSDPKK	QVDTNTKNVF
810	820	830	840	850	860	870	880
GQPRLRASLR	DLRSPRKNYK	STIEDDLKKL	IIMDNLGPEQ	ERDTGQSPQK	GLQRTLSDES	LCSGRREPSF	ASPAGLEPGL
890	900	910	920	930	940	950	960
PSDVLFTSTC	AFPSSTLPAR	RQHQHPHPPV	GPGATPAAGS	GFPEKKSTIS	ASELSLADGR	DRPLRRLDPG	LMPLPDTAAG
970	980	990	1000	1010	1020	1030	1040
LEWSSLVNAA	KAYEVQRAVS	LFSLNDPALS	PDIPPAHSPV	HSHLSLERGP	PTPRTTPTMS	EEPPLDLTGK	VYQLEVMLKQ
1050	1060	1070	1080	1090	1100		
LHTDLQKEKQ	DKVVLQSEVA	SLRQNNQRLQ	EESQAASEQL	RKFAEIFCRE	KKEL		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2765	1	671.8356	35.13	2	63.6	14.6	1	710-721	R.DPPRQPSDMGSR.V	

Detailed Protein Report

Protein 740: kelch-like protein 23 [Homo sapiens]

Accession:	gi|40255071	**Score:**	14.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.9
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|313151204	refseq_human (refseq_human_20140103.fasta)	kelch-like protein 23 [Homo sapiens]

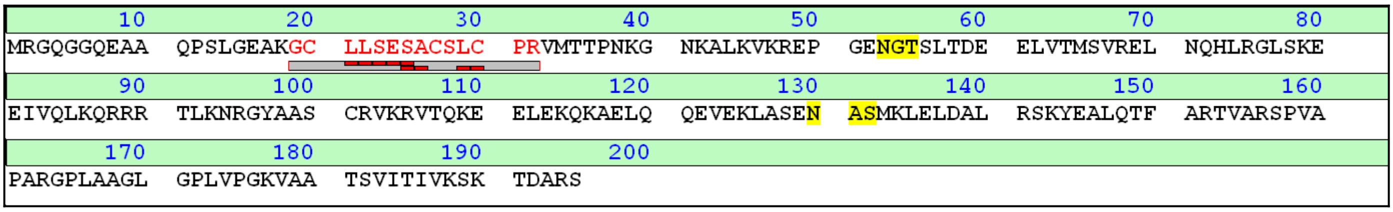
10	20	30	40	50	60	70	80
MALKGQEDYI	YLFKDSTHPV	DFLDAFRTFY	LDGLFTDITL	QCPSGIIFHC	HRAVLAACSN	YFKAMFTADM	KEKFKNKIKL
90	100	110	120	130	140	150	160
SGIHHDILEG	LVNYAYTSQI	EITKRNVQSL	LEAADLLQFL	SVKKACERFL	VRHLDIDNCI	GMHSFAEFHV	CPELEKESRR
170	180	190	200	210	220	230	240
ILCSKFKEVW	QQEEFLEISL	EKFLFILSRK	NLSVWKEEAI	IEPVIKWTAH	DVENRIECLY	NLLSYINIDI	DPVYLKTALG
250	260	270	280	290	300	310	320
LQRSCLLTEN	KIRSLIYNAL	NPMHKEISQR	STATMYIIGG	YYWHPLSEVH	IWDPLTNVWI	QGAEIPDYTR	ESYGVTCLGP
330	340	350	360	370	380	390	400
NIYVTGGYRT	DNIEALDTVW	IYNSESDEWT	EGLPMLNARY	YHCAVTLGGC	VYALGGYRKG	APAEEAEFYD	PLKEKWIPIA
410	420	430	440	450	460	470	480
NMIKGVGNAT	ACVLHDVIYV	IGGHCGYRGS	CTYDKVQSYN	SDINEWSLIT	SSPHPEYGLC	SVPFENKLYL	VGGQTTITEC
490	500	510	520	530	540	550	560
YDPEQNEWRE	IAPMMERRME	CGAVIMNGCI	YVTGGYSYSK	GTYLQSIEKY	DPDLNKWEIV	GNLPSAMRSH	GCVCVYNV

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2946	1	859.1210	79.00	3	66.0	14.6	1	498-520	R.RMECGAVIMNGCIYVTGGYSYSK.G	Carbamidomethyl: 4; Oxidation: 2

Detailed Protein Report

Protein 741: PREDICTED: transcription factor MafG isoform X1 [Homo sapiens]

Accession:	gi|578832019	**Score:**	14.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.2
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	7.2
		No. of unique Peptides:	1



10	20	30	40	50	60	70	80
MRGQGGQEAA	QPSLGEAKGC	LLSESACSLC	PRVMTTPNKG	NKALKVKREP	GENGTSLTDE	ELVTMSVREL	NQHLRGLSKE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
EIVQLKQRRR	TLKNRGYAAS	CRVKRVTQKE	ELEKQKAELQ	QEVEKLASEN	ASMKLELDAL	RSKYEALQTF	ARTVARSPVA
170	**180**	**190**	**200**				
PARGPLAAGL	GPLVPGKVAA	TSVITIVKSK	TDARS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2135	1	719.8043	-32.98	2	55.3	14.5	0	19-32	K.GCLLSESACSLCPR.V	

Detailed Protein Report

Protein 742: 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_huma (refseq_human_20140103.fasta)	arylsulfatase F precursor [Homo sapiens]
gi|319996604	refseq_huma (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

Protein 743: 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

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
2754	1	557.9575	265.47	2	65.6	14.5	1	183-191	K.HPRFSTLTR.N	

Protein 744: neurogenic locus notch homolog protein 4 preproprotein [Homo sapiens]

Accession:	gi|55770876	**Score:**	14.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	209.5
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MQPPSLLLLL	LLLLLLCVSV	VRPRGLLCGS	FPEPCANGGT	CLSLSLGQGT	CQCAPGFLGE	TCQFPDPCQN	AQLCQNGGSC
90	100	110	120	130	140	150	160
QALLPAPLGL	PSSPSPLTPS	FLCTCLPGFT	GERCQAKLED	PCPPSFCSKR	GRCHIQASGR	PQCSCMPGWT	GEQCQLRDFC
170	180	190	200	210	220	230	240
SANPCVNGGV	CLATYPQIQC	HCPPGFEGHA	CERDVNECFQ	DPGPCPKGTS	CHNTLGSFQC	LCPVGQEGPR	CELRAGPCPP
250	260	270	280	290	300	310	320
RGCSNGGTCQ	LMPEKDSTFH	LCLCPPGFIG	PDCEVNPDNC	VSHQCQNGGT	CQDGLDTYTC	LCPETWTGWD	CSEDVDECET
330	340	350	360	370	380	390	400
QGPPHCRNGG	TCQNSAGSFH	CVCVSGWGGT	SCEENLDDCI	AATCAPGSTC	IDRVGSFSCL	CPPGRTGLLC	HLEDMCLSQP
410	420	430	440	450	460	470	480
CHGDAQCSTN	PLTGSTLCLC	QPGYSGPTCH	QDLDECLMAQ	QGPSPCEHGG	SCLNTPGSFN	CLCPPGYTGS	RCEADHNECL
490	500	510	520	530	540	550	560
SQPCHPGSTC	LDLLATFHCL	CPPGLEGQLC	EVETNECASA	PCLNHADCHD	LLNGFQCICL	PGFSGTRCEE	DIDECRSSPC
570	580	590	600	610	620	630	640
ANGGQCQDQP	GAFHCKCLPG	FEGPRCQTEV	DECLSDPCPV	GASCLDLPGA	FFCLCPSGFT	GQLCEVPLCA	PNLCQPKQIC
650	660	670	680	690	700	710	720
KDQKDKANCL	CPDGSPGCAP	PEDNCTCHHG	HCQRSSCVCD	VGWTGPECEA	ELGGCISAPC	AHGGTCYPQP	SGYNCTCPTG
730	740	750	760	770	780	790	800
YTGPTCSEEM	TACHSGPCLN	GGSCNPSPGG	YYCTCPPSHT	GPQCQTSTDY	CVSAPCFNGG	TCVNRPGTFS	CLCAMGFQGP
810	820	830	840	850	860	870	880
RCEGKLRPSC	ADSPCRNRAT	CQDSPQGPRC	LCPTGYTGGS	CQTLMDLCAQ	KPCPRNSHCL	QTGPSFHCLC	LQGWTGPLCN
890	900	910	920	930	940	950	960
LPLSSCQKAA	LSQGIDVSSL	CHNGGLCVDS	GPSYFCHCPP	GFQGSLCQDH	VNPCESRPCQ	NGATCMAQPS	GYLCQCAPGY
970	980	990	1000	1010	1020	1030	1040
DGQNCSKELD	ACQSQPCHNH	GTCTPKPGGF	HCACPPGFVG	LRCEGDVDEC	LDQPCHPTGT	AACHSLANAF	YCQCLPGHTG
1050	1060	1070	1080	1090	1100	1110	1120
QWCEVEIDPC	HSQPCFHGGT	CEATAGSPLG	FICHCPKGFE	GPTCSHRAPS	CGFHHCHHGG	LCLPSPKPGF	PPRCACLSGY
1130	1140	1150	1160	1170	1180	1190	1200
GGPDCLTPPA	PKGCGPPSPC	LYNGSCSETT	GLGGPGFRCS	CPHSSPGPRC	QKPGAKGCEG	RSGDGACDAG	CSGPGGNWDG
1210	1220	1230	1240	1250	1260	1270	1280
GDCSLGVPDP	WKGCPSHSRC	WLLFRDGQCH	PQCDSEECLF	DGYDCETPPA	CTPAYDQYCH	DHFHNGHCEK	GCNTAECGWD
1290	1300	1310	1320	1330	1340	1350	1360
GGDCRPEDGD	PEWGPSLALL	VVLSPPALDQ	QLFALARVLS	LTLRVGLWVR	KDRDGRDMVY	PYPGARAEEK	LGGTRDPTYQ
1370	1380	1390	1400	1410	1420	1430	1440
ERAAPQTQPL	GKETDSLSAG	FVVVMGVDLS	RCGPDHPASR	CPWDPGLLLR	FLAAMAAVGA	LEPLLPGPLL	AVHPHAGTAP
1450	1460	1470	1480	1490	1500	1510	1520
PANQLPWPVL	CSPVAGVILL	ALGALLVLQL	IRRRRREHGA	LWLPPGFTRR	PRTQSAPHRR	RPPLGEDSIG	LKALKPKAEV
1530	1540	1550	1560	1570	1580	1590	1600
DEDGVVMCSG	PEEGEEVGQA	EETGPPSTCQ	LWSLSGGCGA	LPQAAMLTPP	QESEMEAPDL	DTRGPDGVTP	LMSAVCCGEV
1610	1620	1630	1640	1650	1660	1670	1680
QSGTFQGAWL	GCPEPWEPLL	DGGACPQAHT	VGTGETPLHL	AARFSRPTAA	RRLLEAGANP	NQPDRAGRTP	LHAAVAADAR
1690	1700	1710	1720	1730	1740	1750	1760
EVCQLLLRSR	QTAVDARTED	GTTPLMLAAR	LAVEDLVEEL	IAAQADVGAR	DKWGKTALHW	AAAVNNARAA	RSLLQAGADK
1770	1780	1790	1800	1810	1820	1830	1840
DAQDNREQTP	LFLAAREGAV	EVAQLLLGLG	AARELRDQAG	LAPADVAHQR	NHWDLLTLLE	GAGPPEARHK	ATPGREAGPF
1850	1860	1870	1880	1890	1900	1910	1920
PRARTVSVSV	PPHGGGALPR	CRTLSAGAGP	RGGGACLQAR	TWSVDLAARG	GGAYSHCRSL	SGVGAGGGPT	PRGRRFSAGM
1930	1940	1950	1960	1970	1980	1990	2000
RGPRPNPAIM	RGRYGVAAGR	GGRVSTDDWP	CDWVALGACG	SASNIPIPPP	CLTPSPERGS	PQLDCGPPAL	QEMPINQGGE
2010							
GKK							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1028	1	974.6819	-25.27	3	41.4	14.5	0	647-674	K.ANCLCPDGSPGCAPPEDNCTCHHGHCQR.S	

Detailed Protein Report

Protein 745: NHL repeat-containing protein 2 [Homo sapiens]

Accession:	gi|42476013	**Score:**	14.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.4
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.51 **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		QD:QU 0.51

Detailed Protein Report

Protein 746: 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; Oxidation: 12

Detailed Protein Report

Protein 747: PREDICTED: rab-3A-interacting protein isoform X3 [Homo sapiens]

Accession:	gi|578823282	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.2
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MTFSNALAVA GMMGSGFYRI PPLPSPATHT HVVRCIWPRS LRLSYDEAFA MANDPLEGFH EVNLASPTSP DLLGVYESGT
        90        100        110        120        130        140        150        160
QEQTTSPSVI YRPHPSALSS VPIQANALDV SELPTQPVYS SPRRLNCAEI SSISFHVTDP APCSTSGVTA GLTKLTTRKD
       170        180        190        200        210        220        230        240
NYNAEREFLQ GATITEACDG SDDIFGLSTD SLSRLRSPSV LEVREKGYER LKEELAKAQR ELKLKDEECE RLSKVRDQLG
       250        260        270        280        290        300        310        320
QELEELTASL FEEAHKMVRE ANIKQATAEK QLKEAQGKID VLQAEVAALK TLVLSSSPTS PTQEPLPGGK TPFKKGHTRN
       330        340        350        360        370        380        390
KSTSSAMSGS HQDLSVIQPI VKDCKEKPSF TLLNSSPSLI LKKCVCLLNF CMEARSLLNG ITNVNLF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1716	1	637.9569	-8.71	3	50.0	14.4	0	2-19	M.TFSNALAVAGMMGSGFYR.I	Oxidation: 11, 12

Protein 748: F-box only protein 31 isoform 1 [Homo sapiens]

Accession:	gi|83035136	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.6
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.9
		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
2660	1	974.0954	106.87	2	62.0	14.4	0	44-64	R.IEASAGVGGGLCAGPSPPPPR.C	Carbamidomethyl: 12

Detailed Protein Report

Protein 749: 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 750: spliceosome RNA helicase DDX39B [Homo sapiens]

Accession:	gi|4758112	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.0
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|18375623	refseq_human(refseq_human_20140103.fasta)	spliceosome RNA helicase DDX39B [Homo sapiens]

10	20	30	40	50	60	70	80
MAENDVDNEL	LDYEDDEVET	AAGGDGAEAP	AKKDVKGSYV	SIHSSGFRDF	LLKPELLRAI	VDCGFEHPSE	VQHECIPQAI
90	100	110	120	130	140	150	160
LGMDVLCQAK	SGMGKTAVFV	LATLQQLEPV	TGQVSVLVMC	HTRELAFQIS	KEYERFSKYM	PNVKVAVFFG	GLSIKKDEEV
170	180	190	200	210	220	230	240
LKKNCPHIVV	GTPGRILALA	RNKSLNLKHI	KHFILDECDK	MLEQLDMRRD	VQEIFRMTPH	EKQVMMFSAT	LSKEIRPVCR
250	260	270	280	290	300	310	320
KFMQDPMEIF	VDDETKLTLH	GLQQYYVKLK	DNEKNRKLFD	LLDVLEFNQV	VIFVKSVQRC	IALAQLLVEQ	NFPAIAIHRG
330	340	350	360	370	380	390	400
MPQEERLSRY	QQFKDFQRRI	LVATNLFGRG	MDIERVNIAF	NYDMPEDSDT	YLHRVARAGR	FGTKGLAITF	VSDENDAKIL
410	420	430					
NDVQDRFEVN	ISELPDEIDI	SSYIEQTR					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
39	1	625.3631	57.54	2	29.2	14.4	0	164-175	K.NCPHIVVGTPGR.I	

Detailed Protein Report

Protein 751: vacuolar protein sorting-associated protein 13B isoform 1 [Homo sapiens]

Accession:	gi|35493701	**Score:**	14.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	445.7
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.4
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 2.19 **CV:** 0.00 % **No. of Peptides:** 1

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	DHYRSRPGEG	WQSGHFEGVF	LQCKEKSVTT	TKLLDGTHQQ	HGFLSLTYTK	AVTKNVRHKL
1450	1460	1470	1480	1490	1500	1510	1520
TSRNERRSFH	KLSEGLMDGS	PHFLHEILLS	AQAFDIVLYF	PLLNAIASIF	QAKLPKTQKE	KRKSPGQPMR	THTLTSRNLP
1530	1540	1550	1560	1570	1580	1590	1600
LIYVNTSVIR	IFIPKTEEMQ	PTVEANQAAK	EDTVVLKIGS	VAMAPQADNP	LGRSVLRKDI	YQRALNLGIL	RDPGSEIEDR
1610	1620	1630	1640	1650	1660	1670	1680
QYQIDLQSIN	IGTAQWHQLK	PEKESVSGGV	VTETERNSQN	PALEWNMASS	IRRHQERRAI	LTPVLTDFSV	RITGAPAVIF
1690	1700	1710	1720	1730	1740	1750	1760
TKVVSPENLH	TEEILVCGHS	LEVNITTNLD	FFLSVAQVQL	LHQLIVANMT	GLEPSNKAAE	ISKQEQKKVD	IFDGGMAETS
1770	1780	1790	1800	1810	1820	1830	1840
SRYSGAQDSG	IGSDSVKIRI	VQIEQHSGAS	QHRIARPSRQ	SSIVKNLNFI	PFDIFITASR	ISLMTYSCMA	LSKSKSQEQK
1850	1860	1870	1880	1890	1900	1910	1920
NNEKTDKSSL	NLPEVDSDVA	KPNQACISTV	TAEDLLRSSI	SFPSGKKIGV	LSLESLHAST	RSSARQALGI	TIVRQPGRRG
1930	1940	1950	1960	1970	1980	1990	2000
TGDLQLEPFL	YFIVSQPSLL	LSCHHRKQRV	EVSIFDAVLK	GVASDYKCID	PGKTLPEALD	YCTVWLQTVP	GEIDSKSGIP
2010	2020	2030	2040	2050	2060	2070	2080
PSFITLQIKD	FLNGPADVNL	DISKPLKANL	SFTKLDQINL	FLKKIKNAHS	LAHSEETSAM	SNTMVNKDDL	PVSKYYRGKL
2090	2100	2110	2120	2130	2140	2150	2160
SKPKIHGDGV	QKISAQENMW	RAVSCFQKIS	VQTTQIVISM	ETVPHTSKPC	LLASLSNLNG	SLSVKATQKV	PGIILGSSFL
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
1639	1	911.3413	-106.88	2	50.8	14.4	1	2193-2208	K.WCKHSGNPGPEQSIPK.I	Carbamidomethyl: 2	QD:QU 2.19

Detailed Protein Report

Protein 752: protein FAM83G [Homo sapiens]

Accession:	gi|115392150	**Score:**	14.4
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

QD:QU **Median:** 0.45 **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
620	2	492.6384	-237.57	2	36.3	14.4	0	44-51	R.DAFYEVLK.R		QD:QU 0.45

Detailed Protein Report

Protein 753: PREDICTED: dipeptidyl peptidase 9 isoform X2 [Homo sapiens]

Accession: gi|530425489
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 14.4
MW [kDa]: 91.8
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 754: **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 755: 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 756: PREDICTED: inhibitor of Bruton tyrosine kinase isoform X3 [Homo sapiens]

Accession:	gi|578812678	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	148.9
Database Date:	2015-11-30	**pI:**	8.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSPMPDCTS	KCRSLKHALD	VLSVVTKGSE	NQIKAFLSSH	CYNAATIKDV	FGRNALHLVS	SCGKKGVLDW	LIQKGVDLLV
90	100	110	120	130	140	150	160
KDKESGWTAL	HRSIFYGHID	CVWSLLKHGV	SLYIQDKEGL	SALDLVMKDR	PTHVVFKNTD	PTDVYTWGDN	TNFTLGHGSQ
170	180	190	200	210	220	230	240
NSKHHPELVD	LFSRSGIYIK	QVVLCKFHSV	FLSQKGQVYT	CGHGPGGRLG	HGDEQTCLVP	RLVEGLNGHN	CSQVAAAKDH
250	260	270	280	290	300	310	320
TVVLTEDGCV	YTFGLNIFHQ	LGIIPPPSSC	NVPRQIQAKY	LKGRTIIGVA	AGRFHTVLWT	REAVYTMGLN	GGQLGCLLDP
330	340	350	360	370	380	390	400
NGEKCVTAPR	QVSALHHKDI	ALSLVAASDG	ATVCVTTRGD	IYLLADYQCK	KMASKQLNLK	KVLVSGGHME	YKVDPEHLKE
410	420	430	440	450	460	470	480
NGGQKICILA	MDGAGRVFCW	RSVNSSLKQC	RWAYPRQVFI	SDIALNRNEI	LFVTQDGEGF	RGRWFEEKRK	SSEKKEILSN
490	500	510	520	530	540	550	560
LHNSSSDVSY	VSDINSVYER	IRLEKLTFAH	RAVSVSTDPS	GCNFAILQSD	PKTSLYEIPA	VSSSSFFEEF	GKLLREADEM
570	580	590	600	610	620	630	640
DSIHDVTFQV	GNRLFPAHKY	ILAVHSDFFQ	KLFLSDGNTS	EFTDIYQKDE	DSAGCHLFVV	EKVHPDMFEY	LLQFIYTDTC
650	660	670	680	690	700	710	720
DFLTHGFKPR	IHLNKNPEEY	QGTLNSHLNK	VNFHEDDNQK	SAFEVYKSNQ	AQTVSERQKS	KPKSCKKGKN	IREDDPVRML
730	740	750	760	770	780	790	800
QTVAKKFDFS	NLSSRLDGVR	FENEKINVIA	KNTGNKLKLS	QKKCSFLCDV	TMKSVDGKEF	PCHKCVLCAR	LEYFHSMLSS
810	820	830	840	850	860	870	880
SWIEASSCAA	LEMPIHSDIL	KVILDYLYTD	EAVVIKESQN	VDFICSVLVV	ADQLLITRLK	EICEVALTEK	LTLKNAAMLL
890	900	910	920	930	940	950	960
EFAAMYSAKQ	LKLSCLQFIG	LNMAALLEAR	SLDVLSDGVL	KDLSEFYRKM	IPAMDRRVIT	PYQDGPDISY	LEVEDGDIFL
970	980	990	1000	1010	1020	1030	1040
KEEINMEQNH	SETMFKKAKT	KAKKKPRKRS	DSSGGYNLSD	IIQSPSSTEL	LTSDSEGSYA	GVGSPRDLQS	PDFTTGFHSD
1050	1060	1070	1080	1090	1100	1110	1120
KIEAKVKPYV	NGTSPVYSRE	DLKPWEKSPI	LKISAPQPIP	SNRIDTTSSA	SWVAGSFSPV	SPPVVDLRTI	MEIEESRQKC
1130	1140	1150	1160	1170	1180	1190	1200
GATPKSHLGK	TVSHGVKLSQ	KQRKMIALTT	KENNSGMNSM	ETVLFTPSKA	PKPVNAWASS	LHSVSSKSFR	DFLLEEKKSV
1210	1220	1230	1240	1250	1260	1270	1280
TSHSSGDHVK	KVSFKGIENS	QAPKIVRCST	HGTPGPEGNH	ISDLPLLDSP	NPWLSSSVTA	PSMVAPVTFA	SIVEEELQQE
1290	1300	1310	1320	1330	1340		
AALIRSREKP	LALIQIEEHA	IQDLLVFYEA	FGNPEEFVIV	ERTPQGPLAV	PMWNKHGC		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1342	1	388.0955	-190.68	3	45.3	14.3	0	764-773	K.CSFLCDVTMK.S	Oxidation: 9

Detailed Protein Report

Protein 757: 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 758: **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 759: **PREDICTED: arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 3 isoform X4 [Homo sapiens]**

Accession:	gi|530380661	**Score:**	14.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.8
Database Date:	2015-11-30	**pI:**	6.8
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAPQDLDIA	VWLATVHLEQ	YADTFRRHGL	ATAGAARGLG	HEELKQLGIS	ATGHRKRILR	LLQTGTEEGS	LDPKSDSAME
90	100	110	120	130	140	150	160
PSPSPAPQAQ	PPKPVPKPRT	VFGGLSGPAT	TQRPGLSPAL	GGPGVSRSPE	PSPRPPPLPT	SSSEQSSALN	TVEMMPNSIY
170	180	190	200	210	220	230	240
FGLDSRGRAQ	AAQDKAPDSS	QISAPTPALR	PTTGTVHIMD	PGCLYYGVQP	VGTPGAPDRR	ESRGVCQGRA	EHRLSRQDLE
250	260	270	280	290	300	310	320
AREDAGYASL	ELPGDSTLLS	PTLETEETSD	DLISPYASFS	FTADRLTPLL	SGWLDKLSPQ	GNYVFQRRFV	QFNGRSLMYF
330	340	350	360	370	380	390	400
GSDKDPFPKG	VIPLTAIEMT	RSSKDNKFQV	ITGQRVFVFR	TESEAQRDMW	CSTLQSCLKE	QRLLGHPRPP	QPPRPLRTGM
410	420	430	440	450	460	470	480
LELRGHKAKV	FAALSPGELA	LYKSEQAFSL	GIGICFIELQ	GCSVRETKSR	SFDLLTPHRC	FSFTAESGGA	RQSWAAALQE
490	500	510	520	530	540	550	560
AVTETLSDYE	VAEKIWSNRA	NRQCADCGSS	RPDWAAVNLG	VVICKQCAGQ	HRALGSGISK	VQSLKLDTSV	WSNEIVQLFI
570	580	590	600	610	620	630	640
VLGNDRANRF	WAGTLPPGEG	LHPDATPGPR	GEFISRKYRL	GLFRKPHPQY	PDHSQLLQAL	CAAVARPNLL	KNMTQLLCVE
650	660	670	680	690	700	710	720
AFEGEEPWFP	PAPDGSCPGL	LPSDPSPGVY	NEVVVRATYS	GFLYCSPVSN	KAGPSPPRRG	RDAPPRLWCV	LGAALEMFAS
730	740	750	760	770	780	790	800
ENSPEPLSLI	QPQDIVCLGV	SPPPTDPGDR	FPFSFELILA	GGRIQHFGTD	GADSLEAWTS	AVGKWFSPLS	CHQLLGPGLL
810	820	830	840	850	860	870	880
RLGRLWLRSP	SHTAPAPGLW	LSGFGLLRGD	HLFLCSAPGP	GPPAPEDMVH	LRRLQEISVV	SAADTPDKKE	HLVLVETGRT
890	900	910	920	930	940		
LYLQGEGRLD	FTAWNAAIGG	AAGGGGTGLQ	EQQMSRGDIP	IIVDACISFV	TQHG		

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	854-869	R.LQEISVVSAADTPDKK.E	

Detailed Protein Report

Protein 760: **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

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
1967	3	665.2921	-47.52	2	55.0	14.3	0	1151- 1162	R.STPRPPCPSTMR.-	

Detailed Protein Report

Protein 761: visinin-like protein 1 [Homo sapiens]

Accession:	gi|21361559	**Score:**	14.3
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

QD:QU **Median:** 1.14 **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
1504	3	816.2780	-135.09	2	49.0	14.3	1	140-153	K.MNEDGLTPEQRVDK.I		QD:QU 1.14

Detailed Protein Report

Protein 762: 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 763: nuclear receptor coactivator 3 isoform d [Homo sapiens]

Accession:	gi|291490685	**Score:**	14.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	154.3
Database Date:	2015-11-30	**pI:**	7.0
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.82 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MSGLGENLDP	LASDSRKRKL	PCDTPGQGLT	CSGEKRRREQ	ESKYIEELAE	LISANLSDID	NFNVKPDKCA	ILKETVRQIR
90	100	110	120	130	140	150	160
QIKEQGKTIS	NDDDVQKADV	SSTGQGVIDK	DSLGPLLLQA	LDGFLFVVNR	DGNIVFVSEN	VTQYLQYKQE	DLVNTSVYNI
170	180	190	200	210	220	230	240
LHEEDRKDFL	KNLPKSTVNG	VSWTNETQRQ	KSHTFNCRML	MKTPHDILED	INASPEMRQR	YETMQCFALS	QPRAMMEEGE
250	260	270	280	290	300	310	320
DLQSCMICVA	RRITTGERTF	PSNPESFITR	HDLSGKVVNI	DTNSLRSSMR	PGFEDIIRRC	IQRFFSLNDG	QSWSQKRHYQ
330	340	350	360	370	380	390	400
EVTSDGIFSP	TAYLNGHAET	PVYRFSLADG	TIVTAQTKSK	LFRNPVTNDR	HGFVSTHFLQ	REQNGYRPNP	NPVGQGIRPP
410	420	430	440	450	460	470	480
MAGCNSSVGG	MSMSPNQGLQ	MPSSRAYGLA	DPSTTGQMSG	ARYGGSSNIA	SLTPGPGMQS	PSSYQNNNYG	LNMSSPPHGS
490	500	510	520	530	540	550	560
PGLAPNQQNI	MISPRNRGSP	KIASHQFSPV	AGVHSPMASS	GNTGNHSFSS	SSLSALQAIS	EGVGTSLLST	LSSPGPKLDN
570	580	590	600	610	620	630	640
SPNMNITQPS	KVSNQDSKSP	LGFYCDQNPV	ESSMCQSNSR	DHLSDKESKE	SSVEGAENQR	GPLESKGHKK	LLQLLTCSSD
650	660	670	680	690	700	710	720
DRGHSSLTNS	PLDSSCKESS	VSVTSPSGVS	SSTSGGVSST	SNMHGSLLQE	KHRILHKLLQ	NGNSPAEVAK	ITAEATGKDT
730	740	750	760	770	780	790	800
SSITSCGDGN	VVKQEQLSPK	KKENNALLRY	LLDRDDPSDA	LSKELQPQVE	GVDNKMSQCT	SSTIPSSSQE	KDPKIKTETS
810	820	830	840	850	860	870	880
EEGSGDLDNL	DAILGDLTSS	DFYNNSISSN	GSHLGTKQQV	FQGTNSLGLK	SSQSVQSIRP	PYNRAVSLDS	PVSVGSSPPV
890	900	910	920	930	940	950	960
KNISAFPMLP	KQPMLGGNPR	MMDSQENYGS	SMGDWGLPNS	KAGRMEPMNS	NSMGRPGGDY	NTSLPRPALG	GSIPTLPLRS
970	980	990	1000	1010	1020	1030	1040
NSIPGARPVL	QQQQQMLQMR	PGEIPMGMGA	NPYGQAAASN	QLGSWPDGML	SMEQVSHGTQ	NRPLLRNSLD	DLVGPPSNLE
1050	1060	1070	1080	1090	1100	1110	1120
GQSDERALLD	QLHTLLSNTD	ATGLEEIDRA	LGIPELVNQG	QALEPKQDAF	QGQEAAVMMD	QKAGLYGQTY	PAQGPPMQGG
1130	1140	1150	1160	1170	1180	1190	1200
FHLQGQSPSF	NSMMNQMNQQ	GNFPLQGMHP	RANIMRPRTN	TPKQLRMQLQ	QRLQGQQFLN	QSRQALELKM	ENPTAGGAAV
1210	1220	1230	1240	1250	1260	1270	1280
MRPMMQPQQG	FLNAQMVAQR	SRELLSHHFR	QQRVAMMMQQ	QQQQQQQQQQ	QQQQQQQQQQ	QQQQQQQTQA	FSPPPNVTAS
1290	1300	1310	1320	1330	1340	1350	1360
PSMDGLLAGP	TMPQAPPQQF	PYQPNYGMGQ	QPDPAFGRVS	SPPNAMMSSR	MGPSQNPMMQ	HPQAASIYQS	SEMKGWPSGN
1370	1380	1390	1400	1410	1420		
LARNSSFSQQ	QFAHQGNPAV	YSMVHMNGSS	GHMGQMNMNP	MPMSGMPMGP	DQKYC		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
544	1	630.6481	4.75	3	35.4	14.2	2	18-35	K.RKLPCDTPGQGLTCSGEK.R		QD:QU 0.82

Detailed Protein Report

Protein 764: telomerase-binding protein EST1A isoform 3 [Homo sapiens]

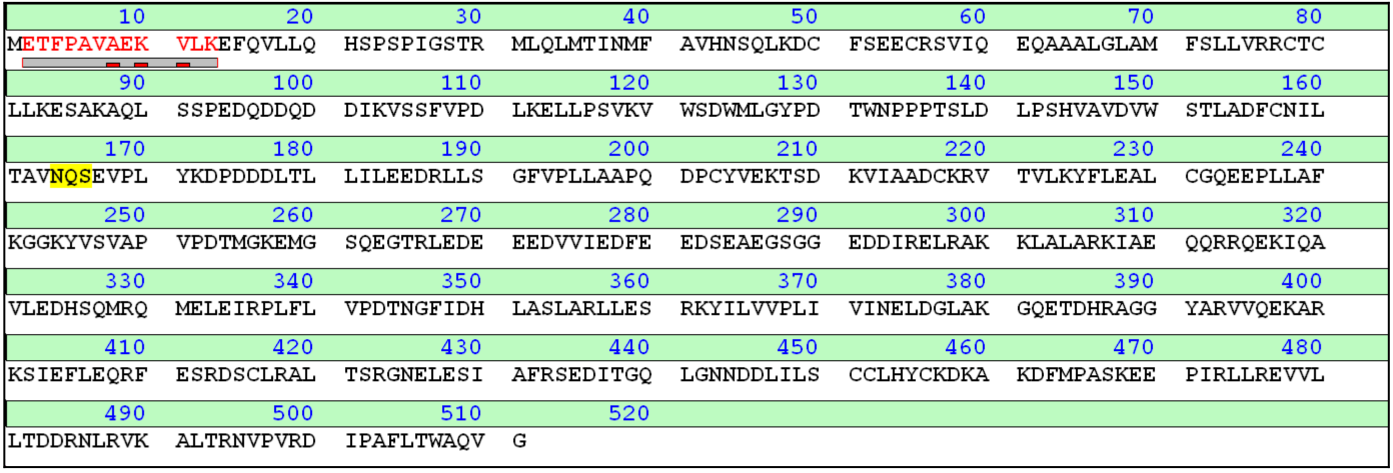
Accession:	gi|378744171	**Score:**	14.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.4
Database Date:	2015-11-30	**pI:**	4.6
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:** 0.70	**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				

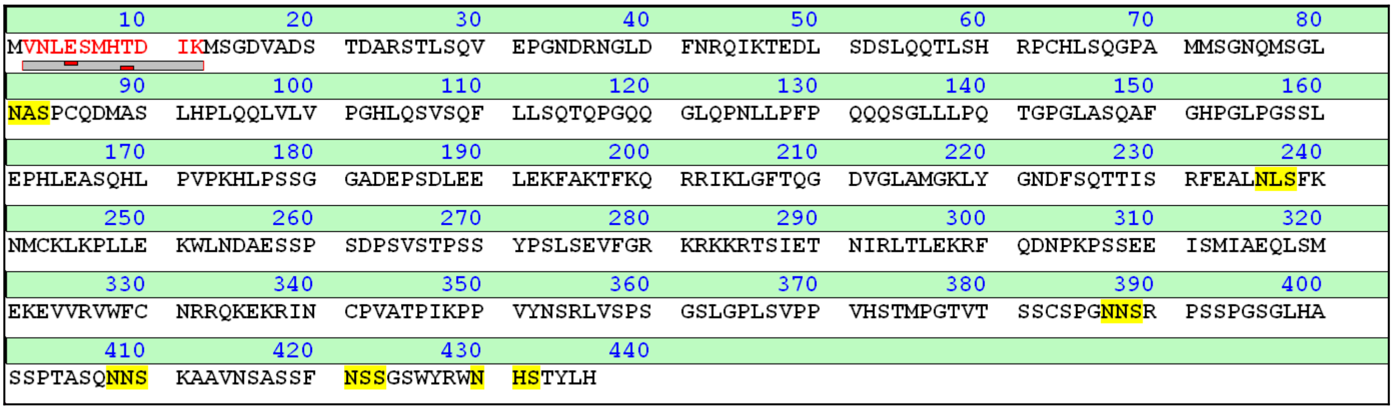
Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2172	1	666.3077	-111.59	2	57.5	14.2	1	2-13	M.ETFPAVAEKVLK.E		QD:QU 0.70

BRUKER

Detailed Protein Report

Protein 765: 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



```
        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
465	1	643.8361	18.68	2	35.8	14.1	0	2-12	M.VNLESMHTDIK.M	

Detailed Protein Report

Protein 766: growth arrest-specific protein 7 isoform a [Homo sapiens]

Accession:	gi|41406076	**Score:**	14.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.2
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	5.1
		No. of unique Peptides:	1

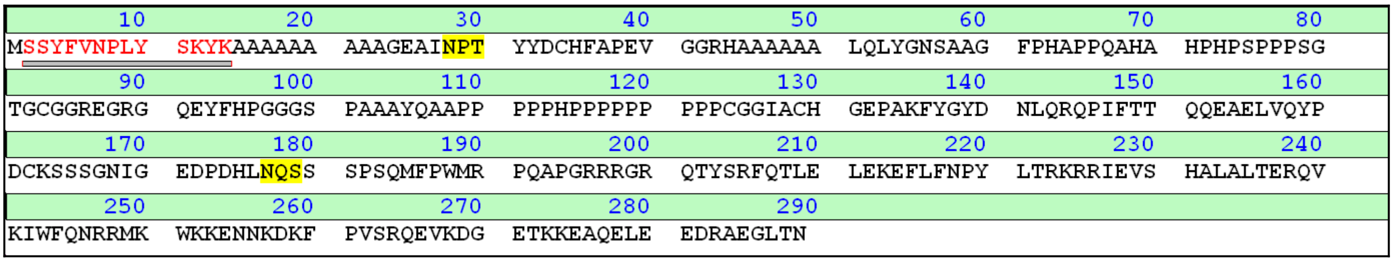
```
        10          20          30          40          50          60          70          80
MSNMENSFDD  VSCLSPQNLG  SSSPSKKQSK  ENTITINCVT  FPHPDTMPEQ  QLLKPTEWSY  CDYFWADKKD  PQGNGTVAGF
        90         100         110         120         130         140         150         160
ELLLQKQLKG  KQMQKEMSEF  IRERIKIEED  YAKNLAKLSQ  NSLASQEEGS  LGEAWAQVKK  SLADEAEVHL  KFSAKLHSEV
       170         180         190         200         210         220         230         240
EKPLMNFREN  FKKDMKKCDH  HIADLRKQLA  SRYASVEKAR  KALTERQRDL  EMKTQQLEIK  LSNKTEEDIK  KARRKSTQAG
       250         260         270         280         290         300         310         320
DDLMRCVDLY  NQAQSKWFEE  MVTTTLELER  LEVERVEMIR  QHLCQYTQLR  HETDMFNQST  VEPVDQLLRK  VDPAKDRELW
       330         340
VREHKTGNIR  PVDMEI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2697	1	596.2791	-61.86	3	62.6	14.1	0	70-86	K.DPQGNGTVAGFELLLQK.Q	

Detailed Protein Report

Protein 767: 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 768: 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

QD:QU **Median:** 0.77 **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		QD:QU 0.77

Detailed Protein Report

Protein 769: PREDICTED: RING finger protein 32 isoform X5 [Homo sapiens]

Accession:	gi|578813915	**Score:**	14.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.1
Database Date:	2015-11-30	**pI:**	10.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.5
		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 770: conserved oligomeric Golgi complex subunit 2 isoform 2 [Homo sapiens]

Accession:	gi|223029519	**Score:**	14.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.1
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEKSRMNLPK	GPDTLCFDKD	EFMKEDFDVD	HFVSDCRKRV	QLEELRDDLE	LYYKLLKTAM	VELINKDYAD	FVNLSTNLVG
90	100	110	120	130	140	150	160
MDKALNQLSV	PLGQLREEVL	SLRSSVSEGI	RAVDERMSKQ	EDIRKKKMCV	LRLIQVIRSV	EKIEKILNSQ	SSKETSALEA
170	180	190	200	210	220	230	240
SSPLLTGQIL	ERIATEFNQL	QFHAVQSKGM	PLLDKVRPRI	AGITAMLQQS	LEGLLLEGLQ	TSDVDIIRHC	LRTYATIDKT
250	260	270	280	290	300	310	320
RDAEALVGQV	LVKPYIDEVI	IEQFVESHPN	GLQVMYNKLL	EFVPHHCRLL	REVTGGAISS	EKGNTVPGYD	FLVNSVWPQI
330	340	350	360	370	380	390	400
VQGLEEKLPS	LFNPGNPDAF	HEKYTISMDF	VRRLERQCGS	QASVKRLRAH	PAYHSFNKKW	NLPVYFQIRF	REIAGSLEAA
410	420	430	440	450	460	470	480
LTDVLEDAPA	ESPYCLLASH	RTWSSLRRCW	SDEMFLPLLV	HRLWRLTLQI	LARYSVFVNE	LSLRPISNES	PKEIKKPLVT
490	500	510	520	530	540	550	560
GSKEPSITQG	NTEDQGSGPS	ETKPVVSISR	TQLVYVVADL	DKLQEQLPEL	LEIIKPKLEM	IGFKNFSSIS	ALEDSQSSFS
570	580	590	600	610	620	630	640
ACVPSLSSKI	IQDLSDSCFG	FLKSALEVPR	LYRRTNKEVP	TTASSYVDSA	LKPLFQLQSG	HKDKLKQAII	QQWLEGTLSE
650	660	670	680	690	700	710	720
STHKYYETVS	DVLNSVKKME	ESLKRLKQAR	KTTPANPVGP	SGGMSDDDKI	RLQLALDVEY	LGEQIQKLGL	QASDIKSFSA
730	740						
LAELVAAAKD	QATAEQP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
103	1	672.4409	120.25	3	30.0	14.1	0	154-172	K.ETSALEASSPLLTGQILER.I	

Detailed Protein Report

Protein 771: 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

Quantitation

QD:QU **Median:** 1.57 **CV:** 0.00 % **No. of 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	Ratios
826	1	737.3742	-17.03	3	40.3	14.0	2	47-67	R. DTARTLLPRGGEGSPACARPK.A	Carbamidomethyl: 17	QD:QU 1.57

Detailed Protein Report

Protein 772: calponin-3 isoform 2 [Homo sapiens]

Accession: gi|554506520
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 14.0
MW [kDa]: 31.4
pI: 6.1
Sequence Coverage [%]: 4.9
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

Protein 773: **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

Quantitation

QD:QU **Median:** 0.82 **CV:** 0.00 % **No. of 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	Ratios	
513	1	746.2002	-160.22	2	36.4	13.9	0	149-162	R.TPATCCHCAAVMAR.S	Carbamidomethyl: 6	QD:QU	0.82

Detailed Protein Report

Protein 774: serine/threonine-protein kinase SBK1 [Homo sapiens]

Accession:	gi|66773086	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.2
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
MSVGCPEPEP	PRSLTCCGPG	TAPGPGAGVP	LLTEDMQALT	LRTLAASDVT	KHYELVRELG	KGTYGKVDLV	VYKGTGTKMA
90	100	110	120	130	140	150	160
LKFVNKSKTK	LKNFLREVSI	TNSLSSSPFI	IKVFDVVFET	EDCYVFAQEY	APAGDLFDII	PPQVGLPEDT	VKRCVQQLGL
170	180	190	200	210	220	230	240
ALDFMHGRQL	VHRDIKPENV	LLFDRECRRV	KLADFGMTRR	VGCRVKRVSG	TIPYTAPEVC	QAGRADGLAV	DTGVDVWAFG
250	260	270	280	290	300	310	320
VLIFCVLTGN	FPWEAASGAD	AFFEEFVRWQ	RGRLPGLPSQ	WRRFTEPALR	MFQRLLALEP	ERRGPAKEVF	RFLKHELTSE
330	340	350	360	370	380	390	400
LRRRPSHRAR	KPPGDRPPAA	GPLRLEAPGP	LKRTVLTESG	SGSRPAPPAV	GSVPLPVPVP	VPVPVPVPVP	EPGLAPQGPP
410	420	430					
GRTDGRADKS	KGQVVLATAI	EICV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2934	1	952.9576	-29.79	2	65.8	13.9	1	207-224	K.RVSGTIPYTAPEVCQAGR.A	

Detailed Protein Report

Protein 775: 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	

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Detailed Protein Report

Protein 776: transmembrane and coiled-coil domain-containing protein 5A [Homo sapiens]

Accession:	gi|34303932	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.2
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530405403	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transmembrane and coiled-coil domain-containing protein 5A isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MEISRLAQSK	RNIISLNMDL	ERDTQRIDEA	NQKLLLKIQE	REDKIQRLES	EIIQTRGLVE	DEEWEKENRT	TMERERALQE
90	100	110	120	130	140	150	160
LEEETARLER	KNKTLVHSIT	ELQQKLTRKS	QKITNCEQSS	PDGALEETKV	KLQQLEASYA	CQEKELLKVM	KEYAFVTQLC
170	180	190	200	210	220	230	240
EDQALYIKKY	QETLKKIEEE	LEALFLEREV	SKLVSMNPVE	KEHTSQNNEG	TPTQKTARLF	SKKIFCCLFF	ITLFFIRLLS
250	260	270	280	290			
YMFFHVRFIN	PDLLVNVLPK	VLGRSTLWKL	RCFFFPSLTL	ETEDMLPH			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1410	1	978.1800	1.91	3	46.2	13.9	2	145-168	K.ELLKVMKEYAFVTQLCEDQALYIK.K	Carbamidomethyl: 16

Detailed Protein Report

Protein 777: 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

QD:QU **Median:** 0.65 **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	QD:QU	0.65

Detailed Protein Report

Protein 778: 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

QD:QU **Median:** 1.41 **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		QD:QU 1.41

Detailed Protein Report

Protein 779: **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 780: **PREDICTED: WD repeat-containing protein 62 isoform X1 [Homo sapiens]**

Accession:	gi|530416321	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	162.6
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAVGSGGYA	RNDAGEKLPS	VMAGVPARRG	QSSPPPAPPI	CLRRRTRLST	ASEETVQNRV	SLEKVLGITA	QNSSGLTCDP
90	100	110	120	130	140	150	160
GTGHVAYLAG	CVVVILDPKE	NKQQHIFNTA	RKSLSALAFS	PDGKYIVTGE	NGHRPAVRIW	DVEEKNQVAE	MLGHKYGVAC
170	180	190	200	210	220	230	240
VAFSPNMKHI	VSMGYQHDMV	LNVWDWKKDI	VVASNKVSCR	VIALSFSEDS	SYFVTVGNRH	VRFWFLEVST	ETKVTSTVPL
250	260	270	280	290	300	310	320
VGRSGILGEL	HNNIFCGVAC	GRGRMAGSTF	CVSYSGLLCQ	FNEKRVLEKW	INLKVSLSSC	LCVSQELIFC	GCTDGIVRIF
330	340	350	360	370	380	390	400
QAHSLHYLAN	LPKPHYLGVD	VAQGLEPSFL	FHRKAEAVYP	DTVALTFDPI	HQWLSCVYKD	HSIYIWDVKD	INRVGKVWSE
410	420	430	440	450	460	470	480
LFHSSYVWNV	EVYPEFEDQR	ACLPSGSFLT	CSSDNTIRFW	NLDSSPDSHW	QKNIFSNTLL	KVVYVENDIQ	HLQDMSHFPD
490	500	510	520	530	540	550	560
RGSENGTPMD	VKAGVRVMQV	SPDGQHLASG	DRSGNLRIHE	LHFMDELVKV	EAHDAEVLCL	EYSKPETGLT	LLASASRDRL
570	580	590	600	610	620	630	640
IHVLNVEKNY	NLEQTLDDHS	SSITAIKFAG	NRDIQMISCG	ADKSIYFRSA	QQGSDGLHFV	RTHHVAEKTT	LYDMDIDITQ
650	660	670	680	690	700	710	720
KYVAVACQDR	NVRVYNTVNG	KQKKCYKGSQ	GDEGSLLKVH	VDPSGTFLAT	SCSDKSISVI	DFYSGECIAK	MFGHSEIITS
730	740	750	760	770	780	790	800
MKFTYDCHHL	ITVSGDSCVF	IWHLGPEITN	CMKQHLLEID	HRQQQHTND	KKRSGHPRQD	TYVSTPSEIH	SLSPGEQTED
810	820	830	840	850	860	870	880
DLEEECEPEE	MLKTPSKDSL	DPDPRCLLTN	GKLPLWAKRL	LGDDDVADGL	AFHAKRSYQP	HGRWAERAGQ	EPLKTILDAQ
890	900	910	920	930	940	950	960
DLDCYFTPMK	PESLENSILD	SLEPQSLASL	LSESESPQEA	GRGHPSFLPQ	QKESSEASEL	ILYSLEAEVT	VTGTDSQYCR
970	980	990	1000	1010	1020	1030	1040
KEVEAGPGDQ	QGDSYLRVSS	DSPKDQSPPE	GCAGPTEDEL	SLPEGPSVPS	SSLPQTPEQE	KFLRHHFETL	TESPCRELFP
1050	1060	1070	1080	1090	1100	1110	1120
AALGDVEASE	AEDHFFNPRL	SISTQFLSSL	QKASRFTHTF	PPRATQCLVK	SPEVKLMDRG	GSQPRAGTGY	ASPDRTHVLA
1130	1140	1150	1160	1170	1180	1190	1200
AGKAEETLEA	WRPPPPCLTS	LASCVPASSV	LPTDRNLPTP	TSAPTPGLAQ	GVHAPSTCSY	MEATASSRAR	ISRSISLGDS
1210	1220	1230	1240	1250	1260	1270	1280
EGPIVATLAQ	PLRRPSSVGE	LASLGQELQA	ITTATTPSLD	SEGQEPALRS	WGNHEARANL	RLTLSSACDG	LLQPPVDTQP
1290	1300	1310	1320	1330	1340	1350	1360
GVTVPAVSFP	APSPVEESAL	RLHGSAFRPS	LPAPESPGLP	AHPSNPQLPE	ARPGIPGGTA	SLLEPTSGAL	GLLQGSPARW
1370	1380	1390	1400	1410	1420	1430	1440
SEPWVPVEAL	PPSPLELSRV	GNILHRLQTT	FQEALDLYRV	LVSSGQVDTG	QQQARTELVS	TFLWIHSQLE	AECLVGTSVA
1450	1460	1470	1480	1490			
PAQALPSPGP	PSPPTLYPLA	SPDLQALLEH	YSELLVQAVR	RKARGH			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2816	1	842.6820	-64.26	3	64.3	13.9	1	146-168	K.NQVAEMLGHKYGVACVAFSPNMK.H	Oxidation: 6, 22

Detailed Protein Report

Protein 781: putative hexokinase HKDC1 [Homo sapiens]

Accession:	gi|156151420	**Score:**	13.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	102.4
Database Date:	2015-11-30	**pI:**	7.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.7
		No. of unique 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
1075	1	947.1189	99.83	2	43.5	13.9	2	147-162	K.KLPLGLTFSFPCRQTK.L	Carbamidomethyl: 12

Detailed Protein Report

Protein 782: 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; Oxidation: 1

Detailed Protein Report

Protein 783: 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

Quantitation

QD:QU **Median:** 0.99 **CV:** 0.00 % **No. of 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	Ratios
413	3	435.7618	34.22	2	35.1	13.8	0	261-268	R.GPLMLSPR.I		QD:QU 0.99

Detailed Protein Report

Protein 784: 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

QD:QU **Median:** 0.78 **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	QD:QU 0.78

Detailed Protein Report

Protein 785: **PREDICTED: thyroid hormone receptor-associated protein 3 isoform X2 [Homo sapiens]**

Accession:	gi|530363679	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.7
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

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	

Detailed Protein Report

Protein 786: PREDICTED: RNA-binding protein 6-like [Homo sapiens]

Accession:	gi|578840146	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.4
Database Date:	2015-11-30	**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 787: **probable E3 ubiquitin-protein ligase HERC6 isoform 2 [Homo sapiens]**

Accession:	gi|259089405	**Score:**	13.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	111.0
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MYFCWGADSR	ELQRRRTAGS	PGAELLQAAS	GERHSLLLLT	NHRVLSCGDN	SRGQLGRRGA	QRGELPEPIQ	ALETLIVDLV
90	100	110	120	130	140	150	160
SCGKEHSLAV	CHKGRVFAWG	AGSEGQLGIG	EFKEISFTPK	KIMTLNDIKI	IQVSCGHYHS	LALSKDSQVF	SWGKNSHGQL
170	180	190	200	210	220	230	240
GLGKEFPSQA	SPQRVRSLEG	IPLAQVAAGG	AHSFALSLCG	TSFGWGSNSA	GQLALSGRNV	PVQSNKPLSV	GALKNLGVVY
250	260	270	280	290	300	310	320
ISCGDAHTAV	LTQDGKVFTF	GDNRSGQLGY	SPTPEKRGPQ	LVERIDGLVS	QIDCGSYHTL	AYVHTTGQVV	SFGHGPSDTS
330	340	350	360	370	380	390	400
KPTHPEALTE	NFDISCLISA	EDFVDVQVKH	IFAGTYANFV	TTHQDTSSTR	APGKTLPEIS	RISQSMAEKW	IAVKRRSTEH
410	420	430	440	450	460	470	480
EMAKSEIRMI	FSSPACLTAS	FLKKRGTGET	TSIDVDLEMA	RDTFKKLTKK	EWISSMITTC	LEDDLLRALP	CHSPHQEALS
490	500	510	520	530	540	550	560
VFLLLPECPV	MHDSKNWKNL	VVPFAKAVCE	MSKQSLQVLK	KCWAFLQESS	LNPLIQMLKA	AIISQLLHQT	KTEQDHCNVK
570	580	590	600	610	620	630	640
ALLGMMKELH	KVNKANCRLP	ENTFNINELS	NLLNFYIDRG	RQLFRDNHLM	SEKKAYMLMH	ETILQKKDEF	PPSPRFILRV
650	660	670	680	690	700	710	720
RRSRLVKDAL	RQLSQAEATD	FCKVLVVEFI	NEICPESGGV	SSEFFHCMFE	EMTKPEYGMF	MYPEMGSCMW	FPAKPKPEKK
730	740	750	760	770	780	790	800
RYFLFGMLCG	LSLFNLNVAN	LPFPLALYKK	LLDQKPSLED	LKELSPRLGK	SLQEVLDDAA	DDIGDALCIR	FSIHWDQNDV
810	820	830	840	850	860	870	880
DLIPNGISIP	VDQTNKRDYV	SKYIDYIFNV	SVKAVYEEFQ	RGFYRVCEKE	ILRHFYPEEL	MTAIIGNTDY	DWKQFEQNSK
890	900	910	920	930	940	950	960
YEQGYQKSHP	TIQLFWKAFH	KLTLDEKKKF	LFFLTGRDRL	HARGIQKMEI	VFRCPETFSE	RDHPTSITCH	NILSLPKYST
970	980	990					
MERMEEALQV	AINNNRGFVS	PMLTQS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2078	1	882.8691	72.62	3	54.5	13.8	2	34-57	R.HSLLLLTNHRVLSCGDNSRGQLGR.R	

Detailed Protein Report

Protein 788: **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

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
1762	1	916.3154	-149.52	2	52.4	13.7	1	179-194	K.MIISAHPNLMSCNTRK.H	Oxidation: 10

Detailed Protein Report

Protein 789: 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

QD:QU **Median:** 1.54 **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		QD:QU 1.54

Detailed Protein Report

Protein 790: **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

Protein 791: E3 ubiquitin-protein ligase RAD18 [Homo sapiens]

Accession: gi|256818821
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 13.7
MW [kDa]: 56.2
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 792: PREDICTED: DNA polymerase beta isoform X5 [Homo sapiens]

Accession:	gi|530387847	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.8
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	5.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578815356	refseq_human (refseq_human_20140103.fasta)	PREDICTED: DNA polymerase beta isoform X7 [Homo sapiens]
gi|530387849	refseq_human (refseq_human_20140103.fasta)	PREDICTED: DNA polymerase beta isoform X6 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MLQMQDIVLN EVKKVDSEYI ATVCGSFRRG AESSGDMDVL LTHPSFTSES TKQPKLLHQV VEQLQKVHFI TDTLSKGETK
        90        100        110        120        130        140        150        160
FMGVCQLPSK NDEKEYPHRR IDIRLIPKDQ YYCGVLYFTG SDIFNKNMRA HALEKGFTIN EYTIRPLGVT GVAGEPLPVD
       170        180        190
SEKDIFDYIQ WKYREPKDRS E
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1505	2	555.1325	-261.58	2	47.3	13.7	0	81-90	K.FMGVCQLPSK.N	

Detailed Protein Report

Protein 793: elongation factor G, mitochondrial [Homo sapiens]

Accession:	gi|18390331	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.4
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
MRLLGAAAVA	ALGRGRAPAS	LGWQRKQVNW	KACRWSSSGV	IPNEKIRNIG	ISAHIDSGKT	TLTERVLYYT	GRIAKMHEVK
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
GKDGVGAVMD	SMELERQRGI	TIQSAATYTM	WKDVNINIID	TPGHVDFTIE	VERALRVLDG	AVLVLCAVGG	VQCQTMTVNR
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
QMKRYNVPFL	TFINKLDRMG	SNPARALQQM	RSKLNHNAAF	MQIPMGLEGN	FKGIVDLIEE	RAIYFDGDFG	QIVRYGEIPA
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
ELRAAATDHR	QELIECVANS	DEQLGEMFLE	EKIPSISDLK	LAIRRATLKR	SFTPVFLGSA	LKNKGVQPLL	DAVLEYLPNP
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
SEVQNYAILN	KEDDSKEKTK	ILMNSSRDNS	HPFVGLAFKL	EVGRFGQLTY	VRSYQGELKK	GDTIYNTRTR	KKVRLQRLAR
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
MHADMMEDVE	EVYAGDICAL	FGIDCASGDT	FTDKANSGLS	MESIHVPDPV	ISIAMKPSNK	NDLEKFSKGI	GRFTREDPTF
490	**500**	**510**	**520**	**530**	**540**	**550**	**560**
KVYFDTENKE	TVISGMGELH	LEIYAQRLER	EYGCPCITGK	PKVAFRETIT	APVPFDFTHK	KQSGGAGQYG	KVIGVLEPLD
570	**580**	**590**	**600**	**610**	**620**	**630**	**640**
PEDYTKLEFS	DETFGSNIPK	QFVPAVEKGF	LDACEKGPLS	GHKLSGLRFV	LQDGAHHMVD	SNEISFIRAG	EGALKQALAN
650	**660**	**670**	**680**	**690**	**700**	**710**	**720**
ATLCILEPIM	AVEVVAPNEF	QGQVIAGINR	RHGVITGQDG	VEDYFTLYAD	VPLNDMFGYS	TELRSCTEGK	GEYTMEYSRY
730	**740**	**750**	**760**				
QPCLPSTQED	VINKYLEATG	QLPVKKGKAK	N				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
64	1	750.8346	-57.46	2	30.7	13.7	0	222-234	R.AIYFDGDFGQIVR.Y	

Detailed Protein Report

Protein 794: **PREDICTED: protein NLRC5 isoform X13 [Homo sapiens]**

Accession:	gi|578829278	**Score:**	13.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	152.2
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.3
		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 795: 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

Protein 796: 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 797: ribosomal protein S6 kinase alpha-1 isoform b [Homo sapiens]

Accession:	gi|55743134	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.9
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEQDPKPPRL	RLWALIPWLP	RKQRPRISQT	SLPVPGPGSG	PQRDSDEGVL	KEISITHHVK	AGSEKADPSH	FELLKVLGQG
90	100	110	120	130	140	150	160
SFGKVFLVRK	VTRPDSGHLY	AMKVLKKATL	KVRDRVRTKM	ERDILADVNH	PFVVKLHYAF	QTEGKLYLIL	DFLRGGDLFT
170	180	190	200	210	220	230	240
RLSKEVMFTE	EDVKFYLAEL	ALGLDHLHSL	GIIYRDLKPE	NILLDEEGHI	KLTDFGLSKE	AIDHEKKAYS	FCGTVEYMAP
250	260	270	280	290	300	310	320
EVVNRQGHSH	SADWWSYGVL	MFEMLTGSLP	FQGKDRKETM	TLILKAKLGM	PQFLSTEAQS	LLRALFKRNP	ANRLGSGPDG
330	340	350	360	370	380	390	400
AEEIKRHVFY	STIDWNKLYR	REIKPPFKPA	VAQPDDTFYF	DTEFTSRTPK	DSPGIPPSAG	AHQLFRGFSF	VATGLMEDDG
410	420	430	440	450	460	470	480
KPRAPQAPLH	SVVQQLHGKN	LVFSDGYVVK	ETIGVGSYSE	CKRCVHKATN	MEYAVKVIDK	SKRDPSEEIE	ILLRYGQHPN
490	500	510	520	530	540	550	560
IITLKDVYDD	GKHVYLVTEL	MRGGELLDKI	LRQKFFSERE	ASFVLHTIGK	TVEYLHSQGV	VHRDLKPSNI	LYVDESGNPE
570	580	590	600	610	620	630	640
CLRICDFGFA	KQLRAENGLL	MTPCYTANFV	APEVLKRQGY	DEGCDIWSLG	ILLYTMLAGY	TPFANGPSDT	PEEILTRIGS
650	660	670	680	690	700	710	720
GKFTLSGGNW	NTVSETAKDL	VSKMLHVDPH	QRLTAKQVLQ	HPWVTQKDKL	PQSQLSHQDL	QLVKGAMAAT	YSALNSSKPT
730	740	750					
PQLKPIESSI	LAQRRVRKLP	STTL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1521	3	839.3771	-86.28	2	47.5	13.6	0	27-43	R.ISQTSLPVPGPGSGPQR.D	

Detailed Protein Report

Protein 798: 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 799: beta-1,3-galactosyltransferase 5 isoform a [Homo sapiens]

Accession:	gi|5174397	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.2
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	7.4
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530418764	refseq_human (refseq_human_20140103.fasta)	PREDICTED: beta-1,3-galactosyltransferase 5 isoform X1 [Homo sapiens]
gi|520975380	refseq_human (refseq_human_20140103.fasta)	beta-1,3-galactosyltransferase 5 isoform a [Homo sapiens]
gi|15451883	refseq_human (refseq_human_20140103.fasta)	beta-1,3-galactosyltransferase 5 isoform a [Homo sapiens]
gi|15451881	refseq_human (refseq_human_20140103.fasta)	beta-1,3-galactosyltransferase 5 isoform a [Homo sapiens]

10	20	30	40	50	60	70	80
MAFPKMRLMY	ICLLVLGALC	LYFSMYSLNP	FKEQSFVYKK	DGNFLKLPDT	DCRQTPPFLV	LLVTSSHKQL	AERMAIRQTW
90	100	110	120	130	140	150	160
GKERMVKGKQ	LKTFFLLGTT	SSAAETKEVD	QESQRHGDII	QKDFLDVYYN	LTLKTMMGIE	WVHRFCPQAA	FVMKTDSDMF
170	180	190	200	210	220	230	240
INVDYLTELL	LKKNRTTRFF	TGFLKLNEFP	IRQPFSKWFV	SKSEYPWDRY	PPFCSGTGYV	FSGDVASQVY	NVSKSVPYIK
250	260	270	280	290	300	310	320
LEDVFVGLCL	ERLNIRLEEL	HSQPTFFPGG	LRFSVCLFRR	IVACHFIKPR	TLLDYWQALE	NSRGEDCPPV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2183	1	848.9946	-106.93	3	55.9	13.6	1	93-115	K.TFFLLGTTSSAAETKEVDQESQR.H	

Detailed Protein Report

Protein 800: 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 801: acyl-protein thioesterase 2 [Homo sapiens]

Accession:	gi|9966764	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.7
Database Date:	2015-11-30	**pI:**	6.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCGNTMSVPL	LTDAATVSGA	ERETAAVIFL	HGLGDTGHSW	ADALSTIRLP	HVKYICPHAP	RIPVTLNMKM	VMPSWFDLMG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LSPDAPEDEA	GIKKAAENIK	ALIEHEMKNG	IPANRIVLGG	FSQGGALSLY	TALTCPHPLA	GIVALSCWLP	LHRAFPQAAN
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
GSAKDLAILQ	CHGELDPMVP	VRFGALTAEK	LRSVVTPARV	QFKTYPGVMH	SSCPQEMAAV	KEFLEKLLPP	V

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1865	2	984.3384	-99.79	2	51.8	13.6	0	204-221	K.TYPGVMHSSCPQEMAAVK.E	Oxidation: 6, 14

Detailed Protein Report

Protein 802: **dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 [Homo sapiens]**

Accession:	gi|4503253	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	12.5
Database Date:	2015-11-30	**pI:**	7.5
		Sequence Coverage [%]:	20.4
		No. of unique Peptides:	1

```
         10         20         30         40         50         60         70         80
MSASVVSVIS RFLEEYLSST PQRLKLLDAY LLYILLTGAL QFGYCLLVGT FPFNSFLSGF ISCVGSFILA VCLRIQINPQ
         90        100        110        120
NKADFQGISP ERAFADFLFA STILHLVVMN FVG
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
391	1	862.7047	-86.41	3	34.9	13.6	1	1-23	-.MSASVVSVISRFLEEYLSSTPQR.L	

Detailed Protein Report

Protein 803: **PREDICTED: F-box only protein 4 isoform X1 [Homo sapiens]**

Accession:	gi|530378774	**Score:**	13.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.6
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAGSEPRSGT	NSPPPPFSDW	GRLEAAILSG	WKTFWQSVSK	ERVARTTSRE	EVDEAASTLT	RLPIDVQLYI	LSFLSPHDLC
90	100	110	120	130	140	150	160
QLGSTNHYWN	ETVRDPILWR	YFLLRDLPSW	SSVDWKSLPD	LEILKKPISE	VTDGAFFDYM	AVYRMCCPYT	RRASKSSRPM
170	180	190	200	210	220	230	240
YGAVTSFLHS	LIIQNEPRFA	MFGPGLEELN	TSLVLSLMSS	EELCPTAGLP	QRQIDGIGSG	VNFQLNNQHK	FNILILYSTT
250	260	270	280	290	300	310	
RKERDRAREE	HTSAVNKMFS	RHNEGDDQQG	SRYSVIPQIQ	KVCEVVDGFI	YVANAEAHKS	PGYRG	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1192	1	491.6248	-261.20	2	43.4	13.6	0	33-40	K.TFWQSVSK.E	

Detailed Protein Report

Protein 804: 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	2	598.7793	9.10	2	46.2	13.6	0	129-138	R.GSPEMPFYPR.V	Oxidation: 5

Detailed Protein Report

Protein 805: 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

Quantitation

QD:QU **Median:** 0.94 **CV:** 0.00 % **No. of 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	Ratios
943	1	660.3451	-9.44	2	41.8	13.5	0	534-546	K.AGALNSNDAFVLK.T		QD:QU 0.94

Detailed Protein Report

Protein 806: **solute carrier family 2, facilitated glucose transporter member 14 isoform c [Homo sapiens]**

Accession:	gi|555943829	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.9
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLLRRRNSML	IVNLLAATGG	CLMGLCKIAE	SVEMLILGRL	VIGLFCGLCT	GFVPMYIGEI	SPTALRGAFG	TLNQLGIVIG
90	100	110	120	130	140	150	160
ILVAQIFGLE	LILGSEELWP	VLLGFTILPA	ILQSAALPCC	PESPRFLLIN	RKKEENATRI	LQRLWGTQDV	SQDIQEMKDE
170	180	190	200	210	220	230	240
SARMSQEKQV	TVLELFRVSS	YRQPIIISIV	LQLSQQLSGI	NAVFYYSTGI	FKDAGVQQPI	YATISAGVVN	TIFTLLSLFL
250	260	270	280	290	300	310	320
VERAGRRTLH	MIGLGGMAFC	STLMTVSLLL	KNHYNGMSFV	CIGAILVFVA	CFEIGPGPIP	WFIVAELFSQ	GPRPAAMAVA
330	340	350	360	370	380	390	400
GCSNWTSNFL	VGLLFPSAAY	YLGAYVFIIF	TGFLITFLAF	TFFKVPETRG	RTFEDITRAF	EGQAHGADRS	GKDGVMGMNS
410	420						
IEPAKETTTN	V						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1827	1	590.7884	36.55	2	53.2	13.5	1	159-168	K.DESARMSQEK.Q	

Detailed Protein Report

Protein 807: protein dispatched homolog 2 [Homo sapiens]

Accession:	gi|25121980	**Score:**	13.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	151.9
Database Date:	2015-11-30	**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
1551	1	1011.7626	204.59	1	49.6	13.5	0	811-818	R.WLLALCHR.A	

Detailed Protein Report

Protein 808: 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 809: PREDICTED: rho GTPase-activating protein 21 isoform X5 [Homo sapiens]

Accession: gi|530392351

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 13.5

MW [kDa]: 163.4

pI: 9.7

Sequence Coverage [%]: 0.7

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MMATRRTGLS	EGDGDKLKAC	EVSKNKDGKE	QSETVSLSED	ETFSWPGPKT	VTLKRTSQGF	GFTLRHFIVY	PPESAIQFSY
90	100	110	120	130	140	150	160
KDEENGNRGG	KQRNRLEPMD	TIFVKQVKEG	GPAFEAGLCT	GDRIIKVNGE	SVIGKTYSQV	IALIQNSDTT	LELSVMPKDE
170	180	190	200	210	220	230	240
DILQVLQFTK	DVTALAYSQD	AYLKGNEAYS	GNARNIPEPP	PICYPWLPSA	PSAMAQPVEI	SPPDSSLSKQ	QTSTPVLTQP
250	260	270	280	290	300	310	320
GRAYRMEIQV	PPSPTDVAKS	NTAVCVCNES	VRTVIVPSEK	VVDLLSNRNN	HTGPSHRTEE	VRYGVSEQTS	LKTVSRTTSP
330	340	350	360	370	380	390	400
PLSIPTTHLI	HQPAGSRSLE	PSGILLKSGN	YSGHSDGISS	SRSQAVEAPS	VSVNHYSPNS	HQHIDWKNYK	TYKEYIDNRR
410	420	430	440	450	460	470	480
LHIGCRTIQE	RLDSLRAASQ	STTDYNQVVP	NRTTLQGRRR	STSHDRVPQS	VQIRQRSVSQ	ERLEDSVLMK	YCPRSASQGA
490	500	510	520	530	540	550	560
LTSPSVSFSN	HRTRSWDYIE	GQDETLENVN	SGTPIPDSNG	EKKQTYKWSG	FTEQDDRRGI	CERPRQQEIH	KSFRGSNFTV
570	580	590	600	610	620	630	640
APSVVNSDNR	RMSGRGVGSV	SQFKKIPPDL	KTLQSNRNFQ	TTCGMSLPRG	ISQDRSPLVK	VRSNSLKAPS	THVTKPSFSQ
650	660	670	680	690	700	710	720
KSFVSIKDQR	PVNHLHQNSL	LNQQTWVRTD	SAPDQQVETG	KSPSLSGASA	KPAPQSSENA	GTSDLELPVS	QRNQDLSLQE
730	740	750	760	770	780	790	800
AETEQSDTLD	NKEAVILREK	PPSGRQTPQP	LRHQSYILAV	NDQETGSDTT	CWLPNDARRE	VHIKRMEERK	ASSTSPPGDS
810	820	830	840	850	860	870	880
LASIPFIDEP	TSPSIDHDIA	HIPASAVISA	STSQVPSIAT	VPPCLTTSAP	LIRRQLSHDH	ESVGPPSLDA	QPNSKTERSK
890	900	910	920	930	940	950	960
SYDEGLDDYR	EDAKLSFKHV	SSLKGIKIAD	SQKSSEDSGS	RKDSSSEVFS	DAAKEGWLHF	RPLVTDKGKR	VGGSIRPWKQ
970	980	990	1000	1010	1020	1030	1040
MYVVLRGHSL	YLYKDKREQT	TPSEEEQPIS	VNACLIDISY	SETKRKNVFR	LTTSDCECLF	QAEDRDDMLA	WIKTIQESSN
1050	1060	1070	1080	1090	1100	1110	1120
LNEEDTGVTN	RDLISRRIKE	YNNLMSKAEQ	LPKTPRQSLS	IRQTLLGAKS	EPKTQSPHSP	KEESERKLLS	KDDTSPPKDK
1130	1140	1150	1160	1170	1180	1190	1200
GTWRKGIPSI	MRKTFEKKPT	ATGTFGVRLD	DCPPAHTNRY	IPLIVDICCK	LVEERGLEYT	GIYRVPGNNA	AISSMQEELN
1210	1220	1230	1240	1250	1260	1270	1280
KGMADIDIQD	DKWRDLNVIS	SLLKSFFRKL	PEPLFTNDKY	ADFIEANRKE	DPLDRLKTLK	RLIHDLPEHH	YETLKFLSAH
1290	1300	1310	1320	1330	1340	1350	1360
LKTVAENSEK	NKMEPRNLAI	VFGPTLVRTS	EDNMTHMVTH	MPDQYKIVET	LIQHHDWFFT	EEGAEEPLIQ	LLVTQQNLRV
1370	1380	1390	1400	1410	1420	1430	1440
LGDLERISIA	GNCLCPPSLQ	LLVARGRSRK	KKHSLAAQKM	NWTMYFLRKK	MWNSVTMILK	RSPKKKVRHW	AENRRSSLPK
1450	1460						
KTALGKTPAR	QKMKRYH						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
160	1	619.8184	1.97	2	30.7	13.5	0	1411-1420	K.MWNSVTMILK.R	Oxidation: 7

Detailed Protein Report

Protein 810: 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 811: 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

QD:QU **Median:** 1.43 **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	QD:QU	1.43

Detailed Protein Report

Protein 812: 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

Protein 813: PREDICTED: centrosomal protein of 68 kDa isoform X2 [Homo sapiens]

Accession:	gi|530367390	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.3
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MALGEEKAEA EASEDTKAQS YGRGSCRERE LDIPGPMSGE QPPRLEAEGG LISPVWGAEG IPAPTCWIGT DPGGPSRAHQ
        90        100        110        120        130        140        150        160
PQASDANREP VAERSEPALS GLPPATMGSG DLLLSGESQV EKTKLSSSEE FPQTLSLPRT TTICSGHDAD TEDDPSLADL
       170        180        190        200        210        220        230        240
PQALDLSQQP HSSGLSCLSQ WKSVLSPGSA AQPSSCSISA SSTGSSLQGH QERAEPRGGS LAKVSSSLEP VVPQEPSSVV
       250        260        270        280        290        300        310        320
GLGPRPQWSP QPVFSGGDAS GLGRRRLSFQ AEYWACVLPD SLPPSPDRHS PLWNPNKEYE DLLDYTYPLR PGPQLPKHLD
       330        340        350        360        370        380        390        400
SRVPADPVLQ DSGVDLDSFS VSPASTLKSP TNVSPNCPPA EATALPFSGP REPSLKQWPS RVPQKQGGMG LASWSQLAST
       410        420        430        440        450        460        470        480
PRAPGSRDAR WERREPALRG AKDRLTIGKH LDMGSPQLRT RDRGWPSPRP EREKRTSQSA RRPTCTESRW KSEEEVESDD
       490        500        510        520        530        540        550        560
EYLALPARLT QVSSLVSYLG SISTLVTLPT GDIKGQSPLE VSDSDGPASF PSSSSQSQLP PGAALQGSGD PEGQNPCFLR
       570        580        590        600        610        620        630        640
SFVRAHDSAG EGSLGSSQAL GVSSGLLKTR PSLPARLDRW PFSDPDVEGQ LPRKGGEQGK ESLVQCVKTF CCQLEELICW
       650        660        670        680        690        700        710        720
LYNVADVTDH GTAARSNLTS LKSSLQLYRQ FKKDIDEHQS LTESVLQKGE ILLQCLLENT PDMYPGSFRL THSPSPSICL
       730
K
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
58	1	819.8353	-70.68	2	29.4	13.4	0	30-44	R.ELDIPGPMSGEQPPR.L	Oxidation: 8

Detailed Protein Report

Protein 814: 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	2	1023.5001	6.47	1	50.2	13.4	2	327-333	R.TRQMRCR.D	Carbamidomethyl: 6; Oxidation: 4

Detailed Protein Report

Protein 815: 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

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
1794	1	872.3077	-114.49	2	52.8	13.4	0	2-17	M.DTTMEADLGATGHRPR.T	Oxidation: 4

Detailed Protein Report

Protein 816: 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; Oxidation: 15

Detailed Protein Report

Protein 817: 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 818: PREDICTED: ankyrin repeat domain-containing protein 17 isoform X7 [Homo sapiens]

Accession:	gi|530376947	**Score:**	13.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	156.1
Database Date:	2015-11-30	**pI:**	4.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

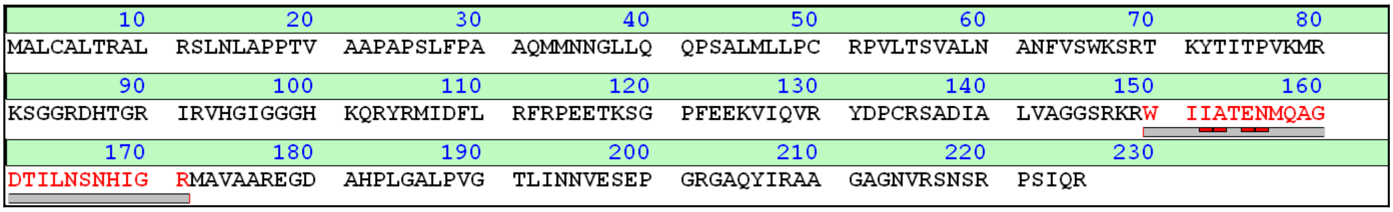
10	20	30	40	50	60	70	80
MEKATVPVAA	ATAAEGEGSP	PAVAAVAGPP	AAAEVGGGVG	GSSRARSASS	PRGMVRVCDL	LLKKKPPQQQ	HHKAKRNRTC
90	100	110	120	130	140	150	160
RPPSSSESSS	DSDNSGGGGG	GGGGGGGGGG	TSSNNSEEEE	DDDDEEEEVS	EVESFILDQD	DLENPMLETA	SKLLLSGTAD
170	180	190	200	210	220	230	240
GADLRTVDPE	TQARLEALLE	AAGIGKLSTA	DGKAFADPEV	LRRLTSSVSC	ALDEAAAALT	RMRAESTANA	GQSDNRSLAE
250	260	270	280	290	300	310	320
ACSEGDVNAV	RKLLIEGRSV	NEHTEEGESL	LCLACSAGYY	ELAQVLLAMH	ANVEDRGIKG	DITPLMAAAN	GGHVKIVKLL
330	340	350	360	370	380	390	400
LAHKADVNAQ	SSTGNTALTY	ACAGGYVDVV	KVLLESGASI	EDHNENGHTP	LMEAGSAGHV	EVARLLLENG	AGINTHSNEF
410	420	430	440	450	460	470	480
KESALTLACY	KGHLEMVRFL	LEAGADQEHK	TDEMHTALME	ACMDGHVEVA	RLLLDSGAQV	NMPADSFESP	LTLAACGGHV
490	500	510	520	530	540	550	560
ELAALLIERG	ASLEEVNDEG	YTPLMEAARE	GHEEMVALLL	GQGANINAQT	EETQETALTL	ACCGGFLEVA	DFLIKAGADI
570	580	590	600	610	620	630	640
ELGCSTPLME	AAQEGHLELV	KYLLAAGANV	HATTATGDTA	LTYACENGHT	DVADVLLQAG	ADLEHESEGG	RTPLMKAARA
650	660	670	680	690	700	710	720
GHVCTVQFLI	SKGANVNRTT	ANNDHTVLSL	ACAGGHLAVV	ELLLAHGADP	THRLKDGSTM	LIEAAKGGHT	SVVCYLLDYP
730	740	750	760	770	780	790	800
NNLLSAPPPD	VTQLTPPSHD	LNRAPRVPVQ	ALPMVVPPQE	PDKPPANVAT	TLPIRNKAAS	KQKSSSHLPA	NSQDVQGYIT
810	820	830	840	850	860	870	880
NQSPESIVEE	AQGKLTELEQ	RIKEAIEKNA	QLQSLELAHA	DQLTKEKIEE	LNKTREEQIQ	KKQKILEELQ	KVERELQLKT
890	900	910	920	930	940	950	960
QQQLKKQYLE	VKAQRIQLQQ	QQQQSCQHLG	LLTPVGVGEQ	LSEGDYARLQ	QVDPVLLKDE	PQQTAAQMGF	APIQPLAMPQ
970	980	990	1000	1010	1020	1030	1040
ALPLAAGPLP	PGSIANLTEL	QGVIVGQPVL	GQAQLAGLGQ	GILTETQQGL	MVASPAQTLN	DTLDDIMAAV	SGRASAMSNT
1050	1060	1070	1080	1090	1100	1110	1120
PTHSIAASIS	QPQTPTPSPI	ISPSAMLPIY	PAIDIDAQTE	SNHDTALTLA	CAGGHEELVQ	TLLERGASIE	HRDKKGFTPL
1130	1140	1150	1160	1170	1180	1190	1200
ILAATAGHVG	VVEILLDNGA	DIEAQSERTK	DTPLSLACSG	GRQEVVELLL	ARGANKEHRN	VSDYTPLSLA	ASGGYVNIIK
1210	1220	1230	1240	1250	1260	1270	1280
ILLNAGAEIN	SRTGSKLGIS	PLMLAAMNGH	TAAVKLLLDM	GSDINAQIET	NRNTALTLAC	FQGRTEVVSL	LLDRKANVEH
1290	1300	1310	1320	1330	1340	1350	1360
RAKTGLTPLM	EAASGGYAEV	GRVLLDKGAD	VNAPPVPSSR	DTALTIAADK	GHYKFCELLI	GRGAHIDVRN	KKGNTPLWLA
1370	1380	1390	1400	1410	1420	1430	1440
ANGGHLDVVQ	LLVQAGADVD	AADNRKITPL	MAAFRKGHVK	VVRYLVKEVN	QFPSDSECMR	YIATITDKEM	LKKCHLCMES
1450	1460	1470	1480	1490			
IVQAKDRQAA	EANKNASILL	EELDLEKADY	NIIPIYSHGE				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2659	1	938.0625	114.26	2	62.0	13.4	2	1433-1447	K.KCHLCMESIVQAKDR.Q	Carbamidomethyl: 2, 5

Detailed Protein Report

Protein 819: **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 820: integrin alpha-E precursor [Homo sapiens]

Accession:	gi|148728188	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	130.1
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
MWLFHTLLCI	ASLALLAAFN	VDVARPWLTP	KGGAPFVLSS	LLHQDPSTNQ	TWLLVTSPRT	KRTPGPLHRC	SLVQDEILCH
90	100	110	120	130	140	150	160
PVEHVPIPKG	RHRGVTVVRS	HHGVLICIQV	LVRRPHSLSS	ELTGTCSLLG	PDLRPQAQAN	FFDLENLLDP	DARVDTGDCY
170	180	190	200	210	220	230	240
SNKEGGGEDD	VNTARQRRAL	EKEEEEDKEE	EEDEEEEEAG	TEIAIILDGS	GSIDPPDFQR	AKDFISNMMR	NFYEKCFECN
250	260	270	280	290	300	310	320
FALVQYGGVI	QTEFDLRDSQ	DVMASLARVQ	NITQVGSVTK	TASAMQHVLD	SIFTSSHGSR	RKASKVMVVL	TDGGIFEDPL
330	340	350	360	370	380	390	400
NLTTVINSPK	MQGVERFAIG	VGEEFKSART	ARELNLIASD	PDETHAFKVT	NYMALDGLLS	KLRYNIISME	GTVGDALHYQ
410	420	430	440	450	460	470	480
LAQIGFSAQI	LDERQVLLGA	VGAFDWSGGA	LLYDTRSRRG	RFLNQTAAAA	ADAEAAQYSY	LGYAVAVLHK	TCSLSYIAGA
490	500	510	520	530	540	550	560
PRYKHHGAVF	ELQKEGREAS	FLPVLEGEQM	GSYFGSELCP	VDIDMDGSTD	FLLVAAPFYH	VHGEEGRVYV	YRLSEQDGSF
570	580	590	600	610	620	630	640
SLARILSGHP	GFTNARFGFA	MAAMGDLSQD	KLTDVAIGAP	LEGFGADDGA	SFGSVYIYNG	HWDGLSASPS	QRIRASTVAP
650	660	670	680	690	700	710	720
GLQYFGMSMA	GGFDISGDGL	ADITVGTLGQ	AVVFRSRPVV	RLKVSMAFTP	SALPIGFNGV	VNVRLCFEIS	SVTTASESGL
730	740	750	760	770	780	790	800
REALLNFTLD	VDVGKQRRRL	QCSDVRSCLG	CLREWSSGSQ	LCEDLLLMPT	EGELCEEDCF	SNASVKVSYQ	LQTPEGQTDH
810	820	830	840	850	860	870	880
PQPILDRYTE	PFAIFQLPYE	KACKNKLFCV	AELQLATTVS	QQELVVGLTK	ELTLNINLTN	SGEDSYMTSM	ALNYPRNLQL
890	900	910	920	930	940	950	960
KRMQKPPSPN	IQCDDPQPVA	SVLIMNCRIG	HPVLKRSSAH	VSVVWQLEEN	AFPNRTADIT	VTVTNSNERR	SLANETHTLQ
970	980	990	1000	1010	1020	1030	1040
FRHGFVAVLS	KPSIMYVNTG	QGLSHHKEFL	FHVHGENLFG	AEYQLQICVP	TKLRGLQVVA	VKKLTRTQAS	TVCTWSQERA
1050	1060	1070	1080	1090	1100	1110	1120
CAYSSVQHVE	EWHSVSCVIA	SDKENVTVAA	EISWDHSEEL	LKDVTELQIL	GEISFNKSLY	EGLNAENHRT	KITVVFLKDE
1130	1140	1150	1160	1170	1180		
KYHSLPIIIK	GSVGGLLVLI	VILVILFKCG	FFKRKYQQLN	LESIRKAQLK	SENLLEEEN		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1655	1	896.8887	87.41	3	49.2	13.3	0	306-330	K.VMVVLTDGGIFEDPLNLTTVINSPK.M	Oxidation: 2

Detailed Protein Report

Protein 821: **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 822: **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

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
233	1	493.3908	201.48	3	32.9	13.3	2	467-479	R.LRNDLAKLHVNGK.S	

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Detailed Protein Report

Protein 823: PREDICTED: BAG family molecular chaperone regulator 3 isoform X1 [Homo sapiens]

Accession:	gi|530394628	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.4
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSAATHSPMM	QVASGNGDRD	PLPPGWEIKI	DPQTGWPFFV	DHNSRTTTWN	DPRVPSEGPK	ETPSSANGPS	REGSRLPPAR
90	100	110	120	130	140	150	160
EGHPVYPQLR	PGYIPIPVLH	EGAENRQVHP	FHVYPQPGMQ	RFRTEAAAAA	PQRSQSPLRG	MPETTQPDKQ	CGQVAAAAAA
170	180	190	200	210	220	230	240
QPPASHGPER	SQSPAASDCS	SSSSSASLPS	SGRSSLGSHQ	LPRGYISIPV	IHEQNVTRPA	AQPSFHQAQK	THYPAQQGEY
250	260	270	280	290	300	310	320
QTHQPVYHKI	QGDDWEPRPL	RAASPFRSSV	QGASSREGSP	ARSSTPLHSP	SPIRVHTVVD	RPQPMTHRET	APVSQPENKP
330	340	350	360	370	380	390	400
ESKPGPVGPE	LPPGHIPIQV	IRKEVDSKPV	SQKPPPPSEK	VEVKVPPAPV	PCPPPSPGPS	AVPSSPKSVA	TEERAAPSTA
410	420	430	440	450	460	470	480
PAEATPPKPG	EAEAPPKHPG	VLKVEAILEK	VQGLEQAVDN	FEGKKTDKKY	LMIEEYLTKE	LLALDSVDPE	GRADVRQARR
490	500	510	520	530	540	550	560
DGVRKVQTIL	EKLEQKAIDV	PGQVQVYELQ	PSNLEADQPL	QAIMEMGAVA	ADKGKKNAGN	AEDPHTETQQ	PEATAAATSN
570	580						
PSSMTDTPGN	PAAP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2079	1	916.9082	4.24	2	54.5	13.3	0	2-19	M.SAATHSPMMQVASGNGDR.D	Oxidation: 8

Detailed Protein Report

Protein 824: **PREDICTED: serine/threonine-protein phosphatase 2A regulatory subunit B'' subunit gamma isoform X7 [Homo sapiens]**

Accession:	gi|578825918	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.3
Database Date:	2015-11-30	**pI:**	7.6
		Sequence Coverage [%]:	8.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MDWKEVLRRR LATPNTCPNK KKSEQELKDE EMDLFTKYYS EWKGGRKNTN EFYKTIPRFY YRLPAEDEVL LQKLREESRA
        90        100        110        120        130        140        150        160
VFLQRKSREL LDNEELQNLW FLLDKHQTPP MIGEEAMINY ENFLKVGEKA GAKCKQFFTA KVFAKLLHTD SYGRISIMQF
       170        180        190        200        210        220        230        240
FNYVMRKVWL HQTRIGLSLY DVAGQGYLRE SDLENYILEL IPTLPQLDGL EKSFYSFYVC TAVRKFFFFL DPLRTGKIKI
       250        260        270        280        290
QDILACSFLD DLLELRDEEL SKESQETNWF SAPSALRVYG L
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2954	1	891.7382	-98.03	3	66.1	13.3	2	167-189	R.KVWLHQTRIGLSLYDVAGQGYLR.E	

Detailed Protein Report

Protein 825: PREDICTED: cirhin isoform X2 [Homo sapiens]

Accession:	gi|530424438	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.7
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIVDRQYMGV	SKRKCIVWGV	AFLSDGTIIS	VDSAGKVQFW	DSATGTLVKS	HLIANADVQS	IAVADQEDSF	VVGTAEGTVF
90	100	110	120	130	140	150	160
HFQLVPVTSN	SSEKQWVRTK	PFQHHTHDVR	TVAHSPTALI	SGGTDTHLVF	RPLMEKVEVK	NYDAALRKIT	FPHRCLISCS
170	180	190	200	210	220	230	240
KKRQLLLFQF	AHHLELWRLG	STVATGKNGD	TLPLSKNADH	LLHLKTKGPE	NIICSCISPC	GSWIAYSTVS	RFFLYRLNYE
250	260	270	280	290	300	310	320
HDNISLKRVS	KMPAFLRSAL	QILFSEDSTK	LFVASNQGAL	HIVQLSGGSF	KHLHAFQPQS	GTVEAMCLLA	VSPDGNWLAA
330	340	350	360	370	380	390	400
SGTSAGVHVY	NVKQLKLHCT	VPAYNFPVTA	MAIAPNTNNL	VIAHSDQQVF	EYSIPDKQYT	DWSRTVQKQG	FHHLWLQRDT
410	420	430	440	450	460	470	480
PITHISFHPK	RPMHILLHDA	YMFCIIDKSL	PLPNDKTLLY	NPFPPTNESD	VIRRRTAHAF	KISKIYKPLL	FMDLLDERTL
490	500	510					
VAVERPLDDI	IAQLPPPIKK	KKFGT					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2470	1	938.4630	-17.91	1	61.4	13.3	1	155-162	R.CLISCSKK.R	Carbamidomethyl: 1

Detailed Protein Report

Protein 826: 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 827: PREDICTED: cytosolic carboxypeptidase 3 isoform X3 [Homo sapiens]

Accession:	gi|578814196	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	99.8
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
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
1532	1	917.3273	-136.49	2	49.4	13.3	1	839-854	K.DEQANKNDGQPTLYLK.F	

Detailed Protein Report

Protein 828: 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 829:	**general transcription factor 3C polypeptide 1 isoform 2 [Homo sapiens]**		
Accession:	gi|555943794	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	236.1
Database Date:	2015-11-30	**pI:**	8.2
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

Detailed Protein Report

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	GNSRLNIWGE	ARVGSELCAG	WEEQFEVDRE
1210	1220	1230	1240	1250	1260	1270	1280
PSLDRNRRVR	GGKSQKRKRL	KKDPGKKIKR	KKKGEFPGEK	SKRLRYHDEA	DQSALQRMTR	LRVTWSMQED	GLLVLCRIAS
1290	1300	1310	1320	1330	1340	1350	1360
NVLNTKVKGP	FVTWQVVRDI	LHATFEESLD	KTSHSVGRRA	RYIVKNPQAY	LNYKVCLAEV	YQDKALVGDF	MNRRGDYDDP
1370	1380	1390	1400	1410	1420	1430	1440
KVCANEFKEF	VEKLKEKFSS	ALRNSNLEIP	DTLQELFARY	RVLAIGDEKD	QTRKEDELNS	VDDIHFLVLQ	NLIQSTLALS
1450	1460	1470	1480	1490	1500	1510	1520
DSQMKSYQSF	QTFRLYREYK	DHVLVKAFME	CQKRSLVNRR	RVNHTLGPKK	NRALPFVPMS	YQLSQTYYRI	FTWRFPSTIC
1530	1540	1550	1560	1570	1580	1590	1600
TESFQFLDRM	RAAGKLDQPD	RFSFKDQDNN	EPTNDMVAFS	LDGPGGNCVA	VLTLFSLGLI	SVDVRIPEQI	IVVDSSMVEN
1610	1620	1630	1640	1650	1660	1670	1680
EVIKSLGKDG	SLEDDEDEED	DLDEGVGGKR	RSMEVKPAQA	SHTNYLLMRG	YYSPGIVSTR	NLNPNDSIVV	NSCQMKFQLR
1690	1700	1710	1720	1730	1740	1750	1760
CTPVPARLRP	AAAPLEELTM	GTSCLPDTFT	KLINPQENTC	SLEEFVLQLE	LSGYSPEDLT	AALEILEAII	ATGCFGIDKE
1770	1780	1790	1800	1810	1820	1830	1840
ELRRRFSALE	KAGGGRTRTF	ADCIQALLEQ	HQVLEVGGNT	ARLVAMGSAW	PWLLHSVRLK	DREDADIQRE	DPQARPLEGS
1850	1860	1870	1880	1890	1900	1910	1920
SSEDSPPEGQ	APPSHSPRGT	KRRASWASEN	GETDAEGTQM	TPAKRPALQD	SNLAPSLGPG	AEDGAEAQAP	SPPPALEDTA
1930	1940	1950	1960	1970	1980	1990	2000
AAGAAQEDQE	GVGFTESFGA	ANISQAARER	DCESVCFIGR	PWRVVDGHLN	LPVCKGMMEA	MLYHIMTRPG	IPESSLLRHY
2010	2020	2030	2040	2050	2060	2070	2080
QGVLQPVAVL	ELLQGLESLG	CIRKRWLRKP	RPVSLFSTPV	VEEVEVPSSL	DESPMAFYEP	TLDCTLRLGR	VFPHEVNWNK
2090							
WIHL							

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1476	1	977.4972	62.60	2	47.0	13.3	0	1183-1199	R.VGSELCAGWEEQFEVDR.E	

Detailed Protein Report

Protein 830: centrin-2 [Homo sapiens]

Accession:	gi|4757902	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	19.7
Database Date:	2015-11-30	**pI:**	4.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASNFKKANM	ASSSQRKRMS	PKPELTEEQK	QEIREAFDLF	DADGTGTIDV	KELKVAMRAL	GFEPKKEEIK	KMISEIDKEG
90	100	110	120	130	140	150	160
TGKMNFGDFL	TVMTQKMSEK	DTKEEILKAF	KLFDDDETGK	ISFKNLKRVA	KELGENLTDE	ELQEMIDEAD	RDGDGEVSEQ
170	180						
EFLRIMKKTS	LY						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2724	1	1028.0424	75.06	2	63.0	13.3	1	84-100	K.MNFGDFLTVMTQKMSEK.D	Oxidation: 1, 10, 14

Detailed Protein Report

Protein 831: vitamin K epoxide reductase complex subunit 1 isoform 2 precursor [Homo sapiens]

Accession:	gi|45827739	**Score:**	13.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	9.9
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	14.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGSTWGSPGW VRLALCLTGL VLSLYALHVK AARARDRDYR ALCDVGTAIS CSRVFSSRLP ADTLGLCPDA AELPGVSRWF
        90        100
CLPGLDPVLR AL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1852	1	676.7559	-92.47	2	51.7	13.3	0	41-53	R.ALCDVGTAISCSR.V	Carbamidomethyl: 3

Detailed Protein Report

Protein 832: PREDICTED: transcriptional regulator ATRX isoform X8 [Homo sapiens]

Accession: gi|578838421

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 13.2

MW [kDa]: 211.9

pI: 6.7

Sequence Coverage [%]: 0.5

No. of unique Peptides: 1

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	

BRUKER

Detailed Protein Report

Protein 833: **multivesicular body subunit 12A [Homo sapiens]**

Accession:	gi|24308440	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.8
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	8.4
		No. of unique Peptides:	1

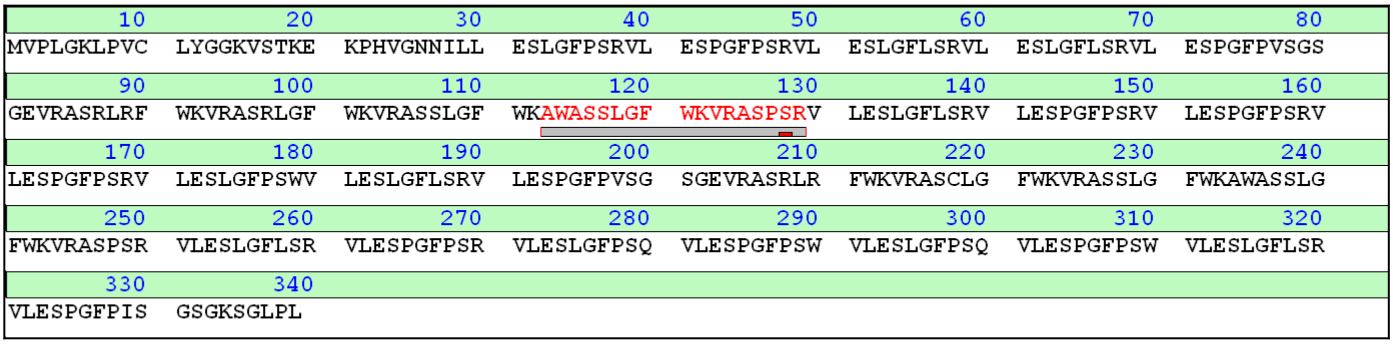
10	20	30	40	50	60	70	80
MDPVPGTDSA	PLAGLAWSSA	SAPPPRGFSA	ISCTVEGAPA	SFGKSFAQKS	GYFLCLSSLG	SLENPQENVV	ADIQIVVDKS
90	100	110	120	130	140	150	160
PLPLGFSPVC	DPMDSKASVS	KKKRMCVKLL	PLGATDTAVF	DVRLSGKTKT	VPGYLRIGDM	GGFAIWCKKA	KAPRPVPKPR
170	180	190	200	210	220	230	240
GLSRDMQGLS	LDAASQPSKG	GLLERTASRL	GSRASTLRRN	DSIYEASSLY	GISAMDGVPF	TLHPRFEGKS	CSPLAFSAFG
250	260	270	280				
DLTIKSLADI	EEEYNYGFVV	EKTAAARLPP	SVS				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2637	1	1145.5118	-44.07	2	61.7	13.2	1	27-49	R.GFSAISCTVEGAPASFGKSFAQK.S	

Detailed Protein Report

Protein 834: **PREDICTED: aggrecan core protein-like isoform X3 [Homo sapiens]**

Accession:	gi|530435186	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.0
Database Date:	2015-11-30	**pI:**	11.6
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1



10	20	30	40	50	60	70	80
MVPLGKLPVC	LYGGKVSTKE	KPHVGNNILL	ESLGFPSRVL	ESPGFPSRVL	ESLGFLSRVL	ESLGFLSRVL	ESPGFPVSGS
90	100	110	120	130	140	150	160
GEVRASRLRF	WKVRASRLGF	WKVRASSLGF	WKAWASSLGF	WKVRASPSRV	LESLGFLSRV	LESPGFPSRV	LESPGFPSRV
170	180	190	200	210	220	230	240
LESPGFPSRV	LESLGFPSWV	LESLGFLSRV	LESPGFPVSG	SGEVRASRLR	FWKVRASCLG	FWKVRASSLG	FWKAWASSLG
250	260	270	280	290	300	310	320
FWKVRASPSR	VLESLGFLSR	VLESPGFPSR	VLESLGFPSQ	VLESPGFPSW	VLESLGFPSQ	VLESPGFPSW	VLESLGFLSR
330	340						
VLESPGFPIS	GSGKSGLPL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2944	1	953.4516	-58.86	2	66.0	13.2	2	113-129	K.AWASSLGFWKVRASPSR.V	

Detailed Protein Report

Protein 835: APITD1-CORT protein isoform 2 [Homo sapiens]

Accession:	gi|302058297	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	9.1
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	23.4
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:** 1.01	**CV:** 0.00 %	**No. of Peptides:** 1

```
         10         20         30         40         50         60         70         80
MEEEAETEEQ QRFSYQQRLK AAVHYTVGCL CEEVALDKEM QFSKQTIAAI SELTFRQCEN FAKDLEMFAS ICRKRQE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
23	1	736.0076	-0.36	3	30.0	13.2	2	57-74	R.QCENFAKDLEMFASICRK.R	Carbamidomethyl: 2; Oxidation: 11	QD:QU 1.01

Detailed Protein Report

Protein 836: 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

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
1950	1	794.7765	-89.11	2	54.8	13.2	1	359-371	K.KFHSSDSEEEEHK.K	

Detailed Protein Report

Protein 837: PREDICTED: neurexin-1-beta isoform X14 [Homo sapiens]

Accession:	gi|578803284	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	46.6
Database Date:	2015-11-30	**pI:**	8.6
		Sequence Coverage [%]:	5.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MYQRMLRCGA	ELGSPGGGGG	GGGGGGAGGR	LALLWIVPLT	LSGLLGVAWG	ASSLGAHHIH	HFHGSSKHHS	VPIAIYRSPA
90	100	110	120	130	140	150	160
SLRGGHAGTT	YIFSKGGGQI	TYKWPPNDRP	STRADRLAIG	FSTVQKEAVL	VRVDSSSGLG	DYLELHIHQG	KIGVKFNVGT
170	180	190	200	210	220	230	240
DDIAIEESNA	IINDGKYHVV	RFTRSGGNAT	LQVDSWPVIE	RYPAGRQLTI	FNSQATIIIG	GKEQGQPFQG	QLSGLYYNGL
250	260	270	280	290	300	310	320
KVLNMAAEND	ANIAIVGNVR	LVGEVPSSMT	TESTATAMQS	EMSTSIMETT	TTLATSTARR	GKPPTKEPIS	QTTDDILVAS
330	340	350	360	370	380	390	400
AECPSDDEDI	DPCEPSSANP	TRAGGREPYP	GSAEVIRESS	STTGMVVGIV	AAAALCILIL	LYAMYKYRNR	DEGSYHVDES
410	420	430	440				
RNYISNSAQS	NGAVVKEKQP	SSAKSSNKNK	KNKDKEYYV				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2237	1	851.3609	-12.43	2	56.6	13.2	0	8-30	R.CGAELGSPGGGGGGGGGGGAGGR.L	

Detailed Protein Report

Protein 838: 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 839: PREDICTED: DNA polymerase zeta catalytic subunit isoform X4 [Homo sapiens]

Accession:	gi|530383948	**Score:**	13.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	301.0
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	0.5
		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
LKPIKDGIQK	SPCSEPQEPL	VISPINTRAR	TGKCESLCFH	STPIIQRKLL	ERLPEAPGLS	PLSTEPKTQK	LSNKKGSNTD
2250	2260	2270	2280	2290	2300	2310	2320
TLRRVLLTQA	KNQFAAVNTP	QKETSQIDGP	SLNNTYGFKV	SIQNLQEAKA	LHEIQNLTLI	SVELHARTRR	DLEPDPEFDP
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
2757	1	710.3801	13.75	2	63.5	13.2	0	136-148	R.ICELLQSGAIMNK.F	

Detailed Protein Report

Protein 840: **retinitis pigmentosa 9 protein [Homo sapiens]**

Accession:	gi|42718020	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.1
Database Date:	2015-11-30	**pI:**	10.4
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSRPGREDV	GAAGARRPRE	PPEQELQRRR	EQKRRRHDAQ	QLQQLKHLES	FYEKPPPGLI	KEDETKPEDC	IPDVPGNEHA
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
REFLAHAPTK	GLWMPLGKEV	KVMQCWRCKR	YGHRTGDKEC	PFFIKGNQKL	EQFRVAHEDP	MYDIIRDNKR	HEKDVRIQQL
170	**180**	**190**	**200**	**210**	**220**	**230**	
KQLLEDSTSD	EDRSSSSSSE	GKEKHKKKKK	KEKHKKRKKE	KKKKKKRKHK	SSKSNEGSDS	E	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2386	1	704.1871	-182.11	2	58.5	13.1	0	162-173	K.QLLEDSTSDEDR.S	

Detailed Protein Report

Protein 841: **PREDICTED: conserved oligomeric Golgi complex subunit 7 isoform X2 [Homo sapiens]**

Accession:	gi|530409377	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.1
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
MPKVLRDVEA	LKQEASFLKE	QMILVKEDIK	KFEQDTSQSM	QVLVEIDQVK	SRMQLAAESL	QEADKWSTLS	ADIEETFKTQ
90	100	110	120	130	140	150	160
DIAVISAKLT	GMQNSLMMLV	DTPDYSEKCV	HLEALKNRLE	ALASPQIVAA	FTSQAVDQSK	VFVKVFTEID	RMPQLLAYYY
170	180	190	200	210	220	230	240
KCHKVQLLAA	WQELCQSDLS	LDRQLTGLYD	ALLGAWHTQI	QWATQVFQKP	HEVVMVLLIQ	TLGALMPSLP	SCLSNGVERA
250	260	270	280	290	300	310	320
GPEQELTRLL	EFYDATAHFA	KGLEMALLPH	LHEHNLVKVT	ELVDAVYDPY	KPYQLKYGDM	EESNLLIQMS	AVPLEHGEVI
330	340	350	360	370	380	390	400
DCVQELSHSV	NKLFGLASAA	VDRCVRFTNG	LGTCGLLSAL	KSLFAKYVSD	FTSTLQSIRK	KCKLDHIPPN	SLFQEDWTAF
410	420	430	440	450	460	470	480
QNSIRIIATC	GELLRHCGDF	EQQLANRILS	TAGKYLSDSC	SPRSLAGFQE	SILTDKKNSA	KNPWQEYNYL	QKDNPAEYAS
490	500	510	520	530	540	550	560
LMEILYTLKE	KGSSNHNLLA	APRAALTRLN	QQAHQLAFDS	VFLRIKQQLL	LISKMDSWNT	AGIGETLTDE	LPAFSLTPLE
570	580	590	600	610	620	630	640
YISNIGQYIM	SLPLNLEPFV	TQEDSALELA	LHAGKLPFPP	EQGDELPELD	NMADNWLGSI	ARATMQTYCD	AILQIPELSP
650	660	670	680	690	700	710	
HSAKQLATDI	DYLINVMDAL	GLQPSRTLQH	IVTLLKTRPE	DYRQVSKGLP	RRLATTVATM	RSVNY	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1449	1	946.3990	-84.94	3	46.6	13.1	2	27-50	K.EDIKKFEQDTSQSMQVLVEIDQVK.S	

Detailed Protein Report

Protein 842: **carcinoembryonic antigen-related cell adhesion molecule 20 isoform 4S precursor [Homo sapiens]**

Accession:	gi|156564388	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	4.1
		No. of unique 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
810	1	770.1691	128.26	3	38.6	13.1	1	122-141	K.ILTILIVQREDSGTYQCEAR.D	

Detailed Protein Report

Protein 843: PREDICTED: ubiquitin carboxyl-terminal hydrolase 11 isoform X2 [Homo sapiens]

Accession:	gi|530421592	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	79.1
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
METRKKDGTW	PSAQLHVMNN	NMSEEDEDFK	GQPGICGLTN	LGNTCFMNSA	LQCLSNVPQL	TEYFLNNCYL	EELNFRNPLG
90	100	110	120	130	140	150	160
MKGEIAEAYA	DLVKQAWSGH	HRSIVPHVFK	NKVGHFASQF	LGYQQHDSQE	LLSFLLDGLH	EDLNRVKKKE	YVELCDAAGR
170	180	190	200	210	220	230	240
PDQEVAQEAW	QNHKRRNDSV	IVDTFHGLFK	STLVCPDCGN	VSVTFDPFCY	LSVPLPISHK	RVLEVFFIPM	DPRRKPEQHR
250	260	270	280	290	300	310	320
LVVPKKGKIS	DLCVALSKHT	GISPERMMVA	DVFSHRFYKL	YQLEEPLSSI	LDRDDIFVYE	VSGRIEAIEG	SREDIVVPVY
330	340	350	360	370	380	390	400
LRERTPARDY	NNSYYGLMLF	GHPLLVSVPR	DRFTWEGLYN	VLMYRLSRYV	TKPNSDDEDD	GDEKEDDEED	KDDVPGPSTG
410	420	430	440	450	460	470	480
GSLRDPEPEQ	AGPSSGVTNR	CPFLLDNCLG	TSQWPPRRRR	KQLFTLQTVN	SNGTSDRTTS	PEEVHAQPYI	AIDWEPEMKK
490	500	510	520	530	540	550	560
RYYDEVEAEG	YVKHDCVGYV	MKKAPVRLQE	CIELFTTVET	LEKENPWYCP	SCKQHQLATK	KLDLWMLPEI	LIIHLKRFSY
570	580	590	600	610	620	630	640
TKFSREKLDT	LVEFPIRDLD	FSEFVIQPQN	ESNPELYKYD	LIAVSNHYGG	MRDGHYTTFA	CNKDSGQWHY	FDDNSVSPVN
650	660	670	680	690	700		
ENQIESKAAY	VLFYQRQDVA	RRLLSPAGSS	GAPASPACSS	PPSSEFMDVN			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
207	1	613.7832	50.78	2	32.6	13.1	0	524-533	K.ENPWYCPSCK.Q	

Detailed Protein Report

Protein 844: CMT1A duplicated region transcript 1 protein isoform b [Homo sapiens]

Accession:	gi|543173106	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	82.0
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Oxidation	**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 845: cartilage intermediate layer protein 2 precursor [Homo sapiens]

Accession:	gi|145699139	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	126.2
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.8
		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 846: 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 847: 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

Protein 848: helicase SRCAP [Homo sapiens]

Accession:	gi|146219843	**Score:**	13.1
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

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
2699	1	973.5249	-63.33	2	62.7	13.1	2	2045-2061	K.LQTLAVLLRQLKAEGHR.V	

Detailed Protein Report

Protein 849: PREDICTED: zinc finger protein 40 isoform X2 [Homo sapiens]

Accession:	gi|578811634	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	222.1
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:** 0.78	**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	PVPGGLQPQI	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
1515	1	719.8406	-37.88	2	49.1	13.1	0	1176-1188	K.VIGISQEESHPSR.D		QD:QU 0.78

Detailed Protein Report

Protein 850: **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 851: selenium-binding protein 1 isoform 2 [Homo sapiens]

Accession:	gi|385137128	**Score:**	13.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.4
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	7.3
		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
827	1	1106.2441	46.85	3	38.8	13.1	2	5-34	K.CGNCGPGYSTPLEAMKGPREEIVYLPCIYR.N	

Detailed Protein Report

Protein 852: **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

Protein 853: mis18-binding protein 1 [Homo sapiens]

Accession: gi|42415492
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 13.0
MW [kDa]: 129.0
pI: 9.9
Sequence Coverage [%]: 1.1
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|530404134	refseq_human (refseq_human_20140103.fasta)	PREDICTED: mis18-binding protein 1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MIATPLKHSR	IYLPPEASSQ	RRNLPMDAIF	FDSIPSGTLT	PVKDLVKYQN	SSLKLNDHKK	NQFLKMTTFN	NKNIFQSTML
90	100	110	120	130	140	150	160
TEATTSNSSL	DISAIKPNKD	GLKNKANYES	PGKIFLRMKE	KVLRDKQEQP	SRNSSLLEPQ	KSGNNETFTP	NRVEKKKLQH
170	180	190	200	210	220	230	240
TYLCEEKENN	KSFQSDDSSL	RASVQGVPLE	SSNNDIFLPV	KQKIQCQQEK	KAPLHNLTYE	LPTLNQEQEN	FLAVEARNKT
250	260	270	280	290	300	310	320
LTRAQLAKQI	FHSKESIVAT	TKSKKDTFVL	ESVDSADEQF	QNTNAETLST	NCIPIKNGSL	LMVSDSERTT	EGTSQQKVKE
330	340	350	360	370	380	390	400
GNGKTVPGET	GLPGSMKDTC	KIVLATPRLH	ITIPRRSKRN	ISKLSPPRIF	QTVTNGLKKN	QVVQLQEWMI	KSINNNTAIC
410	420	430	440	450	460	470	480
VEGKLIDVTN	IYWHSNVIIE	RIEHNKLRTI	SGNVYILKGM	IDQISMKEAG	YPNYLIRKFM	FGFPENWKEH	IDNFLEQLRA
490	500	510	520	530	540	550	560
GEKNREKTKQ	KQKTGRSVRD	IRKSMKNDAR	ENQTDTAQRA	TTTYDFDCDN	LELKSNKHSE	SPGATELNMC	HSNCQNKPTL
570	580	590	600	610	620	630	640
RFPDDQVNNT	IQNGGGDDLS	NQELIGKKEY	KMSSKKLKIG	ERTNERIIKS	QKQETTEELD	VSIDILTSRE	QFFSDEERKY
650	660	670	680	690	700	710	720
MAINQKKAYI	LVTPLKSRKV	IEQRCMRYNL	SAGTIKAVTD	FVIPECQKKS	PISKSMGTLE	NTFEGHKSKN	KEDCDERDLL
730	740	750	760	770	780	790	800
TVNRKIKISN	LEKEQMLTSD	FKKNTRLLPK	LKKIENQVAM	SFYKHQSSPD	LSSEESETEK	EIKRKAEVKK	TKAGNTKEAV
810	820	830	840	850	860	870	880
VHLRKSTRNT	SNIPVILEPE	TEESENEFYI	KQKKARPSVK	ETLQKSGVRK	EFPITEAVGS	DKTNRHPLEC	LPGLIQDKEW
890	900	910	920	930	940	950	960
NEKELQKLHC	AFASLPKHKP	GFWSEVAAAV	GSRSPEECQR	KYMENPRGKG	SQKHVTKKKP	ANSKGQNGKR	GDADQKQTIK
970	980	990	1000	1010	1020	1030	1040
ITAKVGTLKR	KQQMREFLEQ	LPKDDHDDFF	STTPLQHQRI	LLPSFQDSED	DDDILPNMDK	NPTTPSSVIF	PLVKTPQCQH
1050	1060	1070	1080	1090	1100	1110	1120
VSPGMLGSIN	RNDCDKYVFR	MQKYHKSNGG	IVWGNIKKKL	VETDFSTPTP	RRKTPFNTDL	GENSGIGKLF	TNAVESLDEE
1130	1140						
EKDYYFSNSD	SA						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2772	1	733.8764	59.69	2	63.7	13.0	0	695-707	K.SMGTLENTFEGHK.S	Oxidation: 2

Detailed Protein Report

Protein 854: centrosomal protein of 170 kDa protein B isoform 2 [Homo sapiens]

Accession:	gi|326319990	**Score:**	13.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	163.5
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 2.07 **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		QD:QU 2.07

Detailed Protein Report

Protein 855: GTPase NRas [Homo sapiens]

Accession: gi|4505451
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 13.0
MW [kDa]: 21.2
pI: 4.9
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; Oxidation: 13, 20

Detailed Protein Report

Protein 856: 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 857: 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 858: **GDP-fucose protein O-fucosyltransferase 2 isoform A precursor [Homo sapiens]**

Accession:	gi|13273311	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.9
Database Date:	2015-11-30	**pI:**	6.3
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATLSFVFLL	LGAVSWPPAS	ASGQEFWPGQ	SAADILSGAA	SRRRYLLYDV	NPPEGFNLRR	DVYIRIASLL	KTLLKTEEWV
90	100	110	120	130	140	150	160
LVLPPWGRLY	HWQSPDIHQV	RIPWSEFFDL	PSLNKNIPVI	EYEQFIAESG	GPFIDQVYVL	QSYAEGWKEG	TWEEKVDERP
170	180	190	200	210	220	230	240
CIDQLLYSQD	KHEYYRGWFW	GYEETRGLNV	SCLSVQGSAS	IVAPLLLRNT	SARSVMLDRA	ENLLHDHYGG	KEYWDTRRSM
250	260	270	280	290	300	310	320
VFARHLREVG	DEFRSRHLNS	TDDADRIPFQ	EDWMKMKVKL	GSALGGPYLG	VHLRRKDFIW	GHRQDVPSLE	GAVRKIRSLM
330	340	350	360	370	380	390	400
KTHRLDKVFV	ATDAVRKEYE	ELKKLLPEMV	RFEPTWEELE	LYKDGGVAII	DQWICAHARC	LPTSLSAESG	SGGFQRFFCP
410	420	430					
KYSVSEQMVA	CVHSGHFHTV	CLLV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2161	1	1273.4685	-105.69	2	55.6	12.9	0	402-424	K.YSVSEQMVACVHSGHFHTVCLLV.-	

Detailed Protein Report

Protein 859: 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

QD:QU **Median:** 0.62 **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		QD:QU 0.62

Detailed Protein Report

Protein 860: proteasome activator complex subunit 1 isoform 3 [Homo sapiens]

Accession: gi|528078353
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 12.9
MW [kDa]: 26.9
pI: 5.5
Sequence Coverage [%]: 5.2
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MAMLRVQPEA	QAKVDVFRED	LCTKTENLLG	SYFPKKISEL	DAFLKEPALN	EANLSNLKAP	LDIPVPDPVK	EKEKEERKKQ
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
QEKEDKDEKK	KGEDEDKGPP	CGPVNCNEKI	VVLLQRLKPE	IKDVIEQLNL	VTTWLQLQIP	RIEDGNNFGV	AVQEKVFELM
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
TSLHTKLEGF	HTQISKYFSE	RGDAVTKAAK	QPHVGDYRQL	VHELDEAEYR	DIRLMVMEIR	NAYVRRLCYM	TSS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1940	1	698.8096	-96.76	2	52.7	12.9	1	25-36	K.TENLLGSYFPKK.I	

Detailed Protein Report

Protein 861: 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 862: 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

Quantitation

QD:QU **Median:** 0.86 **CV:** 0.00 % **No. of 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	Ratios
1458	1	980.9236	-103.15	2	48.4	12.9	2	25-44	R.DRAPGAAGPPSGQIGNRALR.L		QD:QU 0.86

Protein 863: PREDICTED: uncharacterized protein LOC102723625 [Homo sapiens]

Accession:	gi|578820238	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.3
Database Date:	2015-11-30	**pI:**	11.9
		Sequence Coverage [%]:	10.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MIPRKLGPPP KFGNPIQRSQ ECFPSRHAPP EAPRPEAQPP SRLVPLSRPT LEPAPAPYSL PQDPGPSWEL GWTRSSDPRK
        90        100        110        120        130        140        150        160
AQLWAGQGTL QVGGASGTSL RQLRLEAGNR GDDPGPRPLR TSGGRRLWGR SGVGSRASGP HYPVSARGLP ACPPHPAVPT
       170        180        190        200        210        220        230        240
TRCFPVLRRF SQRTQGALPA FPGLPAGDEV PNLAASPDAA VQVCLGGRSL LQSEISLAGH VSTTLNPGLP WFHYRLHVAD
       250
CPQKVSL
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
266	1	1318.5931	-65.41	2	33.3	12.9	1	137-162	R.ASGPHYPVSARGLPACPPHPAVPTTR.C	

Detailed Protein Report

Protein 864: 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 865: PREDICTED: testis-expressed sequence 2 protein isoform X4 [Homo sapiens]

Accession:	gi|530412523	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	125.0
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 2.13 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MTSLYGRHAE	KTTDMPKPSA	PKVHVQRSVS	RDTIAIHFSA	SGEEEEEEEE	EFREYFEEGL	DDQSIVTGLE	AKEDLYLEPQ
90	100	110	120	130	140	150	160
VGHDPAGPAA	SPVLADGLSV	SQAPAILPVS	KNTVKLLESP	VPAAQVLSTV	PLAVSPGSSS	SGPLASSPSV	SSLSEQKTSS
170	180	190	200	210	220	230	240
SSPLSSPSKS	PILSSSASTS	TLSSAKPFMS	LVKSLSTEVE	PKESPHPARH	RHLMKTLVKS	LSTDTSRQES	DTVSYKPPDS
250	260	270	280	290	300	310	320
KLNLHLFKQF	TQPRNTGGDS	KTAPSSPLTS	PSDTRSFFKV	PEMEAKIEDT	KRRLSEVIYE	PFQLLSKIIG	EESGSHRPKA
330	340	350	360	370	380	390	400
LSSSASELSN	LSSLNGHLES	NNNYSIKEEE	CDSEGDGYGS	DSNIPRSDHP	KSTGEPTREI	ELKSSQGSSL	KDLGLKTSSL
410	420	430	440	450	460	470	480
VLEKCSLSAL	VSKEDEEFCE	LYTEDFDLET	EGESKVDKLS	DIPLKPEVLA	EDGVVLDSED	EVDSAVQHPE	LPVKTLGFFI
490	500	510	520	530	540	550	560
MCVYVYLILP	LPHYVSGLFL	GIGLGFMTAV	CVIWFFTPPS	AHKYHKLHKN	LRHWNTRSLD	IKEPEILKGW	MNEIYNYDPE
570	580	590	600	610	620	630	640
TYHATLTHSV	FVRLEGGTLR	LSKPNKNISR	RASYNEPKPE	VTYISQKIYD	LSDSKIYLVP	KTLARKRIWN	KKYPICIELG
650	660	670	680	690	700	710	720
QQDDFMSKAQ	TDKETSEEKP	PAEGSEDPKK	PPRPQEGTRS	SQRDQILYLF	GRTGREKEEW	FRRFILASKL	KSEIKKSSGV
730	740	750	760	770	780	790	800
SGGKPGLLPA	HSRHNSPSGH	LTHSRSSSKG	SVEEIMSQPK	QKELAGSVRQ	KMLLDYSVYM	GRCVPQESRS	PQRSPLQSAE
810	820	830	840	850	860	870	880
SSPTAGKKLP	EVPPSEEEEQ	EAWVNALLGR	IFWDFLGEKY	WSDLVSKKIQ	MKLSKIKLPY	FMNELTLTEL	DMGVAVPKIL
890	900	910	920	930	940	950	960
QAFKPYVDHQ	GLWIDLEMSY	NGSFLMTLET	KMNLTKLGKE	PLVEALKVGE	IGKEGPRAFC	LADSDEESSS	AGSSEEDDAP
970	980	990	1000	1010	1020	1030	1040
EPSGGDKQLL	PGAEGYVGGH	RTSKIMRFVD	KITKSKYFQK	ATETEFIKKK	IEEVSNTPLL	LTVEVQECRG	TLAVNIPPPP
1050	1060	1070	1080	1090	1100	1110	1120
TDRVWYGFRK	PPHVELKARP	KLGEREVTLV	HVTDWIEKKL	EQEFQKVFVM	PNMDDVYITI	MHSAMDPRST	SCLLKDPPVE
1130							
AADQP							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1076	1	581.1694	-231.84	2	41.9	12.9	1	2-11	M.TSLYGRHAEK.T		QD:QU 2.13

Detailed Protein Report

Protein 866: von Willebrand factor preproprotein [Homo sapiens]

Accession:	gi|89191868	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	309.1
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	0.5
		No. of unique 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

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1234	1	729.1614	-193.04	2	44.0	12.9	0	1944-1956	R.WTCPCVCTGSSTR.H	Carbamidomethyl: 5

Detailed Protein Report

Protein 867: **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 868: **astrotactin-1 isoform 2 precursor [Homo sapiens]**

Accession:	gi|46488921	**Score:**	12.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	135.0
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALAGLCALL	ACCWGPAAVL	ATAAGDVDPS	KELECKLKSI	TVSALPFLRE	NDLSIMHSPS	ASEPKLLFSV	RNDFPGEMVV
90	100	110	120	130	140	150	160
VDDLENTELP	YFVLEISGNT	EDIPLVRWRQ	QWLENGTLLF	HIHHQDGAPS	LPGQDPTEEP	QHESAEEELR	ILHISVMGGM
170	180	190	200	210	220	230	240
IALLLSILCL	VMILYTRRRW	CKRRRVPQPQ	KSASAEAANE	IHYIPSVLIG	GHGRESLRNA	RVQGHNSSGT	LSIRETPILD
250	260	270	280	290	300	310	320
GYEYDITDLR	HHLQRECMNG	GEDFASQVTR	TLDSLQGCNE	KSGMDLTPGS	DNAKLSLMNK	YKDNIIATSP	VDSNHQQATL
330	340	350	360	370	380	390	400
LSHTSSSQRK	RINNKARAGS	AFLNPEGDSG	TEAENDPQLT	FYTDPSRSRR	RSRVGSPRSP	VNKTTLTLIS	ITSCVIGLVC
410	420	430	440	450	460	470	480
SSHVNCPLVV	KITLHVPEHL	IADGSRFILL	EGSQLDASDW	LNPAQVVLFS	QQNSSGPWAM	DLCARRLLDP	CEHQCDPETG
490	500	510	520	530	540	550	560
ECLCYEGYMK	DPVHKHLCIR	NEWGTNQGPW	PYTIFQRGFD	LVLGEQPSDK	IFRFTYTLGE	GMWLPLSKSF	VIPPAELAIN
570	580	590	600	610	620	630	640
PSAKCKTDMT	VMEDAVEVRE	ELMTSSSFDS	LEVLLDSFGP	VRDCSKDNGG	CSKNFRCISD	RKLDSTGCVC	PSGLSPMKDS
650	660	670	680	690	700	710	720
SGCYDRHIGV	DCSDGFNGGC	EQLCLQQMAP	FPDDPTLYNI	LMFCGCIEDY	KLGVDGRSCQ	LITETCPEGS	DCGESRELPM
730	740	750	760	770	780	790	800
NQTLFGEMFF	GYNNHSKEVA	AGQVLKGTFR	QNNFARGLDQ	QLPDGLVVAT	VPLENQCLEE	ISEPTPDPDF	LTGMVNFSEV
810	820	830	840	850	860	870	880
SGYPVLQHWK	VRSVMYHIKL	NQVAISQALS	NALHSLDGAT	SRADFVALLD	QFGNHYIQEA	IYGFEESCSI	WYPNKQVQRR
890	900	910	920	930	940	950	960
LWLEYEDISK	GNSPSDESEE	RERDPKVLTF	PEYITSLSDS	GTKHMAAGVR	MECHSKGRCP	SSCPLCHVTS	SPDTPAEPVL
970	980	990	1000	1010	1020	1030	1040
LEVTKAAPIY	ELVTNNQTQR	LLQEATMSSL	WCSGTGDVIE	DWCRCDSTAF	GADGLPTCAP	LPQPVLRLST	VHEPSSTLVV
1050	1060	1070	1080	1090	1100	1110	1120
LEWEHSEPPI	GVQIVDYLLR	QEKVTDRMDH	SKVETETVLS	FVDDIISGAK	SPCAMPSQVP	DKQLTTISLI	IRCLEPDTIY
1130	1140	1150	1160	1170	1180	1190	1200
MFTLWGVDNT	GRRSRPSDVI	VKTPCPVVDD	VKAQEIADKI	YNLFNGYTSG	KEQQTAYNTL	LDLGSPTLHR	VLYHYNQHYE
1210	1220						
SFGEFTWRCE	DELGPR						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
540	1	457.6284	-304.05	2	35.4	12.9	2	371-378	R.RSRVGSPR.S	

Detailed Protein Report

Protein 869: coiled-coil domain-containing protein 108 isoform 4 [Homo sapiens]

Accession: gi|507144067
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 12.8
MW [kDa]: 81.3
pI: 9.1
Sequence Coverage [%]: 1.6
No. of unique Peptides: 1

Quantitation

QD:QU **Median:** 0.98 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MMLTQAPSSV VRSRNSRNHT VNSGGSCLSA STVAIPAIND SSAAMSACST ISAQPASSMD TQMHSPKKQE RVNKRVIWGI

        90        100        110        120        130        140        150        160
EVAEELHWKG WELGKETTRN LVLKNRSLKL QKMKYRPPKT KFFFTVIPQP IFLSPGITLT LPIVFRPLEA KEYMDQLWFE

       170        180        190        200        210        220        230        240
KAEGMFCVGL RATLPCHRLI CRPPSLQLPM CAVGDTTEAF FCLDNVGDLP TFFTWEFSSP FQMLPATGLL EPGQASQIKV

       250        260        270        280        290        300        310        320
TFQPLTAVIY EVQATCWYGA GSRQRSSIQL QAVAKCAQLL VSIKHKCPED QDAEGFQKLL YFGSVAVGCT SERQIRLHNP

       330        340        350        360        370        380        390        400
SAVNAPFRIE ISPDELAEDQ AFSCPTAHGI VLPGEKKCVS VFFHPKTLDT RTVDYCSIMP SGCASKTLLK VVGFCRGPAV

       410        420        430        440        450        460        470        480
SLQHYCVNFS WVNLGERSEQ PLWIENQSDC TAHFQFAIDC LESVFTIRPA FGTLVGKARM TLHCAFQPTH PIICFRRVAC

       490        500        510        520        530        540        550        560
LIHHQDPLFL DLMGTCHSDS TKPAILKPQH LTWYRTHLAR GLTLYPPDIL DAMLKEKKLA QDQNGALMIP IQDLEDMPAP

       570        580        590        600        610        620        630        640
QYPYIPPMTE FFFDGTSDIT IFPPPISVEP VEVDFGACPG PEAPNPVPLC LMNHTKGKIM VVWTRRSDCP FWVTPESCDV

       650        660        670        680        690        700        710        720
PPLKSMAMRL HFQPPHPNCL YTVELEAFAI YKVCARNERE ECGVSARSLS GLVGWQEVTE GSFRLHPLRA RLSLGWTVTP

       730        740
MSLSPPKLLA
```

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	287-298	K.CPEDQDAEGFQK.L	Carbamidomethyl: 1	QD:QU 0.98

Detailed Protein Report

Protein 870: PREDICTED: coiled-coil domain-containing protein 146 isoform X3 [Homo sapiens]

Accession:	gi|530386260	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.2
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MQTSSPTTRL	FLRIKEKSLK	EEKIIIVKEF	EKITKPGEME	KKMKILREST	EELRKEIMQK	KLEIKNLRED	LASKQKQLLK
90	100	110	120	130	140	150	160
EQKELEELLG	HQVVLKDEVA	HHQTIPVQIG	KEIEKITRKK	VEMEKKKIVL	EQEVKTLNDS	LKKVENKVSA	IVDEKENVIK
170	180	190	200	210	220	230	240
EVEGKRALLE	IKEREHNQLV	KLLELARENE	ATSLTERGIL	DLNLRNSLID	KQNYHDELSR	KQREKERDFR	NLRKMELLLK
250	260	270	280	290	300	310	320
VSWDALRQTQ	ALHQRLLLEM	EAIPKDDSTL	SERRRELHKE	VEVAKRNLAQ	QKIISEMESK	LVEQQLAEEN	KLLKEQENMK
330	340	350	360	370	380	390	400
ELVVNLLRMT	QIKIDEKEQK	SKDFLKAQQK	YTNIVKEMKA	KDLEIRIHKK	KKCEIYRRLR	EFAKLYDTIR	NERNKFVNLL
410	420	430	440	450	460	470	480
HKAHQKVNEI	KERHKMSLNE	LEILRNSAVS	QERKLQNSML	KHANNVTIRE	SMQNDVRKIV	SKLQEMKEKK	EAQLNNIDRL
490	500	510	520	530	540	550	560
ANTITMIEEE	MVQLRKRYEK	AVQHRNESGV	QLIEREEEIC	IFYEKINIQE	KMKLNGEIEI	HLLEEKIQFL	KMKIAEKQRQ
570	580	590	600	610	620	630	640
ICVTQKLLPA	KRSLDADLAV	LQIQFSQCTD	RIKDLEKQFV	KPDGENRARF	LPGKDLTEKE	MIQKLDKLEL	QLAKKEEKLL
650	660	670	680	690	700	710	720
EKDFIYEQVS	RLTDRLCSKT	QGCKQDTLLL	AKKMNGYQRR	IKNATEKMMA	LVAELSMKQA	LTIELQKEVR	EKEDFIFTCN
730	740	750	760	770	780	790	800
SRIEKGLPLN	KEIEKEWLKV	LRDEEMHALA	IAEKSQEFLE	ADNRQLPNGV	YTTAEQRPNA	YIPEADATLP	LPKPYGALAP
810	820	830					
FKPSEPGANM	RHIRKPVIKP	VEI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2135	1	754.0400	192.03	2	57.1	12.8	2	329-340	R.MTQIKIDEKEQK.S	Oxidation: 1

Detailed Protein Report

Protein 871: spermatogenesis-associated protein 31E1 [Homo sapiens]

Accession:	gi|155029550	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	157.0
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

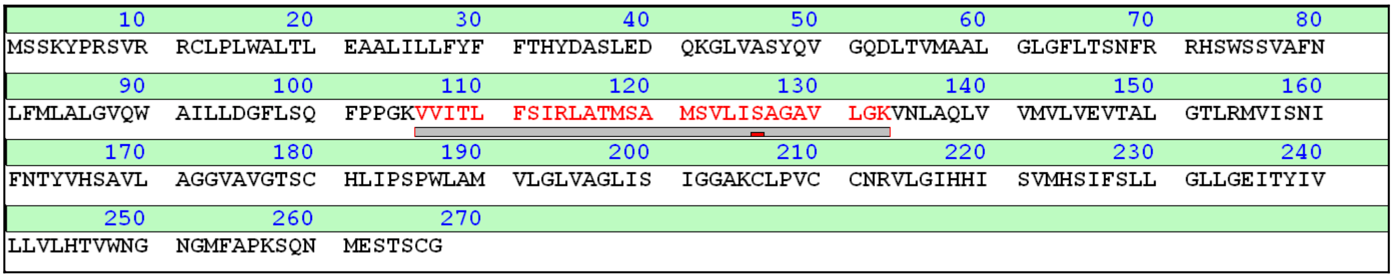
10	20	30	40	50	60	70	80
MGNLVIPLGK	GRAGRVESGQ	RIPPPAPRPS	VECTGDDIAL	QMEKMLFPLK	SPSATWLSPS	STPWMMDFIL	TSVCGLVLLF
90	100	110	120	130	140	150	160
LLLLYVHSDP	PSPPPGRKRS	SREPQRERSG	RSRSRKISAL	KACRILLREL	EETRDLNYLL	ESHLRKLAGE	GSSHLPLGGD
170	180	190	200	210	220	230	240
PLGDVCKPVP	AKAHQPHGKC	MQDPSPASLS	PPAPPAPLAS	TLSPGPMTFS	EPFGPHSTLS	ASGPPEPLLP	LKCPATQPHV
250	260	270	280	290	300	310	320
VFPPSPQPHG	PLASSPPPPD	SSLAGLQCGS	TTCPVPQSSP	LHNQVLPPPT	RVISGLGCSS	DPIWDLYCWR	EAATTWGLST
330	340	350	360	370	380	390	400
YSHGKSQPRH	LPDHTSEASF	WGDPTPKHME	VGGCTFIHPD	VQKLLETLIA	KRALMKMWQE	KERKRADHPH	MTSLGKEWDI
410	420	430	440	450	460	470	480
TTLNPFWNVS	TQPQQLPRPQ	QVSDATTVGN	HLQQKRSQLF	WDLPSLNSES	LATTVWVSRN	PSSQNAHSVP	LDKASTSLPG
490	500	510	520	530	540	550	560
EPEVEASSQL	SQAPPQPHHM	AQPQHFTPAW	PQSQPPPLAE	IQTQAHLSPP	VPSLGCSSPP	QIRGCGASYP	TSQERTQSVI
570	580	590	600	610	620	630	640
PTGKEYLEWP	LKKRPKWKRV	LPSLLKKSQA	VLSQPTAHLP	QERPASWSPK	SAPILPGVVT	SPELPEHWWQ	GRNAIHQEQS
650	660	670	680	690	700	710	720
CGPPSRLQAS	GDLLQPDGEF	PGRPQSQAED	TQQALLPSQP	SDFAGKGRKD	VQKTGFRSSG	RFSDKGCLGS	KLGPDPSRDQ
730	740	750	760	770	780	790	800
GSGRTSVKAL	DEDKEAEGDL	RRSWKYQSVS	STPRDPDKEH	LENKLQIHLA	RKVGEIKEGW	IPMPVRRSWL	MAKCAVPKSD
810	820	830	840	850	860	870	880
THRKPGKLAS	WRGGKAHVNT	SQELSFLHPC	TQQILEVHLV	RFCVRHSWGT	DLQSLEPINV	WSGEAQAPPF	PQSTFTPWAS
890	900	910	920	930	940	950	960
WVSRVESVPK	VPIFLGKRPQ	NGPGDNRTTS	KSVPTVSGPL	AAPPPEQEGV	QRPPRGSQSA	DTHGRSEAFP	TGHKGRGCSQ
970	980	990	1000	1010	1020	1030	1040
PPTCSLVGRT	WQSRTVLESG	KPKPRLEGSM	GSEMAGNEAW	LESESMSPGD	PCSSRALQVL	SIGSQWARAE	DALQALKVGE
1050	1060	1070	1080	1090	1100	1110	1120
KPPTWEVTLG	ASVRASSGSV	QEDLRSTGAL	GTTGNPSASS	VCVAQDPEQL	HLKAQVVSEI	ALIVQVDSEE	QLPGRAPGIL
1130	1140	1150	1160	1170	1180	1190	1200
LQDGATGLCL	PGRHMDMLTA	ADRLPTQAPL	STSQSVSGKN	MTASQGPCAL	LWKGGDSPGQ	QEPGSPKAKA	PQKSQKTLGC
1210	1220	1230	1240	1250	1260	1270	1280
ADKGEAHRRP	RTGEQGHRSK	GPRTSEASGR	SHPAQAREIG	DKQERKYNQL	QLEKGQTPPE	SHFQRKISHH	PQGLHPRKGG
1290	1300	1310	1320	1330	1340	1350	1360
TRWEDVLQKG	KPGADAFQSW	GSGPPRQFMD	CMADKAWTIS	RVVGQILVDK	LGLQWGRGPS	EVNRHKGDFR	AQENVPSCCH
1370	1380	1390	1400	1410	1420	1430	1440
RGHCHQERSR	EMRALACSPK	ATPKGHHCPV	KNRGIRDRDS	SWAPPPREPV	SPAGPHHHRP	RMASTSGGPH	PQLQELMSAQ
1450							
RCLAS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2526	1	574.6432	-239.26	2	60.3	12.8	0	1055-1065	R.ASSGSVQEDLR.S	

Detailed Protein Report

Protein 872: **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



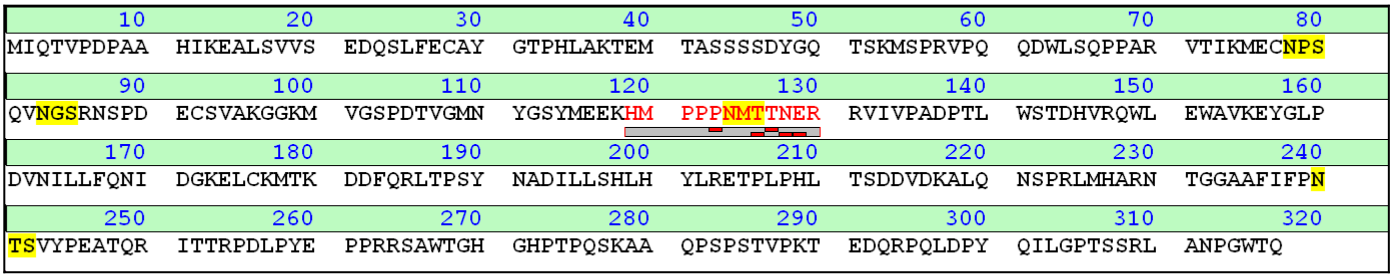
```
        10         20         30         40         50         60         70         80
MSSKYPRSVR RCLPLWALTL EAALILLFYF FTHYDASLED QKGLVASYQV GQDLTVMAAL GLGFLTSNFR RHSWSSVAFN
        90        100        110        120        130        140        150        160
LFMLALGVQW AILLDGFLSQ FPPGKVVITL 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 873: transcriptional regulator ERG isoform 6 [Homo sapiens]

Accession:	gi|343478184	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.3
Database Date:	2015-11-30	**pI:**	6.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1



10	20	30	40	50	60	70	80
MIQTVPDPAA	HIKEALSVVS	EDQSLFECAY	GTPHLAKTEM	TASSSSDYGQ	TSKMSPRVPQ	QDWLSQPPAR	VTIKMECNPS
90	100	110	120	130	140	150	160
QVNGSRNSPD	ECSVAKGGKM	VGSPDTVGMN	YGSYMEEKHM	PPPNMTTNER	RVIVPADPTL	WSTDHVRQWL	EWAVKEYGLP
170	180	190	200	210	220	230	240
DVNILLFQNI	DGKELCKMTK	DDFQRLTPSY	NADILLSHLH	YLRETPLPHL	TSDDVDKALQ	NSPRLMHARN	TGGAAFIFPN
250	260	270	280	290	300	310	320
TSVYPEATQR	ITTRPDLPYE	PPRRSAWTGH	GHPTPQSKAA	QPSPSTVPKT	EDQRPQLDPY	QILGPTSSRL	ANPGWTQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2099	1	720.7086	-156.70	2	54.8	12.8	0	119-130	K.HMPPPNMTTNER.R	Oxidation: 2

Detailed Protein Report

Protein 874: **tyrosine-protein kinase TXK [Homo sapiens]**

Accession:	gi|148596974	**Score:**	12.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.2
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.99 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MILSSYNTIQ	SVFCCCCCCS	VQKRQMRTQI	SLSTDEELPE	KYTQRRRPWL	SQLSNKKQSN	TGRVQPSKRK	PLPPLPPSEV
90	100	110	120	130	140	150	160
AEEKIQVKAL	YDFLPREPCN	LALRRAEEYL	ILEKYNPHWW	KARDRLGNEG	LIPSNYVTEN	KITNLEIYEW	YHRNITRNQA
170	180	190	200	210	220	230	240
EHLLRQESKE	GAFIVRDSRH	LGSYTISVFM	GARRSTEAAI	KHYQIKKNDS	GQWYVAERHA	FQSIPELIWY	HQHNAAGLMT
250	260	270	280	290	300	310	320
RLRYPVGLMG	SCLPATAGFS	YEKWEIDPSE	LAFIKEIGSG	QFGVVHLGEW	RSHIQVAIKA	INEGSMSEED	FIEEAKVMMK
330	340	350	360	370	380	390	400
LSHSKLVQLY	GVCIQRKPLY	IVTEFMENGC	LLNYLRENKG	KLRKEMLLSV	CQDICEGMEY	LERNGYIHRD	LAARNCLVSS
410	420	430	440	450	460	470	480
TCIVKISDFG	MTRYVLDDEY	VSSFGAKFPI	KWSPPEVFLF	NKYSSKSDVW	SFGVLMWEVF	TEGKMPFENK	SNLQVVEAIS
490	500	510	520	530			
EGFRLYRPHL	APMSIYEVMY	SCWHEKPEGR	PTFAELLRAV	TEIAETW			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1026	1	583.6927	-182.21	2	41.3	12.8	0	395-405	R.NCLVSSTCIVK.I		QD:QU	0.99

Detailed Protein Report

Protein 875: 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

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
2176	1	937.3251	-94.18	2	57.6	12.8	0	74-89	R.DSEYETAETMCQILPK.G	Oxidation: 10

Detailed Protein Report

Protein 876: protein KRI1 homolog [Homo sapiens]

Accession: gi|145580615
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 12.7
MW [kDa]: 83.2
pI: 5.0
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 877: 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

```
         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
477	1	686.3590	14.33	2	35.9	12.7	2	90-101	R.RGRDPEMGGKPR.R	Oxidation: 7

Detailed Protein Report

Protein 878: **PREDICTED: thrombospondin type-1 domain-containing protein 7A isoform X4 [Homo sapiens]**

Accession:	gi|578813343	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	169.7
Database Date:	2015-11-30	**pI:**	9.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGLQARRWAS	GSRGAAGPRR	GVLQLLPLPL	PLPLLLLLLL	RPGAGRAAAQ	GEAEAPTLYL	WKTGPWGRCM	GDECGPGGIQ
90	100	110	120	130	140	150	160
TRAVWCAHVE	GWTTLHTNCK	QAERPNNQQN	CFKVCDWHKE	LYDWRLGPWN	QCQPVISKSL	EKPLECIKGE	EGIQVREIAC
170	180	190	200	210	220	230	240
IQKDKDIPAE	DIICEYFEPK	PLLEQACLIP	CQQDCIVSEF	SAWSECSKTC	GSGLQHRTRH	VVAPPQFGGS	GCPNLTEFQV
250	260	270	280	290	300	310	320
CQSSPCEAEE	LRYSLHVGPW	STCSMPHSRQ	VRQARRRGKN	KEREKDRSKG	VKDPEARELI	KKKRNRNRQN	RQENKYWDIQ
330	340	350	360	370	380	390	400
IGYQTREVMC	INKTGKAADL	SFCQQEKLPM	TFQSCVITKE	CQVSEWSEWS	PCSKTCHDMV	SPAGTRVRTR	TIRQFPIGSE
410	420	430	440	450	460	470	480
KECPEFEEKE	PCLSQGDGVV	PCATYGWRTT	EWTECRVDPL	LSQQDKRRGN	QTALCGGGIQ	TREVYCVQAN	ENLLSQLSTH
490	500	510	520	530	540	550	560
KNKEASKPMD	LKLCTGPIPN	TTQLCHIPCP	TECEVSPWSA	WGPCTYENCN	DQQGKKGFKL	RKRRITNEPT	GGSGVTGNCP
570	580	590	600	610	620	630	640
HLLEAIPCEE	PACYDWKAVR	LGNCEPDNGK	ECGPGTQVQE	VVCINSDGEE	VDRQLCRDAI	FPIPVACDAP	CPKDCVLSTW
650	660	670	680	690	700	710	720
STWSSCSHTC	SGKTTEGKQI	RARSILAYAG	EEGGIRCPNS	SALQEVRSCN	EHPCTVYHWQ	TGPWGQCIED	TSVSSFNTTT
730	740	750	760	770	780	790	800
TWNGEASCSV	GMQTRKVICV	RVNVGQVGPK	KCPESLRPET	VRPCLLPCKK	DCIVTPYSDW	TSCPSSCKEG	DSSIRKQSRH
810	820	830	840	850	860	870	880
RVIIQLPANG	GRDCTDPLYE	EKACEAPQAC	QSYRWKTHKW	RRCQLVPWSV	QQDSPGAQEG	CGPGRQARAI	TCRKQDGGQA
890	900	910	920	930	940	950	960
GIHECLQYAG	PVPALTQACQ	IPCQDDCQLT	SWSKFSSCNG	DCGAVRTRKR	TLVGKSKKKE	KCKNSHLYPL	IETQYCPCDK
970	980	990	1000	1010	1020	1030	1040
YNAQPVGNWS	DCILPEGKVE	VLLGMKVQGD	IKECGQGYRY	QAMACYDQNG	RLVETSRCNS	HGYIEEACII	PCPSDCKLSE
1050	1060	1070	1080	1090	1100	1110	1120
WSNWSRCSKS	CGSGVKVRSK	WLREKPYNGG	RPCPKLDHVN	QAQVYEVVPC	HSDCNQYLWV	TEPWSICKVT	FVNMRENCGE
1130	1140	1150	1160	1170	1180	1190	1200
GVQTRKVRCM	QNTADGPSEH	VEDYLCDPEE	MPLGSRVCKL	PCPEDCVISE	WGPWTQCVLP	CNQSSFRQRS	ADPIRQPADE
1210	1220	1230	1240	1250	1260	1270	1280
GRSCPNAVEK	EPCNLNKNCY	HYDYNVTDWS	TCQLSEKAVC	GNGIKTRMLD	CVRSDGKSVD	LKYCEALGLE	KNWQMNTSCM
1290	1300	1310	1320	1330	1340	1350	1360
VECPVNCQLS	DWSPWSECSQ	TCGLTGKMIR	RRTVTQPFQG	DGRPCPSLMD	QSKPCPVKPC	YRWQYGQWSP	CQVQEAQCGE
1370	1380	1390	1400	1410	1420	1430	1440
GTRTRNISCV	VSDGSADDFS	KVVDEEFCAD	IELIIDGNKN	MVLEESCSQP	CPGDCYLKDW	SSWSLCQLTC	VNGEDLGFGG
1450	1460	1470	1480	1490	1500	1510	1520
IQVRSRPVII	QELENQHLCP	EQMLETKSCY	DGQCYEYKWM	ASAWKGSSRT	VWCQRSDGIN	VTAKSQRNPK	EGKTTD

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1536	2	977.3535	-97.31	2	47.7	12.7	1	394-409	R.QFPIGSEKECPEFEEK.E	Carbamidomethyl: 10

Detailed Protein Report

Protein 879: 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; Oxidation: 1

Detailed Protein Report

Protein 880: **tetraspanin-32 [Homo sapiens]**

Accession:	gi|170763493	**Score:**	12.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.6
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	4.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGPWSRVRVA	KCQMLVTCFF	ILLLGLSVAT	MVTLTYFGAH	FAVIRRASLE	KNPYQAVHQW	AFSAGLSLVG	LLTLGAVLSA
90	100	110	120	130	140	150	160
AATVREAQGL	MAGGFLCFSL	AFCAQVQVVF	WRLHSPTQVE	DAMLDTYDLV	YEQAMKGTSH	VRRQELAAIQ	DVFLCCGKKS
170	180	190	200	210	220	230	240
PFSRLGSTEA	DLCQGEEAAR	EDCLQGIRSF	LRTHQQVASS	LTSIGLALTV	SALLFSSFLW	FAIRCGCSLD	RKGKYTLTPR
250	260	270	280	290	300	310	320
ACGRQPQEPS	LLRCSQGGPT	HCLHSEAVAI	GPRGCSGSLR	WLQESDAAPL	PLSCHLAAHR	ALQGRSRGGL	SGCPERGLSD
330							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1946	1	745.7827	-96.21	2	54.7	12.7	2	306-320	R.SRGGLSGCPERGLSD.-	

Detailed Protein Report

Protein 881: **PREDICTED: EGF-containing fibulin-like extracellular matrix protein 1 isoform X2 [Homo sapiens]**

Accession: gi|530367362
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 12.7
MW [kDa]: 59.3
pI: 9.5
Sequence Coverage [%]: 4.2
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MSTCPLWRGV PASLGNEELA REGKRGRQRG PLEQGARTSL RCALYRRARN AGLSARASLS SLLRPPSPSP FPSLSPPPPA
        90        100        110        120        130        140        150        160
AAAAAGLRQI RPTGLPSPAH SPRCPGPERS AAAQVFLLCC ARNSASSRFT MLKALFLTML TLALVKSQDT EETITYTQCT
       170        180        190        200        210        220        230        240
DGYEWDPVRQ QCKDIDECDI VPDACKGGMK CVNHYGGYLC LPKTAQIIVN NEQPQQETQP AEGTSGATTG VVAASSMATS
       250        260        270        280        290        300        310        320
GVLPGGGFVA SAAAVAGPEM QTGRNNFVIR RNPADPQRIP SNPSHRIQCA AGYEQSEHNV CQDIDECTAG THNCRADQVC
       330        340        350        360        370        380        390        400
INLRGSFACQ CPPGYQKRGE QCVDIDECRT SSYLCQYQCV NEPGKFSCMC PQGYQVVRSR TCQDINECET TNECREDEMC
       410        420        430        440        450        460        470        480
WNYHGGFRCY PRNPCQDPYI LTPENRCVCP VSNAMCRELP QSIVYKYMSI RSDRSVPSDI FQIQATTIYA NTINTFRIKS
       490        500        510        520        530        540        550
GNENGEFYLR QTSPVSAMLV LVKSLSGPRE HIVDLEMLTV SSIGTFRTSS VLRLTIIVGP FSF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
952	1	824.0174	-86.17	3	40.4	12.7	2	2-24	M.STCPLWRGVPASLGNEELAREGK.R	

Detailed Protein Report

Protein 882: pre-mRNA-splicing factor CWC22 homolog [Homo sapiens]

Accession:	gi|55749769	**Score:**	12.7
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
868	1	820.4583	123.98	2	40.9	12.7	0	488-501	K.ELCNMILDCCAQQR.T	

Detailed Protein Report

Protein 883: PREDICTED: RING finger protein 17 isoform X9 [Homo sapiens]

Accession: gi|578824965
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 12.7
MW [kDa]: 174.6
pI: 5.1
Sequence Coverage [%]: 1.6
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	WYRAKVIELN	HWESCWKSCI	DRTKQQKLII	QKPVNSSLML
650	660	670	680	690	700	710	720
TVCLSHAILI	VKVQIKGLPG	HQEVEVKYVD	FGNTAKITIK	DVRKIKDEFL	NAPEKAIKCK	LAYIEPYKRT	MQWSKEAKEK
730	740	750	760	770	780	790	800
FEEKAQDKFM	TCSVIKILED	NVLLVELFDS	LGAPEMTTTS	INDQLVKEGL	ASYEIGYILK	DNSQKHIEVW	DPSPEEIISN
810	820	830	840	850	860	870	880
EVHNLNPVSA	KSLPNENFQS	LYNKELPVHI	CNVISPEKIY	VQWLLTENLL	NSLEEKMIAA	YENSKWEPVK	WENDMHCAVK
890	900	910	920	930	940	950	960
IQDKNQWRRG	QIIRMVTDTL	VEVLLYDVGV	ELVVNVDCLR	KLEENLKTMG	RLSLECSLVD	IRPAGGSDKW	TATACDCLSL
970	980	990	1000	1010	1020	1030	1040
YLTGAVATII	LQVDSEENNT	TWPLPVKIFC	RDEKGERVDV	SKYLIKKGLA	LRERRINNLD	NSHSLSEKSL	EVPLEQEDSV
1050	1060	1070	1080	1090	1100	1110	1120
VTNCIKTNFD	PDKKTADIIS	EQKVSEFQEK	ILEPRTTRGY	KPPAIPNMNV	FEATVSCVGD	DGTIFVVPKL	SEFELIKMTN
1130	1140	1150	1160	1170	1180	1190	1200
EIQSNLKCLG	LLEPYFWKKG	EACAVRGSDT	LWYRGKVMEV	VGGAVRVQYL	DHGFTEKIPQ	CHLYPILLYP	DIPQFCIPCQ
1210	1220	1230	1240	1250	1260	1270	1280
LHNTTPVGNV	WQPDAIEVLQ	QLLSKRQVDI	HIMELPKNPW	EKLSIHLYFD	GMSLSYFMAY	YKYCTSEHTE	EMLKEKPRSD
1290	1300	1310	1320	1330	1340	1350	1360
HDKKYEEEQW	EIRFEELLSA	ETDTPLLPPY	LSSSLPSPGE	LYAVQVKHVV	SPNEVYICLD	SIETSNQSNQ	HSDTDDSGVS
1370	1380	1390	1400	1410	1420	1430	1440
GESESESLDE	ALQRVNKKVE	ALPPLTDFRT	EMPCLAEYDD	GLWYRAKIVA	IKEFNPLSIL	VQFVDYGSTA	KLTLNRLCQI
1450	1460	1470	1480	1490	1500	1510	1520
PSHLMRYPAR	AIKVLLAGFK	PPLRDLGETR	IPYCPKWSME	ALWAMIDCLQ	GKQLYAVSMA	PAPEQIVTLY	DDEQHPVHMP
1530	1540						
LVEMGLADKD	E						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2739	1	698.3923	-31.29	4	63.2	12.7	0	628-652	K.LIIQKPVNSSLMLTVCLSHAILIVK.V	Carbamidomethyl: 16

Detailed Protein Report

Protein 884: 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

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
607	1	689.3448	-28.75	2	37.6	12.6	2	438-450	K.TSEAAVKEGKTEK.T	

Detailed Protein Report

Protein 885: PREDICTED: killer cell immunoglobulin-like receptor 2DS5 [Homo sapiens]

Accession:	gi|578847295	**Score:**	12.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.6
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSLMVISMAC	VAFFLLQGAW	PHEGFRRKPS	LLAHPGPLVK	SEETVILQCW	SDVMFEHFLL	HREGTFNHTL	RLIGEHIDGV
90	100	110	120	130	140	150	160
SKGNFSIGRM	TQDLAGTYRC	YGSVTHSPYQ	LSAPSDPLDI	VITGLYEKPS	LSAQPGPTVL	AGESVTLSCS	SRSSYDMYHL
170	180	190	200	210	220	230	240
SREGEAHERR	LPAGPKVNGT	FQADFPLDPA	THGGTYRCFG	SFRDSPYEWS	KSSDPLLVSV	TGNSSNSWPS	PTEPSSKTGN
250	260	270	280	290	300	310	
PRHLHVLIGT	SVVKLPFTIL	LFFLLHRWCS	NKKNASVMDQ	GPAGNRTVNR	EDSDEQDHQE	VSYA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1791	1	991.8058	-8.57	3	50.9	12.6	0	1-26	-.MSLMVISMACVAFFLLQGAWPHEGFR.R	Oxidation: 1, 4

Detailed Protein Report

Protein 886: 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

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
2782	1	729.3683	-4.13	2	65.9	12.6	0	241-253	R.FFCLLLGPCMLGK.G	Oxidation: 10

Detailed Protein Report

Protein 887: 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

QD:QU **Median:** 1.84 **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	QD:QU 1.84

Detailed Protein Report

Protein 888: PREDICTED: serine/threonine-protein kinase 38-like isoform X2 [Homo sapiens]

Accession:	gi|530399087	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.0
Database Date:	2015-11-30	**pI:**	8.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAMTAGTTTT	FPMSNHTRER	VTVAKLTLEN	FYSNLILQHE	ERETRQKKLE	VAMEEEGLAD	EEKKLRRSQH	ARKETEFLRL
90	100	110	120	130	140	150	160
KRTRLGLDDF	ESLKVIGRGA	FGEVRLVQKK	DTGHIYAMKI	LRKSDMLEKE	QVAHIRAERD	ILVEADGAWV	VKMFYSFQDK
170	180	190	200	210	220	230	240
RNLYLIMEFL	PGGDMMTLLM	KKDTLTEEET	QFYISETVLA	IDAIHQLGFI	HRDIKPDNLL	LDAKGHVKLS	DFGLCTGLKK
250	260	270	280	290	300	310	320
AHRTEFYRNL	THNPPSDFSF	QNMNSKRKAE	TWKKNRRQLA	YSTVGTPDYI	APEVFMQTGY	NKLCDWWSLG	VIMYEMLIGY
330	340	350	360	370	380	390	400
PPFCSETPQE	TYRKVMNWKE	TLVFPPEVPI	SEKAKDLILR	FCIDSENRIG	NSGVEEIKGH	PFFEGVDWEH	ISAKYHRTGL
410	420						
QIQRLGFSQL	YL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
260	1	619.6380	39.26	3	32.0	12.5	0	2-18	M.AMTAGTTTTFPMSNHTR.E	Oxidation: 2, 12

BRUKER

Detailed Protein Report

Protein 889: 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

Protein 890: 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 891: 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 892: splicing factor 3B subunit 1 isoform 1 [Homo sapiens]

Accession:	gi|54112117	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	145.7
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAKIAKTHED	IEAQIREIQG	KKAALDEAQG	VGLDSTGYYD	QEIYGGSDSR	FAGYVTSIAA	TELEDDDDDY	SSSTSLLGQK
90	100	110	120	130	140	150	160
KPGYHAPVAL	LNDIPQSTEQ	YDPFAEHRPP	KIADREDEYK	KHRRTMIISP	ERLDPFADGG	KTPDPKMNAR	TYMDVMREQH
170	180	190	200	210	220	230	240
LTKEEREIRQ	QLAEKAKAGE	LKVVNGAAAS	QPPSKRKRRW	DQTADQTPGA	TPKKLSSWDQ	AETPGHTPSL	RWDETPGRAK
250	260	270	280	290	300	310	320
GSETPGATPG	SKIWDPTPSH	TPAGAATPGR	GDTPGHATPG	HGGATSSARK	NRWDETPKTE	RDTPGHGSGW	AETPRTDRGG
330	340	350	360	370	380	390	400
DSIGETPTPG	ASKRKSRWDE	TPASQMGGST	PVLTPGKTPI	GTPAMNMATP	TPGHIMSMTP	EQLQAWRWER	EIDERNRPLS
410	420	430	440	450	460	470	480
DEELDAMFPE	GYKVLPPPAG	YVPIRTPARK	LTATPTPLGG	MTGFHMQTED	RTMKSVNDQP	SGNLPFLKPD	DIQYFDKLLV
490	500	510	520	530	540	550	560
DVDESTLSPE	EQKERKIMKL	LLKIKNGTPP	MRKAALRQIT	DKAREFGAGP	LFNQILPLLM	SPTLEDQERH	LLVKVIDRIL
570	580	590	600	610	620	630	640
YKLDDLVRPY	VHKILVVIEP	LLIDEDYYAR	VEGREIISNL	AKAAGLATMI	STMRPDIDNM	DEYVRNTTAR	AFAVVASALG
650	660	670	680	690	700	710	720
IPSLLPFLKA	VCKSKKSWQA	RHTGIKIVQQ	IAILMGCAIL	PHLRSLVEII	EHGLVDEQQK	VRTISALAIA	ALAEAATPYG
730	740	750	760	770	780	790	800
IESFDSVLKP	LWKGIRQHRG	KGLAAFLKAI	GYLIPLMDAE	YANYYTREVM	LILIREFQSP	DEEMKKIVLK	VVKQCCGTDG
810	820	830	840	850	860	870	880
VEANYIKTEI	LPPFFKHFWQ	HRMALDRRNY	RQLVDTTVEL	ANKVGAAEII	SRIVDDLKDE	AEQYRKMVME	TIEKIMGNLG
890	900	910	920	930	940	950	960
AADIDHKLEE	QLIDGILYAF	QEQTTEDSVM	LNGFGTVVNA	LGKRVKPYLP	QICGTVLWRL	NNKSAKVRQQ	AADLISRTAV
970	980	990	1000	1010	1020	1030	1040
VMKTCQEEKL	MGHLGVVLYE	YLGEEYPEVL	GSILGALKAI	VNVIGMHKMT	PPIKDLLPRL	TPILKNRHEK	VQENCIDLVG
1050	1060	1070	1080	1090	1100	1110	1120
RIADRGAEYV	SAREWMRICF	ELLELLKAHK	KAIRRATVNT	FGYIAKAIGP	HDVLATLLNN	LKVQERQNRV	CTTVAIAIVA
1130	1140	1150	1160	1170	1180	1190	1200
ETCSPFTVLP	ALMNEYRVPE	LNVQNGVLKS	LSFLFEYIGE	MGKDYIYAVT	PLLEDALMDR	DLVHRQTASA	VVQHMSLGVY
1210	1220	1230	1240	1250	1260	1270	1280
GFGCEDSLNH	LLNYVWPNVF	ETSPHVIQAV	MGALEGLRVA	IGPCRMLQYC	LQGLFHPARK	VRDVYWKIYN	SIYIGSQDAL
1290	1300	1310					
IAHYPRIYND	DKNTYIRYEL	DYIL					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2825	1	973.5172	42.86	2	64.5	12.5	2	133-150	R.LDPFADGGKTPDPKMNAR.T	Oxidation: 15

Detailed Protein Report

Protein 893: U8 snoRNA-decapping enzyme isoform 2 [Homo sapiens]

Accession:	gi|285026434	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.3
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	10.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAGARRLELG	EALALGSGWR	HACHALLYAP	DPGMLFGRIP	LRYAILMQMR	FDGRLGFPGG	FVDTQDRSLE	DGLNRELREE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
LGEAAAAFRV	ERTDYRSSHV	GSGPRVVAHF	YAKRLTLEEL	LAVEAGATRA	KDHGLEVLGL	VRVPLYTLRD	GVGGLPTFLE
170	**180**	**190**	**200**				
NSFIGSAREQ	LLEALQDLGL	LQSGSISGLK	IPAHH				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2174	1	1057.4538	-108.03	2	55.8	12.5	2	1-20	-.MAGARRLELGEALALGSGWR.H	

Detailed Protein Report

Protein 894: PREDICTED: ankyrin repeat domain-containing protein 54 isoform X2 [Homo sapiens]

Accession:	gi|578836933	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.6
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPMMWKQCSS	CWKMARIPVQ	LMTRAAQLYT	LPHAMAMTRL	CSCSWTMVLI	LTSEMGWGTR	HCTWRPAPTT	FLSSPHCYEE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
VCGFFPSLSS	FSPSPPECSP	QLVPAGARVD	ALDRAGRTPL	HLAKSKLNIL	QEGHAQCLEA	VRLEVKQIIH	MLREYLERLG
170	**180**	**190**	**200**	**210**			
QHEQRERLDD	LCTRLQMTST	KEQVDEVTDL	LASFTSLSLQ	MQSMEKR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1060	1	839.1982	-168.17	2	41.8	12.5	1	1-13	-.MPMMWKQCSSCWK.M	Oxidation: 3, 4

Detailed Protein Report

Protein 895: PREDICTED: F-box/WD repeat-containing protein 1A isoform X1 [Homo sapiens]

Accession:	gi|530394581	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.0
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTIESNWRCG	RHSLQRIHCR	SETSKGVYCL	QYDDQKIVSG	LRDNTIKIWD	KNTLECKRIL	TGHTGSVLCL	QYDERVIITG
90	100	110	120	130	140	150	160
SSDSTVRVWD	VNTGEMLNTL	IHHCEAVLHL	RFNNGMMVTC	SKDRSIAVWD	MASPTDITLR	RVLVGHRAAV	NVVDFDDKYI
170	180	190	200	210	220	230	240
VSASGDRTIK	VWNTSTCEFV	RTLNGHKRGI	ACLQYRDRLV	VSGSSDNTIR	LWDIECGACL	RVLEGHEELV	RCIRFDNKRI
250	260	270	280	290	300	310	320
VSGAYDGKIK	VWDLVAALDP	RAPAGTLCLR	TLVEHSGRVF	RLQFDEFQIV	SSSHDDTILI	WDFLNDPAAQ	AEPPRSPSRT
330							
YTYISR							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2332	3	596.6903	-176.88	2	57.8	12.5	0	148-158	R.AAVNVVDFDDK.Y	

Detailed Protein Report

Protein 896: **PREDICTED: hydroxyacylglutathione hydrolase-like protein isoform X3 [Homo sapiens]**

Accession:	gi|530409265	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.5
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKVKVIPVLE	DNYMYLVIEE	LTREAVAVDV	AVPKRLLEIV	GREGVSLTAV	LTTHHHWDHA	RGNPELARLR	PGLAVLGADE
90	100	110	120	130	140	150	160
RIFSLTRRLA	HGEELRFGAI	HVRCLLTPGH	TAGHMSYFLW	EDDCPDPPAL	FSGDALSVAG	CGSCLEGSAQ	QMYQSLAELG
170	180	190	200	210	220	230	240
TLPPETKVFC	GHEHTLSNLE	FAQKVEPCND	HVRAKLSWAK	ARPLSRRGKR	VGGEGTGFGV	GGALRQGLMV	TGACGHSRRG
250	260	270	280	290	300		
MRMTCPLCRR	LWARSASTTP	SCGWREYGCC	PGASTVTWTL	RKASGDCVLG			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2023	1	698.7910	-48.75	2	53.8	12.5	2	239-249	R.RGMRMTCPLCR.R	Carbamidomethyl: 10; Oxidation: 5

Detailed Protein Report

Protein 897: A disintegrin and metalloproteinase with thrombospondin motifs 20 preproprotein [Homo sapiens]

Accession:	gi|124430557	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	214.6
Database Date:	2015-11-30	**pI:**	7.2
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

Detailed Protein Report

10	20	30	40	50	60	70	80
MWVAKWLTGL	LYHLSLFITR	SWEVDFHPRQ	EALVRTLTSY	EVVIPERVNE	FGEVFPQSHH	FSRQKRSSEA	LEPMPFRTHY
90	100	110	120	130	140	150	160
RFTAYGQLFQ	LNLTADASFL	AAGYTEVHLG	TPERGAWESD	AGPSDLRHCF	YRGQVNSQED	YKAVVSLCGG	LTGTFKGQNG
170	180	190	200	210	220	230	240
EYFLEPIMKA	DGNEYEDGHN	KPHLIYRQDL	NNSFLQTLKY	CSVSESQIKE	TSLPFHTYSN	MNEDLNVMKE	RVLGHTSKNV
250	260	270	280	290	300	310	320
PLKDERRHSR	KKRLISYPRY	IEIMVTADAK	VVSAHGSNLQ	NYILTLMSIV	ATIYKDPSIG	NLIHIVVVKL	VMIHREEEGP
330	340	350	360	370	380	390	400
VINFDGATTL	KNFCSWQQTQ	NDLDDVHPSH	HDTAVLITRE	DICSSKEKCN	MLGLSYLGTI	CDPLQSCFIN	EEKGLISAFT
410	420	430	440	450	460	470	480
IAHELGHTLG	VQHDDNPRCK	EMKVTKYHVM	APALSFHMSP	WSWSNCSRKY	VTEFLDTGYG	ECLLDKPDEE	IYNLPSELPG
490	500	510	520	530	540	550	560
SRYDGNKQCE	LAFGPGSQMC	PHINICMHLW	CTSTEKLHKG	CFTQHVPPAD	GTDCGPGMHC	RHGLCVNKET	ETRPVNGEWG
570	580	590	600	610	620	630	640
PWEPYSSCSR	TCGGGIESAT	RRCNRPEPRN	GGNYCVGRRM	KFRSCNTDSC	PKGTQDFREK	QCSDFNGKHL	DISGIPSNVR
650	660	670	680	690	700	710	720
WLPRYSGIGT	KDRCKLYCQV	AGTNYFYLLK	DMVEDGTPCG	TETHDICVQG	QCMAAGCDHV	LNSSAKIDKC	GVCGGDNSSC
730	740	750	760	770	780	790	800
KTITGVFNSS	HYGYNVVVKI	PAGATNVDIR	QYSYSGQPDD	SYLALSDAEG	NFLFNGNFLL	STSKKEINVQ	GTRTVIEYSG
810	820	830	840	850	860	870	880
SNNAVERINS	TNRQEKELIL	QVLCVGNLYN	PDVHYSFNIP	LEERSDMFTW	DPYGPWEGCT	KMCQGLQRRN	ITCIHKSDHS
890	900	910	920	930	940	950	960
VVSDKECDHL	PLPSFVTQSC	NTDCELRWHV	IGKSECSSQC	GQGYRTLDIH	CMKYSIHEGQ	TVQVDDHYCG	DQLKPPTQEL
970	980	990	1000	1010	1020	1030	1040
CHGNCVFTRW	HYSEWSQCSR	SCGGGERSRE	SYCMNNFGHR	LADNECQELS	RVTRENCNEF	SCPSWAASEW	SECLVTCGKG
1050	1060	1070	1080	1090	1100	1110	1120
TKQRQVWCQL	NVDHLSDGFC	NSSTKPESLS	PCELHTCASW	QVGPWGPCTT	TCGHGYQMRD	VKCVNELASA	VLEDTECHEA
1130	1140	1150	1160	1170	1180	1190	1200
SRPSDRQSCV	LTPCSFISKL	ETALLPTVLI	KKMAQWRHGS	WTPCSVSCGR	GTQARYVSCR	DALDRIADES	YCAHLPRPAE
1210	1220	1230	1240	1250	1260	1270	1280
IWDCFTPCGE	WQAGDWSPCS	ASCGHGKTTR	QVLCMNYHQP	IDENYCDPEV	RPLMEQECSL	AACPPAHSHF	PSSPVQPSYY
1290	1300	1310	1320	1330	1340	1350	1360
LSTNLPLTQK	LEDNENQVVH	PSVRGNQWRT	GPWGSCSSSC	SGGLQHRAVV	CQDENGQSAS	YCDAASKPPE	LQQCGPGPCP
1370	1380	1390	1400	1410	1420	1430	1440
QWNYGNWGEC	SQTCGGGIKS	RLVICQFPNG	QILEDHNCEI	VNKPPSVIQC	HMHACPADVS	WHQEPWTSCS	ASCGKGRKYR
1450	1460	1470	1480	1490	1500	1510	1520
EVFCIDQFQR	KLEDTNCSQV	QKPPTHKACR	SVRCPSWKAN	SWNECSVTCG	SGVQQRDVYC	RLKGVGQVVE	EMCDQSTRPC
1530	1540	1550	1560	1570	1580	1590	1600
SQRRCWSQDC	VQHKGMERGR	LNCSTSCERK	DSHQRMECTD	NQIRQVNEIV	YNSSTISLTS	KNCRNPPCNY	IVVTADSSQC
1610	1620	1630	1640	1650	1660	1670	1680
ANNCGFSYRQ	RITYCTEIPS	TKKHKLHRLR	PIVYQECPVV	PSSQVYQCIN	SCLHLATWKV	GKWSKCSVTC	GIGIMKRQVK
1690	1700	1710	1720	1730	1740	1750	1760
CITKHGLSSD	LCLNHLKPGA	QKKCYANDCK	SFTTCKEIQV	KNHIRKDGDY	YLNIKGRIIK	IYCADMYLEN	PKEYLTLVQG
1770	1780	1790	1800	1810	1820	1830	1840
EENFSEVYGF	RLKNPYQCPF	NGSRREDCEC	DNGHLAAGYT	VFSKIRIDLT	SMQIKTTDLL	FSKTIFGNAV	PFATAGDCYS
1850	1860	1870	1880	1890	1900	1910	1920
AFRCPQGQFS	INLSGTGMKI	SSTAKWLTQG	SYTSVSIRRS	EDGTRFFGKC	GGYCGKCLPH	MTTGLPIQVI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
692	3	730.1835	-205.23	2	37.2	12.5	0	1741-1752	K.IYCADMYLENPK.E	

Detailed Protein Report

Protein 898: **PREDICTED: exportin-4 isoform X3 [Homo sapiens]**

Accession:	gi|530402602	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	97.1
Database Date:	2015-11-30	**pI:**	4.5
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

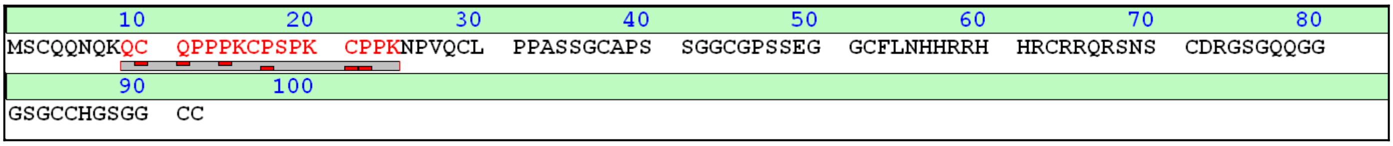
10	20	30	40	50	60	70	80
MAQDSLQCLA	QLASLHGPIF	PDEGSQVDYL	AHFIEGLLNT	INGIEIEDSE	AVGISSIISN	LITVFPRNVL	TAIPSELFSS
90	100	110	120	130	140	150	160
FVNCLTHLTC	SFGRSAALEE	VLDKDDMVYM	EAYDKLLESW	LTLVQDDKHF	HKGFFTQHAV	QVFNSYIQCH	LAAPDGTRNL
170	180	190	200	210	220	230	240
TANGVASREE	EEISELQEDD	RDQFSDQLAS	VGMLGRIAAE	HCIPLLTSLL	EERVTRLHGQ	LQRHQQLLA	SPGSSTVDNK
250	260	270	280	290	300	310	320
MLDDLYEDIH	WLILVTGYLL	ADDTQGETPL	IPPEIMEYSI	KHSSEVDINT	TLQILGSPGE	KASSIPGYNR	TDSVIRLLSA
330	340	350	360	370	380	390	400
ILRVSEVESR	AIRADLTHLL	SPQMGKDIVW	FLKRWAKTYL	LVDEKLYDQI	SLPFSTAFGA	DTEGSQWIIG	YLLQKVISNL
410	420	430	440	450	460	470	480
SVWSSEQDLA	NDTVQLLVTL	VERRERANLV	IQCENWWNLA	KQFASRSPPL	NFLSSPVQRT	LMKALVLGGF	AHMDTETKQQ
490	500	510	520	530	540	550	560
YWTEVLQPLQ	QRFLRVINQE	NFQQMCQQEE	VKQEITATLE	ALCGIAEATQ	IDNVAILFNF	LMDFLTNCIG	LMEVYKNTPE
570	580	590	600	610	620	630	640
TVNLIIEVFV	EVAHKQICYL	GESKAMNLYE	ACLTLLQVYS	KNNLGRQRID	VTAEEEQYQD	LLLIMELLTN	LLSKEFIDFS
650	660	670	680	690	700	710	720
DTDEVFRGHE	PGQAANRSVS	AADVVLYGVN	LILPLMSQDL	LKFPTLCNQY	YKLITFICEI	FPEKIPQLPE	DLFKSLMYSL
730	740	750	760	770	780	790	800
ELGMTSMSSE	VCQLCLEALT	PLAEQCAKAQ	ETDSPLFLAT	RHFLKLVFDM	LVLQKHNTEM	TTAAGEAFYT	LVCLHQAEYS
810	820	830	840	850	860	870	
ELVETLLSSQ	QDPVIYQRLA	DAFNKLTASS	TPPTLDRKQK	MAFLKSLEEF	MANVGGLLCV	K	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2864	1	1132.6268	1.42	2	65.0	12.5	1	197-216	R.IAAEHCIPLLTSLLEERVTR.L	

Detailed Protein Report

Protein 899: late cornified envelope protein 3E [Homo sapiens]

Accession:	gi|30410033	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	9.5
Database Date:	2015-11-30	**pI:**	12.6
		Sequence Coverage [%]:	17.4
		No. of unique Peptides:	1



```
         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
1680	1	867.8636	-74.29	2	49.5	12.5	2	9-24	K.QCQPPPKCPSPKCPPK.N	

Detailed Protein Report

Protein 900: CREB/ATF bZIP transcription factor [Homo sapiens]

Accession:	gi|88900495	**Score:**	12.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	37.1
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	6.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578821635	refseq_human (refseq_human_20140103.fasta)	PREDICTED: CREB/ATF bZIP transcription factor isoform X8 [Homo sapiens]

10	20	30	40	50	60	70	80
MRHSLTKLLA	ASGSNSPTRS	ESPEPAATCS	LPSDLTRAAA	GEEETAAAGS	PGRKQQFGDE	GELEAGRGSR	GGVAVRAPSP
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
EEMEEEAIAS	LPGEETEDMD	FLSGLELADL	LDPRQPDWHL	DPGLSSPGPL	SSSGGGSDSG	GLWRGDDDDE	AAAAEMQRFS
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
DLLQRLLNGI	GGCSSSSDSG	SAEKRRRKSP	GGGGGGGSGN	DNNQAATKSP	RKAAAAAARL	NRLKKKEYVM	GLESRVRGLA
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
AENQELRAEN	RELGKRVQAL	QEESRYLRAV	LANETGLARL	LSRLSGVGLR	LTTSLFRDSP	AGDHDYALPV	GKQKQDLLEE
330	**340**	**350**	**360**				
DDSAGGVCLH	VDKDKVSVEF	CSACARKASS	SLKM				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1905	1	1021.8816	-81.96	2	52.3	12.5	1	189-211	K.SPGGGGGGGSGNDNNQAATKSPR.K	

Detailed Protein Report

Protein 901: ribonuclease pancreatic precursor [Homo sapiens]

Accession:	gi|4506547	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.6
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	14.7
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|38201686	refseq_human (refseq_human_20140103.fasta)	ribonuclease pancreatic precursor [Homo sapiens]
gi|38201684	refseq_human (refseq_human_20140103.fasta)	ribonuclease pancreatic precursor [Homo sapiens]
gi|38201682	refseq_human (refseq_human_20140103.fasta)	ribonuclease pancreatic precursor [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MALEKSLVRL LLLVLILLVL GWVQPSLGKE SRAKKFQRQH MDSDSSPSSS STYCNQMMRR RNMTQGRCKP VNTFVHEPLV
        90        100        110        120        130        140        150        160
DVQNVCFQEK VTCKNGQGNC YKSNSSMHIT DCRLTNGSRY PNCAYRTSPK ERHIIVACEG SPYVPVHFDA SVEDST
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
170	1	1382.5832	10.89	2	30.9	12.4	2	39-61	R.QHMDSDSSPSSSSTYCNQMMRRR.N	Carbamidomethyl: 16; Oxidation: 3

Detailed Protein Report

Protein 902: **PREDICTED: zinc finger protein 449 isoform X1 [Homo sapiens]**

Accession:	gi|530422388	**Score:**	12.4
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

```
        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
2275	1	1130.5320	8.03	2	58.9	12.4	2	215-232	R.THTEERPFKCNYCGKSFR.Q	Carbamidomethyl: 10

Detailed Protein Report

Protein 903: 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 904: transcription factor LBX2 isoform 2 [Homo sapiens]

Accession:	gi|57528437	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.3
Database Date:	2015-11-30	**pI:**	11.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	9.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGKRTSLEVS	LGELGGEKCR	GGRRSFPPLA	ASRPARPGGW	RWARRDLCKT	ASRAENNSQA	CRPQRRAGPD	ALGPGPFGRK
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
RRKSRTAFTA	QQVLELERRF	VFQKYLAPSE	RDGLATRLGL	ANAQVVTWFQ	NRRAKLKRDV	EEMRADVASL	RALSPEVLCS
170	**180**	**190**	**200**				
LALPEGAPDP	GLCLGPAGPD	SRPHLSDEEI	QVDD				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
86	1	1003.1478	137.21	2	29.8	12.4	2	5-23	R.TSLEVSLGELGGEKCRGGR.R	Carbamidomethyl: 15

Detailed Protein Report

Protein 905: **catechol O-methyltransferase isoform S-COMT [Homo sapiens]**

Accession:	gi|6466450	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.4
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGDTKEQRIL NHVLQHAEPG NAQSVLEAID TYCEQKEWAM NVGDKKGKIV DAVIQEHQPS VLLELGAYCG YSAVRMARLL
        90        100        110        120        130        140        150        160
SPGARLITIE INPDCAAITQ RMVDFAGVKD KVTLVVGASQ DIIPQLKKKY DVDTLDMVFL DHWKDRYLPD TLLLEECGLL
       170        180        190        200        210        220        230
RKGTVLLADN VICPGAPDFL AHVRGSSCFE CTHYQSFLEY REVVDGLEKA IYKGPGSEAG P
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1130	1	555.3419	99.52	2	44.3	12.4	1	102-111	R.MVDFAGVKDK.V	

Detailed Protein Report

Protein 906: 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 907: ataxin-7-like protein 1 isoform 3 [Homo sapiens]

Accession:	gi|211971080	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.8
Database Date:	2015-11-30	**pI:**	10.8
		Sequence Coverage [%]:	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCRPSPSPVS	PASNPRTSLV	QVKTKACLSG	HHSASSTSKP	FKTPKDNLLT	SSSKQHTVFP	AKGSRDKPCV	PVPVVSLEKI
90	100	110	120	130	140	150	160
PNLVKADGAN	VKMNSTTTTA	VSASSTSSSA	VSTPPLIKPV	LMSKSVPPSP	EKILNGKGIL	PTTIDKKHQN	GTKNSNKPYR
170	180	190	200	210	220	230	240
RLSEREFDPN	KHCGVLDPET	KKPCTRSLTC	KTHSLSHRRA	VPGRKKQFDL	LLAEHKAKSR	EKEVKDKEHL	LTSTREILPS
250	260	270	280	290	300	310	320
QSGPAQDSLL	GSSGSSGPEP	KVASPAKSRP	PNSVLPRPSS	ANSISSSTSS	NHSGHTPEPP	LPPVGGDLAS	RLSSDEGEMD
330	340	350	360	370	380	390	400
GADESEKLDC	QFSTHHPRPL	AFCSFGSRLM	GRGYYVFDRR	WDRFRFALNS	MVEKHLNSQM	WKKIPPAADS	PLPSPAAHIT
410	420	430	440	450	460	470	480
TPVPASVLQP	FSNPSAVYLP	SAPISSRLTS	SYIMTSAMLS	NAAFVTSPDP	SALMSHTTAF	PHVAATLSIM	DSTFKAPSAV
490	500	510	520	530	540	550	560
SPIPAVIPSP	SHKPSKTKTS	KSSKVKDLST	RSDESPSNKK	RKPQSSTSSS	SSSSSSSLQT	SLSSPLSGPH	KKNCVLNASS
570	580	590	600	610	620	630	640
ALNSYQAAPP	YNSLSVHNSN	NGVSPLSAKL	EPSGRTSLPG	GPADIVRQVG	AVGGSSDSCP	LSVPSLALHA	GDLSLASHNA
650	660	670	680	690	700	710	720
VSSLPLSFDK	SEGKKRKNSS	SSSKACKITK	MPGMNSVHKK	NPPSLLAPVP	DPVNSTSSRQ	VGKNSSLALS	QSSPSSISSP
730	740						
GHSRQKNTNR	TGRIRTLP						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
638	1	776.3466	-53.90	2	36.6	12.4	0	2-16	M.CRPSPSPVSPASNPR.T	

Detailed Protein Report

Protein 908: bisphosphoglycerate mutase [Homo sapiens]

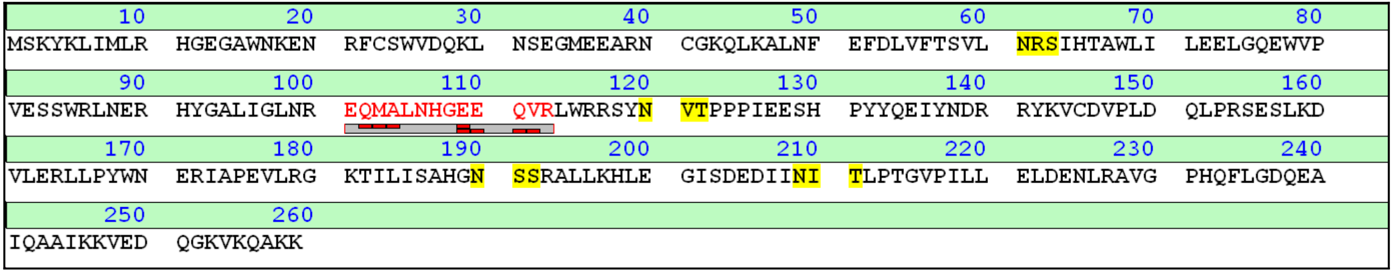
Accession:	gi|4502445	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.0
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:** 1.09	**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
1043	1	770.8455	-21.73	2	41.5	12.4	0	101-113	R.EQMALNHGEEQVR.L		QD:QU 1.09

Detailed Protein Report

Protein 909: **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 910: 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 911: PREDICTED: aspartyl aminopeptidase isoform X4 [Homo sapiens]

Accession:	gi|578803997	**Score:**	12.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.6
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
MAGFSELKET	EKWNIKPESK	YFMTRNSSTI	IAFAVGGQYV	PGNGFSLIGA	HTDSPCLRVK	RRSRRSQVGF	QQVGVETYGG
90	100	110	120	130	140	150	160
GIWSTWFDRD	LTLAGRVIVK	CPTSGRLEQQ	LVHVERPILR	IPHLAIHLQR	NINENFGPNT	EMHLVPILAT	AIQEELEKGT
170	180	190	200	210	220	230	240
PEPGPLNAVD	ERHHSVLMSL	LCAHLGLSPK	DIVEMELCLA	DTQPAVLGGA	YDEFIFAPRL	DNLHSCFCAL	QALIDSCAGP
250	260	270	280	290	300	310	320
GSLATEPHVR	MVTLYDNEEV	GSESAQGAQS	LLTELVLRRI	SASCQHPTAF	EEAIPKSFMI	SADMAHAVHP	NYLDKHEENH
330	340	350	360	370	380	390	400
RPLFHKGPVI	KVNSKQRYAS	NAVSEALIRE	VANKVKVPLQ	DLMVRNDTPC	GTTIGPILAS	RLGLRVLDLG	SPQLAMHSIR
410	420	430	440				
EMACTTGVLQ	TLTLFKGFFE	LFPSLSHNLL	VD				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2198	1	1031.5929	23.90	2	56.1	12.4	2	338-356	R.YASNAVSEALIREVANKVK.V	

Detailed Protein Report

Protein 912: complexin-4 [Homo sapiens]

Accession:	gi|31795561	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.3
Database Date:	2015-11-30	**pI:**	4.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	8.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAFLMKSMIS	NQVKNLGFGG	GSEENKEEGG	ASDPAAAQGM	TREEYEEYQK	QMIEEKMERD	AAFTQKKAER	ACLRVHLREK
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
YRLPKSEMDE	NQIQMAGDDV	DLPEDLRKMV	DEDQEEEEDK	DSILGQIQNL	QNMDLDTIKE	KAQATFTEIK	QTAEQKCSVM
170							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1078	1	820.2655	-85.51	2	42.0	12.3	1	108-120	R.KMVDEDQEEEEDK.D	Oxidation: 2

Detailed Protein Report

Protein 913: PREDICTED: probable tubulin polyglutamylase TTLL2 isoform X1 [Homo sapiens]

Accession:	gi|578812991	**Score:**	12.3
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
531	1	542.2992	-6.22	2	35.3	12.3	1	239-248	K.IKEVIGHGCK.W	

Detailed Protein Report

Protein 914: **PREDICTED: protein-methionine sulfoxide oxidase MICAL3 isoform X15 [Homo sapiens]**

Accession:	gi|578836826	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	153.9
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MELKFLLCCQ	QTYRDLDADN	RGKQSPHHER	KYIKMYTGGV	SSLAEQIANQ	LQRKEQPKAL	LDKKELGSMK	KEFPQNLGGS
90	100	110	120	130	140	150	160
DTCYFCQKRV	YVMERLSAEG	KFFHRSCFKC	EYCATTLRLS	AYAYDIEDGK	FYCKPHYCYR	LSGYAQRKRP	AVAPLSGKEA
170	180	190	200	210	220	230	240
KGPLQDGATT	DANGRANAVA	SSTERTPGSG	VNGLEEPSIA	KRLRGTPERI	ELENYRLSLR	QAEALQEVPE	ETQAEHNLSS
250	260	270	280	290	300	310	320
VLDTGAEEDV	ASSSSESEME	EEGEEEEEEP	RLPPSDLGGV	PWKEAVRIHA	LLKGKSEEEL	EASKSFGPGN	EEEEEEEEEY
330	340	350	360	370	380	390	400
EEEEEEDYDE	EEEESSEAGN	QRLQQVMHAA	DPLEIQADVH	WTHIREREEE	ERMAPASESS	ASGVPDLPSI	RHAAVQAWLE
410	420	430	440	450	460	470	480
TVSGGTPLDE	NDLEEDVDSE	PAEIEGEAAE	DGDPGDTGAE	LDDDQHWSDS	PSDADRELRL	PCPAEGEAEL	ELRVSEDEEK
490	500	510	520	530	540	550	560
LPASPKHQER	GPSQATSPIR	SPQESALLFI	PVHSPSTEGP	QLPPVPAATQ	EKSPEERLFP	EPLLPKEKPK	ADAPSDLKAV
570	580	590	600	610	620	630	640
HSPIRSQPVT	LPEARTPVSP	GSPQPQPPVA	ASTPPPSPLP	ICSQPQPSTE	ATVPSPTQSP	IRFQPAPAKT	STPLAPLPVQ
650	660	670	680	690	700	710	720
SQSDTKDRLG	SPLAVDEALR	RSDLVEEFWM	KSAEIRRSLG	LTPVDRSKGP	EPSFPTPAFR	PVSLKSYSVE	KSPQDEGLHL
730	740	750	760	770	780	790	800
LKPLSIPKRL	GLPKPEGEPL	SLPTPRSPSD	RELRSAQEER	RELSSSSGLG	LHGSSSNMKT	LGSQSFNTSD	SAMLTPPSSP
810	820	830	840	850	860	870	880
PPPPPPGEEP	ATLRRKLREA	EPNASVVPPP	LPATWMRPPR	EPAQPPREEV	RKSFVESVEE	IPFADDVEDT	YDDKTEDSSL
890	900	910	920	930	940	950	960
QEKFFTPPSC	WPRPEKPRHP	PLAKENGRLP	ALEGTLQPQK	RGLPLVSAEA	KELAEERMRA	REKSVKSQAL	RDAMARQLSR
970	980	990	1000	1010	1020	1030	1040
MQQMELASGA	PRPRKASSAP	SQGKERRPDS	PTRPTLRGSE	EPTLKHEATS	EEVLSPPSDS	GGPDGSFTSS	EGSSGKSKKR
1050	1060	1070	1080	1090	1100	1110	1120
SSLFSPRRNK	KEKKSKGEGR	PPEKPSSNLL	EEAAAKPKSL	WKSVFSGYKK	DKKKKADDKS	CPSTPSSGAT	VDSGKHRVLP
1130	1140	1150	1160	1170	1180	1190	1200
VVRAELQLRR	QLSFSEDSDL	SSDDVLEKSS	QKSRRESIYV	PHALAFRRSC	ASKPRTYTEE	ELNAKLTRRV	QKAARRQAKQ
1210	1220	1230	1240	1250	1260	1270	1280
EELKRLHRAQ	IIQRQLQQVE	ERQRRLEERG	VAVEKALRGE	AVEPSGGTPR	RRPLSFCPCC	VQEGMGKKDD	PKLMQEWFKL
1290	1300	1310	1320	1330	1340	1350	1360
VQEKNAMVRY	ESELMIFARE	LELEDRQSRL	QQELRERMAV	EDHLKTEEEL	SEEKQILNEM	LEVVEQRDSL	VALLEEQRLR
1370	1380	1390					
EREEDKDLEA	AMLSKGFSLN	WS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2381	1	937.9548	9.09	2	58.5	12.3	2	15-30	R.DLDADNRGKQSPHHER.K	

Detailed Protein Report

Protein 915: 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 916: 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 917: PREDICTED: 5'-AMP-activated protein kinase catalytic subunit alpha-1 isoform X1 [Homo sapiens]

Accession:	gi|578809939	**Score:**	12.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.4
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVMEYVSGGE	LFDYICKNGR	LDEKESRRLF	QQILSGVDYC	HRHMVVHRDL	KPENVLLDAH	MNAKIADFGL	SNMMSDGEFL
90	100	110	120	130	140	150	160
RTSCGSPNYA	APEVISGRLY	AGPEVDIWSS	GVILYALLCG	TLPFDDDHVP	TLFKKICDGI	FYTPQYLNPS	VISLLKHMLQ
170	180	190	200	210	220	230	240
VDPMKRATIK	DIREHEWFKQ	DLPKYLFPED	PSYSSTMIDD	EALKEVCEKF	ECSEEEVLSC	LYNRNHQDPL	AVAYHLIIDN
250	260	270	280	290	300	310	320
RRIMNEAKDF	YLATSPPDSF	LDDHHLTRPH	PERVPFLVAE	TPRARHTLDE	LNPQKSKHQG	VRKAKWHLGI	RSQSRPNDIM
330	340	350	360	370	380	390	400
AEVCRAIKQL	DYEWKVVNPY	YLRVRRKNPV	TSTYSKMSLQ	LYQVDSRTYL	LDFRSIDDEI	TEAKSGTATP	QRSGSVSNYR
410	420	430	440	450	460		
SCQRSDSDAE	AQGKSSEVSL	TSSVTSLDSS	PVDLTPRPGS	HTIEFFEMCA	NLIKILAQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
274	1	424.1315	-203.85	3	32.2	12.3	1	157-166	K.HMLQVDPMKR.A	Oxidation: 8

Detailed Protein Report

Protein 918: PREDICTED: E3 SUMO-protein ligase PIAS1 isoform X2 [Homo sapiens]

Accession: gi|530406586

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 12.3

MW [kDa]: 70.8

pI: 7.3

Sequence Coverage [%]: 4.2

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MVMSLRVSEL	QVLLGYAGRN	KHGRKHELLT	KALHLLKAGC	SPAVQMKIKE	LYRRRFPQKI	MTPADLSIPN	VHSSPMPATL
90	100	110	120	130	140	150	160
SPSTIPQLTY	DGHPASSPLL	PVSLLGPKHE	LELPHLTSAL	HPVHPDIKLQ	KLPFYDLLDE	LIKPTSLASD	NSQRFRETCF
170	180	190	200	210	220	230	240
AFALTPQQVQ	QISSSMDISG	TKCDFTVQVQ	LRFCLSETSC	PQEDHFPPNL	CVKVNTKPCS	LPGYLPPTKN	GVEPKRPSRP
250	260	270	280	290	300	310	320
INITSLVRLS	TTVPNTIVVS	WTAEIGRNYS	MAVYLVKQLS	STVLLQRLRA	KGIRNPDHSR	ALIKEKLTAD	PDSEIATTSL
330	340	350	360	370	380	390	400
RVSLLCPLGK	MRLTIPCRAL	TCSHLQCFDA	TLYIQMNEKK	PTWVCPVCDK	KAPYEHLIID	GLFMEILKYC	TDCDEIQFKE
410	420	430	440	450	460	470	480
DGTWAPMRSK	KEVQEVSASY	NGVDGCLSST	LEHQVASHHQ	SSNKNKKVEV	IDLTIDSSSD	EEEEEPSAKR	TCPSLSPTSP
490	500	510	520	530	540	550	560
LNNKGILSLP	HQASPVSRTP	SLPAVDTSYI	NTSLIQDYRH	PFHMTPMPYD	LQGLDFFPFL	SGDNQHYNTS	LLAAAAAAVS
570	580	590	600	610	620	630	640
DDQDLLHSSR	FFPYTSSQMF	LDQLSAGGST	SLPTTNGSSS	GSNSSLVSSN	SLRESHSHTV	TNRSSTDTAS	IFGIIPDIIS
650							
LD							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2137	1	1057.0868	-89.61	3	55.3	12.3	1	333-359	R.LTIPCRALTCSHLQCFDATLYIQMNEK.K	Carbamidomethyl: 10

Detailed Protein Report

Protein 919: 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

BRUKER

Detailed Protein Report

Protein 920: 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 921: B-cell CLL/lymphoma 7 protein family member C isoform 2 [Homo sapiens]

Accession:	gi|20336477	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.5
Database Date:	2015-11-30	**pI:**	5.0
		Sequence Coverage [%]:	4.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAGRTVRAET	RSRAKDDIKK	VMATIEKVRR	WEKRWVTVGD	TSLRIFKWVP	VVDPQEEERR	RAGGGAERSR	GRERRGRGAS
90	100	110	120	130	140	150	160
PRGGGPLILL	DLNDENSNQS	FHSEGSLQKG	TEPSPGGTPQ	PSRPVSPAGP	PEGVPEEAQP	PRLGQERDPG	GITAGSTDEP
170	180	190	200	210	220		
PMLTKEEPVP	ELLEAEAPEA	YPVFEPVPPV	PEAAQGDTED	SEGAPPLKRI	CPNAPDP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1204	1	491.6325	-223.38	2	43.6	12.2	1	209-217	K.RICPNAPDP.-	

Detailed Protein Report

Protein 922: PREDICTED: proton-coupled amino acid transporter 4 isoform X4 [Homo sapiens]

Accession:	gi|578821970	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.7
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MHILVRCSHF	LCLRFKKSTL	GYSDTVSFAM	EVSPWSCLQK	QAAWGRSVVD	FFLVITQLGF	CSVYIVFLAE	NVKQVHEGFL
90	100	110	120	130	140	150	160
ESKVFISNST	NSSNPCERRS	VDLRIYMLCF	LPFIILLVFI	RELKNLFVLS	FLANVSMAVS	LVIIYQYVVR	NMPDPHNLPI
170	180	190	200	210	220	230	240
VAGWKKYPLF	FGTAVFAFEG	IGVVLPLENQ	MKESKRFPQA	LNIGMGIVTT	LYVTLATLGY	MCFHDEIKGS	ITLNLPQDVW
250	260	270	280	290	300	310	320
LYQSVKILYS	FGIFVTYSIQ	FYVPAEIIIP	GITSKFHTKW	KQICEFGIRS	FLVSITCAGA	ILIPRLDIVI	SFVGAVSSST
330	340	350	360	370	380	390	400
LALILPPLVE	ILTFSKEHYN	IWMVLKNISI	AFTGVVGFLL	GTYITVEEII	YPTPKVVAGT	PQSPFLNLNS	TCLTSGLK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2948	1	965.1376	114.87	2	66.0	12.2	2	2-16	M.HILVRCSHFLCLRFK.K	Carbamidomethyl: 6

Detailed Protein Report

Protein 923: PREDICTED: mitogen-activated protein kinase kinase kinase 3 isoform X4 [Homo sapiens]

Accession: gi|578830957

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 12.2

MW [kDa]: 60.8

pI: 9.6

Sequence Coverage [%]: 2.2

No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MNNELSILLK NQDDLDKAID ILDRSSSMKS LRILLLSQDR NHNSSSPHSG VSRQVRIKAS QSAGDINTIY QPPEPRSRHL
        90        100        110        120        130        140        150        160
SVSSQNPGRS SPPPGYVPER QQHIARQGSY TSINSEGEFI PETSEQCMLD PLSSAENSLS GSCQSLDRSA DSPSFRKSRM
       170        180        190        200        210        220        230        240
SRAQSFPDNR QEYSDRETQL YDKGVKGGTY PRRYHVSVHH KDYSDGRRTF PRIRRHQGNL FTLVPSSRSL STNGENMGLA
       250        260        270        280        290        300        310        320
VQYLDPRGRL RSADSENALS VQERNVPTKS PSAPINWRRG KLLGQGAFGR VYLCYDVDTG RELASKQVQF DPDSPETSKE
       330        340        350        360        370        380        390        400
VSALECEIQL LKNLQHERIV QYYGCLRDRA EKTLTIFMEY MPGGSVKDQL KAYGALTESV TRKYTRQILE GMSYLHSNMI
       410        420        430        440        450        460        470        480
VHRDIKGANI LRDSAGNVKL GDFGASKRLQ TICMSGTGMR SVTGTPYWMS PEVISGEGYG RKADVWSLGC TVVEMLTEKP
       490        500        510        520        530        540        550
PWAEYEAMAA IFKIATQPTN PQLPSHISEH GRDFLRRIFV EARQRPSAEE LLTHHFAQLM Y
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2789	1	665.3703	103.21	2	63.9	12.2	0	429-440	R.LQTICMSGTGMR.S	Oxidation: 6, 11

Detailed Protein Report

Protein 924: 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 925: PREDICTED: uncharacterized protein LOC144535 [Homo sapiens]

Accession:	gi|578796689	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	322.3
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:** 0.59	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MAAQGSPSSS	PSDDSTTSGS	LPELPPTSTA	TSRSPPESKG	SSRSSLLQWT	CPEDSLPLAV	FYGPLDAKNP	LLASCEKEIQ
90	100	110	120	130	140	150	160
ELLGFMRKKK	ALATTEEEKH	EFRRRCATSL	FNIWTKYAPR	LPADYYNEKL	LKVGDSLCQM	KEYKLALLQC	YGRYLQQFNT
170	180	190	200	210	220	230	240
NFDENKVDVT	QFKATFFPKG	FKDKTAGLTF	HALSGKNMCN	YQLVCDSDEN	LKNKESVVQC	LHILSSLRLI	MQVALPQEHL
250	260	270	280	290	300	310	320
CWIIFNGTIY	IYTICRKLMV	IGQSSKALEY	LLWASMCMES	LVPLLSLRYL	TWRATLYTAV	CQCCYDCHAG	IHGEAFARRA
330	340	350	360	370	380	390	400
LAKIDELRQL	ELMSSSKSQE	ESRRYFREAT	MKMAVMIFKR	GVFESRRKNK	AVFRPKIRIN	LREVQTLSWP	RTVTERLLDE
410	420	430	440	450	460	470	480
MFDSTASQFL	AVLEALSDSN	RRILQTGPIV	TDEVEIHDVV	SELFMAGKEL	LIMSNIGADG	MLDFPKTSLL	ELMIGRKDVI
490	500	510	520	530	540	550	560
SVDAAVKFIK	LAFTYEEWSL	FESSAVHLIY	FLQRQDDPES	KKAEKDLTLL	IAMEPLINVK	RNKGLIFPLE	NYKEGQSAQI
570	580	590	600	610	620	630	640
YFKKIAVHDT	CLKTCGYSED	IFHLAATLYV	CVCTAPQDVQ	PDKEIVVDTI	MFLWQKCKLG	IQRLNISRND	YAKFTQKIST
650	660	670	680	690	700	710	720
NKWIYLLWQI	NEVIHCYKME	DIDIVVVAEV	TLRLSEILES	LGSPGRKFKQ	SLDVPLREGT	NKFPGAPKGI	TEILPILQKN
730	740	750	760	770	780	790	800
PVEQLLFAYK	LLDRAIGGIN	LNCMLTSLPN	GSSVIDHCYA	KRTHHIDGDT	YKPLASNSFM	MDLHLELIQA	QHRIAVVLLD
810	820	830	840	850	860	870	880
KLQVLQTPTV	SKDISTKGPE	KLKQSGSTDC	FTELNIMNKI	KKNTLSKAIY	LMQKALLIFE	KDATSTSSWE	LLMEAYSLIQ
890	900	910	920	930	940	950	960
RIEAEQNALY	SYQKYLESSK	RKKSRVPPPP	ILLSRTHCSV	TLKPAPFTSE	VKVSWYCILG	CKAEGSYGKV	RLNNNHLPNS
970	980	990	1000	1010	1020	1030	1040
GEAIPADGKS	VFEVKGLETN	EKYVFAVAAY	SNNGKLVGGA	IGETTKPILV	YPPLSTITAR	MFLTQVAYQV	GNYELAKKVF
1050	1060	1070	1080	1090	1100	1110	1120
SPVWDYFVAS	PLQDEQSVIC	LSNIITITQR	RLHSDILAET	SSILLYLFLR	NIFVTSDIKI	KEENLFCDNI	KGNEIFPSQQ
1130	1140	1150	1160	1170	1180	1190	1200
IARLIECERV	LVALELSNFL	NDSSYALQAV	TQCYGLLAPI	IYHNIVLVPV	VQILIKCIVV	LQGLPSIVCS	KKHTASFESI
1210	1220	1230	1240	1250	1260	1270	1280
QHMIACCIFY	ITKILRSWRE	YDLAVMIINY	GKKMLDITPG	CKSLFDGSNE	QEEMPEEDSS	KKSLKTKKPQ	QILLPEKINE
1290	1300	1310	1320	1330	1340	1350	1360
QLALLETHLL	KLTKQYVTSE	LSGGEDPIFL	YPVVLNWSVK	GAVKEVMKFK	QKPRFLEFFT	QVMLKCMNEE	KFHLMVEVTT
1370	1380	1390	1400	1410	1420	1430	1440
PVHDFLKRRN	ESLLGLIKVK	YKDSALNKKA	NKSLKFKAAV	MEIGRSAEMQ	QRIRSKKKET	LRDFIFKNPA	ISEMVAHERN
1450	1460	1470	1480	1490	1500	1510	1520
RRTSVRKAAQ	RYLMDYLNPL	ILSYVKRKRF	HRLSLEEMPW	RAQMNLYLAG	AHFNLVLQKL	WECTKMKFGT	SHMMVSFRSC
1530	1540	1550	1560	1570	1580	1590	1600
DPNMFSLYNS	GTVLPTRKLT	VENYKAMLDF	LLTAKKRKAN	LPSDAEEFST	FINSIMSDEN	MSKTQTVYDS	DSQSGSSAKE
1610	1620	1630	1640	1650	1660	1670	1680
KDRGANLCVM	DHFMKIFLYC	RRAMVLAHRG	GYWTLLQNCC	RALWNFTQEL	QILLKQAVDL	DKTFPISQDG	FLCTSVLPFY
1690	1700	1710	1720	1730	1740	1750	1760
LGAELLIDML	IQLQNTSSIK	PIEDKGEFSV	PSCYGNIKND	NGGSSLTFEH	PLDDVNVVDL	KWIHDFVLKS	LEVLYQVEKW
1770	1780	1790	1800	1810	1820	1830	1840
ETLVSLAIQF	NTVSHERYTE	QVTPLLVYAQ	RQLLLRIQKF	KGPDITQQPC	ARYEAEYGEK	ITCRNFIGKQ	LKINSSTIEA
1850	1860	1870	1880	1890	1900	1910	1920
TSNCTDLLKM	LISSEYSRAK	ALVCVPVDVT	DTLRCFRETL	EKSKYHNRSI	RHSRKLLSLF	LAQTQGEKGE	INDSKCTSGK
1930	1940	1950	1960	1970	1980	1990	2000
VEFCLGTEEM	HMSIPPDLSQ	EHFRVFSSVE	KSKLPYSQLG	LVISSYHQTI	DVLQASNQRS	LKVQALHSLG	SLLIFAEKKR
2010	2020	2030	2040	2050	2060	2070	2080
AAFKCWCQAL	DDIFRKPDVL	HTWKEFGPSL	TNVTNSHSPP	GFKDYSEEFL	SRVGIWGCLQ	GAVISAKIAQ	FIKSLNVEKK
2090	2100	2110	2120	2130	2140	2150	2160
TDCCILSALL	FQGLLRTTLP	HPKAERCYAQ	YEITQLLPGI	ELFSDRYRAD	ICSVIASLYY	IIRELHFVRQ	NLIVLPLLAL
2170	2180	2190	2200	2210	2220	2230	2240
YQYFVSGICQ	DITRNLEARI	LKIEVLIDLR	FFSEAFYEIS	QIFYGKNMPC	PIPAGYKATG	KMKIFQSFDS	GKPLTSKENI
2250	2260	2270	2280	2290	2300	2310	2320
QAIDELRNKG	LPAVLVTIGQ	PHLLNKFNFV	KAYFFLSVAA	TINCVPENKF	KTVITNKSKP	NLPNLKEIYS	KDDGSSFYNL
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	Ratios
2780	1	973.5049	-1.76	2	63.8	12.2	2	1398-1414	K.AAVMEIGRSAEMQQRIR.S		QD:QU 0.59

Detailed Protein Report

Protein 926: **PREDICTED: nuclear factor erythroid 2-related factor 1 isoform X6 [Homo sapiens]**

Accession:	gi|530412326	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.1
Database Date:	2015-11-30	**pI:**	4.4
		Sequence Coverage [%]:	1.2
		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
1364	1	945.1721	-308.27	1	45.6	12.2	0	170-178	K.EDIDLGAGR.E	

Detailed Protein Report

Protein 927: 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 928: PREDICTED: cytokine receptor-like factor 1 isoform X1 [Homo sapiens]

Accession: gi|578833719
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 12.2
MW [kDa]: 36.8
pI: 9.9
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 929: vacuolar protein sorting-associated protein 41 homolog isoform 2 [Homo sapiens]

Accession: gi|114199473
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 12.2
MW [kDa]: 95.9
pI: 5.6
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 930: **PREDICTED: phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein isoform X1 [Homo sapiens]**

Accession:	gi|530418228	**Score:**	12.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.0
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

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
946	1	628.3451	-22.84	2	41.9	12.2	1	748-759	K.LPSRLEGGASLR.L	

Detailed Protein Report

Protein 931: putative ankyrin repeat domain-containing protein 31 [Homo sapiens]

Accession:	gi|256574792	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	210.7
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEEGVQAPDW	DSDETVIEGS	VTESDLEEKE	LPWRRLLFDQ	DASLKSEFSL	HPDTRGMCKG	MPSPEIQLGF	KLREDLQEQM
90	100	110	120	130	140	150	160
NKNKMMPVLS	EDTILQSQDE	TERNQALLQT	RKNCSMFIGS	FRQSGLSLNH	QNIEGPEAES	PEVLPHIEKE	LSEGRDSPEV
170	180	190	200	210	220	230	240
SLLSGTAITV	SDTVAVKETS	LVEPEKILAA	PNTFFEPRKE	VTMTMTSEET	KDEESSLETF	VSALESLLTS	PESTQEERLF
250	260	270	280	290	300	310	320
ELVSDFDRKE	LMNPLSDSLS	SISIPLNSWS	ACHRDLLEDA	KDDALPAELL	EALNTLSEAK	VETICHRKEG	GSSLIARNEC
330	340	350	360	370	380	390	400
LEVEFNTSQT	NEDCTQIAET	LQDPNPSGLQ	TLAHQNITSC	EPLSNKRNSN	SVTNSSDQET	ACVLRRSSRL	EKLKVSRDAK
410	420	430	440	450	460	470	480
YSDHMYKMPE	KILPKILGCE	DLTNNNSSAQ	NFRMQDPALM	IDGKEKNMHS	ARFKNGKQIR	KNEQFSGKKE	KMKVNKISLH
490	500	510	520	530	540	550	560
SINRRNIFGE	NLVYKAALHD	DADLVHHCIK	KGGNVNQPSY	AGWTALHEAS	VGGFYRTASE	LLKGGADVNI	KGLYQITPLH
570	580	590	600	610	620	630	640
DAVMNGHYKV	AELLLLNGAD	PLFRNDDGKC	ALDEAKDLCM	KRLLERYIPK	HQKCLTSAQR	SSIDPLDIED	VYQHKKPKFS
650	660	670	680	690	700	710	720
SKSHIWHVYN	ENSNRQKLEH	VKVNKGSKAS	LFINKEDVYE	YYQKDPKNTK	FGKSKHKQST	LDQIYSTGLR	KGNLHNVKDP
730	740	750	760	770	780	790	800
NTNVPKGIGR	RKTQHKRTQV	DDVDCNPRKI	LAVSPSRRIN	RLVTYQQHIP	ETHNDLPEEL	CEPSSLTLSS	LRNGLDSSTE
810	820	830	840	850	860	870	880
ACSVSKEKHI	QNLDLSDSQE	VQCLELESVD	QTEAVSFPGL	LLHKEIKLPV	VTTDKQPHTL	QEQHHVLYKS	HENSNLVPKD
890	900	910	920	930	940	950	960
ERFNKWENSF	LSFVKENSDN	DDDDDCSTSE	KAITSKKVLC	STGGKKHYNF	KENLTNKKEM	GFQQFLLSED	HLSQENELKA
970	980	990	1000	1010	1020	1030	1040
VSLTTLPEQE	AVNFSYSDNA	VISEHVANYE	QCIFGPSFDH	SNGNPEQNSL	ACMRTLLTHE	ASKLTNHVEL	FKKPQDYIPR
1050	1060	1070	1080	1090	1100	1110	1120
APTFLMNQTD	THIVEKMAKN	CDTERNYIDR	DQKIIYSNEP	LSIVAHSQVI	ETTKVEKRRQ	NHLESETIHN	IDSHSTDNMS
1130	1140	1150	1160	1170	1180	1190	1200
KELANISKLS	QREKKEISHK	PGMKAGRINK	RNARGESQLH	LAVRRGNLPL	VKALIESGAD	VNLNDNAGWT	PLHEASNEGS
1210	1220	1230	1240	1250	1260	1270	1280
IDIIVELLKA	GAKVNCENID	GILPLHDAVA	NNHLKAAEIL	LQNGANPNQK	DQKQKSALDE	ADDEKMKELL	RSYGAIETVN
1290	1300	1310	1320	1330	1340	1350	1360
RDESDAIVNE	KIPAVRSKRH	KQCFCDDGKT	IDSSSLSHQE	RSRESLSVHQ	TLSAILQDIE	EKQEYLLEFE	IRNPEDAEQY
1370	1380	1390	1400	1410	1420	1430	1440
IEKMLKIKKI	MDNVLAKQKA	ERDDLAKKYR	VSIESFKHGA	LREQLANLAA	RQKSLLVVAK	KQKKISLKIQ	NCRNVTSLPC
1450	1460	1470	1480	1490	1500	1510	1520
LSLRKLPPRS	EISSEKDSQE	LTSLENLEHP	QSGSLSPVSG	SMQETQLSLE	TWNYSQNTNI	CLNSEAVRRG	EFSGNDMNSK
1530	1540	1550	1560	1570	1580	1590	1600
QNGSDCTLDG	FPKSRHSDGT	EKNKLPSQPV	AFIGQTEYSQ	KENDLTEATD	KDHEFYVSSP	VIGKLNISET	ASVLAENAAH
1610	1620	1630	1640	1650	1660	1670	1680
PSNIICDQDL	SNYDPKRGNR	KTSSQQSPTG	ASESLAHQGI	AVLGSDTVHQ	MKPYLKKSVS	VVPCADDSQI	SSSSGSGQQD
1690	1700	1710	1720	1730	1740	1750	1760
TIKKALNYST	APKKKCIQIK	DLILLGRINP	GNNILEFKTQ	ETTHKASILL	NGKLKVESGQ	IYKNPVTWLK	DLLGGNSYVT
1770	1780	1790	1800	1810	1820	1830	1840
WNYAWSKVTY	LGKELLRYVS	EDAPILPEPN	SVPQQYQPCL	PEVACLDDPV	QEPNKSMFEK	TKFGQGTSRE	SMQSSPRYLQ
1850	1860	1870	1880				
INEILLISDQ	EFLPCHIMDQ	HWKFCVECEE	LTP				

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2612	1	812.4151	42.97	2	61.3	12.1	2	1254-1267	K.QKSALDEADDEKMK.E	Oxidation: 13

Detailed Protein Report

Protein 932: 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

QD:QU	**Median:** 0.34	**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		QD:QU 0.34

Detailed Protein Report

Protein 933: 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 934: **PREDICTED: apoptosis-stimulating of p53 protein 2 isoform X1 [Homo sapiens]**

Accession:	gi|530366444	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	125.2
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFLTVYLSNN	EQHFTEVPVT	PETICRDVVD	LCKEPGESDC	HLAEVWCGSE	RPVADNERMF	DVLQRFGSQR	NEVRFFLRHE
90	100	110	120	130	140	150	160
RPPGRDIVSG	PRSQDPSLKR	NGVKVPGEYR	RKENGVNSPR	MDLTLAELQE	MASRQQQQIE	AQQQLLATKE	QRLKFLKQQD
170	180	190	200	210	220	230	240
QRQQQQVAEQ	EKLKRLKEIA	ENQEAKLKKV	RALKGHVEQK	RLSNGKLVEE	IEQMNNLFQQ	KQRELVLAVS	KVEELTRQLE
250	260	270	280	290	300	310	320
MLKNGRIDSH	HDNQSAVAEL	DRLYKELQLR	NKLNQEQNAK	LQQQRECLNK	RNSEVAVMDK	RVNELRDRLW	KKKAALQQKE
330	340	350	360	370	380	390	400
NLPVSSDGNL	PQQAASAPSR	VAAVGPYIQS	STMPRMPSRP	ELLVKPALPD	GSLVIQASEG	PMKIQTLPNM	RSGAASQTKG
410	420	430	440	450	460	470	480
SKIHPVGPDW	SPSNADLFPS	QGSASVPQST	GNALDQVDDG	EVPLREKEKK	VRPFSMFDAV	DQSNAPPSFG	TLRKNQSSED
490	500	510	520	530	540	550	560
ILRDAQVANK	NVAKVPPPVP	TKPKQINLPY	FGQTNQPPSD	IKPDGSSQQL	STVVPSMGTK	PKPAGQQPRV	LLSPSIPSVG
570	580	590	600	610	620	630	640
QDQTLSPGSK	QESPPAAAVR	PFTPQPSKDT	LLPPFRKPQT	VAASSIYSMY	TQQQAPGKNF	QQAVQSALTK	THTRGPHFSS
650	660	670	680	690	700	710	720
VYGKPVIAAA	QNQQQHPENI	YSNSQGKPGS	PEPETEPVSS	VQENHENERI	PRPLSPTKLL	PFLSNPYRNQ	SDADLEALRK
730	740	750	760	770	780	790	800
KLSNAPRPLK	KRSSITEPEG	PNGPNIQKLL	YQRTTIAAME	TISVPSYPSK	SASVTASSES	PVEIQNPYLH	VEPEKEVVSL
810	820	830	840	850	860	870	880
VPESLSPEDV	GNASTENSDM	PAPSPGLDYE	PEGVPDNSPN	LQNNPEEPNP	EAPHVLDVYL	EEYPPYPPPP	YPSGEPEGPG
890	900	910	920	930	940	950	960
EDSVSMRPPE	ITGQVSLPPG	KRTNLRKTGS	ERIAHGMRVK	FNPLALLLDS	SLEGEFDLVQ	RIIYEVDDPS	LPNDEGITAL
970	980	990	1000	1010	1020	1030	1040
HNAVCAGHTE	IVKFLVQFGV	NVNAADSDGW	TPLHCAASCN	NVQVCKFLVE	SGAAVFAMTY	SDMQTAADKC	EEMEEGYTQC
1050	1060	1070	1080	1090	1100	1110	1120
SQFLYGVQEK	MGIMNKGVIY	ALWDYEPQND	DELPMKEGDC	MTIIHREDED	EIEWWWARLN	DKEGYVPRNL	LGLYPRIKPR
1130							
QRSLA							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1220	1	500.6481	-227.72	2	43.8	12.1	1	112-120	R.KENGVNSPR.M	

Detailed Protein Report

Protein 935: uncharacterized protein C14orf93 isoform c [Homo sapiens]

Accession:	gi|545479143	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSFSATILFS	PPSGSEARCC	CCACKSETNG	GNTGSQGGNP	PPSTPITVTG	HGLAVQSSEQ	LLHVIYQRVD	KAVGLAEAAL
90	100	110	120	130	140	150	160
GLARANNELL	KRLQEEVGDL	RQGKVSIPDE	DGESRAHSSP	PEEPGPLKES	PGEAFKALSA	VEEECDSVGS	GVQVVIEELR
170	180	190	200	210	220	230	240
QLGAASVGPG	PLGFPATQRD	MRLPGCTLAA	SEAAPLLNPL	VDDYVASEGA	VQRVLVPAYA	KQLSPATQLA	IQRATPETGP
250	260	270	280	290	300	310	320
ENGTKLPPPR	PEDMLNAAAA	LDSALEESGP	GSTGELRHSL	GLTVSPCRTR	GSGQKNSRRK	RDLVLSKLVH	NVHNHITNDK
330	340	350	360	370	380	390	400
RFNGSESIKS	SWNISVVKFL	LEKLKQELVT	SPHNYTDKEL	KGACVAYFLT	KRREYRNSLN	PFKGLKEKEE	KKLRSRRYRL
410	420	430	440	450	460	470	480
FANRSSIMRH	FGPEDQRLWN	DVTEELMSDE	EDSLNEPDRL	PSAEAQLLPP	ELYNPNFQEE	EDEGGDENAP	GSPSFDQPHK
490	500						
TCCPDLNSFI	EIKVEKDE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
438	1	847.2141	-29.18	1	34.1	12.1	0	19-25	R.CCCCACK.S	Carbamidomethyl: 1, 3

Detailed Protein Report

Protein 936: 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 937: 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 938: zinc finger protein 77 [Homo sapiens]

Accession:	gi|33438586	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.9
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	3.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MDCVIFEEVA	VNFTPEEWAL	LDHAQRSLYR	DVMLETCRNL	ASLDCYIYVR	TSGSSSQRDV	FGNGISNDEE	IVKFTGSDSW
90	100	110	120	130	140	150	160
SIFGENWRFD	NTGDQHQIPQ	RHLRSQLGRL	CESNEGHQCG	ETLSQTANLL	VHKSYPTEAK	PSECTKCGKA	FENRQRSHTG
170	180	190	200	210	220	230	240
QRPCKECGQA	CSCLSCQSPP	MKTQTVEKPC	NCQDSRTASV	TYVKSLSSKK	SYECQKCGKA	FICPSSFRGH	VNSHHGQKTH
250	260	270	280	290	300	310	320
ACKVCGKTFM	YYSYLTRHVR	THTGEKPYEC	KECGKAFSCP	SYFREHVRTH	TGEKPYECKH	CGKSFSCYSS	FRDHVRTHTG
330	340	350	360	370	380	390	400
EKPCQCKHCG	KAFTCYSSLR	EHGRTHSGEK	PYECKECGKA	FRYPSSLRAH	MRMHTGEKPY	VCKQCGKAFG	CPTYFRRHVK
410	420	430	440	450	460	470	480
THSGVKPYQC	KECGKAYSFS	SSLRIHVRTH	TGEKPFECKH	CGKAFSCHSS	LREHVRTHSG	EKPYECNQCG	KAFSHAQYFQ
490	500	510	520	530	540	550	
KHVRSHSGVK	PYECTECGKA	YSCSSSLRVH	VRTHTGERPY	ECKQCGKTFR	YLASLQAHVR	THAGA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1703	1	1070.9798	-22.91	2	49.8	12.1	2	513-530	R.THTGERPYECKQCGKTFR.Y	

Detailed Protein Report

Protein 939: **glutathione reductase, mitochondrial isoform 4 precursor [Homo sapiens]**

Accession:	gi|305410793	**Score:**	12.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	47.2
Database Date:	2015-11-30	**pI:**	9.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALLPRALSA	GAGPSWRRAA	RAFRGFLLLL	PEPAALTRAL	SRAMACRQEP	QPQGPPPAAG	AVASYDYLVI	GGGSGGLASA
90	100	110	120	130	140	150	160
RRAAELGARA	AVVESHKLGG	TCVNVGCVPK	KVMWNTAVHS	EFMHDHADYG	FPSCEGKFNW	RVIKEKRDAY	VSRLNAIYQN
170	180	190	200	210	220	230	240
NLTKSHIEII	RGHAAFTSDP	KPTIEVSGKK	YTAPHILIAT	GGMPSTPHES	QIPGASLGIT	SDGFFQLEEL	PGRSVIVGAG
250	260	270	280	290	300	310	320
YIAVEMAGIL	SALGSKTSLM	IRHDKGIQTD	DKGHIIVDEF	QNTNVKGIYA	VGDVCGKALL	TPVAIAAGRK	LAHRLFEYKE
330	340	350	360	370	380	390	400
DSKLDYNNIP	TVVFSHPPIG	TVGLTEDEAI	HKYGIENVKT	YSTSFTPMYH	AVTKRKTKCV	MKMVCANKEE	KVVGIHMQGL
410	420	430	440	450			
GCDEMLQGFA	VAVKMGATKA	DFDNTVAIHP	TSSEELVTLR				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2535	1	686.2933	-59.83	2	60.4	12.1	2	377-388	K.TKCVMKMVCANK.E	Oxidation: 5

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Detailed Protein Report

Protein 940: tRNA pseudouridine synthase A, mitochondrial isoform 2 [Homo sapiens]

Accession:	gi|70166599	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.3
Database Date:	2015-11-30	**pI:**	8.7
		Sequence Coverage [%]:	2.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|70166634	refseq_huma (refseq_human_20140103.fasta)	tRNA pseudouridine synthase A, mitochondrial isoform 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MAGNAEPPPA	GAACPQDRRS	CSGRAGGDRV	WEDGEHPAKK	LKSGGDEERR	EKPPKRKIVL	LMAYSGKGYH	GMQRNVGSSQ
90	100	110	120	130	140	150	160
FKTIEDDLVS	ALVRSGCIPE	NHGEDMRKMS	FQRCARTDKG	VSAAGQVVSL	KVWLIDDILE	KINSHLPSHI	RILGLKRVTG
170	180	190	200	210	220	230	240
GFNSKNRCDA	RTYCYLLPTF	AFAHKDRDVQ	DETYRLSAET	LQQVNRLLAC	YKGTHNFHNF	TSQKGPQDPS	ACRYILEMYC
250	260	270	280	290	300	310	320
EEPFVREGLE	FAVIRVKGQS	FMMHQIRKMV	GLVVAIVKGY	APESVLERSW	GTEKVDVPKA	PGLGLVLERV	HFEKYNQRFG
330	340	350	360	370	380	390	400
NDGLHEPLDW	AQEEGKVAAF	KEEHIYPTII	GTERDERSMA	QWLSTLPIHN	FSATALTAGG	TGAKVPSPLE	GSEGDGDTD

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
574	1	512.7132	-190.86	2	35.8	12.0	0	300-309	K.APGLGLVLER.V	

Detailed Protein Report

Protein 941: 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; Oxidation: 2

Detailed Protein Report

Protein 942: nucleosome-remodeling factor subunit BPTF isoform 2 [Homo sapiens]

Accession:	gi|38788260	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	322.0
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.5
		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 943: spermatid maturation protein 1 [Homo sapiens]

Accession:	gi|116268095	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.8
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAMVERPRPE	WASYHNCNSN	SCQDLGNSVL	LLLGLIICIN	ISINIVTLLW	SRFRGVLYQV	FHDTICEKEA	PKSSLLRKQT
90	100	110	120	130	140	150	160
QPPKKQSSPA	VHLRCTMDPV	MMTVSPPPAH	RHRRRGSPTR	CAHCPVAWAP	DTDDEKPHQY	PAICSYHWDV	PEDWEGFQHT
170	180	190	200	210	220	230	240
QGTWVPWSQD	APESPPQTIR	FQPTVEERPL	KTGIWSELGL	RAYVYPVNPP	PPSPEAPSHK	NGGEGAVPEA	EAAQYQPVPA
250	260	270	280	290	300	310	
PTLGPAVIPE	FSRHRSSGRI	VYDARDMRRR	LRELTREVEA	LSGCYPLASG	SSTAEETSKN	WVYRSLTGR	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2077	1	1057.4596	-49.95	3	54.5	12.0	2	86-113	K.QSSPAVHLRCTMDPVMMTVSPPPAHRHR.R	Oxidation: 12, 17

Detailed Protein Report

Protein 944: 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 945: proline-rich protein 9 [Homo sapiens]

Accession: gi|307133761
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 12.0
MW [kDa]: 12.9
pI: 4.8
Sequence Coverage [%]: 9.5
No. of unique Peptides: 1

```
        10         20         30         40         50         60         70         80
MSFSEQQCKQ PCVPPPCLPK TQEQCQAKAE EVCLPTCQHP CQDKCLVQAQ EVCLSQCQES SQEKCPQQGQ EPYLPPCQDQ
        90        100        110        120
CPPQCAEPCQ ELFQTKCVEV CPQKVQEKCS PGKGK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2348	1	646.6880	-216.71	2	58.0	12.0	0	10-20	K.QPCVPPPCLPK.T	Carbamidomethyl: 3, 8

Detailed Protein Report

Protein 946: **PREDICTED: dehydrogenase/reductase SDR family member 7B isoform X1 [Homo sapiens]**

Accession:	gi|578829832	**Score:**	12.0
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 [%]:**	5.1
		No. of unique Peptides:	1

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; Oxidation: 13

Detailed Protein Report

Protein 947: 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	

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Detailed Protein Report

Protein 948: immunoglobulin superfamily member 22 [Homo sapiens]

Accession:	gi|253970427	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	147.9
Database Date:	2015-11-30	**pI:**	9.0
		Sequence Coverage [%]:	2.0
		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 949: laminin subunit beta-3 precursor [Homo sapiens]

Accession:	gi|62868215	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.5
Database Date:	2015-11-30	**pI:**	7.9
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530366188	refseq_human (refseq_human_20140103.fasta)	PREDICTED: laminin subunit beta-3 isoform X1 [Homo sapiens]
gi|189083719	refseq_human (refseq_human_20140103.fasta)	laminin subunit beta-3 precursor [Homo sapiens]
gi|62868217	refseq_human (refseq_human_20140103.fasta)	laminin subunit beta-3 precursor [Homo sapiens]

10	20	30	40	50	60	70	80
MRPFFLLCFA	LPGLLHAQQA	CSRGACYPPV	GDLLVGRTRF	LRASSTCGLT	KPETYCTQYG	EWQMKCCKCD	SRQPHNYYSH
90	100	110	120	130	140	150	160
RVENVASSSG	PMRWWQSQND	VNPVSLQLDL	DRRFQLQEVM	MEFQGPMPAG	MLIERSSDFG	KTWRVYQYLA	ADCTSTFPRV
170	180	190	200	210	220	230	240
RQGRPQSWQD	VRCQSLPQRP	NARLNGGKVQ	LNLMDLVSGI	PATQSQKIQE	VGEITNLRVN	FTRLAPVPQR	GYHPPSAYYA
250	260	270	280	290	300	310	320
VSQLRLQGSC	FCHGHADRCA	PKPGASAGPS	TAVQVHDVCV	CQHNTAGPNC	ERCAPFYNNR	PWRPAEGQDA	HECQRCDCNG
330	340	350	360	370	380	390	400
HSETCHFDPA	VFAASQGAYG	GVCDNCRDHT	EGKNCERCQL	HYFRNRRPGA	SIQETCISCE	CDPDGAVPGA	PCDPVTGQCV
410	420	430	440	450	460	470	480
CKEHVQGERC	DLCKPGFTGL	TYANPQGCHR	CDCNILGSRR	DMPCDEESGR	CLCLPNVVGP	KCDQCAPYHW	KLASGQGCEP
490	500	510	520	530	540	550	560
CACDPHNSLS	PQCNQFTGQC	PCREGFGGLM	CSAAAIRQCP	DRTYGDVATG	CRACDCDFRG	TEGPGCDKAS	GRCLCRPGLT
570	580	590	600	610	620	630	640
GPRCDQCQRG	YCNRYPVCVA	CHPCFQTYDA	DLREQALRFG	RLRNATASLW	SGPGLEDRGL	ASRILDAKSK	IEQIRAVLSS
650	660	670	680	690	700	710	720
PAVTEQEVAQ	VASAILSLRR	TLQGLQLDLP	LEEETLSLPR	DLESLDRSFN	GLLTMYQRKR	EQFEKISSAD	PSGAFRMLST
730	740	750	760	770	780	790	800
AYEQSAQAAQ	QVSDSSRLLD	QLRDSRREAE	RLVRQAGGGG	GTGSPKLVAL	RLEMSSLPDL	TPTFNKLCGN	SRQMACTPIS
810	820	830	840	850	860	870	880
CPGELCPQDN	GTACGSRCRG	VLPRAGGAFL	MAGQVAEQLR	GFNAQLQRTR	QMIRAAEESA	SQIQSSAQRL	ETQVSASRSQ
890	900	910	920	930	940	950	960
MEEDVRRTRL	LIQQVRDFLT	DPDTDAATIQ	EVSEAVLALW	LPTDSATVLQ	KMNEIQAIAA	RLPNVDLVLS	QTKQDIARAR
970	980	990	1000	1010	1020	1030	1040
RLQAEAEEAR	SRAHAVEGQV	EDVVGNLRQG	TVALQEAQDT	MQGTSRSLRL	IQDRVAEVQQ	VLRPAEKLVT	SMTKQLGDFW
1050	1060	1070	1080	1090	1100	1110	1120
TRMEELRHQA	RQQGAEAVQA	QQLAEGASEQ	ALSAQEGFER	IKQKYAELKD	RLGQSSMLGE	QGARIQSVKT	EAEELFGETM
1130	1140	1150	1160	1170	1180		
EMMDRMKDME	LELLRGSQAI	MLRSADLTGL	EKRVEQIRDH	INGRVLYYAT	CK		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2105	1	926.8168	-61.93	2	54.9	12.0	1	523-539	R.TYGDVATGCRACDCDFR.G	

Detailed Protein Report

Protein 950: membrane-bound transcription factor site-1 protease preproprotein [Homo sapiens]

Accession:	gi|4506775	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	117.7
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKLVNIWLLL	LVVLLCGKKH	LGDRLEKKSF	EKAPCPGCSH	LTLKVEFSST	VVEYEYIVAF	NGYFTAKARN	SFISSALKSS
90	100	110	120	130	140	150	160
EVDNWRIIPR	NNPSSDYPSD	FEVIQIKEKQ	KAGLLTLEDH	PNIKRVTPQR	KVFRSLKYAE	SDPTVPCNET	RWSQKWQSSR
170	180	190	200	210	220	230	240
PLRRASLSLG	SGFWHATGRH	SSRRLLRAIP	RQVAQTLQAD	VLWQMGYTGA	NVRVAVFDTG	LSEKHPHFKN	VKERTNWTNE
250	260	270	280	290	300	310	320
RTLDDGLGHG	TFVAGVIASM	RECQGFAPDA	ELHIFRVFTN	NQVSYTSWFL	DAFNYAILKK	IDVLNLSIGG	PDFMDHPFVD
330	340	350	360	370	380	390	400
KVWELTANNV	IMVSAIGNDG	PLYGTLNNPA	DQMDVIGVGG	IDFEDNIARF	SSRGMTTWEL	PGGYGRMKPD	IVTYGAGVRG
410	420	430	440	450	460	470	480
SGVKGGCRAL	SGTSVASPVV	AGAVTLLVST	VQKRELVNPA	SMKQALIASA	RRLPGVNMFE	QGHGKLDLLR	AYQILNSYKP
490	500	510	520	530	540	550	560
QASLSPSYID	LTECPYMWPY	CSQPIYYGGM	PTVVNVTILN	GMGVTGRIVD	KPDWQPYLPQ	NGDNIEVAFS	YSSVLWPWSG
570	580	590	600	610	620	630	640
YLAISISVTK	KAASWEGIAQ	GHVMITVASP	AETESKNGAE	QTSTVKLPIK	VKIIPTPPRS	KRVLWDQYHN	LRYPPGYFPR
650	660	670	680	690	700	710	720
DNLRMKNDPL	DWNGDHIHTN	FRDMYQHLRS	MGYFVEVLGA	PFTCFDASQY	GTLLMVDSEE	EYFPEEIAKL	RRDVDNGLSL
730	740	750	760	770	780	790	800
VIFSDWYNTS	VMRKVKFYDE	NTRQWWMPDT	GGANIPALNE	LLSVWNMGFS	DGLYEGEFTL	ANHDMYYASG	CSIAKFPEDG
810	820	830	840	850	860	870	880
VVITQTFKDQ	GLEVLKQETA	VVENVPILGL	YQIPAEGGGR	IVLYGDSNCL	DDSHRQKDCF	WLLDALLQYT	SYGVTPPSLS
890	900	910	920	930	940	950	960
HSGNRQRPPS	GAGSVTPERM	EGNHLHRYSK	VLEAHLGDPK	PRPLPACPRL	SWAKPQPLNE	TAPSNLWKHQ	KLLSIDLDKV
970	980	990	1000	1010	1020	1030	1040
VLPNFRSNRP	QVRPLSPGES	GAWDIPGGIM	PGRYNQEVGQ	TIPVFAFLGA	MVVLAFFVVQ	INKAKSRPKR	RKPRVKRPQL
1050	1060						
MQQVHPPKTP	SV						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1660	1	612.4256	151.20	3	49.3	12.0	1	387-404	R.MKPDIVTYGAGVRGSGVK.G	

Detailed Protein Report

Protein 951: transmembrane channel-like protein 7 isoform b [Homo sapiens]

Accession:	gi|238550100	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.1
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKYLSEWDQW	KRYSSKSWKR	FLEKAREMTT	HLELWREDIR	SIEGKFGTGI	QSYFSFLRFL	VLLNLVIFLI	IFMLVLLPVL
90	100	110	120	130	140	150	160
LTKYKITNSS	FVLIPFKDMD	KQCTVYPVSS	SGLIYFYSYI	IDLLSGTGFL	EETSLFYGHY	TIDGVKFQNF	TYDLPLAYLL
170	180	190	200	210	220	230	240
STIASLALSL	LWIVKRSVEG	FKINLIRSEE	HFQSYCNKIF	AGWDFCITNR	SMADLKHSSL	RYELRADLEE	ERMRQKIAER
250	260	270	280	290	300	310	320
TSEETIRIYS	LRLFLNCIVL	AVLGACFYAI	YVATVFSQEH	MKKEIDKMVF	GENLFILYLP	SIVITLANFI	TPMIFAKIIR
330	340	350	360	370	380	390	400
YEDYSPGFEI	RLTILRCVFM	RLATICVLVF	TLGSKITSCD	DDTCDLCGYN	QKLYPCWETQ	VGQEMYKLMI	FDFIIILAVT
410	420	430	440	450	460	470	480
LFVDFPRKLL	VTYCSSCKLI	QCWGQQEFAI	PDNVLGIVYG	QTICWIGAFF	SPLLPAIATL	KFIIIFYVKE	WSLLYTCRPS
490	500	510	520	530	540	550	560
PRPFRASNSN	FFFLLVLLIG	LCLAIIPLTI	SISRIPSSKA	CGPFTNFNTT	WEVIPKTVST	FPSSLQSFIH	GVTSEAFAVP
570	580	590	600	610	620		
FFMIICLIMF	YFIALAGAHK	RVVIQLREQL	SLESRDKCYL	IQKLTEAQRD	MRN		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2143	1	1052.3999	-98.15	2	57.2	12.0	1	199-216	K.IFAGWDFCITNRSMADLK.H	Oxidation: 14

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Detailed Protein Report

Protein 952: protein AKNAD1 [Homo sapiens]

Accession:	gi|91754185	**Score:**	12.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.8
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
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
2577	1	1202.2445	83.07	2	60.9	12.0	2	249-269	K.YGQGQVHYQLPDFSKIAPKVK.I	

Detailed Protein Report

Protein 953: 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 954: **DNA helicase MCM8 isoform 4 [Homo sapiens]**

Accession:	gi|528078341	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	88.7
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNGEYRGRGF	GRGRFQSWKR	GRGGGNFSGK	WREREHRPDL	SKTTGKRTSE	QTPQFLLSTK	TPQSMQSTLD	RFIPYKGWKL
90	100	110	120	130	140	150	160
YFSEVYSDSS	PLIEKIQAFE	KFFTRHIDLY	DKDEIERKGS	ILVDFKELTE	GGEVTNLIPD	IATELRDAPE	KTLACMGLAI
170	180	190	200	210	220	230	240
HQVLTKDLER	HAAELQAQEG	LSNDGETMVN	VPHIHARVYN	YEPLTQLKNV	RANYYGKYIA	LRGTVVRVSN	IKPLCTKMAF
250	260	270	280	290	300	310	320
LCAACGEIQS	FPLPDGKYSL	PTKCPVPVCR	GRSFTALRSS	PLTVTMDWQS	IKIQELMSDD	QREAGRIPRT	IECELVHDLV
330	340	350	360	370	380	390	400
DSCVPGDTVT	ITGIVKVSNA	EEGSRNKNDK	CMFLLYIEAN	SISNSKGQKT	KSSEDGCKHG	MLMEFSLKDL	YAIQEIQAEE
410	420	430	440	450	460	470	480
NLFKLIVNSL	CPVIFGHEAA	CNVAPRGVYV	CGNTTTTSGL	TVTLSKDSSS	GDFALEAGAL	VLGDQGICGI	DEFDKMGNQH
490	500	510	520	530	540	550	560
QALLEAMEQQ	SISLAKAGVV	CSLPARTSII	AAANPVGGHY	NKAKTVSENL	KMGSALLSRF	DLVFILLDTP	NEHHDHLLSE
570	580	590	600	610	620	630	640
HVIAIRAGKQ	RTISSATVAR	MNSQDSNTSV	LEVVSEKPLS	ERLKVVPGET	IDPIPHQLLR	KYIGYARQYV	YPRLSTEAAR
650	660	670	680	690	700	710	720
VLQDFYLELR	KQSQRLNSSP	ITTRQLESLI	RLTEARARLE	LREEATKEDA	EDIVEIMKYS	MLGTYSDEFG	NLDFERSQHG
730	740	750	760	770	780	790	800
SGMSNRSTAK	RFISALNNVA	ERTYNNIFQF	HQLRQIAKEL	NIQVADFENF	IGSLNDQGYL	LKKGPKVYQL	QTM

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
527	1	882.7095	306.55	1	35.2	11.9	0	787-793	K.VYQLQTM.-	

Detailed Protein Report

Protein 955: 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

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
1995	1	678.8162	-37.70	2	55.3	11.9	2	141-152	K.DCPHMKEKGALK.Q	

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Detailed Protein Report

Protein 956: follistatin-related protein 1 precursor [Homo sapiens]

Accession:	gi|5901956	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.0
Database Date:	2015-11-30	**pI:**	5.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MWKRWLALAL	ALVAVAWVRA	EEELRSKSKI	CANVFCGAGR	ECAVTEKGEP	TCLCIEQCKP	HKRPVCGSNG	KTYLNHCELH
90	100	110	120	130	140	150	160
RDACLTGSKI	QVDYDGHCKE	KKSVSPSASP	VVCYQSNRDE	LRRRIIQWLE	AEIIPDGWFS	KGSNYSEILD	KYFKNFDNGD
170	180	190	200	210	220	230	240
SRLDSSEFLK	FVEQNETAIN	ITTYPDQENN	KLLRGLCVDA	LIELSDENAD	WKLSFQEFLK	CLNPSFNPPE	KKCALEDETY
250	260	270	280	290	300	310	
ADGAETEVDC	NRCVCACGNW	VCTAMTCDGK	NQKGAQTQTE	EEMTRYVQEL	QKHQETAEKT	KRVSTKEI	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2625	1	671.8235	5.72	2	61.5	11.9	0	72-81	K.TYLNHCELHR.D	Carbamidomethyl: 6

Detailed Protein Report

Protein 957: PREDICTED: clathrin heavy chain 2 isoform X7 [Homo sapiens]

Accession:	gi|578837411	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	177.9
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAQILPVRFQ	EHFQLQNLGI	NPANIGFSTL	TMESDKFICI	REKVGEQAQV	TIIDMSDPMA	PIRRPISAES	AIMNPASKVI
90	100	110	120	130	140	150	160
ALKGAPGFCS	PASNSQSPGS	SLCPAGKTLQ	IFNIEMKSKM	KAHTMAEEVI	FWKWVSVNTV	ALVTETAVYH	WSMEGDSQPM
170	180	190	200	210	220	230	240
KMFDRHTSLV	GCQVIHYRTD	EYQKWLLLVG	ISAQQNRVVG	AMQLYSVDRK	VSQPIEGHAA	AFAEFKMEGN	AKPATLFCFA
250	260	270	280	290	300	310	320
VRNPTGGKLH	IIEVGQPAAG	NQPFVKKAVD	VFFPPEAQND	FPVAMQIGAK	HGVIYLITKY	GYLHLYDLES	GVCICMNRIS
330	340	350	360	370	380	390	400
ADTIFVTAPH	KPTSGIIGVN	KKGQVLSVCV	EEDNIVNYAT	NVLQNPDLGL	RLAVRSNLAG	AEKLFVRKFN	TLFAQGSYAE
410	420	430	440	450	460	470	480
AAKVAASAPK	GILRTRETVQ	KFQSIPAQSG	QASPLLQYFG	ILLDQGQLNK	LESLELCHLV	LQQGRKQLLE	KWLKEDKLEC
490	500	510	520	530	540	550	560
SEELGDLVKT	TDPMLALSVY	LRANVPSKVI	QCFAETGQFQ	KIVLYAKKVG	YTPDWIFLLR	GVMKISPEQG	LQFSRMLVQD
570	580	590	600	610	620	630	640
EEPLANISQI	VDIFMENSLI	QQCTSFLLDA	LKNNRPAEGL	LQTWLLEMNL	VHAPQVADAI	LGNKMFTHYD	RAHIAQLCEK
650	660	670	680	690	700	710	720
AGLLQQALEH	YTDLYDIKRA	VVHTHLLNPE	WLVNFFGSLS	VEDSVECLHA	MLSANIRQNL	QLCVQVASKY	HEQLGTQALV
730	740	750	760	770	780	790	800
ELFESFKSYK	GLFYFLGSIV	NFSQDPDVHL	KYIQAACKTG	QIKEVERICR	ESSCYNPERV	KNFLKEAKLT	DQLPLIIVCD
810	820	830	840	850	860	870	880
RFGFVHDLVL	YLYRNNLQRY	IEIYVQKVNP	SRTPAVIGGL	LDVDCSEEVI	KHLIMAVRGQ	FSTDELVAEV	EKRNRLKLLL
890	900	910	920	930	940	950	960
PWLESQIQEG	CEEPATHNAL	AKIYIDSNNS	PECFLRENAY	YDSSVVGRYC	EKRDPHLACV	AYERGQCDLE	LIKVCNENSL
970	980	990	1000	1010	1020	1030	1040
FKSEARYLVC	RKDPELWAHV	LEETNPSRRQ	LIDQVVQTAL	SETRDPEEIS	VTVKAFMTAD	LPNELIELLE	KIVLDNSVFS
1050	1060	1070	1080	1090	1100	1110	1120
EHRNLQNLLI	LTAIKADRTR	VMEYISRLDN	YDALDIASIA	VSSALYEEAF	TVFHKFDMNA	SAIQVLIEHI	GNLDRAYEFA
1130	1140	1150	1160	1170	1180	1190	1200
ERCNEPAVWS	QLAQAQLQKD	LVKEAINSYI	RGDDPSSYLE	VVQSASRSNN	WEDLVKFLQM	ARKKGRESYI	ETELIFALAK
1210	1220	1230	1240	1250	1260	1270	1280
TSRVSELEDF	INGPNNAHIQ	QVGDRCYEEG	MYEAAKLLYS	NVSNFARLAS	TLVHLGEYQA	AVDNSRKASS	TRTWKEVCFA
1290	1300	1310	1320	1330	1340	1350	1360
CMDGQEFRFA	QLCGLHIVIH	ADELEELMCY	YQDRGYFEEL	ILLLEAALGL	ERAHMGMFTE	LAILYSKFKP	QKMLEHLELF
1370	1380	1390	1400	1410	1420	1430	1440
WSRVNIPKVL	RAAEQAHLWA	ELVFLYDKYE	EYDNAVLTMM	SHPTEAWKEG	QFKDIITKVA	NVELCYRALQ	FYLDYKPLLI
1450	1460	1470	1480	1490	1500	1510	1520
NDLLLVLSPR	LDHTWTVSFF	SKDAMQHAAE	SRDAELAQKL	LQWFLEEGKR	ECFAACLFTC	YDLLRPDMVL	ELAWRHNLVD
1530	1540	1550	1560	1570			
LAMPYFIQVM	REYLSKVDKL	DALESLRKQE	EHVTEPAPLV	FDFDGHE			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
178	1	820.7984	68.97	3	31.0	11.9	1	42-63	R.EKVGEQAQVTIIDMSDPMAPIR.R	Oxidation: 14, 18

Detailed Protein Report

Protein 958: PREDICTED: RNA 3'-terminal phosphate cyclase isoform X1 [Homo sapiens]

Accession:	gi|530363524	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	33.4
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530363526	refseq_human (refseq_human_20140103.fasta)	PREDICTED: RNA 3'-terminal phosphate cyclase isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MIRDLCDGQL	EGAEIGSTEI	TFTPEKIKGG	IHTADTKTAG	SVCLLMQVSM	PCVLFAASPS	ELHLKGGTNA	EMAPQIDYTV
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
MVFKPIVEKF	GFIFNCDIKT	RGYYPKGGGE	VIVRMSPVKQ	LNPINLTERG	CVTKIYGRAF	VAGVLPFKVA	KDMAAAAVRC
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
IRKEIRDLYV	NIQPVQEPKD	QAFGNGNGII	IIAETSTGCL	FAGSSLGKRG	VNADKVGIEA	AEMLLANLRH	GGTVDEYLQD
250	**260**	**270**	**280**	**290**	**300**	**310**	
QLIVFMALAN	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
2681	1	559.7841	-33.68	2	64.6	11.9	1	149-159	K.VAKDMAAAAVR.C	Oxidation: 5

Detailed Protein Report

Protein 959: guanylate-binding protein 7 [Homo sapiens]

Accession: gi|148234215

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Carbamidomethyl

Score: 11.9

MW [kDa]: 72.5

pI: 5.7

Sequence Coverage [%]: 2.0

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MASEIHMPGP	VCLTENTKGH	LVVNSEALEI	LSAITQPVVV	VAIVGLYRTG	KSYLMNKLAG	KNKGFPLGCT	VKSETKGIWM
90	100	110	120	130	140	150	160
WCVPHPSKPN	HTLILLDTEG	LGDMEKSDPK	SDSWIFALAV	LLSSSFVYNS	MGTINHQALE	QLHYVTELTE	LIRAKSCPRP
170	180	190	200	210	220	230	240
DEVEDSSEFV	SFFPDFIWTV	RDFTLELKLD	GHPITEDEYL	ENALKLISGK	NPQIQNSNKP	REWIRHFFPK	QKCFVFDRPI
250	260	270	280	290	300	310	320
NDKKLLLHVE	EVREDQLDSN	FQMQSENFCS	YIFTHAKTKT	LREGILVTGN	RLGMLVETYL	DAINSGATPC	LENAMAVLAQ
330	340	350	360	370	380	390	400
CENSAAVQRA	ANHYSQQMAQ	QVRFPTDTLQ	ELLDVHAVCE	REAIAVFMEY	SFKDKSQEFQ	KKLVDTMEKK	KEDFVLQNEE
410	420	430	440	450	460	470	480
ASAKYCQAEL	KRLSELLTES	ISRGTFFVPG	GHNIYLEAKK	KIEQDYTLVP	RKGVKADEVL	QSFLQSQVVI	EESILQSDKA
490	500	510	520	530	540	550	560
LTAGEKAIAA	KQAKKEAAEK	EQELLRQKQK	EQQQMMEAQE	RSFQENIAQL	KKKMEREREN	YMRELRKMLS	HKMKVLEELL
570	580	590	600	610	620	630	640
TEGFKEIFES	LNEEINRLKE	QIEAAENEEP	SVFSQILDVA	GSIFIAALPG	AAKLVDLGMK	ILSSLCNRLR	NPGKKIIS

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
838	1	712.3324	-47.27	2	39.0	11.9	1	64-76	K.GFPLGCTVKSETK.G	Carbamidomethyl: 6

Detailed Protein Report

Protein 960: 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 961: **regulator of G-protein signaling 16 [Homo sapiens]**

Accession:	gi|156416009	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.7
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	9.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCRTLAAFPT	TCLERAKEFK	TRLGIFLHKS	ELGCDTGSTG	KFEWGSKHSK	ENRNFSEDVL	GWRESFDLLL	SSKNGVAAFH
90	100	110	120	130	140	150	160
AFLKTEFSEE	NLEFWLACEE	FKKIRSATKL	ASRAHQIFEE	FICSEAPKEV	NIDHETHELT	RMNLQTATAT	CFDAAQGKTR
170	180	190	200	210			
TLMEKDSYPR	FLKSPAYRDL	AAQASAASAT	LSSCSLDEPS	HT			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
435	1	1014.5179	31.94	2	34.1	11.9	1	142-160	R.MNLQTATATCFDAAQGKTR.T	

Detailed Protein Report

Protein 962: PREDICTED: zinc finger protein 621 isoform X2 [Homo sapiens]

Accession: gi|530372341
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 11.9
MW [kDa]: 45.1
pI: 10.4
Sequence Coverage [%]: 5.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MKPGDIRHAP	NNLASVAFPF	PKPALISHLE	RGEAPWGPDP	WDTEILRGIS	QGGESWIKNE	GLVIKQEASE	ETELHRMPVG
90	100	110	120	130	140	150	160
GLLRNVSQHF	DFKRKALKQT	FNLNPNLILR	GGMKFYECKE	CGKIFRYNSK	LIRHQMSHTG	EKPFKCKECG	KAFKSSYDCI
170	180	190	200	210	220	230	240
VHEKNHIGEG	PYECKECGKG	LSSNTALTQH	QRIHTGEKPY	ECKECGKAFR	RSAAYLQHQR	LHTGEKLYKC	KECWKAFGCR
250	260	270	280	290	300	310	320
SLFIVHQRIH	TGEKPYQCKE	CGKAFTQKIA	SIQHQRVHTG	EKPYECKVCG	KAFKWYGSFV	QHQKLHPVEK	KPVKVLGPSL
330	340	350	360	370	380	390	400
VSPQCSSPAI	PPVLLQGSCS	ASAVAVPSLT	FPHAVLIPTS	GNFFMLLPTS	GIPSSSAQIV	RVFQGLTPTV	KPSPVILTPS
410							
SHSS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1346	1	956.6771	-101.46	3	45.4	11.9	2	152-175	K.AFKSSYDCIVHEKNHIGEGPYECK.E	Carbamidomethyl: 8, 23

Detailed Protein Report

Protein 963: interferon-induced transmembrane protein 10 [Homo sapiens]

Accession:	gi|334848153	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	24.6
Database Date:	2015-11-30	**pI:**	7.5
		Sequence Coverage [%]:	5.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MREGKRGPPC	ILSFRGTLER	VEAQWELEAQ	GPGQCPAPLG	DPASTTDGAQ	EARVPLDGAF	WIPRPPAGSP	KGCFACVSKP
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
PALQAPAAPA	PEPSASPPMA	PTLFPMESKS	SKTDSVRAAG	APPACKHLAE	KKTMTNPTTV	IEVYPDTTEV	NDYYLWSIFN
170	**180**	**190**	**200**	**210**	**220**	**230**	
FVYLNFCCLG	FIALAYSLKV	RDKKLLNDLN	GAVEDAKTAR	LFNITSSALA	ASCIILVFIF	LRYPLTDY	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1913	1	686.2353	-180.69	2	52.4	11.9	0	185-197	K.LLNDLNGAVEDAK.T	

Detailed Protein Report

Protein 964: armadillo repeat-containing protein 7 [Homo sapiens]

Accession:	gi|13375770	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.9
Database Date:	2015-11-30	**pI:**	5.7
		Sequence Coverage [%]:	10.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MAQKPKVDPH VGRLGYLQAL VTEFQETQSQ DAKEQVLANL ANFAYDPSNY EYLRQLQVLD LFLDSLSEEN ETLVEFAIGG
        90        100        110        120        130        140        150        160
LCNLCPDRAN KEHILHAGGV PLIINCLSSP NEETVLSAIT TLMHLSPPGR SFLPELTATP VVQCMLRFSL SASARLRNLA
       170        180        190        200
QIFLEDFCSP RQVAEARSRQ AHSALGIPLP RSVAPRQR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1187	1	757.1449	125.66	3	43.4	11.9	0	14-33	R.LGYLQALVTEFQETQSQDAK.E	

Detailed Protein Report

Protein 965: PNMA-like protein 2 [Homo sapiens]

Accession:	gi|146219841	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.6
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
MAMSLLQDWC	RSLDVDAHRA	LLVTGIPEGL	EQADVEAVLQ	PTLLPLGTFR	LRHMKALMNE	KAQAALVEFV	EDVNHAAIPR
90	100	110	120	130	140	150	160
EIPGKDGVWR	VLWKDRAQDT	RVLRQMRRLL	LDDGPTQAAE	AGTPGEAPTP	PASETQAQDS	GEVTGQAGSL	LGAARNPRRG
170	180	190	200	210	220	230	240
RRGRRNRTRR	NRLTQKGKKR	SRGGRPSAPA	RSEAEDSSDE	SLGIVIEEID	QGDLSGEEDQ	SALYATLQAA	ARELVRQWAP
250	260	270	280	290	300	310	320
CNSEGEEDGP	REFLALVTVT	DKSKKEEAEK	EPAGAESIRL	NTKEDKNGVP	DLVALLAVRD	TPDEEPVDSD	TSESDSQESG
330	340	350	360	370	380	390	400
DQETEELDNP	EFVAIVAYTD	PSDPWAREEM	LKIASVIESL	GWSDEKDKRD	PLRQVLSVMS	KDTNGTRVKV	EEAGREVDAV
410	420	430	440	450	460	470	480
VLRKAGDDGD	LRECISTLAQ	PDLPPQAKKA	GRGLFGGWSE	HREDEGGLLE	LVALLAAQDM	AEVMKEEKEN	AWEGGKYKYP
490	500	510	520	530	540	550	560
KGKLGEVLAL	LAARENMGSN	EGSEEASDEQ	SEEESEDTES	EASEPEDRAS	RKPRAKRART	APRGLTPAGA	PPTASGARKT
570	580	590	600	610	620	630	640
RAGGRGRGRG	VTPEKKAGSR	GSAQDDAAGS	RKKKGSAGAG	AHARAGEAKG	QAPTGSKAAR	GKKARRGRRL	PPKCR

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1644	1	662.3238	-46.15	2	49.1	11.9	0	544-558	R.GLTPAGAPPTASGAR.K	

Detailed Protein Report

Protein 966: vinexin isoform 2 [Homo sapiens]

Accession:	gi|65301112	**Score:**	11.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.7
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	5.2
		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
1992	1	857.8267	-95.65	2	55.3	11.9	2	22-38	R.DPSASNGGGSPARREEK.K	

Detailed Protein Report

Protein 967: PREDICTED: synaptotagmin-7 isoform X7 [Homo sapiens]

Accession:	gi|530397581	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	44.5
Database Date:	2015-11-30	**pI:**	10.7
		Sequence Coverage [%]:	3.4
		No. of unique 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	PRLSLNGTLL	SGAKVAAAAG	LAVEREGRLG	EKPAPVPPPG	EDALRSGGAA
170	180	190	200	210	220	230	240
PSEPGSGGKA	GRGRWRTVQS	HLAAGKLNLS	NFEDSTLSTA	TTLESIPSST	GEPKCQRPRT	LMRQQSLQQP	LSQHQRGRQP
250	260	270	280	290	300	310	320
SQPTTSQSLG	QLQAHMASAP	GPNPRAYGRG	QARQGTSAGS	KYRAAGGRSR	SNPGSWDHVV	GQIRNRGLDM	KSFLPWGLFP
330	340	350	360	370	380	390	400
SPRSSLGALF	TEQETSTLSL	GEEKGRRKGK	HWQDIGILKA	SKFLGASCLS	SETSARASRA	DGSTALGETP	HPKRPCHASF
410	420						
PYPCEWPMAS	KTCCL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
285	1	733.8676	-12.20	2	33.5	11.8	2	270-283	R.GQARQGTSAGSKYR.A	

Detailed Protein Report

Protein 968: 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	

Detailed Protein Report

Protein 969: puratrophin-1 isoform 2 [Homo sapiens]

Accession:	gi|193211603	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.8
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
MERPLENGDE	SPDSQGHATD	WRFAVCSFRD	AWEEEEPASQ	MHVKDPGPPR	PPAGATQDEE	LQGSPLSRKF	QLPPAADESG
90	100	110	120	130	140	150	160
DAQRGTVESS	SVLSEGPGPS	GVESLLCPMS	SHLSLAQGTR	DVQGRAVLLL	CAHSPAWLQS	ECSSQELIRL	LLYLRSIPRP
170	180	190	200	210	220	230	240
EVQALGLTVL	VDARICAPSS	SLFSGLSQLQ	EAAPGAVYQV	LLVGSTLLKE	VPSGLQLEQL	PSQSLLTHIP	TAGLPTSLGG
250	260	270	280	290	300	310	320
GLPYCHQAWL	DFRRRLEALL	QNCQAACALL	QGAIESVKAV	PQPMEPGEVG	QLLQQTEVLM	QQVLDSPWLA	WLQCQGGREL
330	340	350	360	370	380	390	400
TWLKQEVPEV	TLSPDYRTAM	DKADELYDRV	DGLLHQLTLQ	SNQRIQALEL	VQTLEARESG	LHQIEVWLQQ	VGWPALEEAG
410	420	430	440	450	460	470	480
EPSLDMLLQA	QGSFQELYQV	AQEQVRQGEK	FLQPLTGWEA	AELDPPGARF	LALRAQLTEF	SRALAQRCQR	LADAERLFQL
490	500	510	520	530	540	550	560
FREALTWAEE	GQRVLAELEQ	ERPGVVLQQL	QLHWTRHPDL	PPAHFRKMWA	LATGLGSEAI	RQECRWAWAR	CQDTWLALDQ
570	580	590	600	610	620	630	640
KLEASLKLPP	VGSTASLCVS	QVPAAPAHPP	LRKAYSFDRN	LGQSLSEPAC	HCHHAATIAA	CRRPEAGGGA	LPQASPTVPP
650	660	670	680	690	700	710	720
PGSSDPRSLN	RLQLVLAEMV	ATEREYVRAL	EYTMENYFPE	LDRPDVPQGL	RGQRAHLFGN	LEKLRDFHCH	FFLRELEACT
730	740	750	760	770	780	790	800
RHPPRVAYAF	LRHRVQFGMY	ALYSKNKPRS	DALMSSYGHT	FFKDKQQALG	DHLDLASYLL	KPIQRMGKYA	LLLQELARAC
810	820	830	840	850	860	870	880
GGPTQELSAL	REAQSLVHFQ	LRHGNDLLAM	DAIQGCDVNL	KEQGQLVRQD	EFVVRTGRHK	SVRRIFLFEE	LLLFSKPRHG
890	900	910	920	930	940	950	960
PTGVDTFAYK	RSFKMADLGL	TECCGNSNLR	FEIWFRRRKA	RDTFVLQASS	LAIKQAWTAD	ISHLLWRQAV	HNKEVRMAEM
970	980	990	1000	1010	1020	1030	1040
VSMGVGNKAF	RDIAPSEEAI	NDRTVNYVLK	CREVRSRASI	AVAPFDHDSL	YLGASNSLPG	DPASCSVLGS	LNLHLYRDPA
1050	1060	1070	1080	1090	1100	1110	1120
LLGLRCPLYP	SFPEEAALEA	EAELGGQPSL	TAEDSEISSQ	CPSASGSSGS	DSSCVSGQAL	GRGLEDLPCV	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2738	1	665.3700	78.60	2	63.2	11.8	0	972-983	R.DIAPSEEAINDR.T	

Detailed Protein Report

Protein 970: 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 971: **PREDICTED: connector enhancer of kinase suppressor of ras 2 isoform X2 [Homo sapiens]**

Accession:	gi|530421010	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	98.2
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
MALIMEPVSK	WSPSQVVDWM	KGLDDCLQQY	IKNFEREKIS	GDQLLRITHQ	ELEDLGVSRI	GHQELILEAV	DLLCALNYGL
90	100	110	120	130	140	150	160
ETENLKTLSH	KLNASAKNLQ	NFITGRRRSG	HYDGRTSRKL	PNDFLTSVVD	LIGAAKSLLA	WLDRSPFAAV	TDYSVTRNNV
170	180	190	200	210	220	230	240
IQLCLELTTI	VQQDCTVYET	ENKILHVCKT	LSGVCDHIIS	LSSDPLVSQS	AHLEVIQLAN	IKPSEGLGMY	IKSTYDGLHV
250	260	270	280	290	300	310	320
ITGTTENSPA	DRCKKIHAGD	EVIQVNHQTV	VGWQLKNLVN	ALREDPSGVI	LTLKKRPQSM	LTSAPALLKN	MRWKPLALQP
330	340	350	360	370	380	390	400
LIPRSPTSSV	ATPSSTISTP	TKRDSSALQD	LYIPPPPAEP	YIPRDEKGNL	PCEDLRGHMV	GKPVHKGSES	PNSFLDQEYR
410	420	430	440	450	460	470	480
KRFNIVEEDT	VLYCYEYEKG	RSSSQGRRES	TPTYENSLLR	YMSNEKIAQE	EYMFQRNSKK	DTGKKSKKKG	DKSNSPTHYS
490	500	510	520	530	540	550	560
LLPSLQMDAL	RQDIMGTPVP	ETTLYHTFQQ	SSLQHKSKKK	NKGPIAGKSK	RRISCKDLGR	GDCEGWLWKK	KDAKSYFSQK
570	580	590	600	610	620	630	640
WKKYWFVLKD	ASLYWYINEE	DEKAEGFISL	PEFKIDRASE	CRKKYAFKAC	HPKIKSFYFA	AEHLDDMNRW	LNRINMLTAG
650	660	670	680	690	700	710	720
YAERERIKQE	QDYWSESDKE	EADTPSTPKQ	DSPPPPYDTY	PRPPSMSCAS	PYVEAKHSRL	SSTETSQSQS	SHEEFRQEVT
730	740	750	760	770	780	790	800
GSSAVSPIRK	TASQRRSWQD	LIETPLTSSG	LHYLQTLPLE	DSVFSDSAAI	SPEHRRQSTL	PTQKCHLQDH	YGPYPLAESE
810	820	830	840	850	860	870	
RMQVLNGNGG	KPRSFTLPRD	SGFNHCCLNA	PVSACDPQDD	VQPPEVEEEE	EEEEEEGEAA	GENIGEKS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2618	1	973.4719	-48.48	2	61.4	11.8	1	296-312	K.RPQSMLTSAPALLKNMR.W	Oxidation: 5, 16

Detailed Protein Report

Protein 972: PREDICTED: extended synaptotagmin-3 isoform X2 [Homo sapiens]

Accession:	gi|578807790	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	91.8
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.6
		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

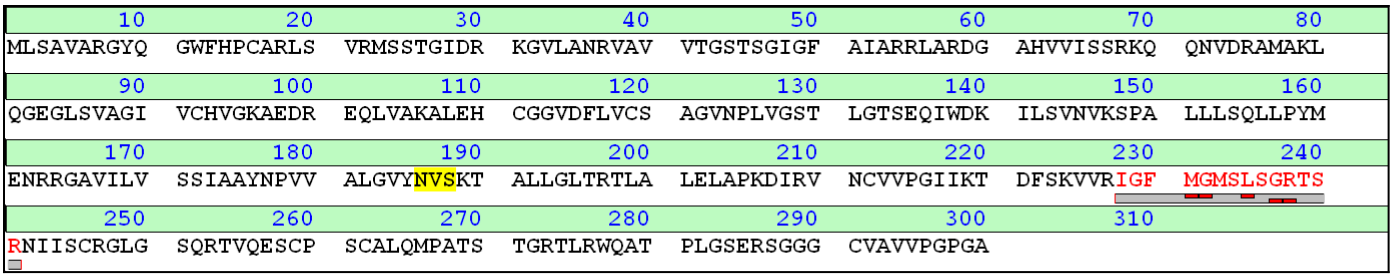
Detailed Protein Report

Protein 973: **dehydrogenase/reductase SDR family member 2, mitochondrial isoform 1 [Homo sapiens]**

Accession:	gi|33667109	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.5
Database Date:	2015-11-30	**pI:**	11.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.7
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 1.78 **CV:** 0.00 % **No. of Peptides:** 1



```
        10         20         30         40         50         60         70         80
MLSAVARGYQ GWFHPCARLS VRMSSTGIDR KGVLANRVAV VTGSTSGIGF AIARRLARDG AHVVISSRKQ QNVDRAMAKL
        90        100        110        120        130        140        150        160
QGEGLSVAGI VCHVGKAEDR EQLVAKALEH CGGVDFLVCS AGVNPLVGST LGTSEQIWDK ILSVNVKSPA LLLSQLLPYM
       170        180        190        200        210        220        230        240
ENRRGAVILV SSIAAYNPVV ALGVYNVSKT ALLGLTRTLA LELAPKDIRV NCVVPGIIKT DFSKVVRIGF MGMSLSGRTS
       250        260        270        280        290        300        310
RNIISCRGLG SQRTVQESCP SCALQMPATS TGRTLRWQAT PLGSERSGGG CVAVVPGPGA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
767	1	766.4829	145.43	2	38.1	11.8	1	228-241	R.IGFMGMSLSGRTSR.N	Oxidation: 4, 6	QD:QU	1.78

Detailed Protein Report

Protein 974: 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 975: 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

QD:QU **Median:** 17.80 **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	QD:QU 17.80

Detailed Protein Report

Protein 976: zinc finger protein 12 isoform b [Homo sapiens]

Accession:	gi|110349775	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.1
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNKSLGPVSF	KDVAVDFTQE	EWQQLDPEQK	ITYRDVMLEN	YSNLVSVGYH	IIKPDVISKL	EQGEEPWIVE	GEFLLQSYPD
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
EVWQTDDLIE	RIQEEENKPS	RQTVFIETLI	EEREYISSDG	SYARMKADEC	SGCGKSLLHI	KLEKTHPGDQ	AYEFNQNGEP
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
YTLNEESLYQ	KIRILEKPFE	YIECQKAFQK	DTVFVNHMEE	KPYKWNGSEI	AFLQMSDLTV	HQTSHMEMKP	YECSECGKSF
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
CKKSKFIIHQ	RTHTGEKPYE	CNQCGKSFCQ	KGTLTVHQRT	HTGEKPYECN	ECGKNFYQKL	HLIQHQRTHS	GEKPYECSYC
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
GKSFCQKTHL	TQHQRTHSGE	RPYVCHDCGK	TFSQKSALND	HQKIHTGVKL	YKCSECGKCF	CRKSTLTTHL	RTHTGEKPYE
410	**420**	**430**	**440**	**450**	**460**	**470**	**480**
CNECGKFFSR	LSYLTVHYRT	HSGEKPYECN	ECGKTFYLNS	ALMRHQRVHT	GEKPYECNEC	GKLFSQLSYL	TIHHRTHSGV
490	**500**	**510**	**520**	**530**	**540**	**550**	**560**
KPYECSECGK	TFYQNSALCR	HRRIHKGEKP	YECYICGKFF	SQMSYLTIHH	RIHSGEKPYE	CSECGKTFCQ	NSALNRHQRT
570	**580**	**590**	**600**	**610**	**620**	**630**	**640**
HTGEKAYECY	ECGKCFSQMS	YLTIHHRIHS	GEKPFECNEC	GKAFSRMSYL	TVHYRTHSGE	KPYECTECGK	KFYHKSAFNS
650	**660**						
HQRIHRRGNM	NVIDVGRLL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
516	1	717.8729	114.29	2	36.4	11.8	2	373-383	K.CSECGKCFCRK.S	Carbamidomethyl: 1, 4, 7

Detailed Protein Report

Protein 977: potassium voltage-gated channel subfamily H member 4 [Homo sapiens]

Accession:	gi|6912446	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	111.6
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPVMKGLLAP	QNTFLDTIAT	RFDGTHSNFL	LANAQGTRGF	PIVYCSDGFC	ELTGYGRTEV	MQKTCSCRFL	YGPETSEPAL
90	100	110	120	130	140	150	160
QRLHKALEGH	QEHRAEICFY	RKDGSAFWCL	LDMMPIKNEM	GEVVLFLFSF	KDITQSGSPG	LGPQGGRGDS	NHENSLGRRG
170	180	190	200	210	220	230	240
ATWKFRSARR	RSRTVLHRLT	GHFGRRGQGG	MKANNNVFEP	KPSVPEYKVA	SVGGSRCLLL	HYSVSKAIWD	GLILLATFYV
250	260	270	280	290	300	310	320
AVTVPYNVCF	SGDDDTPITS	RHTLVSDIAV	EMLFILDIIL	NFRTTYVSQS	GQVISAPRSI	GLHYLATWFF	IDLIAALPFD
330	340	350	360	370	380	390	400
LLYIFNITVT	SLVHLLKTVR	LLRLLRLLQK	LERYSQCSAV	VLTLLMSVFA	LLAHWMACIW	YVIGRREMEA	NDPLLWDIGW
410	420	430	440	450	460	470	480
LHELGKRLEV	PYVNGSVGGP	SRRSAYIAAL	YFTLSSLTSV	GFGNVCANTD	AEKIFSICTM	LIGALMHAVV	FGNVTAIIQR
490	500	510	520	530	540	550	560
MYSRRSLYHS	RMKDLKDFIR	VHRLPRPLKQ	RMLEYFQTTW	AVNSGIDANE	LLRDFPDELR	ADIAMHLNRE	ILQLPLFGAA
570	580	590	600	610	620	630	640
SRGCLRALSL	HIKTSFCAPG	EYLLRRGDAL	QAHYYVCSGS	LEVLRDNMVL	AILGKGDLIG	ADIPEPGQEP	GLGADPNFVL
650	660	670	680	690	700	710	720
KTSADVKALT	YCGLQQLSSR	GLAEVLRLYP	EYGAAFRAGL	PRDLTFNLRQ	GSDTSGLSRF	SRSPRLSQPR	SESLGSSSDK
730	740	750	760	770	780	790	800
TLPSITEAES	GAEPGGGPRP	RRPLLLPNLS	PARPRGSLVS	LLGEELPPFS	ALVSSPSLSP	SLSPALAGQG	HSASPHGPPR
810	820	830	840	850	860	870	880
CSAAWKPPQL	LIPPLGTFGP	PDLSPRIVDG	IEDSGSTAEA	PSFRFSRRPE	LPRPRSQAPP	TGTRPSPELA	SEAEEVKEKV
890	900	910	920	930	940	950	960
CRLNQEISRL	NQEVSQLSRE	LRHIMGLLQA	RLGPPGHPAG	SAWTPDPPCP	QLRPPCLSPC	ASRPPPSLQD	TTLAEVHCPA
970	980	990	1000	1010	1020		
SVGTMETGTA	LLDLRPSILP	PYPSEPDPLG	PSPVPEASPP	TPSLLRHSFQ	SRSDTFH		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2599	1	610.2335	-156.17	2	61.2	11.8	0	217-226	R.CLLLHYSVSK.A	Carbamidomethyl: 1

Detailed Protein Report

Protein 978: bifunctional glutamate/proline--tRNA ligase [Homo sapiens]

Accession: gi|62241042
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 11.8
MW [kDa]: 170.5
pI: 7.2
Sequence Coverage [%]: 1.2
No. of unique Peptides: 1

Quantitation

QD:QU **Median:** 0.54 **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	QD:QU 0.54

Detailed Protein Report

Protein 979: proline dehydrogenase 1, mitochondrial isoform 1 precursor [Homo sapiens]

Accession: gi|304766736
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.8
MW [kDa]: 67.9
pI: 8.8
Sequence Coverage [%]: 2.5
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 980: **heterogeneous nuclear ribonucleoprotein U isoform b [Homo sapiens]**

Accession: gi|14141161
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.8
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
436	1	658.3678	-41.71	2	35.4	11.8	2	11-21	K.LKVSELKEELK.K	

Detailed Protein Report

Protein 981: 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 982: ataxin-1 [Homo sapiens]

Accession: gi|51479158
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.8
MW [kDa]: 86.9
pI: 9.2
Sequence Coverage [%]: 1.5
No. of unique Peptides: 1

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
1222	1	612.4331	130.26	2	45.4	11.8	0	698-709	K.GQPVDPASVLLK.H	

Detailed Protein Report

Protein 983: **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

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
1754	2	577.2577	-85.92	2	52.2	11.8	0	473-483	R.STRPPGANPTR.R	

Detailed Protein Report

Protein 984: signal-regulatory protein beta-2 isoform 1 precursor [Homo sapiens]

Accession:	gi|171906611	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	36.9
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.8
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.67 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MCSTMSAPTC	LAHLPPCFLL	LALVLVPSDA	SGQSSRNDWQ	VLQPEGPMLV	AEGETLLLRC	MVVGSCTDGM	IKWVKVSTQD
90	100	110	120	130	140	150	160
QQEIYNFKRG	SFPGVMPMIQ	RTSEPLNCDY	SIYIHNVTRE	HTGTYHCVRF	DGLSEHSEMK	SDEGTSVLVK	GAGDPEPDLW
170	180	190	200	210	220	230	240
IIQPQELVLG	TTGDTVFLNC	TVLGDGPPGP	IRWFQGAGLS	REAIYNFGGI	SHPKETAVQA	SNNDFSILLQ	NVSSEDAGTY
250	260	270	280	290	300	310	320
YCVKFQRKPN	RQYLSGQGTS	LKVKAKSTSS	KEAEFTSEPA	TEMSPTGLLV	VFAPVVLGLK	AITLAALLLA	LATSRRSPGQ
330	340	350					
EDVKTTGPAG	AMNTLAWSKG	QE					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
555	1	708.8400	52.03	2	35.5	11.8	0	60-72	R.CMVVGSCTDGMIK.W	Carbamidomethyl: 7; Oxidation: 2	QD:QU 0.67

Detailed Protein Report

Protein 985: 39S ribosomal protein L52, mitochondrial isoform e [Homo sapiens]

Accession:	gi|31083085	**Score:**	11.8
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
2730	1	877.9630	30.30	2	63.1	11.8	1	14-28	R.RLHCSVAAWAGGQWR.L	Carbamidomethyl: 4

Detailed Protein Report

Protein 986: 60S ribosomal protein L35a [Homo sapiens]

Accession:	gi|16117791	**Score:**	11.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	12.5
Database Date:	2015-11-30	**pI:**	11.7
		Sequence Coverage [%]:	11.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530375914	refseq_human(refseq_human_20140103.fasta)	PREDICTED: 60S ribosomal protein L35a isoform X2 [Homo sapiens]

```
         10         20         30         40         50         60         70         80
MSGRLWSKAI FAGYKRGLRN QREHTALLKI EGVYARDETE FYLGKRCAYV YKAKNNTVTP GGKPNKTRVI WGKVTRAHGN
         90        100        110        120
SGMVRAKFRS NLPAKAIGHR IRVMLYPSRI
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2762	1	733.8633	-77.98	2	63.6	11.8	2	88-100	K.FRSNLPAKAIGHR.I	

Detailed Protein Report

Protein 987: 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

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
675	1	690.3561	-24.67	2	38.4	11.8	1	146-157	K.NAKEEINVLHGR.L	

Detailed Protein Report

Protein 988: **liprin-beta-2 isoform 3 [Homo sapiens]**

Accession:	gi|375151575	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	83.1
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGKLITRMWK	LLRRRSAPKE	LLSRTSLETQ	KLDLMTEVSE	LKLKLVGMEK	EQREQEEKQR	KAEELLQELR	HLKIKVEELE
90	100	110	120	130	140	150	160
NERNQYEWKL	KATKAEVAQL	QEQVALKDAE	IERLHSQLSR	TAALHSESHT	ERDQEIQRLK	MGMETLLLAN	EDKDRRIEEL
170	180	190	200	210	220	230	240
TGLLNQYRKV	KEIVMVTQGP	SERTLSINEE	EPEGGFSKWN	ATNKDPEELF	KQEMPPRCSS	PTVGPPPLPQ	KSLETRAQKK
250	260	270	280	290	300	310	320
LSCSLEDLRS	ESVDKCMDGN	QPFPVLEPKD	SPFLAEHKYP	TLPGKLSGAT	PNGEAAKSPP	TICQPDATGS	SLLRLRDTES
330	340	350	360	370	380	390	400
GWDDTAVVND	LSSTSSGTES	GPQSPLTPDG	KRNPKGIKKF	WGKIRRTQSG	NFYTDTLGMA	EFRRGGLRAT	AGPRLSRTRD
410	420	430	440	450	460	470	480
SKGQKSDANA	PFAQWSTERV	CAWLEDFGLA	QYVIFARQWV	SSGHTLLTAT	PQDMEKELGI	KHPLHRKKLV	LAVKAINTKQ
490	500	510	520	530	540	550	560
EEKSALLDHI	WVTRWLDDIG	LPQYKDQFHE	SRVDGRMLQY	LTVNDLLFLK	VTSQLHHLSI	KCAIHVLHVN	KFNPHCLHRR
570	580	590	600	610	620	630	640
PADESNLSPS	EVVQWSNHRV	MEWLRSVDLA	EYAPNLRGSG	VHGGLIILEP	RFTGDTLAML	LNIPPQKTLL	RRHLTTKFNA
650	660	670	680	690	700	710	720
LIGPEAEQEK	REKMASPAYT	PLTTTAKVRP	RKLGFSHFGN	IRKKKFDEST	DYICPMEPSD	GVSDSHRVYS	GYRGLSPLDA
730	740						
PELDGLDQVG	QIS						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2166	1	977.4261	-10.11	2	55.7	11.7	0	367-383	R.TQSGNFYTDTLGMAEFR.R	Oxidation: 13

Detailed Protein Report

Protein 989: **PREDICTED: regulator of G-protein signaling 7-binding protein isoform X2 [Homo sapiens]**

Accession:	gi|578810352	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.7
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.8
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.35 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MSSAPNGRKK RPSRSTRSSI FQISKPPLQS GDWERRGSGS ESAHKTQRAL DDCKMLVQEF NTQVALYREL VISIGDVSVS
        90        100        110        120        130        140        150        160
CPSLRAEMHK TRTKGCEMAR QAHQKLAAIS GPEDGEIHPE ICRLYIQLQC CLEMYTTEML KSICLLGSLQ FHRKGKEPGG
       170        180        190        200        210
GTKSLDCKIE ESAETPALED SSSSPVDSQQ HSWQVSTDIE NTER
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
1047	1	973.9236	-30.05	2	41.6	11.7	2	37-54	R.GSGSESAHKTQRALDDCK.M	Carbamidomethyl: 17	QD:QU	0.35

Detailed Protein Report

Protein 990: 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 991: **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 992: pancreatic lipase-related protein 2 precursor [Homo sapiens]

Accession:	gi|106507261	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	52.0
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	2.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMLPPWTLGL	LLLATVRGKE	VCYGQLGCFS	DEKPWAGTLQ	RPVKLLPWSP	EDIDTRFLLY	TNENPNNFQL	ITGTEPDTIE
90	100	110	120	130	140	150	160
ASNFQLDRKT	RFIIHGFLDK	AEDSWPSDMC	KKMFEVEKVN	CICVDWRHGS	RAMYTQAVQN	IRVVGAETAF	LIQALSTQLG
170	180	190	200	210	220	230	240
YSLEDVHVIG	HSLGAHTAAE	AGRRLGGRVG	RITGLDPAGP	CFQDEPEEVR	LDPSDAVFVD	VIHTDSSPIV	PSLGFGMSQK
250	260	270	280	290	300	310	320
VGHLDFFPNG	GKEMPGCKKN	VLSTITDIDG	IWEGIGGFVS	CNHLRSFEYY	SSSVLNPDGF	LGYPCASYDE	FQESKCFPCP
330	340	350	360	370	380	390	400
AEGCPKMGHY	ADQFKGKTSA	VEQTFFLNTG	ESGNFTSWRY	KVSVTLSGKE	KVNGYIRIAL	YGSNENSKQY	EIFKGSLKPD
410	420	430	440	450	460	470	480
ASHTCAIDVD	FNVGKIQKVK	FLWNKRGINL	SEPKLGASQI	TVQSGEDGTE	YNFCSSDTVE	ENVLQSLYPC	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1225	1	671.3731	171.64	2	43.8	11.7	0	101-111	K.AEDSWPSDMCK.K	Carbamidomethyl: 10; Oxidation: 9

Detailed Protein Report

Protein 993: **vesicle transport protein GOT1B [Homo sapiens]**

Accession:	gi|7705636	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.4
Database Date:	2015-11-30	**pI:**	10.8
		Sequence Coverage [%]:	9.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MISLTDTQKI GMGLTGFGVF FLFFGMILFF DKALLAIGNV LFVAGLAFVI GLERTFRFFF QKHKMKATGF FLGGVFVVLI
        90        100        110        120        130        140
GWPLIGMIFE IYGFFLLFRG FFPVVVGFIR RVPVLGSLLN LPGIRSFVDK VGESNNMV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2030	1	713.2881	-69.27	2	53.9	11.7	1	126-138	R.SFVDKVGESNNMV.-	

Detailed Protein Report

Protein 994: metastasis-associated protein MTA2 [Homo sapiens]

Accession:	gi|14141170	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	75.0
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAANMYRVGD	YVYFENSSSN	PYLVRRIEEL	NKTANGNVEA	KVVCLFRRRD	ISSSLNSLAD	SNAREFEEES	KQPGVSEQQR
90	100	110	120	130	140	150	160
HQLKHRELFL	SRQFESLPAT	HIRGKCSVTL	LNETDILSQY	LEKEDCFFYS	LVFDPVQKTL	LADQGEIRVG	CKYQAEIPDR
170	180	190	200	210	220	230	240
LVEGESDNRN	QQKMEMKVWD	PDNPLTDRQI	DQFLVVARAV	GTFARALDCS	SSIRQPSLHM	SAAAASRDIT	LFHAMDTLQR
250	260	270	280	290	300	310	320
NGYDLAKAMS	TLVPQGGPVL	CRDEMEEWSA	SEAMLFEEAL	EKYGKDFNDI	RQDFLPWKSL	ASIVQFYYMW	KTTDRYIQQK
330	340	350	360	370	380	390	400
RLKAAEADSK	LKQVYIPTYT	KPNPNQIISV	GSKPGMNGAG	FQKGLTCESC	HTTQSAQWYA	WGPPNMQCRL	CASCWIYWKK
410	420	430	440	450	460	470	480
YGGLKTPTQL	EGATRGTTEP	HSRGHLSRPE	AQSLSPYTTS	ANRAKLLAKN	RQTFLLQTTK	LTRLARRMCR	DLLQPRRAAR
490	500	510	520	530	540	550	560
RPYAPINANA	IKAECSIRLP	KAAKTPLKIH	PLVRLPLATI	VKDLVAQAPL	KPKTPRGTKT	PINRNQLSQN	RGLGGIMVKR
570	580	590	600	610	620	630	640
AYETMAGAGV	PFSANGRPLA	SGIRSSSQPA	AKRQKLNPAD	APNPVVFVAT	KDTRALRKAL	THLEMRRAAR	RPNLPLKVKP
650	660	670					
TLIAVRPPVP	LPAPSHPAST	NEPIVLED					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1808	1	780.2935	-154.53	2	51.1	11.7	1	139-152	K.TLLADQGEIRVGCK.Y	Carbamidomethyl: 13

Detailed Protein Report

Protein 995: membrane-spanning 4-domains subfamily A member 14 isoform 2 [Homo sapiens]

Accession: gi|119226220
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.7
MW [kDa]: 74.6
pI: 5.2
Sequence Coverage [%]: 1.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MESTSQDRRA	THVITIKPNE	TVLTAFPYRP	HSSLLDFLKG	EPRVLGATQI	LLALIIVGFG	TIFALNYIGF	SQRLPLVVLT
90	100	110	120	130	140	150	160
GYPFWGALIG	QGVTGMNVIS	SLVAITGITF	TILSYRHQDK	YCQMPSFEEI	CVFSRTLFIV	LFFLPSDVTQ	NSEQPAPEEN
170	180	190	200	210	220	230	240
DQLQFVLQEE	FSSDDSTTNA	QSVIFGGYAF	FKLTLSRSPL	VSQPGNKGRE	FVPDEQKQSI	LPSPKFSEEE	IEPLPPTLEK
250	260	270	280	290	300	310	320
KPSENMSIQL	DSTFKQMKDE	DLQSAIVQPS	QMQTKLLQDQ	AASLQVFPSH	SALKLEDISP	EDLPSQALPV	EGLSEQTMPS
330	340	350	360	370	380	390	400
KSTSSHVKQS	SNLTANDLPP	QGILSQDTSS	QDMLFHDMTS	QDMQSLDMLS	QDTPSHAMPP	QDIPSQDMLS	QALSAHAILP
410	420	430	440	450	460	470	480
EASTSHIVQF	PEIQHLLQQP	PDLQPENTEP	QNQQILQMSY	QDIRSEVMEE	TKEWKSEEEL	HRRKSSRRHS	LNQQTKALQY
490	500	510	520	530	540	550	560
LRRHSLDVQA	KGQKSSKRHS	LDQQSKGWQS	PKQKSLDQQI	KDWLSPKRHS	VDKQAQLNQT	KEQLPDQQAE	DQQAKGEQYP
570	580	590	600	610	620	630	640
EGQSKDGQVK	DQQTDKEQNS	KKQTQDQQTE	DQPAQEKKSP	KGQFQNVQAE	GQQAQVEKVP	KLLCQDSESQ	IQQYQFWQFH
650	660	670					
KGNLQAGQPR	TVNLLAKNPL	TG					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
974	1	555.2031	-91.32	2	40.7	11.7	1	1-9	-.MESTSQDRR.A	

Detailed Protein Report

Protein 996: zinc finger protein 26 isoform 3 [Homo sapiens]

Accession:	gi|372266178	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.6
Database Date:	2015-11-30	**pI:**	10.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATSFRTASC	WGLLSFKDIS	MEFTWDEWQL	LDSTQKYLYR	DVILENYHNL	ISVDGWEEWY	QNNQDELESI	ERSYACSVLG
90	100	110	120	130	140	150	160
RLNLSKTHDS	SRQRLYNTRG	KSLTQNSAPS	RSYLRKNPDK	FHGYEEPYFL	KHQRAHSIEK	NCVCSECGKA	FRCKSQLIVH
170	180	190	200	210	220	230	240
LRIHTGERPY	ECSKCERAFS	AKSNLNAHQR	VHTGEKPYSC	SECEKVFSFR	SQLIVHQEIH	TGGKPYGCSE	CGKAYSWKSQ
250	260	270	280	290	300	310	320
LLLHQRSHTG	VKPYECSECG	KAFSLKSPFV	VHQRTHTGVK	PHKCSECGKA	FRSKSYLLVH	IRMHTGEKPY	QCSDCGKAFN
330	340	350	360	370	380	390	400
MKTQLIVHQG	VHTGNNPYQC	GECGKAFGRK	EQLTAHLRAH	AGEKPYGCSE	CGKAFSSKSY	LVIHRRTHTG	ERPYECSLCE
410	420	430	440	450	460	470	480
RAFCGKSQLI	IHQRTHSTEK	PYECNECEKA	YPRKASLQIH	QKTHSGEKPF	KCSECGKAFT	QKSSLSEHQR	VHTGEKPWKC
490	500	510					
SECGKSFCWN	SGLRIHRKTH	K					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2652	1	665.3901	129.73	3	61.9	11.7	1	386-401	R.RTHTGERPYECSLCER.A	Carbamidomethyl: 14

Detailed Protein Report

Protein 997: 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

Quantitation

QD:QU	**Median:** 0.93	**CV:** 0.00 %	**No. of Peptides:** 1

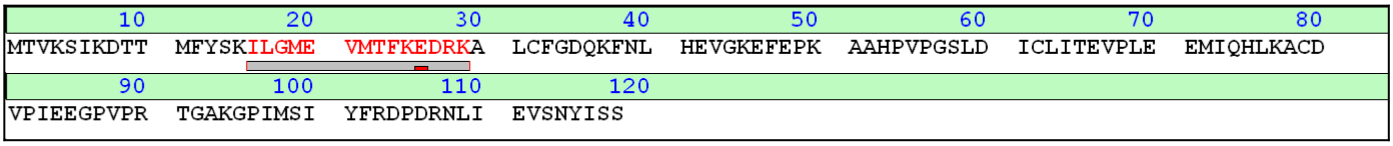
10	20	30	40	50	60	70	80
MAQWNQLQQL	DTRYLEQLHQ	LYSDSFPMEL	RQFLAPWIES	QDWAYAASKE	SHATLVFHNL	LGEIDQQYSR	FLQESNVLYQ
90	100	110	120	130	140	150	160
HNLRRIKQFL	QSRYLEKPME	IARIVARCLW	EESRLLQTAA	TAAQQGGQAN	HPTAAVVTEK	QQMLEQHLQD	VRKRVQDLEQ
170	180	190	200	210	220	230	240
KMKVVENLQD	DFDFNYKTLK	SQGDMQDLNG	NNQSVTRQKM	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	Ratios
1378	1	977.5477	34.77	2	47.4	11.7	0	216-233	R.SIVSELAGLLSAMEYVQK.T	Oxidation: 13	QD:QU 0.93

Detailed Protein Report

Protein 998: PREDICTED: glyoxalase domain-containing protein 5 isoform X1 [Homo sapiens]

Accession:	gi|578838023	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.3
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	11.9
		No. of unique Peptides:	1



```
        10         20         30         40         50         60         70         80
MTVKSIKDTT MFYSKILGME VMTFKEDRKA LCFGDQKFNL HEVGKEFEPK AAHPVPGSLD ICLITEVPLE EMIQHLKACD
        90        100        110        120
VPIEEGPVPR TGAKGPIMSI YFRDPDRNLI EVSNYISS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2512	1	856.9301	-10.53	2	62.0	11.7	2	16-29	K.ILGMEVMTFKEDRK.A	Oxidation: 4

Detailed Protein Report

Protein 999: **mitochondrial intermediate peptidase [Homo sapiens]**

Accession:	gi|156105687	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.6
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MLCVGRLGGL GARAAALPPR RAGRGSLEAG IRARRVSTSW SPVGAAFNVK PQGSRLDLFG ERRGLFGVPE LSAPEGFHIA
        90        100        110        120        130        140        150        160
QEKALRKTEL LVDRACSTPP GPQTVLIFDE LSDSLCRVAD LADFVKIAHP EPAFREAAEE ACRSIGTMVE KLNTNVDLYQ
       170        180        190        200        210        220        230        240
SLQKLLADKK LVDSLDPETR RVAELFMFDF EISGIHLDKE KRKRAVDLNV KILDLSSTFL MGTNFPNKIE KHLLPEHIRR
       250        260        270        280        290        300        310        320
NFTSAGDHII IDGLHAESPD DLVREAAYKI FLYPNAGQLK CLEELLSSRD LLAKLVGYST FSHRALQGTI AKNPETVMQF
       330        340        350        360        370        380        390        400
LEKLSDKLSE RTLKDFEMIR GMKMKLNPQN SEVMPWDPPY YSGVIRAERY NIEPSLYCPF FSLGACMEGL NILLNRLLGI
       410        420        430        440        450        460        470        480
SLYAEQPAKG EVWSEDVRKL AVVHESEGLL GYIYCDFFQR ADKPHQDCHF TIRGGRLKED GDYQLPVVVL MLNLPRSSRS
       490        500        510        520        530        540        550        560
SPTLLTPGMM ENLFHEMGHA MHSMLGRTRY QHVTGTRCPT DFAEVPSILM EYFANDYRVV NQFARHYQTG QPLPKNMVSR
       570        580        590        600        610        620        630        640
LCESKKVCAA ADMQLQVFYA TLDQIYHGKH PLRNSTTDIL KETQEKFYGL PYVPNTAWQL RFSHLVGYGA RYYSYLMSRA
       650        660        670        680        690        700        710        720
VASMVWKECF LQDPFNRAAG ERYRREMLAH GGGREPMLMV EGMLQKCPSV DDFVSALVSD LDLDFETFLM DSE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2189	1	993.8848	-92.03	2	56.0	11.7	1	632-647	R.YYSYLMSRAVASMVWK.E	Oxidation: 6, 13

Detailed Protein Report

Protein 1000: centrosomal protein kizuna isoform 3 [Homo sapiens]

Accession:	gi|247301334	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.2
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	2.8
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.98 **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		QD:QU	0.98

Detailed Protein Report

Protein 1001: PREDICTED: sperm-associated antigen 8 isoform X4 [Homo sapiens]

Accession:	gi|578816456	**Score:**	11.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.4
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MTVPGFRNLV ADRVPNYTSW SQHCPWEPQK QPPWEFLQVL EPGARGLWKP PDIKGKLMVC YETLPRGQCL LYNWEEERAT
        90        100        110        120        130        140        150        160
NHLDQVPSMQ DGSESFFFRH GHRGLLTMQL KSPMPSSTTQ KDSYQPPGNV YWPLRGKREA MLEMLLQHQI CKEVQAEQEP
       170        180        190        200        210        220        230        240
TRKLFEVESV THHDYRMELA QAGTPAPTKP HDYRQEQPET FWIQRAPQLP GVSNIRTLDT PFRKNCSFST PVPLSLGKLL
       250        260        270        280
PYEPENYPYQ LGEISSLPCP GGRLGGGGGR MTPF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2737	1	753.8991	19.19	2	63.2	11.7	0	225-238	K.NCSFSTPVPLSLGK.L	Carbamidomethyl: 2

Detailed Protein Report

Protein 1002: regulator of G-protein signaling 9 isoform 2 [Homo sapiens]

Accession:	gi|126366080	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	76.6
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	1.8
		No. of unique 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
461	1	626.3269	-12.81	2	35.8	11.6	1	596-607	R.LSPKCPAVSHGR.V	

Detailed Protein Report

Protein 1003: 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

Protein 1004: PREDICTED: TRAF3-interacting protein 1 isoform X3 [Homo sapiens]

Accession:	gi|578804055	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	71.4
Database Date:	2015-11-30	**pI:**	9.4
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MNAAVVRRTQ	EALGKVIRRP	PLTEKLLSKP	PFRYLHDIIT	EVIRMTGFMK	GLYTDAEMKS	DNVKDKDAKI	SFLQKAIDVV
90	100	110	120	130	140	150	160
VMVSGEPLLA	KPARIVAGHE	PERTNELLQI	IGKCCLNKLS	SDDAVRRVLA	GEKGEVKGRA	SLTSRSQELD	NKNVREEESR
170	180	190	200	210	220	230	240
VHKNTEDRGD	AEIKERSTSR	DRKQKEELKE	DRKPREKDKD	KEKAKENGGN	RHREGERERA	KARARPDNER	QKDRGNRERD
250	260	270	280	290	300	310	320
RDSERKKETE	RKSEGGKEKE	RLRDRDRERD	RDKGKDRDRR	RVKNGEHSWD	LDREKNREHD	KPEKKSASSG	EMSKKLSDGT
330	340	350	360	370	380	390	400
FKDSKAETET	EISTRASKSL	TTKTSKRRSK	NSVEGDSTSD	AGDAGPAGQD	KSEVPETPEI	PNELSSNIRR	IPRPGSARPA
410	420	430	440	450	460	470	480
PPRVKRQDSM	EALQMDRSGS	GKTVSNVITE	SHNSDNEEDD	QFVVEAAPQL	SEMSEIEMVT	AVELEEEEKH	GGLVKKILET
490	500	510	520	530	540	550	560
KKDYEKLQQS	PKPGEKERSL	FESAWKKEKD	IVSKEIEKLR	TSIQTLCKSA	LPLGKIMDYI	QEDVDAMQNE	LQMWHSENRQ
570	580	590	600	610	620	630	
HAEALQQEQR	ITDCAVEPLK	AELAELEQLI	KDQQDKICAV	KANILKNEEK	IQKMVYSINL	TSRR	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
515	1	686.3549	-44.18	2	36.4	11.6	0	34-44	R.YLHDIITEVIR.M	

Detailed Protein Report

Protein 1005: PREDICTED: gamma-adducin isoform X7 [Homo sapiens]

Accession:	gi|530393082	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.8
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	2.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578818929	refseq_human (refseq_human_20140103.fasta)	PREDICTED: gamma-adducin isoform X11 [Homo sapiens]

10	20	30	40	50	60	70	80
MKKGHNPTGL	LALQQIADYI	MANSFSGFSS	PPLSLGMVTP	INDLPGADTS	SYVKGEKLTR	CKLASLYRLV	DLFGWAHLAN
90	100	110	120	130	140	150	160
TYISVRISKE	QDHIIIIPRG	LSFSEATASN	LVKVNIIGEV	VDQGSTNLKI	DHTGFSPHAA	IYSTRPDVKC	VIHIHTLATA
170	180	190	200	210	220	230	240
AVSSMKCGIL	PISQESLLLG	DVAYYDYQGS	LEEQEERIQL	QKVLGPSCKV	LVLRNHGVVA	LGETLEEAFH	YIFNVQLACE
250	260	270	280	290	300	310	320
IQVQALAGAG	GVDNLHVLDF	QKYKAFTYTV	AASGGGGVNM	GSHQKWKVGE	IEFEGLMRTL	DNLGYRTGYA	YRHPLIREKP
330	340	350	360	370	380	390	400
RHKSDVEIPA	TVTAFSFEDD	TVPLSPLKYM	AQRQQREKTR	WLNSPNTYMK	VNVPEESRNG	ETSPRTKITW	MKAEDSSKVS
410	420	430	440	450	460	470	480
GGTPIKIEDP	NQFVPLNTNP	NEVLEKRNKI	REQNRYDLKT	AGPQSQLLAG	IVVDKPPSTM	QFEDDDHGPP	APPNPFSHLT
490	500	510	520	530	540	550	560
EGELEEYKRT	IERKQQGLED	AEQELLSDDA	SSVSQIQSQT	QSPQNVPEKL	EENHELFSKS	FISMEVPVMV	VNGKDDMHDV
570	580	590	600	610	620	630	
EDELAKRVSR	LSTSTTIENI	EITIKSPEKI	EEVLSPEGSP	SKSPSKKKKK	FRTPSFLKKN	KKKEKVEA	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
734	1	712.3429	-45.01	2	39.2	11.6	0	100-113	R.GLSFSEATASNLVK.V	

Detailed Protein Report

Protein 1006: 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 1007: 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 1008: cell division cycle-associated protein 4 [Homo sapiens]

Accession:	gi|22027509	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.1
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	7.5
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|22027511	refseq_human (refseq_human_20140103.fasta)	cell division cycle-associated protein 4 [Homo sapiens]

10	20	30	40	50	60	70	80
MFARGLKRKC	VGHEEDVEGA	LAGLKTVSSY	SLQRQSLLDM	SLVKLQLCHM	LVEPNLCRSV	LIANTVRQIQ	EEMTQDGTWR
90	100	110	120	130	140	150	160
TVAPQAAERA	PLDRLVSTEI	LCRAAWGQEG	AHPAPGLGDG	HTQGPVSDLC	PVTSAQAPRH	LQSSAWEMDG	PRENRGSFHK
170	180	190	200	210	220	230	240
SLDQIFETLE	TKNPSCMEEL	FSDVDSPYYD	LDTVLTGMMG	GARPGPCEGL	EGLAPATPGP	SSSCKSDLGE	LDHVVEILVE
250							
T							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2120	1	955.8719	-124.82	2	55.1	11.6	2	8-25	K.RKCVGHEEDVEGALAGLK.T	

Detailed Protein Report

Protein 1009: kazrin isoform C [Homo sapiens]

Accession: gi|63999741
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 11.6
MW [kDa]: 37.0
pI: 7.9
Sequence Coverage [%]: 3.7
No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|65301128	refseq_human (refseq_human_20140103.fasta)	kazrin isoform C [Homo sapiens]

10	20	30	40	50	60	70	80
MKEMLAKDLE	ESQGGKSSEV	LSATELRVQL	AQKEQELARA	KEALQAMKAD	RKRLKGEKTD	LVSQMQQLYA	TLESREEQLR
90	100	110	120	130	140	150	160
DFIRNYEQHR	KESEDAVKAL	AKEKDLLERE	KWELRRQAKE	ATDHATALRS	QLDLKDNRMK	ELEAELAMAK	QSLATLTKDV
170	180	190	200	210	220	230	240
PKRHSLAMPG	ETVLNGNQEW	VVQADLPLTA	AIRQSQQTLY	HSHPPHPADR	QAVRVSPCHS	RQPSVISDAS	AAEGDRSSTP
250	260	270	280	290	300	310	320
SDINSPRHRT	HSLCNGDSPG	PVQKNLHNPI	VQSLEDLEDQ	KRKKKKEKMG	FGSISRVFAR	GKQRKSLDPG	LFDGTAPDYY
330							
IEEDADW							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2651	1	698.3866	57.31	2	61.9	11.6	1	139-150	R.MKELEAELAMAK.Q	Oxidation: 1, 10

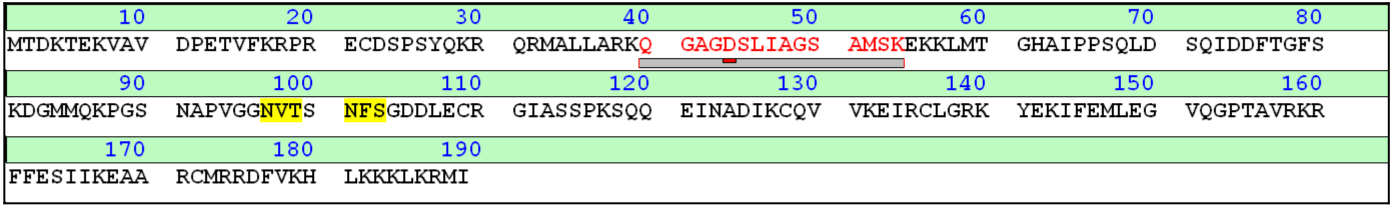
Detailed Protein Report

Protein 1010: cancer/testis antigen family 45 member A5 [Homo sapiens]

Accession:	gi|56090473	**Score:**	11.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.1
Database Date:	2015-11-30	**pI:**	10.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.9
		No. of unique 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
309	1	704.8671	37.75	2	33.9	11.6	0	40-54	K.QGAGDSLIAGSAMSK.E	Oxidation: 13

Detailed Protein Report

Protein 1011: 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 1012: protein phosphatase 1M isoform b [Homo sapiens]

Accession: gi|171460934
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 11.6
MW [kDa]: 27.9
pI: 5.3
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; Oxidation: 18

Detailed Protein Report

Protein 1013: 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 1014: PREDICTED: bile acid receptor isoform X2 [Homo sapiens]

Accession:	gi|578824525	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.5
Database Date:	2015-11-30	**pI:**	10.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVMQFQGLEN	PIQISPHCSC	TPSGFFMEMM	SMKPAKGVLT	EQVAGPLGQN	LEVEPYSQYS	NVQFPQVQPQ	ISSSSYYSNL
90	100	110	120	130	140	150	160
GFYPQQPEEW	YSPGIYELRR	MPAETLYQGE	TEVAEMPVTK	KPRMGASAGR	IKGDELCVVC	GDRASGYHYN	ALTCEGCKGF
170	180	190	200	210	220	230	240
FRRSITKNAV	YKCKNGGNCV	MDMYMRRKCQ	ECRLRKCKEM	GMLAECMYTG	LLTEIQCKSK	RLRKNVKQHA	DQTVNEDSEG
250	260	270	280	290			
RDLRQVTSTT	KSCRCRRKLN	SPQINRLFYI	LLWIHITNRG	CLRK			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1939	1	917.8148	-77.02	2	54.6	11.5	2	173-187	K.CKNGGNCVMDMYMRR.K	Carbamidomethyl: 7

Detailed Protein Report

Protein 1015: **PREDICTED: transmembrane and coiled-coil domains protein 3 isoform X1 [Homo sapiens]**

Accession:	gi|530400601	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.1
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.0
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530400605	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transmembrane and coiled-coil domains protein 3 isoform X3 [Homo sapiens]
gi|530400603	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transmembrane and coiled-coil domains protein 3 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MNTLSLPLNI	RRGGSDTNLN	FDVPDGILDF	HKVKLTADSL	KQKILKVTEQ	IKIEQTSRDG	NVAEYLKLVN	NADKQQAGRI
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
KQVFEKKNQK	SAHSIAQLQK	KLEQYHRKLR	EIEQNGASRS	SKDISKDHLK	DIHRSLKDAH	VKSRTAPHCM	ESSKSGMPGV
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
SLTPPVFVFN	KSREFANLIR	NKFGSADNIA	HLKNSLEEFR	PEASARAYGG	SATIVNKPKY	GSDDECSSGT	SGSADSNGNQ
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
SFGAGGASTL	DSQGKLAVIL	EELREIKDTQ	AQLAEDIEAL	KVQFKREYGF	ISQTLQEERY	RYERLEDQLH	DLTDLHQHET
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
ANLKQELASI	EEKVAYQAYE	RSRDIQEALE	SCQTRISKLE	LHQQEQQALQ	TDTVNAKVLL	GRCINVILAF	MTVILVCVST
410	**420**	**430**	**440**	**450**			
IAKFVSPMMK	SRCHILGTFF	AVTLLAIFCK	NWDHILCAIE	RMIIPR			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2855	1	1027.5252	-26.05	2	64.9	11.5	0	413-430	R.CHILGTFFAVTLLAIFCK.N	Carbamidomethyl: 1

Detailed Protein Report

Protein 1016: 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

Quantitation

QD:QU **Median:** 0.95 **CV:** 0.00 % **No. of 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	Ratios
880	1	695.3494	-29.98	2	41.1	11.5	1	101-113	K.LQKLGEGDSSVTR.E		QD:QU 0.95

Detailed Protein Report

Protein 1017: PREDICTED: serine/threonine-protein kinase 31 isoform X3 [Homo sapiens]

Accession:	gi|578813577	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	95.7
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
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
414	1	592.2979	34.39	2	35.1	11.5	0	581-591	K.GYSVDVDTEAK.V	

Detailed Protein Report

Protein 1018: UDP-glucuronosyltransferase 2A3 precursor [Homo sapiens]

Accession:	gi|193211427	**Score:**	11.5
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
2124	1	652.6392	15.16	3	55.1	11.5	1	123-137	K.MMCESFIYNQTLMKK.L	Carbamidomethyl: 3; Oxidation: 1, 13

Detailed Protein Report

Protein 1019: melanotransferrin isoform 2 precursor [Homo sapiens]

Accession:	gi|16163666	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	32.7
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	6.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRGPSGALWL	LLALRTVLGG	MEVRWCATSD	PEQHKCGNMS	EAFREAGIQP	SLLCVRGTSA	DHCVQLIAAQ	EADAITLDGG
90	100	110	120	130	140	150	160
AIYEAGKEHG	LKPVVGEVYD	QEVGTSYYAV	AVVRRSSHVT	IDTLKGVKSC	HTGINRTVGW	NVPVGYLVES	GRLSVMGCDV
170	180	190	200	210	220	230	240
LKAVSDYFGG	SCVPGAGETS	YSESLCRLCR	GDSSGEGVCD	KSPLERYYDY	SGAFRCLAEG	AGDVAFVKHS	TVLENTDESP
250	260	270	280	290	300	310	
SRRQTWTRSE	EEEGECPAHE	EARRTMRSSA	GQAWKWAPVH	RPQDESDKGE	FGKRAKSRDM	LG	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2850	1	754.6730	23.67	3	64.8	11.5	2	249-267	R.SEEEEGECPAHEEARRTMR.S	Oxidation: 18

Detailed Protein Report

Protein 1020: WAP four-disulfide core domain protein 2 precursor [Homo sapiens]

Accession:	gi|56699495	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.0
Database Date:	2015-11-30	**pI:**	4.5
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	17.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPACRLGPLA	AALLLSLLLF	GFTLVSGTGA	EKTGVCPELQ	ADQNCTQECV	SDSECADNLK	CCSAGCATFC	SLPNDKEGSC
90	**100**	**110**	**120**	**130**			
PQVNINFPQL	GLCRDQCQVD	SQCPGQMKCC	RNGCGKVSCV	TPNF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2885	1	1287.8628	-110.66	2	65.2	11.5	2	95-116	R.DQCQVDSQCPGQMKCCRNGCGK.V	Carbamidomethyl: 9, 15, 16; Oxidation: 13

Detailed Protein Report

Protein 1021: 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

QD:QU **Median:** 0.44 **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		QD:QU 0.44

Detailed Protein Report

Protein 1022: 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 1023: **transmembrane protein 191B [Homo sapiens]**

Accession:	gi|334085264	**Score:**	11.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	39.0
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
MCRATLGLPL	PPIVIQPARR	SLPPIVTPAS	RRLGPRGGRH	LGSVSTAMAA	TQELLLQLQK	DNRDGRQRKQ	ELEKLMRGLE
90	100	110	120	130	140	150	160
AESESLNQRL	QDLSERERSL	LRRRSQAAQP	LQGEAREAAR	ERAERVRRRL	EEAERHKEDL	EQHSRQLQEQ	WEELSSQLFY
170	180	190	200	210	220	230	240
GGEPQSQKST	EQQLAAQLVT	LQNELELAET	KCALQEEKLQ	QDALQTAEAW	AIFQEQTVVL	QVRPHSDAKV	PPASPPPDLG
250	260	270	280	290	300	310	320
RCDGQLRGVQ	YSTESLMEEM	ARADRETRLF	GGPRALAIRR	CVLGALQVLL	TLPLLFLGLS	LLWTVLLDPG	AVSAWLWSLT
330	340	350					
SETTLRRLRY	TLSPLLELRA	NGLLPT					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1263	1	714.0054	-115.37	3	45.9	11.5	2	328-346	R.LRYTLSPLLELRANGLLPT.-	

Detailed Protein Report

Protein 1024: 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 1025: cyclin-dependent kinase 14 isoform a [Homo sapiens]

Accession:	gi|560231615	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.0
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MCDLIEPQPA	EKIGKMKKLR	RTLSESFSRI	ALKKDDTTFD	EICVTKMSTR	NCQGMDSVIK	PLDTIPEDKK	VRVQRTQSTF
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
DPFEKPANQV	KRVHSENNAC	INFKTSSTGK	ESPKVRRHSS	PSSPTSPKFG	KADSYEKLEK	LGEGSYATVY	KGKSKVNGKL
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
VALKVIRLQE	EEGTPFTAIR	EASLLKGLKH	ANIVLLHDII	HTKETLTLVF	EYVHTDLCQY	MDKHPGGLHP	DNVKLFLFQL
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
LRGLSYIHQR	YILHRDLKPQ	NLLISDTGEL	KLADFGLARA	KSVPSHTYSN	EVVTLWYRPP	DVLLGSTEYS	TCLDMWGVGC
330	**340**	**350**	**360**	**370**	**380**	**390**	**400**
IFVEMIQGVA	AFPGMKDIQD	QLERIFLVLG	TPNEDTWPGV	HSLPHFKPER	FTLYSSKNLR	QAWNKLSYVN	HAEDLASKLL
410	**420**	**430**	**440**	**450**	**460**	**470**	
QCSPKNRLSA	QAALSHEYFS	DLPPRLWELT	DMSSIFTVPN	VRLQPEAGES	MRAFGKNNSY	GKSLSNSKH	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1903	1	676.2591	-182.65	2	52.3	11.4	1	22-33	R.TLSESFSRIALK.K	

Detailed Protein Report

Protein 1026: **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 1027: **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 1028: 3-keto-steroid reductase [Homo sapiens]

Accession:	gi|7705421	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.2
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
MRKVVLITGA	SSGIGLALCK	RLLAEDDELH	LCLACRNMSK	AEAVCAALLA	SHPTAEVTIV	QVDVSNLQSV	FRASKELKQR
90	100	110	120	130	140	150	160
FQRLDCIYLN	AGIMPNPQLN	IKALFFGLFS	RKVIHMFSTA	EGLLTQGDKI	TADGLQEVFE	TNVFGHFILI	RELEPLLCHS
170	180	190	200	210	220	230	240
DNPSQLIWTS	SRSARKSNFS	LEDFQHSKGK	EPYSSSKYAT	DLLSVALNRN	FNQQGLYSNV	ACPGTALTNL	TYGILPPFIW
250	260	270	280	290	300	310	320
TLLMPAILLL	RFFANAFTLT	PYNGTEALVW	LFHQKPESLN	PLIKYLSATT	GFGRNYIMTQ	KMDLDEDTAE	KFYQKLLELE
330	340	350					
KHIRVTIQKT	DNQARLSGSC	L					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1650	1	682.3648	78.06	3	50.9	11.4	1	295-311	R.NYIMTQKMDLDEDTAEK.F	

Protein 1029: transcription initiation factor TFIID subunit 1-like [Homo sapiens]

Accession: gi|24429572
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.4
MW [kDa]: 207.2
pI: 5.1
Sequence Coverage [%]: 0.9
No. of unique Peptides: 1

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	m/z meas.	Δ m/z	z	Rt	Score	P	Range	Sequence	Modification

	Cmpds.		[ppm]		[min]					
1183	1	839.3834	23.08	2	44.9	11.4	0	1050- 1065	R.TMSTEQAHSGEGPMSK.F	

Detailed Protein Report

Protein 1030: sushi domain-containing protein 1 isoform 3 precursor [Homo sapiens]

Accession:	gi|544063419	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.4
Database Date:	2015-11-30	**pI:**	6.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		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 1031: tumor suppressor candidate gene 1 protein [Homo sapiens]

Accession:	gi|51944974	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.4
Database Date:	2015-11-30	**pI:**	11.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	8.0
		No. of unique Peptides:	1

```
        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
474	1	775.3888	94.96	2	35.9	11.4	1	15-31	R.GSCCGGDGAADGRGPGR.S	Carbamidomethyl: 3

Detailed Protein Report

Protein 1032: double-stranded RNA-specific adenosine deaminase isoform d [Homo sapiens]

Accession:	gi|70167113	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	103.6
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

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	

Detailed Protein Report

Protein 1033: guanine nucleotide-binding protein subunit beta-5 isoform a [Homo sapiens]

Accession:	gi|5729852	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.7
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MATEGLHENE	TLASLKSEAE	SLKGKLEEER	AKLHDVELHQ	VAERVEALGQ	FVMKTRRTLK	GHGNKVLCMD	WCKDKRRIVS
90	100	110	120	130	140	150	160
SSQDGKVIVW	DSFTTNKEHA	VTMPCTWVMA	CAYAPSGCAI	ACGGLDNKCS	VYPLTFDKNE	NMAAKKKSVA	MHTNYLSACS
170	180	190	200	210	220	230	240
FTNSDMQILT	ASGDGTCALW	DVESGQLLQS	FHGHGADVLC	LDLAPSETGN	TFVSGGCDKK	AMVWDMRSGQ	CVQAFETHES
250	260	270	280	290	300	310	320
DINSVRYYPS	GDAFASGSDD	ATCRLYDLRA	DREVAIYSKE	SIIFGASSVD	FSLSGRLLFA	GYNDYTINVW	DVLKGSRVSI
330	340	350	360				
LFGHENRVST	LRVSPDGTAF	CSGSWDHTLR	VWA				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2176	1	994.3487	-118.16	2	55.8	11.4	1	129-145	K.CSVYPLTFDKNENMAAK.K	Carbamidomethyl: 1

Detailed Protein Report

Protein 1034: interleukin-17F precursor [Homo sapiens]

Accession: gi|16418375
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl, Oxidation

Score: 11.4
MW [kDa]: 18.0
pI: 10.3
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; Oxidation: 23

Detailed Protein Report

Protein 1035: PREDICTED: formin-like protein 1 isoform X8 [Homo sapiens]

Accession:	gi|578831370	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	119.1
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGNAAGSAEQ	PAGPAAPPPK	QPAPPKQPMP	AAGELEERFN	RALNCMNLPP	DKVQLLSQYD	NEKKWELICD	QERFQVKNPP
90	100	110	120	130	140	150	160
AAYIQKLKSY	VDTGGVSRKV	AADWMSNLGF	KRRVQESTQV	LRELETSLRT	NHIGWVQEFL	NEENRGLDVL	LEYLAFAQCS
170	180	190	200	210	220	230	240
VTYDMESTDN	GASNSEKNKP	LEQSVEDLSK	GPPSSVPKSR	HLTIKCPPSP	RLTPAHSRKA	LRNSRIVSQK	DDVHVCIMCL
250	260	270	280	290	300	310	320
RAIMNYQSGF	SLVMNHPACV	NEIALSLNNK	NPRTKALVLE	LLAAVCLVRG	GHDIILAAFD	NFKEVCGEQH	RFEKLMEYFR
330	340	350	360	370	380	390	400
NEDSNIDFMV	ACMQFINIVV	HSVENMNFRV	FLQYEFTHLG	LDLYLERLRL	TESDKLQVQI	QAYLDNIFDV	GALLEDTETK
410	420	430	440	450	460	470	480
NAVLEHMEEL	QEQVALLTER	LRDAENESMA	KIAELEKQLS	QARKELETLR	ERFSESTAMG	PSRRPPEPEK	APPAAPTRPS
490	500	510	520	530	540	550	560
ALELKVEELE	EKGLIRILRG	PGDAVSIEIL	PVAVATPSGG	DAPTPGVPTG	SPSPDLAPAA	EPAPGAAPPP	PPPLPGLPSP
570	580	590	600	610	620	630	640
QEAPPSAPPQ	APPLPGSPEP	PPAPPLPGDL	PPPPPPPPPP	PGTDGPVPPP	PPPPPPPPGG	PPDALGRRDS	ELGPGVKAKK
650	660	670	680	690	700	710	720
PIQTKFRMPL	LNWVALKPSQ	ITGTVFTELN	DEKVLQELDM	SDFEEQFKTK	SQGPSLDLSA	LKSKAAQKAP	SKATLIEANR
730	740	750	760	770	780	790	800
AKNLAITLRK	GNLGAERICQ	AIEAYDLQAL	GLDFLELLMR	FLPTEYERSL	ITRFEREQRP	MEELSEEDRF	MLCFSRIPRL
810	820	830	840	850	860	870	880
PERMTTLTFL	GNFPDTAQLL	MPQLNAIIAA	SMSIKSSDKL	RQILEIVLAF	GNYMNSSKRG	AAYGFRLQSL	DALLEMKSTD
890	900	910	920	930	940	950	960
RKQTLLHYLV	KVIAEKYPQL	TGFHSDLHFL	DKAGSVSLDS	VLADVRSLQR	GLELTQREFV	RQDDCMVLKE	FLRANSPTMD
970	980	990	1000	1010	1020	1030	1040
KLLADSKTAQ	KAEQEVEQWK	KEAAAQEAGA	DTPGKGEPPA	PKSPPKARRP	QMDLISELKR	RQQKEPLIYE	SDRDGAIEDI
1050	1060	1070	1080				
ITDLRNQPYI	RADTGRRSAR	RRPPGPPLQV	TSDLSL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2052	1	937.3073	-130.77	2	54.2	11.4	0	674-688	K.VLQELDMSDFEEQFK.T	Oxidation: 7

Detailed Protein Report

Protein 1036: paired box protein Pax-8 isoform PAX8E [Homo sapiens]

Accession:	gi|7669542	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.0
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	6.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK ILGRYYETGS IRPGVIGGSK
        90        100        110        120        130        140        150        160
PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND TVPSVSSINR IIRTKVQQPF NLPMDSCVAT KSLSPGHTLI
       170        180        190        200        210        220        230        240
PSSAVTPPES PQSDSLGSTY SINGLLGIAQ PGSDKRKMDD SDQDSCRLSI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF
       250        260        270        280        290
ERQHYPEAYA SPSHTKGEQE VNTLAMPMAT PPTPPTARPG ASPTPAC
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1475	1	954.9298	-86.64	2	47.0	11.4	0	65-82	R.YYETGSIRPGVIGGSKPK.V	

Detailed Protein Report

Protein 1037: 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 1038: PREDICTED: cip1-interacting zinc finger protein isoform X8 [Homo sapiens]

Accession:	gi|578817288	**Score:**	11.4
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

Quantitation

QD:QU	**Median:** 0.39	**CV:** 0.00 %	**No. of 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	Ratios
86	1	837.3356	-111.08	2	31.0	11.4	2	12-27	R.QTDLGLRASPSRCGGR.G		QD:QU 0.39

Detailed Protein Report

Protein 1039: PREDICTED: serine protease 23 isoform X1 [Homo sapiens]

Accession:	gi|530396226	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	51.4
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	5.0
		No. of unique Peptides:	1

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	

Detailed Protein Report

Protein 1040: **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 1041: ataxin-7-like protein 2 [Homo sapiens]

Accession:	gi|93277115	**Score:**	11.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.1
Database Date:	2015-11-30	**pI:**	10.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAVRERAAAA	MAALERRVPS	LDDFAGQSWS	SWVERADLPA	ADGAELEESS	KNTKKLDAMT	LIKEDMSIFG	HCPAHDDFYL
90	100	110	120	130	140	150	160
VVCNHCSQVV	KPQAFQKHCE	RRHGPLSKLY	GRAPPPPPAP	ASSQKCHVVN	GQGPACRAPG	STKTSSREKG	QGSRSRGHQP
170	180	190	200	210	220	230	240
PEKTQKDNLC	QPGGLTKDSP	GKPPMAPPSK	EPPGRENIEI	IPSEGSSHWA	EGSPPEKEPS	GTRLPPKTHR	KMARKECDLN
250	260	270	280	290	300	310	320
RQCGVINPET	KKICTRLLTC	KIHSVHQRRE	VQGRAKDFDV	LVAELKANSR	KGESPKEKSP	GRKEQVLERP	SQELPSSVQV
330	340	350	360	370	380	390	400
VAAVAAPSST	FSVRAKQTYP	YCALPRSRAS	SESELDDEGP	CGGDGDPGLF	PFPMPRGGTQ	ASSEESEEEG	TSDDLHPPPD
410	420	430	440	450	460	470	480
CHYATRPPRP	QAFCTFGSRL	VSPGCYVFSR	RLDRFCSALS	SMLERHLSTH	MWKKIPPAAE	PPAHLVNSPL	SAPLSPSSTG
490	500	510	520	530	540	550	560
TCPRLPGPTL	RPACPASMPP	TKDNLVPSYP	AGSPSVAAAC	SQAECMGGSQ	AITSPLPANT	PSPSFSKLPP	SKASKSSKGK
570	580	590	600	610	620	630	640
DGVEVEAPSR	KRKLSPGPTT	LKRTCILEPT	GKGKPSGCRG	LSAKTKTALS	MGLNGTMGPR	VKRAGPLDCR	GSPHQLPTPV
650	660	670	680	690	700	710	720
KASQLENRGA	AGHPAKALPT	NCLSEEEVAK	KRKNLATYCR	PVKAKHCQAG	APADVACSVR	RKKPGPALAF	EEKCSTLKSK
730							
AH							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
796	2	509.7026	-123.40	2	38.5	11.4	0	584-592	R.TCILEPTGK.G	Carbamidomethyl: 2

Detailed Protein Report

Protein 1042: repressor of RNA polymerase III transcription MAF1 homolog [Homo sapiens]

Accession:	gi|110349740	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.8
Database Date:	2015-11-30	**pI:**	4.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKLLENSSFE	AINSQLTVET	GDAHIIGRIE	SYSCKMAGDD	KHMFKQFCQE	GQPHVLEALS	PPQTSGLSPS	RLSKSQGGEE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
EGPLSDKCSR	KTLFYLIATL	NESFRPDYDF	STARSHEFSR	EPSLSWVVNA	VNCSLFSAVR	EDFKDLKPQL	WNAVDEEICL
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
AECDIYSYNP	DLDSDPFGED	GSLWSFNYFF	YNKRLKRIVF	FSCRSISGST	YTPSEAGNEL	DMELGEEEVE	EESRSGGSGA
250	**260**						
EETSTMEEDR	VPVICI						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
418	1	731.6703	-195.14	2	33.9	11.3	1	29-41	R.IESYSCKMAGDDK.H	Oxidation: 8

Detailed Protein Report

Protein 1043: probable G-protein coupled receptor 150 [Homo sapiens]

Accession: gi|40385873
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 11.3
MW [kDa]: 46.3
pI: 11.9
Sequence Coverage [%]: 4.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MEDLFSPSIL	PPAPNISVPI	LLGWGLNLTL	GQGAPASGPP	SRRVRLVFLG	VILVVAVAGN	TTVLCRLCGG	GGPWAGPKRR
90	100	110	120	130	140	150	160
KMDFLLVQLA	LADLYACGGT	ALSQLAWELL	GEPRAATGDL	ACRFLQLLQA	SGRGASAHLV	VLIALERRRA	VRLPHGRPLP
170	180	190	200	210	220	230	240
ARALAALGWL	LALLLALPPA	FVVRGDSPSP	LPPPPPPTSL	QPGAPPAARA	WPGERRCHGI	FAPLPRWHLQ	VYAFYEAVAG
250	260	270	280	290	300	310	320
FVAPVTVLGV	ACGHLLSVWW	RHRPQAPAAA	APWSASPGRA	PAPSALPRAK	VQSLKMSLLL	ALLFVGCELP	YFAARLAAAW
330	340	350	360	370	380	390	400
SSGPAGDWEG	EGLSAALRVV	AMANSALNPF	VYLFFQAGDC	RLRRQLRKRL	GSLCCAPQGG	AEDEEGPRGH	QALYRQRWPH
410	420	430	440				
PHYHHARREP	LDEGGLRPPP	PRPRPLPCSC	ESAF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2711	1	973.5265	106.80	2	62.8	11.3	0	370-388	R.LGSLCCAPQGGAEDEEGPR.G	Carbamidomethyl: 6

Detailed Protein Report

Protein 1044: heterogeneous nuclear ribonucleoprotein L isoform a [Homo sapiens]

Accession: gi|52632383
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.3
MW [kDa]: 64.1
pI: 9.2
Sequence Coverage [%]: 3.7
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MSRRLLPRAE	KRRRRLEQRQ	QPDEQRRRSG	AMVKMAAAGG	GGGGGRYYGG	GSEGGRAPKR	LKTDNAGDQH	GGGGGGGGGA
90	100	110	120	130	140	150	160
GAAGGGGGGE	NYDDPHKTPA	SPVVHIRGLI	DGVVEADLVE	ALQEFGPISY	VVVMPKKRQA	LVEFEDVLGA	CNAVNYAADN
170	180	190	200	210	220	230	240
QIYIAGHPAF	VNYSTSQKIS	RPGDSDDSRS	VNSVLLFTIL	NPIYSITTDV	LYTICNPCGP	VQRIVIFRKN	GVQAMVEFDS
250	260	270	280	290	300	310	320
VQSAQRAKAS	LNGADIYSGC	CTLKIEYAKP	TRLNVFKNDQ	DTWDYTNPNL	SGQGDPGSNP	NKRQRQPPLL	GDHPAEYGGP
330	340	350	360	370	380	390	400
HGGYHSHYHD	EGYGPPPPHY	EGRRMGPPVG	GHRRGPSRYG	PQYGHPPPPP	PPPEYGPHAD	SPVLMVYGLD	QSKMNCDRVF
410	420	430	440	450	460	470	480
NVFCLYGNVE	KVKFMKSKPG	AAMVEMADGY	AVDRAITHLN	NNFMFGQKLN	VCVSKQPAIM	PGQSYGLEDG	SCSYKDFSES
490	500	510	520	530	540	550	560
RNNRFSTPEQ	AAKNRIQHPS	NVLHFFNAPL	EVTEENFFEI	CDELGVKRPS	SVKVFSGKSE	RSSSGLLEWE	SKSDALETLG
570	580	590					
FLNHYQMKNP	NGPYPYTLKL	CFSTAQHAS					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2243	1	951.4429	25.12	2	56.7	11.3	1	35-56	K.MAAAGGGGGGGRYYGGGSEGGR.A	

Detailed Protein Report

Protein 1045: protein kinase C theta type isoform 3 [Homo sapiens]

Accession:	gi|544063437	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	77.9
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
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
1283	1	729.3578	39.18	2	46.2	11.3	0	1-12	-.MSNQNGQMYIQK.K	Oxidation: 1

Detailed Protein Report

Protein 1046: 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 1047: diphthamide biosynthesis protein 7 [Homo sapiens]

Accession: gi|24308452
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 11.3
MW [kDa]: 50.5
pI: 6.1
Sequence Coverage [%]: 4.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MMGCFALQTV	DTELTADSVE	WCPLQGCRHL	LACGTYQLRR	PEDRPAGPQN	KGGMEVKEPQ	VRLGRLFLYS	FNDNNSIHPL
90	100	110	120	130	140	150	160
VEVQRKDTSA	ILDMKWCHIP	VAGHALLGLA	DASGSIQLLR	LVESEKSHVL	EPLSSLALEE	QCLALSLDWS	TGKTGRAGDQ
170	180	190	200	210	220	230	240
PLKIISSDST	GQLHLLMVNE	TRPRLQKVAS	WQAHQFEAWI	AAFNYWHPEI	VYSGGDDGLL	RGWDTRVPGK	FLFTSKRHTM
250	260	270	280	290	300	310	320
GVCSIQSSPH	REHILATGSY	DEHILLWDTR	NMKQPLADTP	VQGGVWRIKW	HPFHHHLLLA	ACMHSGFKIL	NCQKAMEERQ
330	340	350	360	370	380	390	400
EATVLTSHTL	PDSLVYGADW	SWLLFRSLQR	APSWSFPSNL	GTKTADLKGA	SELPTPCHEC	REDNDGEGHA	RPQSGMKPLT
410	420	430	440	450	460		
EGMRKNGTWL	QATAATTRDC	GVNPEEADSA	FSLLATCSFY	DHALHLWEWE	GN		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1360	1	991.6333	137.20	2	45.5	11.3	1	40-57	R.RPEDRPAGPQNKGGMEVK.E	Oxidation: 15

Detailed Protein Report

Protein 1048: **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 1049: EH domain-binding protein 1 isoform 3 [Homo sapiens]

Accession:	gi|217330572	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	132.2
Database Date:	2015-11-30	**pI:**	5.6
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.77 **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	
778	1	830.6256	153.36	1	39.7	11.3	0	210-216	K.ITELINK.L		QD:QU	0.77

Detailed Protein Report

Protein 1050: sister chromatid cohesion protein PDS5 homolog A isoform 3 [Homo sapiens]

Accession:	gi|155030220	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.0
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		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
504	1	699.9329	104.76	2	34.9	11.3	1	416-427	R.KEAMMGLAQLYK.K	Oxidation: 4

Detailed Protein Report

Protein 1051: glycine receptor subunit alpha-2 isoform C [Homo sapiens]

Accession:	gi|284925161	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.0
Database Date:	2015-11-30	**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 1052: spectrin beta chain, non-erythrocytic 5 [Homo sapiens]

Accession:	gi|485837026	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	416.5
Database Date:	2015-11-30	**pI:**	6.2
		Sequence Coverage [%]:	0.3
		No. of unique Peptides:	1

Detailed Protein Report

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
1262	1	598.7915	-6.95	2	45.9	11.3	0	1334-1345	K.GLMAAHEPSGAR.R	

Detailed Protein Report

Protein 1053: 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

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
1531	2	698.8072	-95.99	2	49.3	11.3	2	1-11	-.MVVLRGPHRCR.H	Carbamidomethyl: 10; Oxidation: 1

Detailed Protein Report

Protein 1054: PREDICTED: hypoxia-inducible factor 3-alpha isoform X4 [Homo sapiens]

Accession:	gi|530417039	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	63.4
Database Date:	2015-11-30	**pI:**	7.2
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:**	0.22	**CV:**	0.00 %	**No. of Peptides:**	1	

Alias proteins:

Accession	Name	Description
gi|530417041	refseq_human (refseq_human_20140103.fasta)	PREDICTED: hypoxia-inducible factor 3-alpha isoform X5 [Homo sapiens]

10	20	30	40	50	60	70	80
MALGLQRARP	ALSCGVISPP	CAPTRNSHPG	PGCTASPPAP	PGWPFSQRGP	GRWSTTELRK	EKSRDAARSR	RSQETEVLYQ
90	100	110	120	130	140	150	160
LAHTLPFARG	VSAHLDKASI	MRLTISYLRM	HRLCAAGEWN	QVGAGGEPLD	ACYLKALEGF	VMVLTAEGDM	AYLSENVSKH
170	180	190	200	210	220	230	240
LGLSQLELIG	HSIFDFIHPC	DQEELQDALT	PQQTLSRRKV	EAPTERCFSL	RMKSTLTSRG	RTLNLKAATW	KVLNCSGHMR
250	260	270	280	290	300	310	320
AYKPPAQTSP	AGSPDSEPPL	QCLVLICEAI	PHPGSLEPPL	GRGAFLSRHS	LDMKFTYCDD	RIAEVAGYSP	DDLIGCSAYE
330	340	350	360	370	380	390	400
YIHALDSDAV	SKSIHTLLSK	GQAVTGQYRF	LARSGGYLWT	QTQATVVSGG	RGPQSESIVC	VHFLISQVEE	TGVVLSLEQT
410	420	430	440	450	460	470	480
EQHSRRPIQR	GAPSQKDTPN	PGDSLDTPGP	RILAFLHPPS	LSEAALAADP	RRFCSPDLRR	LLGPILDGAS	VAATPSTPLA
490	500	510	520	530	540	550	560
TRHPQSPLSA	DLPDELPVGT	ENVHRLFTSG	KDTEAVETDL	DIAQDPGPEL	RGRGRGSGAA	GSETSQKVPQ	PRTRKLSALS
570	580	590					
SQPEFPSDRR	TSPREPAGPQ	HPTPEPE					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
2337	1	646.6647	-229.39	2	57.9	11.3	1	534-547	R.GRGSGAAGSETSQK.V		QD:QU 0.22

Detailed Protein Report

Protein 1055: **PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 isoform X9 [Homo sapiens]**

Accession:	gi|530380539	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.5
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
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	

Detailed Protein Report

Protein 1056: telomerase protein component 1 [Homo sapiens]

Accession:	gi|21536371	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	290.3
Database Date:	2015-11-30	**pI:**	9.2
		Sequence Coverage [%]:	0.6
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530404542	refseq_human (refseq_human_20140103.fasta)	PREDICTED: telomerase protein component 1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MEKLHGHVSA	HPDILSLENR	CLAMLPDLQP	LEKLHQHVST	HSDILSLKNQ	CLATLPDLKT	MEKPHGYVSA	HPDILSLENQ
90	100	110	120	130	140	150	160
CLATLSDLKT	MEKPHGHVSA	HPDILSLENR	CLATLSSLKS	TVSASPLFQS	LQISHMTQAD	LYRVNNSNCL	LSEPPSWRAQ
170	180	190	200	210	220	230	240
HFSKGLDLST	CPIALKSISA	TETAQEATLG	RWFDSEEKKG	AETQMPSYSL	SLGEEEEVED	LAVKLTSGDS	ESHPEPTDHV
250	260	270	280	290	300	310	320
LQEKKMALLS	LLCSTLVSEV	NMNNTSDPTL	AAIFEICREL	ALLEPEFILK	ASLYARQQLN	VRNVANNILA	IAAFLPACRP
330	340	350	360	370	380	390	400
HLRRYFCAIV	QLPSDWIQVA	ELYQSLAEGD	KNKLVPLPAC	LRTAMTDKFA	QFDEYQLAKY	NPRKHRAKRH	PRRPPRSPGM
410	420	430	440	450	460	470	480
EPPFSHRCFP	RYIGFLREEQ	RKFEKAGDTV	SEKKNPPRFT	LKKLVQRLHI	HKPAQHVQAL	LGYRYPSNLQ	LFSRSRLPGP
490	500	510	520	530	540	550	560
WDSSRAGKRM	KLSRPETWER	ELSLRGNKAS	VWEELIENGK	LPFMAMLRNL	CNLLRVGISS	RHHELILQRL	QHAKSVIHSR
570	580	590	600	610	620	630	640
QFPFRFLNAH	DAIDALEAQL	RNQALPFPSN	ITLMRRILTR	NEKNRPRRRF	LCHLSRQQLR	MAMRIPVLYE	QLKREKLRVH
650	660	670	680	690	700	710	720
KARQWKYDGE	MLNRYRQALE	TAVNLSVKHS	LPLLPGRTVL	VYLTDANADR	LCPKSNPQGP	PLNYALLLIG	MMITRAEQVD
730	740	750	760	770	780	790	800
VVLCGGDTLK	TAVLKAEEGI	LKTAIKLQAQ	VQEFDENDGW	SLNTFGKYLL	SLAGQRVPVD	RVILLGQSMD	DGMINVAKQL
810	820	830	840	850	860	870	880
YWQRVNSKCL	FVGILLRRVQ	YLSTDLNPND	VTLSGCTDAI	LKFIAEHGAS	HLLEHVGQMD	KIFKIPPPPG	KTGVQSLRPL
890	900	910	920	930	940	950	960
EEDTPSPLAP	VSQQGWRSIR	LFISSTFRDM	HGERDLLLRS	VLPALQARAA	PHRISLHGID	LRWGVTEEET	RRNRQLEVCL
970	980	990	1000	1010	1020	1030	1040
GEVENAQLFV	GILGSRYGYI	PPSYNLPDHP	HFHWAQQYPS	GRSVTEMEVM	QFLNRNQRLQ	PSAQALIYFR	DSSFLSSVPD
1050	1060	1070	1080	1090	1100	1110	1120
AWKSDFVSES	EEAARRISEL	KSYLSRQKGI	TCRRYPCEWG	GVAAGRPYVG	GLEEFGQLVL	QDVWNMIQKL	YLQPGALLEQ
1130	1140	1150	1160	1170	1180	1190	1200
PVSIPDDDLV	QATFQQLQKP	PSPARPRLLQ	DTVQRLMLPH	GRLSLVTGQS	GQGKTAFLAS	LVSALQAPDG	AKVASLVFFH
1210	1220	1230	1240	1250	1260	1270	1280
FSGARPDQGL	ALTLLRRLCT	YLRGQLKEPG	ALPSTYRSLV	WELQQRLLPK	SAESLHPGQT	QVLIIDGADR	LVDQNGQLIS
1290	1300	1310	1320	1330	1340	1350	1360
DWIPKKLPRC	VHLVLSVSSD	AGLGETLEQS	QGAHVLALGP	LEASARARLV	REELALYGKR	LEESPFNNQM	RLLLVKRESG
1370	1380	1390	1400	1410	1420	1430	1440
RPLYLRLVTD	HLRLFTLYEQ	VSERLRTLPA	TVPLLLQHIL	STLEKEHGPD	VLPQALTALE	VTRSGLTVDQ	LHGVLSVWRT
1450	1460	1470	1480	1490	1500	1510	1520
LPKGTKSWEE	AVAAGNSGDP	YPMGPFACLV	QSLRSLLGEG	PLERPGARLC	LPDGPLRTAA	KRCYGKRPGL	EDTAHILIAA
1530	1540	1550	1560	1570	1580	1590	1600
QLWKTCDADA	SGTFRSCPPE	ALGDLPYHLL	QSGNRGLLSK	FLTNLHVVAA	HLELGLVSRL	LEAHALYASS	VPKEEQKLPE
1610	1620	1630	1640	1650	1660	1670	1680
ADVAVFRTFL	RQQASILSQY	PRLLPQQAAN	QPLDSPLCHQ	ASLLSRRWHL	QHTLRWLNKP	RTMKNQQSSS	LSLAVSSSPT
1690	1700	1710	1720	1730	1740	1750	1760
AVAFSTNGQR	AAVGTANGTV	YLLDLRTWQE	EKSVVSGCDG	ISACLFLSDD	TLFLTAFDGL	LELWDLQHGC	RVLQTKAHQY
1770	1780	1790	1800	1810	1820	1830	1840
QITGCCLSPD	CRLLATVCLG	GCLKLWDTVR	GQLAFQHTYP	KSLNCVAFHP	EGQVIATGSW	AGSISFFQVD	GLKVTKDLGA
1850	1860	1870	1880	1890	1900	1910	1920
PGASIRTLAF	NVPGGVVAVG	RLDSMVELWA	WREGARLAAF	PAHHGFVAAA	LFLHAGCQLL	TAGEDGKVQV	WSGSLGRPRG
1930	1940	1950	1960	1970	1980	1990	2000
HLGSLSLSPA	LSVALSPDGD	RVAVGYRADG	IRIYKISSGS	QGAQGQALDV	AVSALAWLSP	KVLVSGAEDG	SLQGWALKEC
2010	2020	2030	2040	2050	2060	2070	2080
SLQSLWLLSR	FQKPVLGLAT	SQELLASASE	DFTVQLWPRQ	LLTRPHKAED	FPCGTELRGH	EGPVSCCSFS	TDGGSLATGG
2090	2100	2110	2120	2130	2140	2150	2160
RDRSLLCWDV	RTPKTPVLIH	SFPACHRDWV	TGCAWTKDNL	LISCSSDGSV	GLWDPESGQR	LGQFLGHQSA	VSAVAAVEEH
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
1409	1	630.7535	142.03	3	46.2	11.3	2	610-624	R.FLCHLSRQQLRMAMR.I	

Detailed Protein Report

Protein 1057: PREDICTED: germinal-center associated nuclear protein isoform X6 [Homo sapiens]

Accession:	gi|578836729	**Score:**	11.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	165.4
Database Date:	2015-11-30	**pI:**	5.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

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        10          20          30          40          50          60          70          80
MAIFWHRKKI  SPNKKPFSLK  EKKPGDGEVS  PSTEDAPFQH  SPLGKAAGRT  GASSLLNKSS  PVKKPSLLKA  HQFEGDSFDS
        90         100         110         120         130         140         150         160
ASEGSEGLGP  CVLSLSTLIG  TVAETSKEKY  RLLDQRDRIM  RQARVKRTDL  DKARTFVGTC  LDMCPEKERY  MRETRSQLSV
       170         180         190         200         210         220         230         240
FEVVPGTDQV  DHAAAVKEYS  RSSADQEEPL  PHELRPLPVL  SRTMDYLVTQ  IMDQKEGSLR  DWYDFVWNRT  RGIRKDITQQ
       250         260         270         280         290         300         310         320
HLCDPLTVSL  IEKCTRFHIH  CAHFMCEEPM  SSFDAKINNE  NMTKCLQSLK  EMYQDLRNKG  VFCASEAEFQ  GYNVLLSLNK
       330         340         350         360         370         380         390         400
GDILREVQQF  HPAVRNSSEV  KFAVQAFAAL  NSNNFVRFFK  LVQSASYLNA  CLLHCYFSQI  RKDALRALNF  AYTVSTQRST
       410         420         430         440         450         460         470         480
IFPLDGVVRM  LLFRDCEEAT  DFLTCHGLTV  SDGCVELNRS  AFLEPEGLSK  TRKSVFITRK  LTVSVGEIVN  GGPLPPVPRH
       490         500         510         520         530         540         550         560
TPVCSFNSQN  KYIGESLAAE  LPVSTQRPGS  DTVGGGRGEE  CGVEPDAPLS  SLPQSLPAPA  PSPVPLPPVL  ALTPSVAPSL
       570         580         590         600         610         620         630         640
FQLSVQPEPP  PPEPVPMYSD  EDLAQVVDEL  IQEALQRDCE  EVGSAGAAYA  AAALGVSNAA  MEDLLTAATT  GILRHIAAEE
       650         660         670         680         690         700         710         720
VSKERERREQ  ERQRAEEERL  KQERELVLSE  LSQGLAVELM  ERVMMEFVRE  TCSQELKNAV  ETDQRVRVAR  CCEDVCAHLV
       730         740         750         760         770         780         790         800
DLFLVEEIFQ  TAKETLQELQ  CFCKYLQRWR  EAVTARKKLR  RQMRAFPAAP  CCVDVSDRLR  ALAPSAECPI  AEENLARGLL
       810         820         830         840         850         860         870         880
DLGHAGRLGI  SCTRLRRLRN  KTAHQMKVQH  FYQQLLSDVA  WASLDLPSLV  AEHLPGRQEH  VFWKLVLVLP  DVEEQSPESC
       890         900         910         920         930         940         950         960
GRILANWLKV  KFMGDEGSVD  DTSSDAGGIQ  TLSLFNSLSS  KGDQMISVNV  CIKVAHGALS  DGAIDAVETQ  KDLLGASGLM
       970         980         990        1000        1010        1020        1030        1040
LLLPPKMKSE  DMAEEDVYWL  SALLQLKQLL  QAKPFQPALP  LVVLVPSPGG  DAVEKEVEDG  LMLQDLVSAK  LISDYTVTEI
      1050        1060        1070        1080        1090        1100        1110        1120
PDTINDLQGS  TKVLQAVQWL  VSHCPHSLDL  CCQTLIQYVE  DGIGHEFSGR  FFHDRRERRL  GGLASQEPGA  IIELFNSVLQ
      1130        1140        1150        1160        1170        1180        1190        1200
FLASVVSSEQ  LCDLSWPVTE  FAEAGGSRLL  PHLHWNAPEH  LAWLKQAVLG  FQLPQMDLPP  LGAPWLPVCS  MVVQYASQIP
      1210        1220        1230        1240        1250        1260        1270        1280
SSRQTQPVLQ  SQVENLLHRT  YCRWKSKSPS  PVHGAGPSVM  EIPWDDLIAL  CINHKLRDWT  PPRLPVTSEA  LSEDGQICVY
      1290        1300        1310        1320        1330        1340        1350        1360
FFKNDLKKYD  VPLSWEQARL  QTQKELQLRE  GRLAIKPFHP  SANNFPIPLL  HMHRNWKRST  ECAQEGRIPS  TEDLMRGASA
      1370        1380        1390        1400        1410        1420        1430        1440
EELLAQCLSS  SLLLEKEENK  RFEDQLQQWL  SEDSGAFTDL  TSLPLYLPQT  LVSLSHTIEP  VMKTSVTTSP  QSDMMREQLQ
      1450        1460        1470        1480        1490
LSEATGTCLG  ERLKHLERLI  RSSREEEVAS  ELHLSALLDM  VDI
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Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
101	1	707.1277	128.95	3	30.0	11.3	0	1357-1376	R.GASAEELLAQCLSSSLLLEK.E	Carbamidomethyl: 11

Detailed Protein Report

Protein 1058: adenylate cyclase type 9 [Homo sapiens]

Accession:	gi|50959205	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	150.6
Database Date:	2015-11-30	**pI:**	7.3
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MASPPHQQLL	HHHSTEVSCD	SSGDSNSVRV	KINPKQLSSN	SHPKHCKYSI	SSSCSSSGDS	GGVPRRVGGG	GRLRRQKKLP
90	100	110	120	130	140	150	160
QLFERASSRW	WDPKFDSVNL	EEACLERCFP	QTQRRFRYAL	FYIGFACLLW	SIYFAVHMRS	RLIVMVAPAL	CFLLVCVGFF
170	180	190	200	210	220	230	240
LFTFTKLYAR	HYAWTSLALT	LLVFALTLAA	QFQVLTPVSG	RGDSSNLTAT	ARPTDTCLSQ	VGSFSMCIEV	LFLLYTVMHL
250	260	270	280	290	300	310	320
PLYLSLCLGV	AYSVLFETFG	YHFRDEACFP	SPGAGALHWE	LLSRGLLHGC	IHAIGVHLFV	MSQVRSRSTF	LKVGQSIMHG
330	340	350	360	370	380	390	400
KDLEVEKALK	ERMIHSVMPR	IIADDLMKQG	DEESENSVKR	HATSSPKNRK	KKSSIQKAPI	AFRPFKMQQI	EEVSILFADI
410	420	430	440	450	460	470	480
VGFTKMSANK	SAHALVGLLN	DLFGRFDRLC	EETKCEKIST	LGDCYYCVAG	CPEPRADHAY	CCIEMGLGMI	KAIEQFCQEK
490	500	510	520	530	540	550	560
KEMVNMRVGV	HTGTVLCGIL	GMRRFKFDVW	SNDVNLANLM	EQLGVAGKVH	ISEATAKYLD	DRYEMEDGKV	IERLGQSVVA
570	580	590	600	610	620	630	640
DQLKGLKTYL	ISGQRAKESR	CSCAEALLSG	FEVIDGSQVS	SGPRGQGTAS	SGNVSDLAQT	VKTFDNLKTC	PSCGITFAPK
650	660	670	680	690	700	710	720
SEAGAEGGAP	QNGCQDEHKN	STKASGGPNP	KTQNGLLSPP	QEEKLTNSQT	SLCEILQEKG	RWAGVSLDQS	ALLPLRFKNI
730	740	750	760	770	780	790	800
REKTDAHFVD	VIKEDSLMKD	YFFKPPINQF	SLNFLDQELE	RSYRTSYQEE	VIKNSPVKTF	ASPTFSSLLD	VFLSTTVFLT
810	820	830	840	850	860	870	880
LSTTCFLKYE	AATVPPPPAA	LAVFSAALLL	EVLSLAVSIR	MVFFLEDVMA	CTKRLLEWIA	GWLPRHCIGA	ILVSLPALAV
890	900	910	920	930	940	950	960
YSHVTSEYET	NIHFPVFTGS	AALIAVVHYC	NFCQLSSWMR	SSLATVVGAG	PLLLLYVSLC	PDSSVLTSPL	DAVQNFSSER
970	980	990	1000	1010	1020	1030	1040
NPCNSSVPRD	LRRPASLIGQ	EVVLVFFLLL	LLVWFLNREF	EVSYRLHYHG	DVEADLHRTK	IQSMRDQADW	LLRNIIPYHV
1050	1060	1070	1080	1090	1100	1110	1120
AEQLKVSQTY	SKNHDSGGVI	FASIVNFSEF	YEENYEGGKE	CYRVLNELIG	DFDELLSKPD	YSSIEKIKTI	GATYMAASGL
1130	1140	1150	1160	1170	1180	1190	1200
NTAQAQDGSH	PQEHLQILFE	FAKEMMRVVD	DFNNNMLWFN	FKLRVGFNHG	PLTAGVIGTT	KLLYDIWGDT	VNIASRMDTT
1210	1220	1230	1240	1250	1260	1270	1280
GVECRIQVSE	ESYRVLSKMG	YDFDYRGTVN	VKGKGQMKTY	LYPKCTDHRV	IPQHQLSISP	DIRVQVDGSI	GRSPTDEIAN
1290	1300	1310	1320	1330	1340	1350	1360
LVPSVQYVDK	TSLGSDSSTQ	AKDAHLSPKR	PWKEPVKAEE	RGRFGKAIEK	DDCDETGIEE	ANELTKLNVS	KSV

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1876	1	612.7873	-6.31	2	53.8	11.2	0	629-640	K.TCPSCGITFAPK.S	

Detailed Protein Report

Protein 1059: 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; Oxidation: 5

Detailed Protein Report

Protein 1060: tripartite motif-containing protein 38 [Homo sapiens]

Accession:	gi|5454014	**Score:**	11.2
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 [%]:**	3.4
		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; Oxidation: 15

Detailed Protein Report

Protein 1061: 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 1062: D-3-phosphoglycerate dehydrogenase [Homo sapiens]

Accession:	gi|23308577	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.6
Database Date:	2015-11-30	**pI:**	6.3
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAFANLRKVL	ISDSLDPCCR	KILQDGGLQV	VEKQNLSKEE	LIAELQDCEG	LIVRSATKVT	ADVINAAEKL	QVVGRAGTGV
90	100	110	120	130	140	150	160
DNVDLEAATR	KGILVMNTPN	GNSLSAAELT	CGMIMCLARQ	IPQATASMKD	GKWERKKFMG	TELNGKTLGI	LGLGRIGREV
170	180	190	200	210	220	230	240
ATRMQSFGMK	TIGYDPIISP	EVSASFGVQQ	LPLEEIWPLC	DFITVHTPLL	PSTTGLLNDN	TFAQCKKGVR	VVNCARGGIV
250	260	270	280	290	300	310	320
DEGALLRALQ	SGQCAGAALD	VFTEEPPRDR	ALVDHENVIS	CPHLGASTKE	AQSRCGEEIA	VQFVDMVKGK	SLTGVVNAQA
330	340	350	360	370	380	390	400
LTSAFSPHTK	PWIGLAEALG	TLMRAWAGSP	KGTIQVITQG	TSLKNAGNCL	SPAVIVGLLK	EASKQADVNL	VNAKLLVKEA
410	420	430	440	450	460	470	480
GLNVTTSHSP	AAPGEQGFGE	CLLAVALAGA	PYQAVGLVQG	TTPVLQGLNG	AVFRPEVPLR	RDLPLLLFRT	QTSDPAMLPT
490	500	510	520	530	540		
MIGLLAEAGV	RLLSYQTSLV	SDGETWHVMG	ISSLLPSLEA	WKQHVTEAFQ	FHF		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1642	1	634.8441	11.21	2	49.1	11.2	2	136-146	R.KKFMGTELNGK.T	Oxidation: 4

Detailed Protein Report

Protein 1063: putative uncharacterized protein ENSP00000383407 [Homo sapiens]

Accession:	gi|375151595	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.5
Database Date:	2015-11-30	**pI:**	9.1
		Sequence Coverage [%]:	8.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSSRTDSPIP PFGESEQTPN NLFVGVSNLE NAKPKKRKLF RRFMSENKIF EGKTVNDKIW QEHSKHKNDS HIRRPCQLKD
        90        100        110        120        130        140
LNENDFLSNN IHTYQGKTLQ GTSYQVTSEC WSPFHYQRHV ETTVDELAQE FM
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2759	1	665.3721	64.79	2	63.5	11.2	1	43-53	R.FMSENKIFEGK.T	

Detailed Protein Report

Protein 1064: 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; Oxidation: 9, 16

Detailed Protein Report

Protein 1065: 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

Protein 1066: zinc finger and BTB domain-containing protein 5 [Homo sapiens]

Accession:	gi|7662074	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.2
Database Date:	2015-11-30	**pI:**	5.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.7
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530390257	refseq_human (refseq_human_20140103.fasta)	PREDICTED: zinc finger and BTB domain-containing protein 5 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MDFPGHFEQI	FQQLNYQRLH	GQLCDCVIVV	GNRHFKAHRS	VLAACSTHFR	ALFSVAEGDQ	TMNMIQLDSE	VVTAEAFAAL
90	100	110	120	130	140	150	160
IDMMYTSTLM	LGESNVMDVL	LAASHLHLNS	VVKACKHYLT	TRTLPMSPPS	ERVQEQSARM	QRSFMLQQLG	LSIVSSALNS
170	180	190	200	210	220	230	240
SQNGEEQPAP	MSSSMRSNLD	QRTPFPMRRL	HKRKQSAEER	ARQRLRPSID	ESAISDVTPE	NGPSGVHSRE	EFFSPDSLKI
250	260	270	280	290	300	310	320
VDNPKADGMT	DNQEDSAIMF	DQSFGTQEDA	QVPSQSDNSA	GNMAQLSMAS	RATQVETSFD	QEAAPEKSSF	QCENPEVGLG
330	340	350	360	370	380	390	400
EKEHMRVVVK	SEPLSSPEPQ	DEVSDVTSQA	EGSESVEVEG	VVVSAEKIDL	SPESSDRSFS	DPQSSTDRVG	DIHILEVTNN
410	420	430	440	450	460	470	480
LEHKSTFSIS	NFLNKSRGNN	FTANQNNDDN	IPNTTSDCRL	ESEAPYLLSP	EAGPAGGPSS	APGSHVENPF	SEPADSHFVR
490	500	510	520	530	540	550	560
PMQEVMGLPC	VQTSGYQGGE	QFGMDFSRSG	LGLHSSFSRV	MIGSPRGGAS	NFPYYRRIAP	KMPVVTSVRS	SQIPENSTSS
570	580	590	600	610	620	630	640
QLMMNGATSS	FENGHPSQPG	PPQLTRASAD	VLSKCKKALS	EHNVLVVEGA	RKYACKICCK	TFLTLTDCKK	HIRVHTGEKP
650	660	670	680				
YACLKCGKRF	SQSSHLYKHS	KTTCLRWQSS	NLPSTLL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2671	1	699.0932	93.54	3	62.2	11.2	1	19-36	R.LHGQLCDCVIVVGNRHFK.A	Carbamidomethyl: 6

Detailed Protein Report

Protein 1067: **PREDICTED: receptor-interacting serine/threonine-protein kinase 2 isoform X1 [Homo sapiens]**

Accession:	gi|530389383	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	45.6
Database Date:	2015-11-30	**pI:**	6.4
		Sequence Coverage [%]:	3.2
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.15 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MTPPLLHHDL KTQNILLDNE FHVKIADFGL SKWRMMSLSQ SRSSKSAPEG GTIIYMPPEN YEPGQKSRAS IKHDIYSYAV
        90        100        110        120        130        140        150        160
ITWEVLSRKQ PFEDVTNPLQ IMYSVSQGHR PVINEESLPY DIPHRARMIS LIESGWAQNP DERPSFLKCL IELEPVLRTF
       170        180        190        200        210        220        230        240
EEITFLEAVI QLKKTKLQSV SSAIHLCDKK KMELSLNIPV NHGPQEESCG SSQLHENSGS PETSRSLPAP QDNDFLSRKA
       250        260        270        280        290        300        310        320
QDCYFMKLHH CPGNHSWDST ISGSQRAAFC DHKTTPCSSA IINPLSTAGN SERLQPGIAQ QWIQSKREDI VNQMTEACLN
       330        340        350        360        370        380        390        400
QSLDALLSRD LIMKEDYELV STKPTRTSKV RQLLDTTDIQ GEEFAKVIVQ KLKDNKQMGL QPYPEILVVS RSPSLNLLQN
       410
KSM
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
676	1	730.2232	-190.60	2	37.0	11.2	0	226-238	R.SLPAPQDNDFLSR.K		QD:QU	0.15

Detailed Protein Report

Protein 1068: PREDICTED: tudor domain-containing protein 7 isoform X1 [Homo sapiens]

Accession:	gi|578817238	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	115.3
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MACTETARIA	QLVARQRSSK	RKTGRQVNCQ	MRVKKTMPFF	LEGKPKATLR	QPGFASNFSV	GKKPNPAPLR	DKGNSVGVKP
90	100	110	120	130	140	150	160
DAEMSPYMLH	TTLGNEAFKD	IPVQRHVTMS	TNNRFSPKAS	LQPPLQMHLS	RTSTKEMSDN	LNQTVEKPNV	KPPASYTYKM
170	180	190	200	210	220	230	240
DEVQNRIKEI	LNKHNNGIWI	SKLPHFYKEL	YKEDLNQGIL	QQFEHWPHIC	TVEKPCSGGQ	DLLLYPAKRK	QLLRSELDTE
250	260	270	280	290	300	310	320
KVPLSPLPGP	KQTPPLKGCP	TVMAGDFKEK	VADLLVKYTS	GLWASALPKA	FEEMYKVKFP	EDALKNLASL	SDVCSIDYIS
330	340	350	360	370	380	390	400
GNPQKAILYA	KLPLPTDKIQ	KDAGQAHGDN	DIKAMVEQEY	LQVEESIAES	ANTFMEDITV	PPLMIPTEAS	PSVLVVELSN
410	420	430	440	450	460	470	480
TNEVVIRYVG	KDYSAAQELM	EDEMKEYYSK	NPKITPVQAV	NVGQLLAVNA	EEDAWLRAQV	ISTEENKIKV	CYVDYGFSEN
490	500	510	520	530	540	550	560
VEKSKAYKLN	PKFCSLSFQA	TKCKLAGLEV	LSDDPDLVKV	VESLTCGKIF	AVEILDKADI	PLVVLYDTSG	EDDININATC
570	580	590	600	610	620	630	640
LKAICDKSLE	VHLQVDAMYT	NVKVTNICSD	GTLYCQVPCK	GLNKLSDLLR	KIEDYFHCKH	MTSECFVSLP	FCGKICLFHC
650	660	670	680	690	700	710	720
KGKWLRVEIT	NVHSSRALDV	QFLDSGTVTS	VKVSELREIP	PRFLQEMIAI	PPQAIKCCLA	DLPQSIGMWT	PDAVLWLRDS
730	740	750	760	770	780	790	800
VLNCSDCSIK	VTKVDETRGI	AHVYLFTPKN	FPDPHRSINR	QITNADLWKH	QKDVFLSAIS	SGADSPNSKN	GNMPMSGNTG
810	820	830	840	850	860	870	880
ENFRKNLTDV	IKKSMVDHTS	AFSTEELPPP	VHLSKPGEHM	DVYVPVACHP	GYFVIQPWQE	IHKLEVLMEE	MILYYSVSEE
890	900	910	920	930	940	950	960
RHIAVEKDQV	YAAKVENKWH	RVLLKGILTN	GLVSVYELDY	GKHELVNIRK	VQPLVDMFRK	LPFQAVTAQL	AGVKCNQWSE
970	980	990	1000	1010	1020	1030	
EASMVFRNHV	EKKPLVALVQ	TVIENANPWD	RKVVVYLVDT	SLPDTDTWIH	DFMSEYLIEL	SKVN	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2184	1	955.9047	-109.56	2	55.9	11.2	1	119-135	K.ASLQPPLQMHLSRTSTK.E	Oxidation: 9

Detailed Protein Report

Protein 1069: probable palmitoyltransferase ZDHHC8 isoform 2 [Homo sapiens]

Accession:	gi|32698692	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.4
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPRSPGTRLK	PAKYIPVATA	AALLVGSSTL	FFVFTCPWLT	RAVSPAVPVY	NGIIFLFVLA	NFSMATFMDP	GVFPRADEDE
90	100	110	120	130	140	150	160
DKEDDFRAPL	YKNVDVRGIQ	VRMKWCATCH	FYRPPRCSHC	SVCDNCVEDF	DHHCPWVNNC	IGRRNYRYFF	LFLLSLSAHM
170	180	190	200	210	220	230	240
VGVVAFGLVY	VLNHAEGLGA	AHTTITMAVM	CVAGLFFIPV	IGLTGFHVVL	VTRGRTTNEQ	VTGKFRGGVN	PFTRGCCGNV
250	260	270	280	290	300	310	320
EHVLCSPLAP	RYVVEPPRLP	LAVSLKPPFL	RPELLDRAAP	LKVKLSDNGL	KAGLGRSKSK	GSLDRLDEKP	LDLGPPLPPK
330	340	350	360	370	380	390	400
IEAGTFSSDL	QTPRPGSAES	ALSVQRTSPP	TPAMYKFRPA	FPTGPKVPFC	GPGEQVPGPD	SLTLGDDSIR	SLDFVSEPSL
410	420	430	440	450	460	470	480
DLPDYGPGGL	HAAYPPSPPL	SASDAFSGAL	RSLSLKASSR	RGGDHVALQP	LRSEGGPPTP	HRSIFAPHAL	PNRNGSLSYD
490	500	510	520	530	540	550	560
SLLNPGSPGG	HACPAHPAVG	VAGYHSPYLH	PGATGDPPRP	LPRSFSPVLG	PRPREPSPVR	YDNLSRTIMA	SIQERKDREE
570	580	590	600	610	620	630	640
RERLLRSQAD	SLFGDSGVYD	APSSYSLQQA	SVLSEGPRGP	ALRYGSRDDL	VAGPGFGGAR	NPALQTSLSS	LSSSVSRAPR
650	660	670	680	690	700	710	720
TSSSSLQADQ	ASSNAPGPRP	SSGSHRSPAR	QGLPSPPGTP	HSPSYAGPKA	VAFIHTDLPE	PPPSLTVQRD	HPQLKTPPSK
730	740	750	760	770			
LNGQSPGLAR	LGPATGPPGP	SASPTRHTLV	KKVSGVGGTT	YEISV			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1760	1	727.3946	-63.07	2	50.5	11.2	2	278-291	R.AAPLKVKLSDNGLK.A	

Detailed Protein Report

Protein 1070: PREDICTED: monocarboxylate transporter 10 isoform X1 [Homo sapiens]

Accession:	gi|530383357	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.9
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:** 2.32	**CV:** 0.00 %	**No. of Peptides:** 1

10	20	30	40	50	60	70	80
MVLSQEEPDS	ARGTSEAQPL	GPAPTGAAPP	PGPGPSDSPE	AAVEKVEVEL	AGPATAEPHE	PPEPPEGGWG	WLVMLAAMWC
90	100	110	120	130	140	150	160
NGSVFGIQNA	CGVLFVSMLE	TFGSKDDDKM	VFKTAWVGSL	SMGMIFFCCP	IVSVFTDLFG	CRKTAVVGAA	VGFVGLMSSS
170	180	190	200	210	220	230	240
FVSSIEPLYL	TYGIIFACGC	SFAYQPSLVI	LGHYFKKRLG	LVNGIVTAGS	SVFTILLPLL	LRVLIDSVGL	FYTLRVLCIF
250	260	270	280	290	300	310	320
MFVLFLAGFT	YRPLATSTKD	KESGGSGSSL	FSRKKFSPPK	KIFNFAIFKV	TAYAVWAVGI	PLALFGYFVP	YVHLMKHVNE
330	340	350	360	370	380	390	400
RFQDEKNKEV	VLMCIGVTSG	VGRLLFGRIA	DYVPGVKKVY	LQGYFVTNWA	PMMWHSTSLE	SLPLLEVLCF	VLSRGSIVRS
410	420	430	440	450	460		
KERSVKPLEK	KRWRKCWKTR	TLCCQVHLEC	SRKNLTLLFN	ILHTSTRLDL	LFEF		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1828	1	945.8179	-148.57	2	51.4	11.2	2	419-433	K.TRTLCCQVHLECSRK.N	Carbamidomethyl: 5, 6	QD:QU 2.32

Detailed Protein Report

Protein 1071: zinc finger protein 85 isoform d [Homo sapiens]

Accession:	gi|371873730	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	61.2
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MKRHEIMVAK	PTVMCSHFAQ	DLWPEQNIKD	SFQKVTLKRY	GKCRHENLPL	RKGCESMDEC	KMHKGGCNGL	NQCLTATQSK
90	100	110	120	130	140	150	160
IFQCDKYVKV	AHKFSNSNRH	EIRHTKKKPF	KCTKCGKSFG	MISCLTEHSR	IHTRVNFYKC	EECGKAFNWS	STLTKHKRIH
170	180	190	200	210	220	230	240
TGEKPYKCEE	CGKAFNQSSN	LIKHKKIHTG	EKPYKCEECG	KTFNRFSTLT	THKIIHTGEK	PYKCKECGKA	FNRSSTLTTH
250	260	270	280	290	300	310	320
RKIHTGEKPY	KCEECGKAFK	QSSNLTTHKI	IHTGEKPYKC	KKCGKAFNQS	AHLTTHEVIH	TGEKPYKCEK	CGKAFNHFSH
330	340	350	360	370	380	390	400
LTTHKIIHTG	EKPYKCKECG	KAFKHSSTLT	KHKIIHTGEK	PYKCKECEKA	FNQSSKLTEH	KKIHTGEKPY	ECEKCGKAFN
410	420	430	440	450	460	470	480
QSSNLTRHKK	SHTEEKPYKC	EECGKGFKWP	STLTIHKIIH	TGEKPYKCEE	CGKAFNQSSK	LTKHKKIHTG	EKPYTCEECG
490	500	510	520	530	540		
KAFNQSSNLT	KHKRIHTGEK	PYKCEECDKA	FKWSSVLTKH	KIIHTGEKLQ	I		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2022	1	765.7797	-170.72	2	55.7	11.2	2	482-494	K.AFNQSSNLTKHKR.I	

Detailed Protein Report

Protein 1072: AT-hook DNA-binding motif-containing protein 1 [Homo sapiens]

Accession:	gi|71274144	**Score:**	11.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	168.2
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	1.1
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530361060	refseq_human (refseq_human_20140103.fasta)	PREDICTED: AT-hook DNA-binding motif-containing protein 1 isoform X6 [Homo sapiens]
gi|530361058	refseq_human (refseq_human_20140103.fasta)	PREDICTED: AT-hook DNA-binding motif-containing protein 1 isoform X5 [Homo sapiens]
gi|530361056	refseq_human (refseq_human_20140103.fasta)	PREDICTED: AT-hook DNA-binding motif-containing protein 1 isoform X4 [Homo sapiens]
gi|530361054	refseq_human (refseq_human_20140103.fasta)	PREDICTED: AT-hook DNA-binding motif-containing protein 1 isoform X3 [Homo sapiens]
gi|530361052	refseq_human (refseq_human_20140103.fasta)	PREDICTED: AT-hook DNA-binding motif-containing protein 1 isoform X2 [Homo sapiens]
gi|530361050	refseq_human (refseq_human_20140103.fasta)	PREDICTED: AT-hook DNA-binding motif-containing protein 1 isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MRVKPQGLVV	TSSAVCSSPD	YLREPKYYPG	GPPTPRPLLP	TRPPASPPDK	AFSTHAFSEN	PRPPPRRDPS	TRRPPVLAKG
90	100	110	120	130	140	150	160
DDPLPPRAAR	PVSQARCPTP	VGDGSSSRRC	WDNGRVNLRP	VVQLIDIMKD	LTRLSQDLQH	SGVHLDCGGL	RLSRPPAPPP
170	180	190	200	210	220	230	240
GDLQYSFFSS	PSLANSIRSP	EERATPHAKS	ERPSHPLYEP	EPEPRDSPQP	GQGHSPGATA	AATGLPPEPE	PDSTDYSELA
250	260	270	280	290	300	310	320
DADILSELAS	LTCPEAQLLE	AQALEPPSPE	PEPQLLDPQP	RFLDPQALEP	LGEALELPPL	QPLADPLGLP	GLALQALDTL
330	340	350	360	370	380	390	400
PDSLESQLLD	PQALDPLPKL	LDVPGRRLEP	QQPLGHCPLA	EPLRLDLCSP	HGPPGPEGHP	KYALRRTDRP	KILCRRRKAG
410	420	430	440	450	460	470	480
RGRKADAGPE	GRLLPLPMPT	GLVAALAEPP	PPPPPPPPAL	PGPGPVSVPE	LKPESSQTPV	VSTRKGKCRG	VRRMVVKMAK
490	500	510	520	530	540	550	560
IPVSLGRRNK	TTYKVSSLSS	SLSVEGKELG	LRVSAEPTPL	LKMKNNGRNV	VVVFPPGEMP	IILKRKRGRP	PKNLLLGPGK
570	580	590	600	610	620	630	640
PKEPAVVAAE	AATVAAATMA	MPEVKKRRRR	KQKLASPQPS	YAADANDSKA	EYSDVLAKLA	FLNRQSQCAG	RCSPPRCWTP
650	660	670	680	690	700	710	720
SEPESVHQAP	DTQSISHFLH	RVQGFRRRGG	KAGGFGGRGG	GHAAKSARCS	FSDFFEGIGK	KKKVVAVAAA	GVGGPGLTEL
730	740	750	760	770	780	790	800
GHPRKRGRGE	VDAVTGKPKR	KRRSRKNGTL	FPEQVPSGPG	FGEAGAEWAG	DKGGGWAPHH	GHPGGQAGRN	CGFQGTEARA
810	820	830	840	850	860	870	880
FASTGLESGA	SGRGSYYSTG	APSGQTELSQ	ERQNLFTGYF	RSLLDSDDSS	DLLDFALSAS	RPESRKASGT	YAGPPTSALP
890	900	910	920	930	940	950	960
AQRGLATFPS	RGAKASPVAV	GSSGAGADPS	FQPVLSARQT	FPPGRAASYG	LTPAASDCRA	AETFPKLVPP	PSAMARSPTT
970	980	990	1000	1010	1020	1030	1040
HPPANTYLPQ	YGGYGAGQSV	FAPTKPFTGQ	DCANSKDCSF	AYGSGNSLPA	SPSSAHSAGY	APPPTGGPCL	PPSKASFFSS
1050	1060	1070	1080	1090	1100	1110	1120
SEGAPFSGSA	PTPLRCDSRA	STVSPGGYMV	PKGTTASATS	AASAASSSSS	SFQPSPENCR	QFAGASQWPF	RQGYGGLDWA
1130	1140	1150	1160	1170	1180	1190	1200
SEAFSQLYNP	SFDCHVSEPN	VILDISNYTP	QKVKQQTAVS	ETFSESSSDS	TQFNQPVGGG	GFRRANSEAS	SSEGQSSLSS
1210	1220	1230	1240	1250	1260	1270	1280
LEKLMMDWNE	ASSAPGYNWN	QSVLFQSSSK	PGRGRRKKVD	LFEASHLGFP	TSASAAASGY	PSKRSTGPRQ	PRGGRGGGAC
1290	1300	1310	1320	1330	1340	1350	1360
SAKKERGGAA	AKAKFIPKPQ	PVNPLFQDSP	DLGLDYYSGD	SSMSPLPSQS	RAFGVGERDP	CDFIGPYSMN	PSTPSDGTFG
1370	1380	1390	1400	1410	1420	1430	1440
QGFHCDSPSL	GAPELDGKHF	PPLAHPPTVF	DAGLQKAYSP	TCSPTLGFKE	ELRPPPTKLA	ACEPLKHGLQ	GASLGHAAAA
1450	1460	1470	1480	1490	1500	1510	1520
QAHLSCRDLP	LGQPHYDSPS	CKGTAYWYPP	GSAARSPPYE	GKVGTGLLAD	FLGRTEAACL	SAPHLASPPA	TPKADKEPLE
1530	1540	1550	1560	1570	1580	1590	1600
MARPPGPPRG	PAAAAAGYGC	PLLSDLTLSP	VPRDSLLPLQ	DTAYRYPGFM	PQAHPGLGGG	PKSGFLGPMA	EPHPEDTFTV
1610							
TSL							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1735	1	945.9132	-52.92	2	50.2	11.2	1	592-609	K.QKLASPQPSYAADANDSK.A	

Detailed Protein Report

Protein 1073: 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 1074: **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

Quantitation

QD:QU **Median:** 1.28 **CV:** 0.00 % **No. of 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	Ratios
1124	1	593.6547	-238.34	2	44.2	11.2	0	265-274	R.SVDWEAVPQR.K		QD:QU 1.28

Detailed Protein Report

Protein 1075: neuronal migration protein doublecortin isoform c [Homo sapiens]

Accession:	gi|30181240	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.0
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	6.4
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|30181244	refseq_huma (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
1003	1	797.6785	-61.53	3	42.6	11.1	2	152-174	K.TSANMKAPQSLASSNSAQARENK.D	

Detailed Protein Report

Protein 1076: keratin, type II cytoskeletal 8 isoform 2 [Homo sapiens]

Accession:	gi|4504919	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.7
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:**	1.22	**CV:**	0.00 %	**No. of Peptides:**	1

Alias proteins:

Accession	Name	Description
gi|372466577	refseq_human (refseq_human_20140103.fasta)	keratin, type II cytoskeletal 8 isoform 2 [Homo sapiens]

10	20	30	40	50	60	70	80
MSIRVTQKSY	KVSTSGPRAF	SSRSYTSGPG	SRISSSSFSR	VGSSNFRGGL	GGGYGGASGM	GGITAVTVNQ	SLLSPLVLEV
90	100	110	120	130	140	150	160
DPNIQAVRTQ	EKEQIKTLNN	KFASFIDKVR	FLEQQNKMLE	TKWSLLQQQK	TARSNMDNMF	ESYINNLRRQ	LETLGQEKLK
170	180	190	200	210	220	230	240
LEAELGNMQG	LVEDFKNKYE	DEINKRTEME	NEFVLIKKDV	DEAYMNKVEL	ESRLEGLTDE	INFLRQLYEE	EIRELQSQIS
250	260	270	280	290	300	310	320
DTSVVLSMDN	SRSLDMDSII	AEVKAQYEDI	ANRSRAEAES	MYQIKYEELQ	SLAGKHGDDL	RRTKTEISEM	NRNISRLQAE
330	340	350	360	370	380	390	400
IEGLKGQRAS	LEAAIADAEQ	RGELAIKDAN	AKLSELEAAL	QRAKQDMARQ	LREYQELMNV	KLALDIEIAT	YRKLLEGEES
410	420	430	440	450	460	470	480
RLESGMQNMS	IHTKTTSGYA	GGLSSAYGGL	TSPGLSYSLG	SSFGSGAGSS	SFSRTSSSRA	VVVKKIETRD	GKLVSESSDV
490							
LPK							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
447	1	738.2345	-160.13	2	34.2	11.1	0	402-414	R.LESGMQNMSIHTK.T		QD:QU	1.22

Detailed Protein Report

Protein 1077: 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 1078: 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 1079: 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	1	682.2633	-103.38	3	54.5	11.1	0	474-492	K.GGQNSLAGPQECWLLTASR.L	Carbamidomethyl: 12

Detailed Protein Report

Protein 1080: uncharacterized protein CXorf22 [Homo sapiens]

Accession: gi|90963001
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 11.1
MW [kDa]: 110.3
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 1081: PREDICTED: uncharacterized protein LOC100996273 [Homo sapiens]

Accession:	gi|397137819	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.1
Database Date:	2015-11-30	**pI:**	12.1
		Sequence Coverage [%]:	8.0
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|410173446	refseq_human(refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein LOC100996273 [Homo sapiens]
gi|397139660	refseq_human(refseq_human_20140103.fasta)	PREDICTED: uncharacterized protein LOC100996273 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MSPKCAETAQ QLRCLTENVQ RPLCPTMPAW GRPSLGLLRV SPACQPKGGR SCGCSQPLLK VGLWVEMWAA SGRHSYKCIP
        90        100        110        120        130        140        150        160
ALRTTFLLPS PFLRTPMQKR GRQLTKDREG YCSWHLMGSI CCIPLGCCPG WIGKELAGRL SSVLTTWLGG GRGAWQEQSA
       170        180        190        200        210        220
GPGNWGLVHV CTHVCVCVRA CWVGREEAVK PHPLLSAAVL LCVSAARGCH HTS
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2595	1	973.1975	143.11	2	61.1	11.1	1	78-94	K.CIPALRTTFLLPSPFLR.T	

Detailed Protein Report

Protein 1082: PREDICTED: peroxisomal acyl-coenzyme A oxidase 2 isoform X2 [Homo sapiens]

Accession:	gi|530373234	**Score:**	11.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.7
Database Date:	2015-11-30	**pI:**	8.8
		Sequence Coverage [%]:	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTQNERYKAA	MRRAFHIRLI	ARRLGWLEDG	RELGYAYRAL	SGDVALNIHR	VFVRALRSLG	SEEQIAKWDP	LCKNIQIIAT
90	100	110	120	130	140	150	160
YAQTELGHGT	YLQGLETEAT	YDAATQEFVI	HSPTLTATKW	WPGDLGRSAT	HALVQAQLIC	SGARRGMHAF	IVPIRSLQDH
170	180	190	200	210	220	230	240
TPLPGIIIGD	IGPKMDFDQT	DNGFLQLNHV	RVPRENMLSR	FAQVLPDGTY	VKLGTAQSNY	LPMVVVRVEL	LSGEILPILQ
250	260	270	280	290	300	310	320
KACVIAMRYS	VIRRQSRLRP	SDPEAKVLDY	QTQQQKLFPQ	LAISYAFHFL	AVSLLEFFQH	SYTAILNQDF	SFLPELHALS
330	340	350	360	370	380	390	400
TGMKAMMSEF	CTQGAEMCRR	ACGGHGYSKL	SGLPSLVTKL	SASCTYEGEN	TVLYLQVARF	LVKSYLQTQM	SPGSTPQRSL
410	420	430	440	450	460	470	480
SPSVAYLTAP	DLARCPAQRA	ADFLCPELYT	TAWAHVAVRL	IKDSVQHLQT	LTQSGADQHE	AWNQTTVIHL	QAAKVHCYYV
490	500	510	520	530	540	550	560
TVKGFTEALE	KLENEPAIQQ	VLKRLCDLHA	IHGILTNSGD	FLHDAFLSGA	QVDMARTAYL	DLLRLIRKDA	ILLTDAFDFT
570	580	590	600	610	620		
DQCLNSALGC	YDGNVYERLF	QWAQKSPTNT	QENPAYEEYI	RPLLQSWRSK	L		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1349	1	945.2230	-270.57	1	45.4	11.1	0	24-31	R.LGWLEDGR.E	

Detailed Protein Report

Protein 1083: 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

QD:QU **Median:** 1.87 **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		QD:QU 1.87

Protein 1084: nucleolar protein of 40 kDa isoform f [Homo sapiens]

Accession:	gi|543173125	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	20.4
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	6.1
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGPLSKSQAV GSKMKNDRIK VSLSMKVVNQ GTGKDLDPNN VIIEQEERRR RSFQDYTGQK ITLEAVLNTT CKKCGCKGHF
        90        100        110        120        130        140        150        160
AKDCFMQPGG TKYSLIPDEE EEKEEAKSAE FEKPDPTRNP SRKRKKEKKK KKHRDRKSSD SDSSDSESDT GKRARHTSKD
       170        180
SKAAKKKKKK KKHKKKHKE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1952	1	676.2626	-80.17	2	52.9	11.0	0	93-103	K.YSLIPDEEEEK.E	

Detailed Protein Report

Protein 1085: 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

Quantitation

QD:QU **Median:** 0.96 **CV:** 0.00 % **No. of 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	Ratios	
728	1	839.4181	42.29	2	39.1	11.0	1	1-16	-.MSFVLSRMAACGGTCK.N	Oxidation: 1	QD:QU	0.96

Protein 1086: 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

```
        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
2156	1	841.3920	-93.73	2	57.3	11.0	1	360-378	R.RVAAAASGANTLAGGLGPK.A	

Detailed Protein Report

Protein 1087: 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

Quantitation

QD:QU **Median:** 3.28 **CV:** 0.00 % **No. of 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	Ratios
2286	1	665.3174	-11.91	2	59.0	11.0	0	16-28	R.GPDVETSPFGAPR.A		QD:QU 3.28

Detailed Protein Report

Protein 1088: 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

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
1830	1	961.3217	-133.49	2	53.2	11.0	1	25-42	R.AGGCNETGMLERLPLCGK.A	Carbamidomethyl: 4; Oxidation: 9

Detailed Protein Report

Protein 1089: RNA-binding protein MEX3A [Homo sapiens]

Accession:	gi|147902746	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.1
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
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
977	1	737.1785	119.61	3	40.7	11.0	2	208-229	R.NKSGAAFGVAPALPGQVTIRVR.V	

Detailed Protein Report

Protein 1090: **PREDICTED: proline synthase co-transcribed bacterial homolog protein isoform X1 [Homo sapiens]**

Accession:	gi|530387555	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.6
Database Date:	2015-11-30	**pI:**	11.0
Modification(s):	Oxidation	**Sequence Coverage [%]:**	9.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MMSNDWFTRR	KLGGTGRWCE	PRAAGGLGLG	VGPRGMWRAG	SMSAELGVGC	ALRAVNERVQ	QAVARRPRDL	PAIQPRLVAV
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
SKTKPADMVI	EAYGHGQRTF	GENYVQELLE	KASNPKILSL	CPEIKWHFIG	HLQKQNVNKL	MGKSEFLIKR	ENIMPRTE

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1926	1	719.2731	-99.81	2	52.6	11.0	0	39-53	R.AGSMSAELGVGCALR.A	Oxidation: 4

Detailed Protein Report

Protein 1091: 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	

Detailed Protein Report

Protein 1092: PREDICTED: polypyrimidine tract-binding protein 3 isoform X5 [Homo sapiens]

Accession:	gi|578818044	**Score:**	11.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.5
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 1.37 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MNSSTPSTAN	GNDSKKFKRD	RPPCSPSRVL	HLRKIPCDVT	EAEIISLGLP	FGKVTNLLML	KGKSQAFLEM	ASEEAAVTMV
90	100	110	120	130	140	150	160
NYYTPITPHL	RSQPVYIQYS	NHRELKTDNL	PNQARAQAAL	QAVSAVQSGS	LALSGGPSNE	GTVLPGQSPV	LRIIIENLFY
170	180	190	200	210	220	230	240
PVTLEVLHQI	FSKFGTVLKI	ITFTKNNQFQ	ALLQYADPVN	AHYAKMALDG	QNIYNACCTL	RIDFSKLTSL	NVKYNNDKSR
250	260	270	280	290	300	310	320
DFTRLDLPTG	DGQPSLEPPM	AAAFGAPGII	SSPYAGAAGF	APAIGFPQAT	GLSVPAVPGA	LGPLTITSSA	VTGRMAIPGA
330	340	350	360	370	380	390	400
SGIPGNSVLL	VTNLNPDLIT	PHGLFILFGV	YGDVHRVKIM	FNKKENALVQ	MADANQAQLA	MNHLSGQRLY	GKVLRATLSK
410	420	430	440	450	460	470	480
HQAVQLPREG	QEDQGLTKDF	SNSPLHRFKK	PGSKNFQNIF	PPSATLHLSN	IPPSVTVDDL	KNLFIEAGCS	VKAFKFFQKD
490	500	510	520	530			
RKMALIQLGS	VEEAIQALIE	LHNHDLGENH	HLRVSFSKST	I			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
266	1	977.4418	-97.99	3	32.1	11.0	1	35-61	K. IPCDVTEAEIISLGLPFGKVTNLLMI G	Oxidation: 25	QD:QU 1.37

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Detailed Protein Report

Protein 1093: PREDICTED: protein ECT2 isoform X6 [Homo sapiens]

Accession:	gi|530374050	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.9
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGGVIRKDFN	SKVTHLVANC	TQGEKFRVAV	SLGTPIMKPE	WIYKAWERRN	EQDFYAAVDD	FRNEFKVPPF	QDCILSFLGF
90	100	110	120	130	140	150	160
SDEEKTNMEE	MTEMQGGKYL	PLGDERCTHL	VVEENIVKDL	PFEPSKKLYV	VKQEWFWGSI	QMDARAGETM	YLYEKANTPE
170	180	190	200	210	220	230	240
LKKSVSMLSL	NTPNSNRKRR	RLKETLAQLS	RETDVSPFPP	RKRPSAEHSL	SIGSLLDISN	TPESSINYGD	TPKSCTKSSK
250	260	270	280	290	300	310	320
SSTPVPSKQS	ARWQVAKELY	QTESNYVNIL	ATIIQLFQVP	LEEEGQRGGP	ILAPEEIKTI	FGSIPDIFDV	HTKIKDDLED
330	340	350	360	370	380	390	400
LIVNWDESKS	IGDIFLKYSK	DLVKTYPPFV	NFFEMSKETI	IKCEKQKPRF	HAFLKINQAK	PECGRQSLVE	LLIRPVQRLP
410	420	430	440	450	460	470	480
SVALLLNDLK	KHTADENPDK	STLEKAIGSL	KEVMTHINED	KRKTEAQKQI	FDVVYEVDGC	PANLLSSHRS	LVQRVETISL
490	500	510	520	530	540	550	560
GEHPCDRGEQ	VTLFLFNDCL	EIARKRHKVI	GTFRSPHGQT	RPPASLKHIH	LMPLSQIKKV	LDIRETEDCH	NAFALLVRPP
570	580	590	600	610	620	630	640
TEQANVLLSF	QMTSDELPKE	NWLKMLCRHV	ANTICKADAE	NLIYTADPES	FEVNTKDMDS	TLSRASRAIK	KTSKKVTRAF
650	660	670	680	690	700	710	720
SFSKTPKRAL	RRALMTSHGS	VEGRSPSSND	KHVMSRLSST	SSLAITHSVS	TSNVIGFTKH	VYVQRLNSTG	GRSQYSWFQS
730	740	750	760				
VRHSAFRASF	SEILEGNTDF	SNFKKVLSKS	SLTFVKN				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1030	2	700.2304	-175.90	2	41.4	10.9	0	13-25	K.VTHLVANCTQGEK.F	

Detailed Protein Report

Protein 1094: 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 1095: 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

QD:QU	**Median:** 1.47	**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		QD:QU	1.47

Detailed Protein Report

Protein 1096: PREDICTED: serine/threonine-protein kinase N3 isoform X4 [Homo sapiens]

Accession:	gi|578817399	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	92.9
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEEGAPRQPG	PSQWPPEDEK	EVIRRAIQKE	LKIKEGVENL	RRVATDRRHL	GHVQQLLRSS	NRRLEQLHGE	LRELHARILL
90	100	110	120	130	140	150	160
PGPGPGPAEP	VASGPRPWAE	QLRARHLEAL	RRQLHVELKV	KQGAENMTHT	CASGTPKERK	LLAAAQQMLR	DSQLKVALLR
170	180	190	200	210	220	230	240
MKISSLEASG	SPEPGPELLA	EELQHRLHVE	AAVAEGAKNV	VKLLSSRRTQ	DRKALAEAQA	QLQESSQKLD	LLRLALEQLL
250	260	270	280	290	300	310	320
EQLPPAHPLR	SRVTRELRAA	VPGYPQPSGT	PVKPTALTGT	LQVRLLGCEQ	LLTAVPGRSP	AAALASSPSE	GWLRTKAKHQ
330	340	350	360	370	380	390	400
RGRGELASEV	LAVLKVDNRV	VGQTGWGQVA	EQSWDQTFVI	PLERARELEI	GVHWRDWRQL	CGVAFLRLED	FLDNACHQLS
410	420	430	440	450	460	470	480
LSLVPQGLLF	AQVTFCDPVI	ERRPRLQRQE	RIFSKRRGQD	FLRASQMNLG	MAAWGRLVMN	LLPPCSSPST	ISPPKGCPRT
490	500	510	520	530	540	550	560
PTTLREASDP	ATPSNFLPKK	TPLGEEMTPP	PKPPRLYLPQ	EPTSEETPRT	KRPHMEPRTR	RGPSPPASPT	RKPPRLQDFR
570	580	590	600	610	620	630	640
CLAVLGRGHF	GKVLLVQFKG	TGKYYAIKAL	KKQEVLSRDE	IESLYCEKRI	LEAVGCTGHP	FLLSLLACFQ	TSSHACFVTE
650	660	670	680	690	700	710	720
FVPGGDLMMQ	IHEDVFPEPQ	ARFYVACVVL	GLQFLHEKKI	IYRDLKLDNL	LLDAQGFLKI	ADFGLCKEGI	GFGDRTSTFC
730	740	750	760	770	780	790	800
GTPEFLAPEV	LTQEAYTRAV	DWWGLGVLLY	EMLVGECPFP	GDTEEEVFDC	IVNMDAPYPG	FLSVQGLEFI	QKLLQKCPEK
810	820	830	840				
RLGADHQLAS	PARPHHPAPL	RAYPVWPCGP	ALL				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
242	1	566.5934	-38.74	3	31.8	10.9	1	700-715	K.IADFGLCKEGIGFGDR.T	

Detailed Protein Report

Protein 1097: PREDICTED: E3 ubiquitin-protein ligase TRAF7 isoform X1 [Homo sapiens]

Accession:	gi|530409257	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	74.3
Database Date:	2015-11-30	**pI:**	6.9
		Sequence Coverage [%]:	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSGKSARYN	RFSGGPSNLP	TPDVTTGTRM	ETTFGPAFSA	VTTITKADGT	STYKQHCRTP	SSSSTLAYSP	RDEEDSMPPI
90	100	110	120	130	140	150	160
STPRRSDSAI	SVRSLHSESS	MSLRSTFSLP	EEEEEPEPLV	FAEQPSVKLC	CQLCCSVFKD	PVITTCGHTF	CRRCALKSEK
170	180	190	200	210	220	230	240
CPVDNVKLTV	VVNNIAVAEQ	IGELFIHCRH	GCRVAGSGKP	PIFEVDPRGC	PFTIKLSARK	DHEGSCDYRP	VRCPNNPSCP
250	260	270	280	290	300	310	320
PLLRMNLEAH	LKECEHIKCP	HSKCTFIGNQ	DTYETHLETC	RFEGLKEFLQ	QTDDRFHEMH	VALAQKDQEI	AFLRSMLGKL
330	340	350	360	370	380	390	400
SEKIDQLEKS	LELKFDVLDE	NQSKLSEDLM	EFRRDASMLN	DELSHINARL	NMGILGSYDP	QQIFKCKGTF	VGHQGPVWCL
410	420	430	440	450	460	470	480
CVYSMGDLLF	SGSSDKTIKV	WDTCTTYKCQ	KTLEGHDGIV	LALCIQGCKL	YSGSADCTII	VWDIQNLQKV	NTIRAHDNPV
490	500	510	520	530	540	550	560
CTLVSSHNVL	FSGSLKAIKV	WDIVGTELKL	KKELTGLNHW	VRALVAAQSY	LYSGSYQTIK	IWDIRTLDCI	HVLQTSGGSV
570	580	590	600	610	620	630	640
YSIAVTNHHI	VCGTYENLIH	VWDIESKEQV	RTLTGHVGTV	YALAVISTPD	QTKVFSASYD	RSLRVWSMDN	MICTQTLLRH
650	660	670					
QGSVTALAVS	RGRLFSGAVD	STVKVWTC					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1965	1	676.7537	-179.62	2	53.1	10.9	1	512-522	K.KELTGLNHWVR.A	

Detailed Protein Report

Protein 1098: 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 1099: 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 1100: peroxisome proliferator-activated receptor delta isoform 2 [Homo sapiens]

Accession:	gi|29171750	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.4
Database Date:	2015-11-30	**pI:**	8.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.3
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.73 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEQPQEEAPE	VREEEEKEEV	AEAEGAPELN	GGPQHALPSS	SYTDLSRSSS	PPSLLDQLQM	GCDGASCGSL	NMECRVCGDK
90	100	110	120	130	140	150	160
ASGFHYGVHA	CEGCKGFFRR	TIRMKLEYEK	CERSCKIQKK	NRNKCQYCRF	QKCLALGMSH	NAIRFGRMPE	AEKRKLVAGL
170	180	190	200	210	220	230	240
TANEGSQYNP	QVADLKAFSK	HIYNAYLKNF	NMTKKKARSI	LTGKASHTAP	FVIHDIETLW	QAEKGLVWKQ	LVNGLPPYKE
250	260	270	280	290	300	310	320
ISVHVFYRCQ	CTTVETVREL	TEFAKSIPSF	SSLFLNDQVT	LLKYGVHEAI	FAMLASIVNK	DGLLVANGSG	FVTREFLRSL
330	340	350	360	370			
RKPFSDIIEP	KFEFAVKFNA	LELDDSDLAL	FIAAIILCGG	E			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
217	1	679.7025	-197.92	2	31.5	10.9	0	133-144	K.CLALGMSHNAIR.F	Carbamidomethyl: 1; Oxidation: 6	QD:QU 0.73

Detailed Protein Report

Protein 1101: 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

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
364	1	529.8113	176.64	2	34.5	10.9	0	473-481	K.MYIEQNACS.-	

Detailed Protein Report

Protein 1102: 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 1103: retinoic acid receptor responder protein 3 [Homo sapiens]

Accession:	gi|149588791	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	18.2
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	6.7
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.15 **CV:** 0.00 % **No. of 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	Ratios
826	1	607.1581	-185.27	2	38.8	10.9	0	65-75	R.LEDVVGGCCYR.V		QD:QU 0.15

Detailed Protein Report

Protein 1104: mitochondrial 10-formyltetrahydrofolate dehydrogenase precursor [Homo sapiens]

Accession:	gi|238814322	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.7
Database Date:	2015-11-30	**pI:**	6.1
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLRRGSQALR	RFSTGRVYFK	NKLKLALIGQ	SLFGQEVYSH	LRKEGHRVVG	VFTVPDKDGK	ADPLALAAEK	DGTPVFKLPK
90	100	110	120	130	140	150	160
WRVKGKTIKE	VAEAYRSVGA	ELNVLPFCTQ	FIPMDIIDSP	KHGSIIYHPS	ILPRHRGASA	INWTLIMGDK	KAGFSVFWAD
170	180	190	200	210	220	230	240
DGLDTGPILL	QRSCDVEPND	TVDALYNRFL	FPEGIKAMVE	AVQLIADGKA	PRIPQPEEGA	TYEGIQKKEN	AEISWDQSAE
250	260	270	280	290	300	310	320
VLHNWIRGHD	KVPGAWTEIN	GQMVTFYGST	LLNSSVPPGE	PLEIKGAKKP	GLVTKNGLVL	FGNDGKALTV	RNLQFEDGKM
330	340	350	360	370	380	390	400
IPASQYFSTG	ETSVVELTAE	EVKVAETIKV	IWAGILSNVP	IIEDSTDFFK	SGASSMDVAR	LVEEIRQKCG	GLQLQNEDVY
410	420	430	440	450	460	470	480
MATKFEGFIQ	KVVRKLRGED	QEVELVVDYI	SKEVNEIMVK	MPYQCFINGQ	FTDADDGKTY	DTINPTDGST	ICKVSYASLA
490	500	510	520	530	540	550	560
DVDKAVAAAK	DAFENGEWGR	MNARERGRLM	YRLADLLEEN	QEELATIEAL	DSGAVYTLAL	KTHIGMSVQT	FRYFAGWCDK
570	580	590	600	610	620	630	640
IQGSTIPINQ	ARPNRNLTFT	KKEPLGVCAI	IIPWNYPLMM	LAWKSAACLA	AGNTLVLKPA	QVTPLTALKF	AELSVKAGFP
650	660	670	680	690	700	710	720
KGVINIIPGS	GGIAGQRLSE	HPDIRKLGFT	GSTPIGKQIM	KSCAVSNLKK	VSLELGGKSP	LIIFNDCELD	KAVRMGMGAV
730	740	750	760	770	780	790	800
FFNKGENCIA	AGRLFVEESI	HDEFVTRVVE	EIKKMKIGDP	LDRSTDHGPQ	NHKAHLEKLL	QYCETGVKEG	ATLVYGGRQV
810	820	830	840	850	860	870	880
QRPGFFMEPT	VFTDVEDYMY	LAKEESFGPI	MVISKFQNGD	IDGVLQRANS	TEYGLASGVF	TRDINKAMYV	SEKLEAGTVF
890	900	910	920	930			
INTYNKTDVA	APFGGVKQSG	FGKDLGEEAL	NEYLKTKTVT	LEY			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
935	1	838.8802	82.27	3	40.2	10.9	2	21-42	K.NKLKLALIGQSLFGQEVYSHLR.K	

Protein 1105: 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 1106: **PREDICTED: arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2-like [Homo sapiens]**

Accession:	gi|578805484	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.5
Database Date:	2015-11-30	**pI:**	12.7
		Sequence Coverage [%]:	6.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTGFSFENLN	TEKKSGENEP	PAHNPFRSAA	RLRCLLALRA	FPAPPNMPKL	LAALGPLPLP	RISSGTRAPG	LRTAGDPRSG
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
RSLLWLAVRA	RLERRDLRQR	CCGRLCSVNE	PPNGSASFPL	CVPRKSLLSK	PSQLRRARVA	LARPNPGVLG	QARGAGVRRG
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
RAGPGAPSGL	RAHAPHLGEA	RCAGAQRGGS	GRALKPGAGK	SWTVQGPRRA	ELSPAPPPPP	PLLPPPPPPG	LQQIAGERLR
250	**260**	**270**	**280**	**290**	**300**		
EAPVQPWRDR	SNHRSVSNSF	PAGGATAPRA	RGPRAELLRC	SQPPELPTAS	FVGGNPTV		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2203	1	956.9064	-68.85	2	56.2	10.9	1	251-269	R.SNHRSVSNSFPAGGATAPR.A	

Detailed Protein Report

Protein 1107: 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 1108: kinesin-like protein KIF1C [Homo sapiens]

Accession:	gi|40254834	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	122.9
Database Date:	2015-11-30	**pI:**	6.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	0.9
		No. of unique Peptides:	1

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

Detailed Protein Report

Protein 1109: 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 1110: PREDICTED: cell adhesion molecule 4 isoform X1 [Homo sapiens]

Accession:	gi|530415930	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	38.3
Database Date:	2015-11-30	**pI:**	5.9
		Sequence Coverage [%]:	4.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGRARRFQWP	LLLLWAAAAG	PGAGQEVQTE	NVTVAEGGVA	EITCRLHQYD	GSIVVIQNPA	RQTLFFNGTR	ALKDERFQLE
90	100	110	120	130	140	150	160
EFSPRRVRIR	LSDARLEDEG	GYFCQLYTED	THHQIATLTV	LVAPENPVVE	VREQAVEGGE	VELSCLVPRS	RPAATLRWYR
170	180	190	200	210	220	230	240
DRKELKGVSS	SQENGKVWSV	ASTVRFRVDR	KDDGGIIICE	AQNQALPSGH	SKQTQYVLDV	QYSPTARIHA	SQAVVREGDT
250	260	270	280	290	300	310	320
LVLTCAVTGN	PRPNQIRWNR	GNESLPERAE	AVGETLTLPG	LVSADNGTYT	CEASNKHGHA	RALYVLVVYG	SYLTHEASGL
330	340	350					
DEQGEAREAF	LNGSDGHKRK	EEFFI					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1674	1	905.3397	-159.27	2	49.4	10.9	0	46-61	R.LHQYDGSIVVIQNPAR.Q	

Detailed Protein Report

Protein 1111: pro-neuregulin-1, membrane-bound isoform isoform HRG-gamma3 [Homo sapiens]

Accession:	gi|236464356	**Score:**	10.9
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	19.3
Database Date:	2015-11-30	**pI:**	10.6
		Sequence Coverage [%]:	10.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MSERKEGRGK GKGKKKERGS GKKPESAAGS QSPALPPRLK EMKSQESAAG SKLVLRCETS SEYSSLRFKW FKNGNELNRK
        90        100        110        120        130        140        150        160
NKPQNIKIQK KPGKSELRIN KASLADSGEY MCKVISKLGN DSASANITIV ESNATSTSTT GTSHLVKCAE KEKTFCVNGG
       170        180
ECFMVKDLSN PSRYLCK
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2745	1	917.4783	-37.51	2	63.3	10.9	1	23-40	K.KPESAAGSQSPALPPRLK.E	

Detailed Protein Report

Protein 1112: polymerase delta-interacting protein 3 isoform 2 [Homo sapiens]

Accession:	gi|30089919	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.9
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	5.4
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MADISLDELI	RKRGAAAKGR	LNARPGVGGV	RSRVGIQQGL	LSQSTRTATF	QQRFDARQKI	GLSDARLKLG	VKDAREKLLQ
90	100	110	120	130	140	150	160
KDARFRIKGK	VQDAREMLNS	RKQQTTVPQK	PRQVADAREK	ISLKRSSPAA	FINPPIGTVT	PALKLTKTIQ	NLYDLDEDDD
170	180	190	200	210	220	230	240
GIASVPTKQM	KFAASGGFLH	HMAGLSSSKL	SMSKALPLTK	VVQNDAYTAP	ALPSSIRTKA	LTNMSRTLVN	KEEPPKELPA
250	260	270	280	290	300	310	320
AEPVLSPLEG	TKMTVNNLHP	RVTEEDIVEL	FCVCGALKRA	RLVHPGVAEV	VFVKKDDAIT	AYKKYNNRCL	DGQPMKCNLH
330	340	350	360	370	380	390	400
MNGNVITSDQ	PILLRLSDSP	SMKKESELPR	RVNSASSSNP	PAEVDPDTIL	KALFKSSGAS	VTTQPTEFKI	KL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
119	1	731.4478	116.11	3	30.2	10.8	1	169-189	K.QMKFAASGGFLHHMAGLSSSK.L	

Detailed Protein Report

Protein 1113: uncharacterized protein C9orf172 [Homo sapiens]

Accession:	gi|148762978	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	106.6
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	1.7
		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
2104	1	977.4132	-55.55	2	54.9	10.8	1	945-961	R.RTGRPFMCMIMAASEPR.A	

Detailed Protein Report

Protein 1114: 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

QD:QU **Median:** 0.52 **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	QD:QU	0.52

Detailed Protein Report

Protein 1115: tripartite motif-containing protein 47 [Homo sapiens]

Accession:	gi|54792146	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	69.5
Database Date:	2015-11-30	**pI:**	6.0
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.47 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MDGSGPFSCP	ICLEPLREPV	TLPCGHNFCL	ACLGALWPHR	GASGAGGPGG	AARCPLCQEP	FPDGLQLRKN	HTLSELLQLR
90	100	110	120	130	140	150	160
QGSGPGSGPG	PAPALAPEPS	APSALPSVPE	PSAPCAPEPW	PAGEEPVRCD	ACPEGAALPA	ALSCLSCLAS	FCPAHLGPHE
170	180	190	200	210	220	230	240
RSPALRGHRL	VPPLRRLEES	LCPRHLRPLE	RYCRAERVCL	CEACAAQEHR	GHELVPLEQE	RALQEAEQSK	VLSAVEDRMD
250	260	270	280	290	300	310	320
ELGAGIAQSR	RTVALIKSAA	VAERERVSRL	FADAAAALQG	FQTQVLGFIE	EGEAAMLGRS	QGDLRRQEEQ	RSRLSRARQN
330	340	350	360	370	380	390	400
LSQVPEADSV	SFLQELLALR	LALEDGCGPG	PGPPRELSFT	KSSQAVRAVR	DMLAVACVNQ	WEQLRGPGGN	EDGPQKLDSE
410	420	430	440	450	460	470	480
ADAEPQDLES	TNLLESEAPR	DYFLKFAYIV	DLDSDTADKF	LQLFGTKGVK	RVLCPINYPL	SPTRFTHCEQ	VLGEGALDRG
490	500	510	520	530	540	550	560
TYYWEVEIIE	GWVSMGVMAE	DFSPQEPYDR	GRLGRNAHSC	CLQWNGRSFS	VWFHGLEAPL	PHPFSPTVGV	CLEYADRALA
570	580	590	600	610	620	630	640
FYAVRDGKMS	LLRRLKASRP	RRGGIPASPI	DPFQSRLDSH	FAGLFTHRLK	PAFFLESVDA	HLQIGPLKKS	CISVLKRR

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
669	1	706.3289	-44.12	3	36.9	10.8	1	231-250	K.VLSAVEDRMDELGAGIAQSR.R		QD:QU 0.47

Detailed Protein Report

Protein 1116: 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 1117: sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 precursor [Homo sapiens]

Accession:	gi|148886654	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	389.9
Database Date:	2015-11-30	**pI:**	5.2
		Sequence Coverage [%]:	0.4
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:** 0.97	**CV:** 0.00 %	**No. of Peptides:** 1

```
        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
```

Detailed Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios	
281	1	743.8595	-21.15	2	33.5	10.8	0	1214-1227	R.GYVCLCPLGYTGLK.C		QD:QU	0.97

Detailed Protein Report

Protein 1118: PREDICTED: NMDA receptor-regulated protein 2 isoform X4 [Homo sapiens]

Accession:	gi|530406441	**Score:**	10.8
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	86.5
Database Date:	2015-11-30	**pI:**	6.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.3
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSKMVISEP	GLNWDISPKN	GLKTFFSREN	YKDHSMAPSL	KELRVLSNRR	IGENLNASAS	SVENEPAVSS	ATQAKEKVKT
90	100	110	120	130	140	150	160
TIGMVLLPKP	RVPYPRFSRF	SQREQRSYVD	LLVKYAKIPA	NSKAVGINKN	DYLQYLDMKK	HVNEEVTEFL	KFLQNSAKKC
170	180	190	200	210	220	230	240
AQDYNMLSDD	ARLFTEKILR	ACIEQVKKYS	EFYTLHEVTS	LMGFFPFRVE	MGLKLEKTLL	ALGSVKYVKT	VFPSMPIKLQ
250	260	270	280	290	300	310	320
LSKDDIATIE	TSEQTAEAMH	YDISKDPNAE	KLVSRYHPQI	ALTSQSLFTL	LNNHGPTYKE	QWEIPVCIQV	IPVAGSKPVK
330	340	350	360	370	380	390	400
VIYINSPLPQ	KKMTMRERNQ	IFHEVPLKFM	MSKNTSVPVS	AVFMDKPEEF	ISEMDMSCEV	NECRKIESLE	NLYLDFDDDV
410	420	430	440	450	460	470	480
TELETFGVTT	TKVSKSPSPA	STSTVPNMTD	APTAPKAGTT	TVAPSAPDIS	ANSRSLSQIL	MEQLQKEKQL	VTGMDGGPEE
490	500	510	520	530	540	550	560
CKNKDDQGFE	SCEKVSNSDK	PLIQDSDLKT	SDALQLENSQ	EIETSNKNDM	TIDILHADGE	RPNVLENLDN	SKEKTVGSEA
570	580	590	600	610	620	630	640
AKTEDTVLCS	SDTDEECLII	DTECKNNSDG	KTAVVGSNLS	SRPASPNSSS	GQASVGNQTN	TACSPEESCV	LKKPIKRVYK
650	660	670	680	690	700	710	720
KFDPVGEILK	MQDELLKPIS	RKVPELPLMN	LENSKQPSVS	EQLSGPSDSS	SWPKSGWPSA	FQKPKGRLPY	ELQDYVEDTS
730	740	750	760	770	780		
EYLAPQEGNF	VYKLFSLQDL	LLLVRCSVQR	IETRPRSKKR	KKIRRLTALR	NC		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1355	1	607.6081	-208.99	2	45.5	10.8	0	485-494	K.DDQGFESCEK.V	Carbamidomethyl: 8

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Detailed Protein Report

Protein 1119: 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 1120: interphotoreceptor matrix proteoglycan 2 precursor [Homo sapiens]

Accession: gi|57242793
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.8
MW [kDa]: 138.5
pI: 4.4
Sequence Coverage [%]: 1.1
No. of unique Peptides: 1

Quantitation

QD:QU **Median:** 4.25 **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		QD:QU	4.25

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Detailed Protein Report

Protein 1121: 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 1122: PREDICTED: AT-rich interactive domain-containing protein 2 isoform X2 [Homo sapiens]

Accession:	gi|578823400	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	191.1
Database Date:	2015-11-30	**pI:**	7.1
		Sequence Coverage [%]:	0.4
		No. of unique Peptides:	1

Quantitation

QD:QU	**Median:**	0.39	**CV:**	0.00 %	**No. of Peptides:**	1

Detailed Protein Report

```
        10         20         30         40         50         60         70         80
MANSTGKAPP DERRKGLAFL DELRQFHHSR GSPFKKIPAV GGKELDLHGL YTRVTTLGGF AKVSEKNQWG EIVEEFNFPR

        90        100        110        120        130        140        150        160
SCSNAAFALK QYYLRYLEKY EKVHHFGEDD DEVPPGNPKP QLPIGAIPSS YNYQQHSVSD YLRQSYGLSM DFNSPNDYNK

       170        180        190        200        210        220        230        240
LVLSLLSGLP NEVDFAINVC TLLSNESKHV MQLEKDPKII TLLLANAGVF DDTLGSFSTV FGEEWKEKTD RDFVKFWKDI

       250        260        270        280        290        300        310        320
VDDNEVRDLI SDRNKSHEGT SGEWIWESLF HPPRKLGIND IEGQRLLLDP VDFKTTHLMF HTVTKCLMSR DRFLKMRGME

       330        340        350        360        370        380        390        400
ILGNLCKAED NGVLICEYVD QDSYREIICH LTLPDVLLVI STLEVLYMLT EMGDVACTKI AKVEKSIDML VCLVSMDIQM

       410        420        430        440        450        460        470        480
FGPDALAAVK LIEHPSSSHQ MLSEIRPQAI EQVQTQTHVA SAPASRAVVA QHVAPPPGIV EIDSEKFACQ WLNAHFEVNP

       490        500        510        520        530        540        550        560
DCSVSRAEMY SEYLSTCSKL ARGGILTSTG FYKCLRTVFP NHTVKRVEDS SSNGQAHIHV VGVKRRAIPL PIQMYYQQQP

       570        580        590        600        610        620        630        640
VSTSVVRVDS VPDVSPAPSP AGIPHGSQTI GNHFQRTPVA NQSSNLTATQ MSFPVQGVHT VAQTVSRIPQ NPSPHTHQQQ

       650        660        670        680        690        700        710        720
NAPVTVIQSK APIPCEVVKA TVIQNSIPQT GVPVSIAVGG GPPQSSVVQN HSTGPQPVTV VNSQTLLHHP SVIPQQSPLH

       730        740        750        760        770        780        790        800
TVVPGQIPSG TPVTVIQQAV PQSHMFGRVQ NIPACTSTVS QGQQLITTSP QPVQTSSQQT SAGSQSQDTV IIAPPQYVTT

       810        820        830        840        850        860        870        880
SASNIVSATS VQNFQVATGQ MVTIAGVPSP QASRVGFQNI APKPLPSQQV SSTVVQQPIQ QPQQPTQQSV VIVSQPAQQG

       890        900        910        920        930        940        950        960
QTYAPAIHQI VLANPAALPA GQTVQLTGQP NITPSSSPSP VPATNNQVPT AMSSSSTPQS QGPPPTVSQM LSVKRQQQQQ

       970        980        990       1000       1010       1020       1030       1040
HSPAPPPQQV QVQVQQPQQV QMQVQPQQSN AGVGQPASGE SSLIKQLLLP KRGPSTPGGK LILPAPQIPP PNNARAPSPQ

      1050       1060       1070       1080       1090       1100       1110       1120
VVYQVASNQA AGFGVQGQTP AQQLLVGQQN VQLVPSAMPP SGGVQTVPIS NLQILPGPLI SNSPATIFQG TSGNQVTITV

      1130       1140       1150       1160       1170       1180       1190       1200
VPNTSFAPAT VSQGNATQLI APAGITMSGT QTGVGLPVQT LPATQASPAG QSSCTTATPP FKGDKIICQK EEEAKEATGL

      1210       1220       1230       1240       1250       1260       1270       1280
HVHERKIEVM ENPSCRRGAT NTSNGDTKEN EMHVGSLLNG RKYSDSSLPP SNSGKIQSET NQCSLISNGP SLELGENGAS

      1290       1300       1310       1320       1330       1340       1350       1360
GKQNSEQIDM QDIKSDLRKP LVNGICDFDK GDGSHLSKNI PNHKTSNHVG NGEISPMEPQ GTLDITQQDT AKGDQLERIS

      1370       1380       1390       1400       1410       1420       1430       1440
NGPVLTLGGS SVSSIQEASN AATQQFSGTD LLNGPLASSL NSDVPQQRPS VVVSPHSTTS VIQGHQIIAV PDSGSKVSHS

      1450       1460       1470       1480       1490       1500       1510       1520
PALSSDVRST NGTAECKTVK RPAEDTDRET VAGIPNKVGV RIVTISDPNN AGCSATMVAV PAGADPSTVA KVAIESAVQQ

      1530       1540       1550       1560       1570       1580       1590       1600
KQQHPPTYVQ NVVPQNTPMP PSPAVQVQGQ PNSSQPSPFS GSSQPGDPMR KPGQNFMCLW QSCKKWFQTP SQVFYHAATE

      1610       1620       1630       1640       1650       1660       1670       1680
HGGKDVYPGQ CLWEGCEPFQ RQRFSFITHL QDKHCSKDAL LAGLKQDEPG QAGSQKSSTK QPTVGGTSST PRAQKAIVNH

      1690       1700       1710       1720       1730       1740       1750       1760
PSAALMALRR GSRNLVFRDF TDEKEGPITK HIRLTAALIL KNIGKYSECG RRLLKRHENN LSVLAISNME ASSTLAKCLY

      1770       1780
ELNFTVQSKE QEKDSEMLQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
198	1	486.6257	-266.72	2	31.2	10.7	1	96-102	R.YLEKYEK.V		QD:QU 0.39

Detailed Protein Report

Protein 1123: 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 KAQKKKKSED 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 1124: 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 1125: **PREDICTED: pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16 isoform X2 [Homo sapiens]**

Accession:	gi|530424571	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	136.2
Database Date:	2015-11-30	**pI:**	5.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.0
		No. of unique Peptides:	1

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
1651	1	720.3147	-23.44	2	50.9	10.7	0	1037-1048	K.CICAAYFHQAAK.L	Carbamidomethyl: 1, 3

Detailed Protein Report

Protein 1126: PREDICTED: cytochrome P450 4A22 isoform X2 [Homo sapiens]

Accession:	gi|530362418	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.1
Database Date:	2015-11-30	**pI:**	9.2
Modification(s):	Oxidation	**Sequence Coverage [%]:**	7.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSVSVLSPSR	RLGGVSGILQ	VTSLLILLLL	LIKAAQLYLH	RQWLLKALQQ	FPCPPSHWLF	GHIQEFQHDQ	ELQRIQERVK
90	100	110	120	130	140	150	160
TFPSACPYWI	WGGKVRVQLY	DPDYMKVILG	RSDPKSHGSY	KFLAPRIGYG	LLLLNGQTWF	QHRRMLTPAF	HNDILKPYVG
170	180	190	200	210	220	230	240
LMADSVRVML	DKWEELLGQD	SPLEVFQHVS	LMTLDTIMKS	AFSHQGSIQV	DRPSDPTEEG	STTEGGGAGE	DQEEEALGFS
250	260	270	280	290	300	310	320
GHPPLGQRAP	GLPRPCWCSG	WNCFRNHLDQ	MPYTTMCIKE	ALRLYPPVPG	IGRELSTPVT	FPDGRSLPKG	IMVLLSIYGL
330	340	350	360				
HHNPKVWPNL	EVFDPSRFAP	GSAQHSHAFL	PFSGGSR				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
9	1	1083.3275	79.88	3	28.6	10.7	1	310-337	K.GIMVLLSIYGLHHNPKVWPNLEVFDPSR.F	Oxidation: 3

Detailed Protein Report

Protein 1127: **disintegrin and metalloproteinase domain-containing protein 19 preproprotein [Homo sapiens]**

Accession:	gi|15451844	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	100.8
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	1.5
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPGGAGAARL	CLLAFALQPL	RPRAAREPGW	TRGSEEGSPK	LQHELIIPQW	KTSESPVREK	HPLKAELRVM	AEGRELILDL
90	100	110	120	130	140	150	160
EKNEQLFAPS	YTETHYTSSG	NPQTTTRKLE	DHCFYHGTVR	ETELSSVTLS	TCRGIRGLIT	VSSNLSYVIE	PLPDSKGQHL
170	180	190	200	210	220	230	240
IYRSEHLKPP	PGNCGFEHSK	PTTRDWALQF	TQQTKKRPRR	MKREDLNSMK	YVELYLVADY	LEFQKNRRDQ	DATKHKLIEI
250	260	270	280	290	300	310	320
ANYVDKFYRS	LNIRIALVGL	EVWTHGNMCE	VSENPYSTLW	SFLSWRRKLL	AQKYHDNAQL	ITGMSFHGTT	IGLAPLMAMC
330	340	350	360	370	380	390	400
SVYQSGGVNM	DHSENAIGVA	ATMAHEMGHN	FGMTHDSADC	CSASAADGGC	IMAAATGHPF	PKVFNGCNRR	ELDRYLQSGG
410	420	430	440	450	460	470	480
GMCLSNMPDT	RMLYGGRRCG	NGYLEDGEEC	DCGEEEECNN	PCCNASNCTL	RPGAECAHGS	CCHQCKLLAP	GTLCREQARQ
490	500	510	520	530	540	550	560
CDLPEFCTGK	SPHCPTNFYQ	MDGTPCEGGQ	AYCYNGMCLT	YQEQCQQLWG	PGARPAPDLC	FEKVNVAGDT	FGNCGKDMNG
570	580	590	600	610	620	630	640
EHRKCNMRDA	KCGKIQCQSS	EARPLESNAV	PIDTTIIMNG	RQIQCRGTHV	YRGPEEEGDM	LDPGLVMTGT	KCGYNHICFE
650	660	670	680	690	700	710	720
GQCRNTSFFE	TEGCGKKCNG	HGVCNNNQNC	HCLPGWAPPF	CNTPGHGGSI	DSGPMPPESV	GPVVAGVLVA	ILVLAVLMLM
730	740	750	760	770	780	790	800
YYCCRQNNKL	GQLKPSALPS	KLRQQFSCPF	RVSQNSGTGH	ANPTFKLQTP	QGKRKVINTP	EILRKPSQPP	PRPPPDYLRG
810	820	830	840	850	860	870	880
GSPPAPLPAH	LSRAARNSPG	PGSQIERTES	SRRPPPSRPI	PPAPNCIVSQ	DFSRPRPPQK	ALPANPVPGR	RSLPRPGGAS
890	900	910	920				
PLRPPGAGPQ	QSRPLAALAP	KFPEYRSQRA	GGMISSKI				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2074	1	720.2852	-119.33	2	54.5	10.7	1	814-827	R.AARNSPGPGSQIER.T	

Detailed Protein Report

Protein 1128: PREDICTED: uncharacterized protein LOC388210 [Homo sapiens]

Accession:	gi|578846031	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.1
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MRQNLTYERH	WPSQPDKIIM	EATLEHVLGA	SCTRQSFWGE	VQTDYARWLR	HSLHLGLCDL	PRALLVVGEH	TLGQGGLLLR
90	100	110	120	130	140	150	160
SRCHLGLAPD	PDHGLHLSLT	LQNHSRPRSA	DFSGALELRG	SKAQRVGLLG	RVSTSTSQSL	VRLEGSVDNR	EEKVRLSVFR
170	180	190	200	210	220	230	240
APSCLQASVA	HEEGGREESV	VLRACAHGRT	AEAEVLFRDG	RQPSQPLGRL	TLQAANQSLL	LAARGCQGGL	LGHVESRIAA
250	260	270	280	290	300	310	320
VGSQVQARLE	EKVQGLGASV	RRFQQLVQPA	GTLDGVAGLL	LQLSQAGREA	MQASGWAVAT	LWARSQALTQ	HLPLYLEWLQ
330	340	350	360	370	380	390	400
VGLEQLREEL	EWPLATLKDA	YLEVTLRPLE	EVWRERAEEA	MRRLQAWVPG	MPGNGGPRPI	RAALGAMKGA	LELAAHQMLS
410	420	430	440	450	460	470	480
WAEATFSRAL	KRLCKPLLDL	YSLSARNRSV	VVMLPLLPAG	DEPLDVARVT	SYLMEEKLLR	PLRELSGANV	LAEYYWLRRR
490	500	510	520	530	540	550	560
LLAGPWEYHA	LVAGAQHVVT	FDGRVWDLST	QCGSILLAQD	FAHNTFSLTL	SRTGSGLTAL	FVELNHKTLI	LYPSLQAYRL
570	580	590	600	610	620	630	640
YNSSLPGDSC	PDLKLHPATT	RKDVSRIELA	SEDGVSVSCD	VPTGLCSLTL	GLWQHGISAG	LLGTNDNEAG	NELMLPDGSM
650	660	670	680	690	700	710	720
ARSLEELSLA	WQVGGDCRAT	EKPQQEQACP	GQLPACWAFF	EGPHSSLRDC	FRVVDPTPFL	SLCVQVPCGT	QELQPACNLA
730	740	750					
AAYIHLCARG	FVPLAPPPQC	V					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2653	1	1058.0400	-59.79	2	61.9	10.7	2	123-142	K.AQRVGLLGRVSTSTSQSLVR.L	

Detailed Protein Report

Protein 1129: testis-specific serine/threonine-protein kinase 6 [Homo sapiens]

Accession:	gi|14042966	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.3
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	6.6
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 1.00 **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		QD:QU	1.00

Detailed Protein Report

Protein 1130: PREDICTED: collagen alpha-1(III) chain-like [Homo sapiens]

Accession:	gi|530356951	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	22.6
Database Date:	2015-11-30	**pI:**	12.4
		Sequence Coverage [%]:	7.3
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530434069	refseq_human (refseq_human_20140103.fasta)	PREDICTED: collagen alpha-1(III) chain-like [Homo sapiens]
gi|530365851	refseq_human (refseq_human_20140103.fasta)	PREDICTED: collagen alpha-1(III) chain-like [Homo sapiens]

10	20	30	40	50	60	70	80
MEAPLGCTIA	QKGCQGQPRP	PSCSNHKVRR	QGSAEPPRKL	RALSRLAARQ	RRQQPEPELV	AATTTERCGE	GEQGPDETLR
90	100	110	120	130	140	150	160
LKTGGGRGTR	LTTAPREWKG	SSPLAAAHTS	SPRGGSARPG	CRTVPSRAVE	PPRRGAREPK	AHPGGPGSPG	AGAGAPGRPG
170	180	190	200	210	220		
SRLDPPGASP	LCGHDIPMGT	VARNAPLCRT	QTLQTPSFPG	RPRPPASPSA	AEGPRRTQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2841	1	913.4679	-6.42	2	64.7	10.7	1	52-67	R.RQQPEPELVAATTTER.C	

Detailed Protein Report

Protein 1131: tyrosine-protein kinase HCK isoform d [Homo sapiens]

Accession:	gi|287326622	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	57.2
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
MGCMKSKFLQ	VGGNTFSKTE	TSASPHCPVY	VPDPTSTIKP	GPNSHNSNTP	GIREGSEDII	VVALYDYEAI	HHEDLSFQKG
90	100	110	120	130	140	150	160
DQMVVLEESG	EWWKARSLAT	RKEGYIPSNY	VARVDSLETE	EWFFKGISRK	DAERQLLAPG	NMLGSFMIRD	SETTKGSYSL
170	180	190	200	210	220	230	240
SVRDYDPRQG	DTVKHYKIRT	LDNGGFYISP	RSTFSTLQEL	VDHYKKGNDG	LCQKLSVPCM	SSKPQKPWEK	DAWEIPRESL
250	260	270	280	290	300	310	320
KLEKKLGAGQ	FGEVWMATYN	KHTKVAVKTM	KPGSMSVEAF	LAEANVMKTL	QHDKLVKLHA	VVTKEPIYII	TEFMAKGSLL
330	340	350	360	370	380	390	400
DFLKSDEGSK	QPLPKLIDFS	AQIAEGMAFI	EQRNYIHRDL	RAANILVSAS	LVCKIADFGL	ARVIEDNEYT	AREGAKFPIK
410	420	430	440	450	460	470	480
WTAPEAINFG	SFTIKSDVWS	FGILLMEIVT	YGRIPYPGMS	NPEVIRALER	GYRMPRPENC	PEELYNIMMR	CWKNRPEERP
490	500	510					
TFEYIQSVLD	DFYTATESQY	QQQP					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1840	1	698.8088	-79.84	2	51.5	10.7	1	102-113	R.KEGYIPSNYVAR.V	

Detailed Protein Report

Protein 1132: sodium-dependent multivitamin transporter [Homo sapiens]

Accession:	gi|256985183	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.6
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	2.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578803248	refseq_human (refseq_human_20140103.fasta)	PREDICTED: sodium-dependent multivitamin transporter isoform X3 [Homo sapiens]
gi|578803246	refseq_human (refseq_human_20140103.fasta)	PREDICTED: sodium-dependent multivitamin transporter isoform X2 [Homo sapiens]
gi|578803244	refseq_human (refseq_human_20140103.fasta)	PREDICTED: sodium-dependent multivitamin transporter isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MSVGVSTSAP	LSPTSGTSVG	MSTFSIMDYV	VFVLLLVLSL	AIGLYHACRG	WGRHTVGELL	MADRKMGCLP	VALSLLATFQ
90	100	110	120	130	140	150	160
SAVAILGVPS	EIYRFGTQYW	FLGCCYFLGL	LIPAHIFIPV	FYRLHLTSAY	EYLELRFNKT	VRVCGTVTFI	FQMVIYMGVV
170	180	190	200	210	220	230	240
LYAPSLALNA	VTGFDLWLSV	LALGIVCTVY	TALGGLKAVI	WTDVFQTLVM	FLGQLAVIIV	GSAKVGGLGR	VWAVASQHGR
250	260	270	280	290	300	310	320
ISGFELDPDP	FVRHTFWTLA	FGGVFMMLSL	YGVNQAQVQR	YLSSRTEKAA	VLSCYAVFPF	QQVSLCVGCL	IGLVMFAYYQ
330	340	350	360	370	380	390	400
EYPMSIQQAQ	AAPDQFVLYF	VMDLLKGLPG	LPGLFIACLF	SGSLSTISSA	FNSLATVTME	DLIRPWFPEF	SEARAIMLSR
410	420	430	440	450	460	470	480
GLAFGYGLLC	LGMAYISSQM	GPVLQAAISI	FGMVGGPLLG	LFCLGMFFPC	ANPPGAVVGL	LAGLVMAFWI	GIGSIVTSMG
490	500	510	520	530	540	550	560
SSMPPSPSNG	SSFSLPTNLT	VATVTTLMPL	TTFSKPTGLQ	RFYSLSYLWY	SAHNSTTVIV	VGLIVSLLTG	RMRGRSLNPA
570	580	590	600	610	620	630	640
TIYPVLPKLL	SLLPLSCQKR	LHCRSYGQDH	LDTGLFPEKP	RNGVLGDSRD	KEAMALDGTA	YQGSSSTCIL	QETSL

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2810	1	813.4027	-85.59	2	64.3	10.7	1	554-568	R.GRSLNPATIYPVLPK.L	

Detailed Protein Report

Protein 1133: kanadaptin [Homo sapiens]

Accession: gi|155722990
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Carbamidomethyl

Score: 10.7
MW [kDa]: 88.8
pI: 5.0
Sequence Coverage [%]: 2.0
No. of unique 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
2813	1	973.4922	-45.30	2	64.3	10.7	2	249-264	R.IPPRTYCRVHVGHVVR.F	Carbamidomethyl: 7

Detailed Protein Report

Protein 1134: 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

QD:QU **Median:** 1.18 **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		QD:QU 1.18

Detailed Protein Report

Protein 1135: PREDICTED: calcium-responsive transcription factor isoform X7 [Homo sapiens]

Accession:	gi|530370982	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.5
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MECQYGPRRK	GFQLKKVSEQ	ESRSCQLYKA	TCPARIYIKK	VQKFPEYRVP	TDPKIDKKII	RMEQEKAFNM	LKKNLVDAGG
90	100	110	120	130	140	150	160
VLRWYVQLPT	QQAHQYHELE	TPCLTLSPSP	FPVSSLEEEE	TAVRDENCAL	PSRLHPQVAH	KIQELVSQGI	EQVYAVRKQL
170	180	190	200	210	220	230	240
RKFVERELFK	PDEVPERHNL	SFFPTVNDIK	NHIHEVQKSL	RNGDTVYNSE	IIPATLQWTT	DSGNILKETM	TVTFAEGNSP
250	260	270	280	290	300	310	320
GESITTKVET	NQTRGSLSPE	PTHLLSSLSS	FQPKIFTQLQ	GLQLQPRYTS	PDESPAVVSV	NNQPSSSPSG	LLDTIGSAVM
330	340	350	360	370	380	390	400
NNNSLLLGQS	HSLQRDTCLT	QNNSTASTMG	NLPEPDQNLV	AMDELVEVGD	VEDTGNLEGT	VHRILLGDVQ	TIPIQIIDNH
410	420	430	440	450			
SALIEENPES	TISVSQVKQE	PKEPALSMEA	KKTVDYKKLS	AT			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1348	1	991.6617	186.83	1	45.4	10.7	0	423-431	K.EPALSMEAK.K	Oxidation: 6

Detailed Protein Report

Protein 1136: protein FAM111B isoform b [Homo sapiens]

Accession: gi|218156273

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 10.7

MW [kDa]: 81.1

pI: 9.7

Sequence Coverage [%]: 1.8

No. of unique Peptides: 1

Alias proteins:

Accession	Name	Description
gi|218156275	refseq_human (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

Protein 1137: cell division cycle-associated protein 2 [Homo sapiens]

Accession:	gi|44681484	**Score:**	10.7
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	112.6
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	0.8
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.71 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MDANSKDKPP	ETKESAMNNA	GNASFILGTG	KIVTPQKHAE	LPPNPCTPDT	FKSPLNFSTV	TVEQLGITPE	SFVRNSAGKS
90	100	110	120	130	140	150	160
SSYLKKCRRR	SAVGARGSPE	TNHLIRFIAR	QQNIKNARKS	PLAQDSPSQG	SPALYRNVNT	LRERISAFQS	AFHSIKENEK
170	180	190	200	210	220	230	240
MTGCLEFSEA	GKESEMTDLT	RKEGLSACQQ	SGFPAVLSSK	RRRISYQRDS	DENLTDAEGK	VIGLQIFNID	TDRACAVETS
250	260	270	280	290	300	310	320
VDLSEISSKL	GSTQSGFLVE	ESLPLSELTE	TSNALKVADC	VVGKGSSDAV	SPDTFTAEVS	SDAVPDVRSP	ATPACRRDLP
330	340	350	360	370	380	390	400
TPKTFVLRSV	LKKPSVKMCL	ESLQEHCNNL	YDDDGTHPSL	ISNLPNCCKE	KEAEDEENFE	APAFLNMRKR	KRVTFGEDLS
410	420	430	440	450	460	470	480
PEVFDESLPA	NTPLRKGGTP	VCKKDFSGLS	SLLLEQSPVP	EPLPQPDFDD	KGENLENIEP	LQVSFAVLSS	PNKSSISETL
490	500	510	520	530	540	550	560
SGTDTFSSSN	NHEKISSPKV	GRITRTSNRR	NQLVSVVEES	VCNLLNTEVQ	PCKEKKINRR	KSQETKCTKR	ALPKKSQVLK
570	580	590	600	610	620	630	640
SCRKKKGKGK	KSVQKSLYGE	RDIASKKPLL	SPIPELPEVP	EMTPSIPSIR	RLGSGYFSSN	GKLEEVKTPK	NPVKRKDLLR
650	660	670	680	690	700	710	720
HDPDLHMHQG	YDKYDVSEFC	SYIKSSSSLG	NATSDEDPNT	NIMNINENKN	IPKAKNKSES	ENEPKAGTDS	PVSCASVTEE
730	740	750	760	770	780	790	800
RVASDSPKPA	LTLQQGQEFS	AGGQNAENLC	QFFKISPDLN	IKCERKDDFL	GAAEGKLQCN	RLMPNSQKDC	HCLGDVLIEN
810	820	830	840	850	860	870	880
TKESKSQSED	LGRKPMESSS	VVSCRDRKDR	RRSMCYSDGR	SLHLEKNGNH	TPSSSVGSSV	EISLENSELF	KDLSDAIEQT
890	900	910	920	930	940	950	960
FQRRNSETKV	RRSTRLQKDL	ENEGLVWISL	PLPSTSQKAK	RRTICTFDSS	GFESMSPIKE	TVSSRQKPQM	APPVSDPENS
970	980	990	1000	1010	1020	1030	
QGPAAGSSDE	PGKRRKSFCI	STLANTKATS	QFKGYRRRSS	LNGKGESSLT	ALERIEHNGE	RKQ	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1156	1	491.6232	-271.81	2	43.0	10.7	1	1015-1022	R.IEHNGERK.Q		QD:QU 0.71

Detailed Protein Report

Protein 1138: 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

Protein 1139: 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 1140: 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 1141: 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

QD:QU **Median:** 2.85 **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	QD:QU 2.85

Detailed Protein Report

Protein 1142: E3 ubiquitin-protein ligase HECW1 isoform b [Homo sapiens]

Accession:	gi|559098413	**Score:**	10.6
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
2069	1	731.3290	-70.89	2	56.3	10.6	1	1387-1400	R.ELKSGGANTQVTEK.N	

Detailed Protein Report

Protein 1143: 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

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
1920	2	785.8075	-102.14	2	54.4	10.6	0	443-457	R.GKPPSPTPWSGSNMK.S	

Detailed Protein Report

Protein 1144: PREDICTED: gamma-tubulin complex component 5 isoform X1 [Homo sapiens]

Accession:	gi|578839948	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.3
Database Date:	2015-11-30	**pI:**	5.5
Modification(s):	Oxidation	**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 1145: proline-rich protein 15 [Homo sapiens]

Accession:	gi|28557711	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	13.7
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	12.4
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|530384560	refseq_human (refseq_human_20140103.fasta)	PREDICTED: proline-rich protein 15 isoform X2 [Homo sapiens]
gi|530384558	refseq_human (refseq_human_20140103.fasta)	PREDICTED: proline-rich protein 15 isoform X1 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MADSGDAGSS GPWWKSLTNS RKKSKEAAVG VPPPAQPAPG EPTPPAPPSP DWTSSSRENQ HPNLLGGAGE PPKPDKLYGD
        90        100        110        120        130
KSGSSRRNLK ISRSGRFKEK RKVRATLLPE AGRSPEEAGF PGDPHEDKQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
351	1	870.3997	23.73	2	33.1	10.6	1	114-129	R.SPEEAGFPGDPHEDKQ.-	

Detailed Protein Report

Protein 1146: PREDICTED: macrophage mannose receptor 1 [Homo sapiens]

Accession: gi|578844889
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.6
MW [kDa]: 88.9
pI: 5.9
Sequence Coverage [%]: 1.4
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 1147: PREDICTED: mitogen-activated protein kinase kinase kinase 10 isoform X2 [Homo sapiens]

Accession:	gi|530416611	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	78.9
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEEEEGAVAK	EWGTTPAGPV	WTAVFDYEAA	GDEELTLRRG	DRVQVLSQDC	AVSGDEGWWT	GQLPSGRVGV	FPSNYVAPGA
90	100	110	120	130	140	150	160
PAAPAGLQLP	QEIPFHELQL	EEIIGVGGFG	KVYRALWRGE	EVAVKAARLD	PEKDPAVTAE	QVCQEARLFG	ALQHPNIIAL
170	180	190	200	210	220	230	240
RGACLNPPHL	CLVMEYARGG	ALSRVLAGRR	VPPHVLVNWA	VQVARGMNYL	HNDAPVPIIH	RDLKSINILI	LEAIENHNLA
250	260	270	280	290	300	310	320
DTVLKITDFG	LAREWHKTTK	MSAAGTYAWM	APEVIRLSLF	SKSSDVWSFG	VLLWELLTGE	VPYREIDALA	VAYGVAMNKL
330	340	350	360	370	380	390	400
TLPIPSTCPE	PFARLLEECW	DPDPHGRPDF	GSILKRLEVI	EQSALFQMPL	ESFHSLQEDW	KLEIQHMFDD	LRTKEKELRS
410	420	430	440	450	460	470	480
REEELLRAAQ	EQRFQEEQLR	RREQELAERE	MDIVERELHL	LMCQLSQEKP	RVRKRKGNFK	RSRLLKLREG	GSHISLPSGF
490	500	510	520	530	540	550	560
EHKITVQASP	TLDKRKGSDG	ASPPASPSII	PRLRAIRLTP	VDCGGSSSGS	SSGGSGTWSR	GGPPKKEELV	GGKKKGRTWG
570	580	590	600	610	620	630	640
PSSTLQKERV	GGEERLKGLG	EGSKQWSSSA	PNLGKSPKHT	PIAPGFASLN	EMDSRTMLVG	LGLAVGGVIG	GCPLAQVPVG
650	660	670	680	690	700	710	720
PWPALQRSDG	PLRLQRSSRR	QRMEAAACPL	PPTRPRPTSQ	CHCLPSPPRG	RGRRGSRRRP	RPPLGGDTAP	GGAATWRC

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2664	1	731.3710	-12.27	3	62.1	10.6	2	698-718	R.RRPRPPLGGDTAPGGAATWRC.-	

Detailed Protein Report

Protein 1148: PREDICTED: heterogeneous nuclear ribonucleoprotein K isoform X7 [Homo sapiens]

Accession:	gi|530391071	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	48.5
Database Date:	2015-11-30	**pI:**	5.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	1

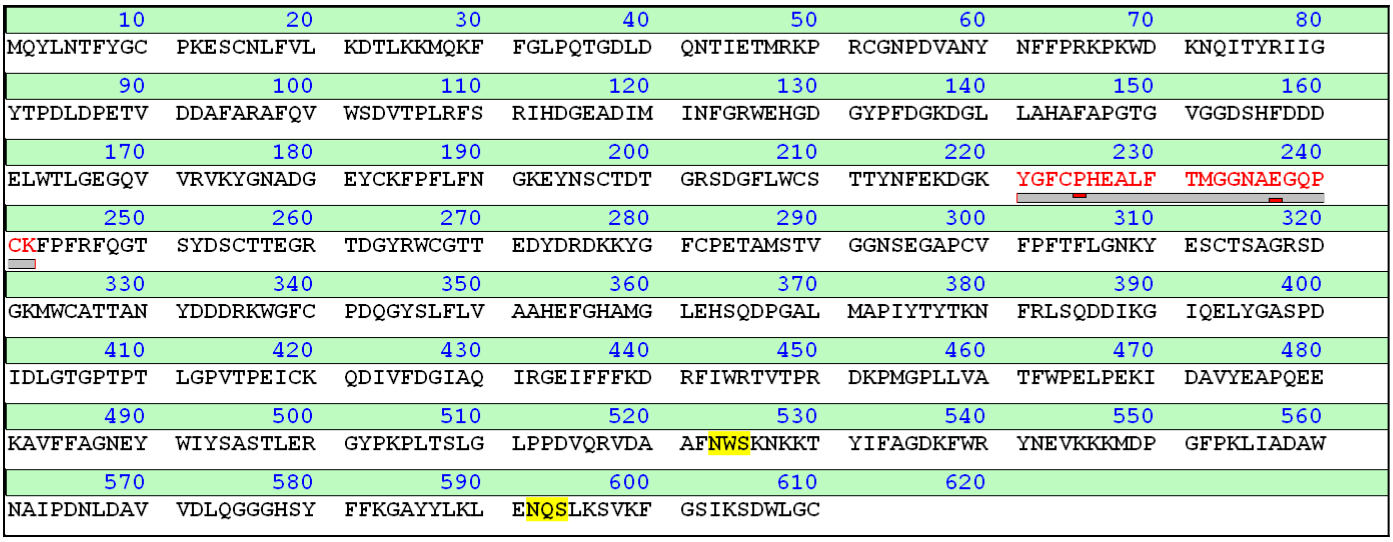
10	20	30	40	50	60	70	80
METEQPEETF	PNTETNGEFG	KRPAEDMEEE	QAFKRSRNTD	EMVELRILLQ	SKNAGAVIGK	GGKNIKALRT	DYNASVSVPD
90	100	110	120	130	140	150	160
SSGPERILSI	SADIETIGEI	LKKIIPTLEE	YQHYKGSDFD	CELRLLIHQS	LAGGIIGVKG	AKIKELRENT	QTTIKLFQEC
170	180	190	200	210	220	230	240
CPHSTDRVVL	IGGKPDRVVE	CIKIILDLIS	ESPIKGRAQP	YDPNFYDETY	DYGGFTMMFD	DRRGRPVGFP	MRGRGGFDRM
250	260	270	280	290	300	310	320
PPGRGGRPMP	PSRRDYDDMS	PRRGPPPPPP	GRGGRGGSRA	RNLPLPPPPP	PRGGDLMAYD	RRGRPGDRYD	GMVGFSADET
330	340	350	360	370	380	390	400
WDSAIDTWSP	SEWQMAYEPQ	GGSGYDYSYA	GGRGSYGDLG	GPIITTQVTI	PKDLAGSIIG	KGGQRIKQIR	HESGASIKID
410	420	430	440				
EPLEGSEDRI	ITITGTQDQI	QNAQYLLQNS	VKQYSGKFF				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
294	1	936.0541	-63.02	3	32.4	10.6	2	145-167	K.ELRENTQTTIKLFQECCPHSTDR.V	Carbamidomethyl: 16

Detailed Protein Report

Protein 1149: 72 kDa type IV collagenase isoform b [Homo sapiens]

Accession:	gi|189217853	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.8
Database Date:	2015-11-30	**pI:**	5.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	3.6
		No. of unique Peptides:	1



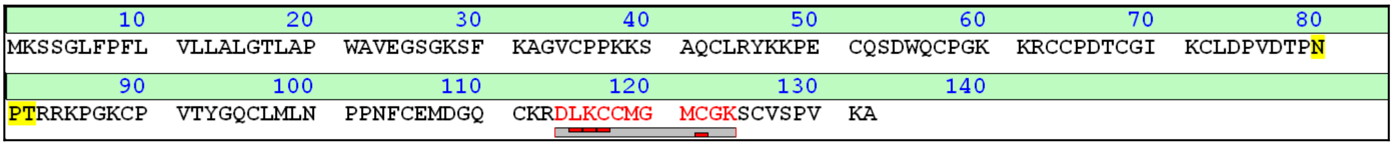
10	20	30	40	50	60	70	80
MQYLNTFYGC	PKESCNLFVL	KDTLKKMQKF	FGLPQTGDLD	QNTIETMRKP	RCGNPDVANY	NFFPRKPKWD	KNQITYRIIG
90	100	110	120	130	140	150	160
YTPDLDPETV	DDAFARAFQV	WSDVTPLRFS	RIHDGEADIM	INFGRWEHGD	GYPFDGKDGL	LAHAFAPGTG	VGGDSHFDDD
170	180	190	200	210	220	230	240
ELWTLGEGQV	VRVKYGNADG	EYCKFPFLFN	GKEYNSCTDT	GRSDGFLWCS	TTYNFEKDGK	YGFCPHEALF	TMGGNAEGQP
250	260	270	280	290	300	310	320
CKFPFRFQGT	SYDSCTTEGR	TDGYRWCGTT	EDYDRDKKYG	FCPETAMSTV	GGNSEGAPCV	FPFTFLGNKY	ESCTSAGRSD
330	340	350	360	370	380	390	400
GKMWCATTAN	YDDDRKWGFC	PDQGYSLFLV	AAHEFGHAMG	LEHSQDPGAL	MAPIYTYTKN	FRLSQDDIKG	IQELYGASPD
410	420	430	440	450	460	470	480
IDLGTGPTPT	LGPVTPEICK	QDIVFDGIAQ	IRGEIFFFKD	RFIWRTVTPR	DKPMGPLLVA	TFWPELPEKI	DAVYEAPQEE
490	500	510	520	530	540	550	560
KAVFFAGNEY	WIYSASTLER	GYPKPLTSLG	LPPDVQRVDA	AFNWSKNKKT	YIFAGDKFWR	YNEVKKKMDP	GFPKLIADAW
570	580	590	600	610	620		
NAIPDNLDAV	VDLQGGGHSY	FFKGAYYLKL	ENQSLKSVKF	GSIKSDWLGC			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
928	1	824.4253	82.38	3	40.1	10.6	0	221-242	K.YGFCPHEALFTMGGNAEGQPCK.F	Carbamidomethyl: 4, 21

Detailed Protein Report

Protein 1150: antileukoproteinase precursor [Homo sapiens]

Accession:	gi|4507065	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.3
Database Date:	2015-11-30	**pI:**	10.7
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	8.3
		No. of unique Peptides:	1



```
        10         20         30         40         50         60         70         80
MKSSGLFPFL VLLALGTLAP WAVEGSGKSF KAGVCPPKKS AQCLRYKKPE CQSDWQCPGK KRCCPDTCGI KCLDPVDTPN
        90        100        110        120        130        140
PTRRKPGKCP VTYGQCLMLN PPNFCEMDGQ CKRDLKCCMG MCGKSCVSPV KA
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2384	1	696.1781	-126.02	2	58.5	10.6	1	114-124	R.DLKCCMGMCGK.S	Carbamidomethyl: 4, 5, 9; Oxidation: 6, 8

Detailed Protein Report

Protein 1151: interferon alpha responsive protein isoform a [Homo sapiens]

Accession:	gi|11641255	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.3
Database Date:	2015-11-30	**pI:**	7.8
		Sequence Coverage [%]:	13.0
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MFSDNSHCPD	CGQQWFPSLE	LGHWLYQTEL	VENECYQVFL	DRINRADYCP	ECYPDNPANR	SLVLPWSFPL	EWAPQNLTRW
90	100	110	120	130	140		
TFEKACHPFL	LGPPLVRKRI	HDSRVAGFNP	ALQLILTRTD	KTLNKKLGQN	K		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
248	1	619.6295	-99.62	3	31.8	10.6	1	105-121	R.VAGFNPALQLILTRTDK.T	

Detailed Protein Report

Protein 1152: PREDICTED: G-protein coupled receptor 124 isoform X2 [Homo sapiens]

Accession:	gi|530387709	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	87.6
Database Date:	2015-11-30	**pI:**	9.3
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGAGGRRMRG	APARLLLPLL	PWLLLLLAPE	ARGAPGCPLS	IRSCKCSGER	PKGLSGGVPG	PARRRVVCSG	GDLPEPPEPG
90	100	110	120	130	140	150	160
LLPNGTVTLL	LSNNKITGLR	NGSFLGLSLL	EKLDLRNNII	STVQPGAFLG	LGELKRLDLS	NNRIGCLTSE	TFQGLPRLLR
170	180	190	200	210	220	230	240
LNISGNIFSS	LQPGVFDELP	ALKVVDLGTE	FLTCDCHLRW	LLPWAQNRSL	QLSEHTLCAY	PSALHAQALG	SLQEAQLCCE
250	260	270	280	290	300	310	320
GALELHTHHL	IPSLRQVVFQ	GDRLPFQCSA	SYLGNDTRIR	WYHNRAPVEG	DEQAGILLAE	SLIHDCTFIT	SELTLSHIGV
330	340	350	360	370	380	390	400
WASGEWECTV	SMAQGNASKK	VEIVVLETSA	SYCPAERVAN	NRGDFRWPRT	LAGITAYQSC	LQYPFTSVPL	GGGAPGTRAS
410	420	430	440	450	460	470	480
RRCDRAGRWE	PGDYSHCLYT	NDITRVLYTF	VLMPINASNA	LTLAHQLRVY	TAEAASFSDM	MDVVYVAQMI	QKFLGYVDQI
490	500	510	520	530	540	550	560
KELVEVMVDM	ASNLMLVDEH	LLWLAQREDK	ACSRIVGALE	RIGGAALSPH	AQHISVNARN	VALEAYLIKP	HSYVGLTCTA
570	580	590	600	610	620	630	640
FQRREGGVPG	TRPGSPGQNP	PPEPEPPADQ	QLRFRCTTGR	PNVSLSSFHI	KNSVALASIQ	LPPSLFSSLP	AALAPPVPPD
650	660	670	680	690	700	710	720
CTLQLLVFRN	GRLFHSHSNT	SRPGAAGPGK	RRGVATPVIF	AGTSGCGVGN	LTEPVAVSLR	HWAEGAEPVA	AWWSQEGPGE
730	740	750	760	770	780	790	800
AGGWTSEGCQ	LRSSQPNVSA	LHCQHLGNVA	VLMELSAFPR	EVGGAGAGLH	PVVYPCTALL	LLCLFATIIT	YILNHRYVPA
810	820						
PRGSPSGLET	PWA						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2631	1	673.3555	23.93	2	63.7	10.6	1	33-45	R.GAPGCPLSIRSCK.C	Carbamidomethyl: 12

Detailed Protein Report

Protein 1153: 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 1154: PREDICTED: exonuclease GOR-like [Homo sapiens]

Accession:	gi|578844508	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.8
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	2.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLRATAPCWF	PPGYPEAKKV	AEEAALEASR	HLGGEQSQAG	APEGSKMLRA	TAPCWFRPGY	PEAKKVAKEA	APEASRHLGA
90	100	110	120	130	140	150	160
GQSPAGAPEG	SKMLRATAPC	WFPPGYPEAK	KVAEEAALEA	PEFPLPSHQP	AQSFGLWVPQ	MHKQASAFVD	IQAEPQNRGP
170	180	190	200	210	220	230	240
AVPPAWPKMV	TESCYFPAQR	GSACRLPAAP	RLTERPSGVR	ISAPRKRKTI	AHSSSPCLVT	GYTDAKRTRV	ASSSQRSRVS
250	260	270	280	290	300	310	320
KVGRQPGKTR	NRSGMACKTT	ATTSSKRIVR	RASLPSLSLK	KPIILRSSGC	QVPTVLRRGY	LQLFTEECLK	FCASKQEAEE
330	340	350	360	370	380	390	400
KALNEEKVAY	DCSPNKNRYL	NVVLNTLKRL	KGLTPSSMPG	LSRAALYSRL	QEFLLTQDQL	KENGYPFPHP	ERPGGAVLFT
410	420	430	440	450	460	470	480
GQGKGPGDSS	CRVCCRCGTE	YLVSSSGRCV	RDQLCYYHWG	RVRSSQVAGG	RVSQYTCCAA	APGSVGCQVA	KQHVRDGRKE
490	500	510	520	530	540	550	560
SLDGFVETFK	KELSRDAYPG	IYALDCEMCY	TTHGLELTRV	TVVDADMRVV	YDTFVKPDNE	IVDYNTRFSG	VTEADVAKTS
570	580	590	600	610	620	630	640
ITLPQVQAIL	LSFFSAQTIL	IGHSLESDLL	ALKLIHSTVV	DTAVLFPHYL	GFPYKRSLRN	LAADYLAQII	QDSQDGHNSS
650	660	670	680				
EDANACLQLV	MWKVRQRAQI	QPRHRSASPA	ALACP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1968	1	932.3760	-123.26	2	53.1	10.6	1	352-369	K.GLTPSSMPGLSRAALYSR.L	

Detailed Protein Report

Protein 1155: nudC domain-containing protein 3 [Homo sapiens]

Accession: gi|122939165
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.6
MW [kDa]: 40.8
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

Protein 1156: PREDICTED: AP-3 complex subunit beta-2 isoform X2 [Homo sapiens]

Accession:	gi|578827454	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	114.4
Database Date:	2015-11-30	**pI:**	5.4
		Sequence Coverage [%]:	1.2
		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 1157: PREDICTED: collagen alpha-1(III) chain-like [Homo sapiens]

Accession:	gi|530361513	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.3
Database Date:	2015-11-30	**pI:**	12.5
		Sequence Coverage [%]:	7.2
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 8.79 **CV:** 0.00 % **No. of Peptides:** 1

```
        10         20         30         40         50         60         70         80
MIPAVSSAER PGPVFVFSPP PTPPRGGPGT GGLEGARQQP GRREPESERG PSPAPCLPSP AAAWVEAAAR QRAGEQAVGR
        90        100        110        120        130        140        150        160
TERLERPTLL RVPLTPTRGS ALPFYPAPSR PPGKPGVESG AGAGRGTDSL PSLHKGGGER TSRGGGRPSA AFARQRRRRR
       170        180        190        200        210        220        230        240
LRRKPGPEPA HLWSLRRLPP GVPIQVCPLP AVPRGAGSVN FTRGCKIGQS LRPRPPRPSP DPLAAGPVRW LLLSTSTALF
       250
VFKAFYGPR
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1452	1	637.0769	50.03	3	46.7	10.6	1	177-194	R.RLPPGVPIQVCPLPAVPR.G		QD:QU 8.79

Detailed Protein Report

Protein 1158: 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 1159: transcriptional repressor p66-alpha [Homo sapiens]

Accession:	gi|164519146	**Score:**	10.6
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	68.0
Database Date:	2015-11-30	**pI:**	10.6
		Sequence Coverage [%]:	3.2
		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 1160: PREDICTED: zinc finger protein 181 isoform X5 [Homo sapiens]

Accession:	gi|578834388	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	65.3
Database Date:	2015-11-30	**pI:**	10.0
		Sequence Coverage [%]:	3.4
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MPQVTFNDVA IDFTHEEWGW LSSAQRDLYK DVMVQNYENL VSVGLSVTKP YVITLLEDGK EPWMMEKKLS KDWESRWENK
        90        100        110        120        130        140        150        160
ELSTKKDNYD EDSPQTVIIE KVVKQSYEFS NSKKNLEYIE KLEGKHGSQV DHFRPAILTS RESPTADSVY KYNIFRSTFH
       170        180        190        200        210        220        230        240
SKSTLSEPQK ISAEGNSHKY DILKKNLPKK SVIKNEKVNG GKKLLNSNKS GAAFSQGKSL TLPQTCNREK IYTCSECGKA
       250        260        270        280        290        300        310        320
FGKQSILNRH WRIHTGEKPY ECRECGKTFS HGSSLTRHLI SHSGEKPYKC IECGKAFSHV SSLTNHQSTH TGEKPYECMN
       330        340        350        360        370        380        390        400
CGKSFSRVSH LIEHLRIHTQ EKLYECRICG KAFIHRSSLI HHQKIHTGEK PYECRECGKA FCCSSHLTRH QRIHTMEKQY
       410        420        430        440        450        460        470        480
ECNKCLKVFS SLSFLVQHQS IHTEEKPFEC QKCRKSFNQL ESLNMHLRNH IRLKPYECSI CGKAFSHRSS LLQHHRIHTG
       490        500        510        520        530        540        550        560
EKPYECIKCG KTFSCSSNLT VHQRIHTGEK PYKCNECGKA FSKGSNLTAH QRVHNGEKPN SVVSVEKPLD YMNHYTCEKS
       570
YRRETV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1323	1	740.7826	87.27	3	45.1	10.5	2	86-104	K.KDNYDEDSPQTVIIEKVVK.Q	

Detailed Protein Report

Protein 1161: PREDICTED: pleckstrin homology domain-containing family H member 1 isoform X9 [Homo sapiens]

Accession: gi|578826005
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.5
MW [kDa]: 99.6
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 1162: zinc finger and BTB domain-containing protein 1 isoform 2 [Homo sapiens]

Accession:	gi|182509178	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.6
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	2.3
		No. of unique Peptides:	1

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	MASGEIGPSK
650							
PVEK							

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

Protein 1163: cytochrome P450 2S1 precursor [Homo sapiens]

Accession:	gi|13449277	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	55.8
Database Date:	2015-11-30	**pI:**	9.5
		Sequence Coverage [%]:	2.6
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.22 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MEATGTWALL	LALALLLLLT	LALSGTRARG	HLPPGPTPLP	LLGNLLQLRP	GALYSGLMRL	SKKYGPVFTI	YLGPWRPVVV
90	100	110	120	130	140	150	160
LVGQEAVREA	LGGQAEEFSG	RGTVAMLEGT	FDGHGVFFSN	GERWRQLRKF	TMLALRDLGM	GKREGEELIQ	AEARCLVETF
170	180	190	200	210	220	230	240
QGTEGRPFDP	SLLLAQATSN	VVCSLLFGLR	FSYEDKEFQA	VVRAAGGTLL	GVSSQGGQTY	EMFSWFLRPL	PGPHKQLLHH
250	260	270	280	290	300	310	320
VSTLAAFTVR	QVQQHQGNLD	ASGPARDLVD	AFLLKMAQEE	QNPGTEFTNK	NMLMTVIYLL	FAGTMTVSTT	VGYTLLLLMK
330	340	350	360	370	380	390	400
YPHVQKWVRE	ELNRELGAGQ	APSLGDRTRL	PYTDAVLHEA	QRLLALVPMG	IPRTLMRTTR	FRGYTLPQGT	EVFPLLGSIL
410	420	430	440	450	460	470	480
HDPNIFKHPE	EFNPDRFLDA	DGRFRKHEAF	LPFSLGKRVC	LGEGLAKAEL	FLFFTTILQA	FSLESPCPPD	TLSLKPTVSG
490	500	510					
LFNIPPAFQL	QVRPTDLHST	TQTR					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
263	1	424.1265	-215.05	3	32.0	10.5	0	335-347	R.ELGAGQAPSLGDR.T		QD:QU 0.22

Detailed Protein Report

Protein 1164: 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; Oxidation: 13

Detailed Protein Report

Protein 1165: zinc finger protein 687 [Homo sapiens]

Accession:	gi|24308227	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	129.4
Database Date:	2015-11-30	**pI:**	9.8
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGDMKTPDFD	DLLAAFDIPD	IDANEAIHSG	PEENEGPGGP	GKPEPGVGSE	SEDTAAASAG	DGPGVPAQAS	DHGLPPPDIS
90	100	110	120	130	140	150	160
VVSVIVKNTV	CPEQSEALAG	GSAGDGAQAA	GVTKEGPVGP	HRMQNGFGSP	EPSLPGTPHS	PAPPSGGTWK	EKGMEGKTPL
170	180	190	200	210	220	230	240
DLFAHFGPEP	GDHSDPLPPS	APSPTREGAL	TPPPFPSSFE	LAQENGPGMQ	PPVSSPPLGA	LKQESCSPHH	PQVLAQQGSG
250	260	270	280	290	300	310	320
SSPKATDIPA	SASPPPVAGV	PFFKQSPGHQ	SPLASPKVPV	CQPLKEEDDD	EGPVDKSSPG	SPQSPSSGAE	AADEDSNDSP
330	340	350	360	370	380	390	400
ASSSSRPLKV	RIKTIKTSCG	NITRTVTQVP	SDPDPPAPLA	EGAFLAEASL	LKLSPATPTS	EGPKVVSVQL	GDGTRLKGTV
410	420	430	440	450	460	470	480
LPVATIQNAS	TAMLMAASVA	RKAVVLPGGT	ATSPKMIAKN	VLGLVPQALP	KADGRAGLGT	GGQKVNGASV	VMVQPSKTAT
490	500	510	520	530	540	550	560
GPSTGGGTVI	SRTQSSLVEA	FNKILNSKNL	LPAYRPNLSP	PAEAGLALPP	TGYRCLECGD	AFSLEKSLAR	HYDRRSMRIE
570	580	590	600	610	620	630	640
VTCNHCARRL	VFFNKCSLLL	HAREHKDKGL	VMQCSHLVMR	PVALDQMVGQ	PDITPLLPVA	VPPVSGPLAL	PALGKGEGAI
650	660	670	680	690	700	710	720
TSSAITTVAA	EAPVLPLSTE	PPAAPATSAY	TCFRCLECKE	QCRDKAGMAA	HFQQLGPPAP	GATSNVCPTC	PMMLPNRCSF
730	740	750	760	770	780	790	800
SAHQRMHKNR	PPHVCPECGG	NFLQANFQTH	LREACLHVSR	RVGYRCPSCS	VVFGGVNSIK	SHIQTSHCEV	FHKCPICPMA
810	820	830	840	850	860	870	880
FKSGPSAHAH	LYSQHPSFQT	QQAKLIYKCA	MCDTVFTHKP	LLSSHFDQHL	LPQRVSVFKC	PSCPLLFAQK	RTMLEHLKNT
890	900	910	920	930	940	950	960
HQSGRLEETA	GKGAGGALLT	PKTEPEELAV	SQGGAAPATE	ESSSSSEEEE	VPSSPEPPRP	AKRPRRELGS	KGLKGGGGGP
970	980	990	1000	1010	1020	1030	1040
GGWTCGLCHS	WFPERDEYVA	HMKKEHGKSV	KKFPCRLCER	SFCSAPSLRR	HVRVNHEGIK	RVYPCRYCTE	GKRTFSSRLI
1050	1060	1070	1080	1090	1100	1110	1120
LEKHVQVRHG	LQLGAQSPGR	GTTLARGSSA	RAQGPGRKRR	QSSDSCSEEP	DSTTPPAKSP	RGGPGSGGHG	PLRYRSSSST
1130	1140	1150	1160	1170	1180	1190	1200
EQSLMMGLRV	EDGAQQCLDC	GLCFASPGSL	SRHRFISHKK	RRGVGKASAL	GLGDGEEEAP	PSRSDPDGGD	SPLPASGGPL
1210	1220	1230	1240				
TCKVCGKSCD	SPLNLKTHFR	THGMAFIRAR	QGAVGDN				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2742	1	937.4585	-79.17	2	63.3	10.5	2	569-583	R.RLVFFNKCSLLLHAR.E	Carbamidomethyl: 8

Detailed Protein Report

Protein 1166: 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

QD:QU **Median:** 1.78 **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		QD:QU 1.78

Detailed Protein Report

Protein 1167: **immediate early response gene 5-like protein [Homo sapiens]**

Accession:	gi|148727370	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	42.1
Database Date:	2015-11-30	**pI:**	6.5
		Sequence Coverage [%]:	5.2
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MECALDAQSL ISISLRKIHS SRTQRGGIKL HKNLLVSYVL RNARQLYLSE RYAELYRRQQ QQQQQQPPHH QHQHLAYAAP
        90        100        110        120        130        140        150        160
GMPASAADFG PLQLGGGGDA EAREPAARHQ LHQLHQLHQL HLQQQLHQHQ HPAPRGCAAA AAAGAPAGGA GALSELPGCA
       170        180        190        200        210        220        230        240
ALQPPHGAPH RGQPLEPLQP GPAPLPLPLP PPAPAALCPR DPRAPAACSA PPGAAPPAAA ASPPASPAPA SSPGFYRGAY
       250        260        270        280        290        300        310        320
PTPSDFGLHC SSQTTVLDLD THVVTTVENG YLHQDCCASA HCPCCGQGAP GPGLASAAGC KRKYYPGQEE EEDDEEDAGG
       330        340        350        360        370        380        390        400
LGAEPPGGAP FAPCKRARFE DFCPDSSPDA SNISNLISIF GSGFSGLVSR QPDSSEQPPP LNGQLCAKQA LASLGAWTRA
       410
IVAF
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1295	1	1164.2240	81.89	2	44.7	10.5	2	2-22	M.ECALDAQSLISISLRKIHSSR.T	

Detailed Protein Report

Protein 1168: RAD52 motif-containing protein 1 isoform 2 [Homo sapiens]

Accession:	gi|77873934	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.4
Database Date:	2015-11-30	**pI:**	9.8
		Sequence Coverage [%]:	3.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAELVPFAVP	IESDKTLLVW	ELSSGPTAEA	LHHSLFTAFS	QFGLLYSVRV	FPNAAVAHPG	FYAVIKFYSA	RAAHRAQKAC
90	100	110	120	130	140	150	160
DRKQLFQKSP	VKVRLGTRHK	AVQHQALALN	SSKCQELANY	YFGFNGCSKR	IIKLQELSDL	EERENEDSMV	PLPKQSLKFF
170	180	190	200	210	220	230	240
CALEVVLPSC	DCRSPGIGLV	EEPMDKVEEG	PLSFLMKRKT	AQKLAIQKAL	SDAFQKLLIV	VLGKTVLIIL	EVLQFQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1615	1	500.6665	-288.74	2	48.7	10.5	1	200-208	K.TAQKLAIQK.A	

Detailed Protein Report

Protein 1169: PREDICTED: coiled-coil domain-containing protein 57 isoform X3 [Homo sapiens]

Accession:	gi|530413473	**Score:**	10.5
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	85.4
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	2.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLPLGSEPAL	NELLLRKEEE	WRALQAHRTQ	LQEAALQDTR	SQLEEAQGKL	RCLQEDFVYN	LQVLEERDLE	LERYDAAFAQ
90	100	110	120	130	140	150	160
AREWEEARRA	EVSELKIEAA	KLRQALAREA	RKVEELQQQQ	QLAFQEHRLE	LERVHSDKNG	EIDHHREQYE	NLKWTLERKL
170	180	190	200	210	220	230	240
EELDGELALQ	RQELLLEFES	KMRKREHEFR	LQADNMSNTA	LSRELKVKLL	HKELEALKEA	GAKAAESLQR	AEATNAELER
250	260	270	280	290	300	310	320
KLQSRAGELQ	DLEAMSRARV	KDLEDKLHSV	QLTRKKEEET	FKRKHEELDR	LAREKDAVLV	AVKGAHVEQL	QELQTRVLEL
330	340	350	360	370	380	390	400
QAHCETLEAQ	LRRAEWRQAD	TAKEKDAAID	QLREDASTVK	SAWDAQIAQL	SKEMVSRDLQ	IQTLQEEEVK	LKAQVARSQQ
410	420	430	440	450	460	470	480
DIERYKQQLS	LAVERERSLE	RDQVQLGLDW	QRRCDDIERD	QIQKSEALIQ	GLSMAKSQVA	AKLQETEQAL	QEQEVVLKAV
490	500	510	520	530	540	550	560
TLERDQAVQA	LRMHGLPRPG	AQMLLRQHEE	EISKDFPSSE	IQRLREQNTS	LRNAIAQMRK	EMEALSHQIP	PPIQTAAEST
570	580	590	600	610	620	630	640
DANQPDPEAG	GDAATPDYVL	ALEAEIRTLK	HKFKTLEKHL	EDVLDPLKMS	SPHAESQPSV	RTSTETTGGS	AQAGQAGGSV
650	660	670	680	690	700	710	720
QAGQAGGSVQ	AGPVSSGLAL	RKLGDRVQLL	NLLVTRLRQK	VLREPLEPAA	LQRELPREVD	QVHLEVLELR	KQVAELGKHL
730	740	750	760				
RIAQHGGAEP	SGRKQPPASD	AVALGREVGA	R				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1662	1	857.6109	168.48	2	49.3	10.5	2	719-734	K.HLRIAQHGGAEPSGRK.Q	

Detailed Protein Report

Protein 1170: 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

QD:QU **Median:** 0.57 **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		QD:QU 0.57

Detailed Protein Report

Protein 1171: 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

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
31	1	668.3030	-47.78	3	30.2	10.4	2	140-156	R.VNTLKTCSDDVVDYFKR.Q	

Detailed Protein Report

Protein 1172: T-box transcription factor TBX4 [Homo sapiens]

Accession:	gi|18129690	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	60.2
Database Date:	2015-11-30	**pI:**	7.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MLQDKGLSES	EEAFRAPGPA	LGEASAANAP	EPALAAPGLS	GAALGSPPGP	GADVVAAAAA	EQTIENIKVG	LHEKELWKKF
90	100	110	120	130	140	150	160
HEAGTEMIIT	KAGRRMFPSY	KVKVTGMNPK	TKYILLIDIV	PADDHRYKFC	DNKWMVAGKA	EPAMPGRLYV	HPDSPATGAH
170	180	190	200	210	220	230	240
WMRQLVSFQK	LKLTNNHLDP	FGHIILNSMH	KYQPRLHIVK	ADENNAFGSK	NTAFCTHVFP	ETSFISVTSY	QNHKITQLKI
250	260	270	280	290	300	310	320
ENNPFAKGFR	GSDDSDLRVA	RLQSKEYPVI	SKSIMRQRLI	SPQLSATPDV	GPLLGTHQAL	QHYQHENGAH	SQLAEPQDLP
330	340	350	360	370	380	390	400
LSTFPTQRDS	SLFYHCLKRR	DGTRHLDLPC	KRSYLEAPSS	VGEDHYFRSP	PPYDQQMLSP	SYCSEVTPRE	ACMYSGSGPE
410	420	430	440	450	460	470	480
IAGVSGVDDL	PPPPLSCNMW	TSVSPYTSYS	VQTMETVPYQ	PFPTHFTATT	MMPRLPTLSA	QSSQPPGNAH	FSVYNQLSQS
490	500	510	520	530	540	550	
QVRERGPSAS	FPRERGLPQG	CERKPPSPHL	NAANEFLYSQ	TFSLSRESSL	QYHSGMGTVE	NWTDG	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1587	1	902.9302	-46.68	2	48.3	10.4	2	79-94	K.KFHEAGTEMIITKAGR.R	Oxidation: 9

Detailed Protein Report

Protein 1173: 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	

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Detailed Protein Report

Protein 1174: PREDICTED: protein CROC-4 isoform X6 [Homo sapiens]

Accession:	gi|578800428	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	14.5
Database Date:	2015-11-30	**pI:**	11.0
Modification(s):	Oxidation	**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 1175: PREDICTED: kalirin isoform X8 [Homo sapiens]

Accession:	gi|578807885	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	176.6
Database Date:	2015-11-30	**pI:**	5.5
		Sequence Coverage [%]:	0.7
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 0.50 **CV:** 0.00 % **No. of Peptides:** 1

10	20	30	40	50	60	70	80
MNPPEGAAEE	GGAADSDVDA	FFRTGSFRND	GLKASDVLPI	LKEKVAFVSG	GRDKRGGPIL	TFPARSNHDR	IRQEDLRKLV
90	100	110	120	130	140	150	160
TYLASVPSED	VCKRGFTVII	DMRGSKWDLI	KPLLKTLQEA	FPAEIHVALI	IKPDNFWQKQ	KTNFGSSKFI	FETSMVSVEG
170	180	190	200	210	220	230	240
LTKLVDPSQL	TEEFDGSLDY	NHEEWIELRL	SLEEFFNSAV	HLLSRLEDLQ	EMLARKEFPV	DVEGSRRLID	EHTQLKKKVL
250	260	270	280	290	300	310	320
KAPVEELDRE	GQRLLQCIRC	SDGFSGRNCI	PGSADFQSLV	PKITSLLDKL	HSTRQHLHQM	WHVRKLKLDQ	CFQLRLFEQD
330	340	350	360	370	380	390	400
AEKMFDWISH	NKELFLQSHT	EIGVSYQYAL	DLQTQHNHFA	MNSMNAYVNI	NRIMSVASRL	SEAGHYASQQ	IKQISTQLDQ
410	420	430	440	450	460	470	480
EWKSFAAALD	ERSTILAMSA	VFHQKAEQFL	SGVDAWCKMC	SEGGLPSEMQ	DLELAIHHHQ	TLYEQVTQAY	TEVSQDGKAL
490	500	510	520	530	540	550	560
LDVLQRPLSP	GNSESLTATA	NYSKAVHQVL	DVVHEVLHHQ	RRLESIWQHR	KVRLHQRLQL	CVFQQDVQQV	LDWIENHGEA
570	580	590	600	610	620	630	640
FLSKHTGVGK	SLHRARALQK	RHDDFEEVAQ	NTYTNADKLL	EAAEQLAQTG	ECDPEEIYKA	ARHLEVRIQD	FVRRVEQRKL
650	660	670	680	690	700	710	720
LLDMSVSFHT	HTKELWTWME	DLQKEMLEDV	CADSVDAVQE	LIKQFQQQT	ATLDATLNVI	KEGEDLIQQL	RSAPPSLGEP
730	740	750	760	770	780	790	800
SEARDSAVSN	NKTPHSSSIS	HIESVLQQLD	DAQVQMEELF	HERKIKLDIF	LQLRIFEQYT	IEVTAELDAW	NEDLLRQMND
810	820	830	840	850	860	870	880
FNTEDLTLAE	QRLQRHTERK	LAMNNMTFEV	IQQGQDLHQY	ITEVQASGIE	LICEKDIDLA	AQVQELLEFL	HEKQHELELN
890	900	910	920	930	940	950	960
AEQTHKRLEQ	CLQLRHLQAE	VKQVLGWIRN	GESMLNASLV	NASSLSEAEQ	LQREHEQFQL	AIESLFHATS	LQKTHQSALQ
970	980	990	1000	1010	1020	1030	1040
VQQKAEVLLQ	AGHYDADAIR	ECAEKVALHW	QQLMLKMEDR	LKLVNASVAF	YKTSEQVCSV	LESLEQEYRR	DEDWCGGRDK
1050	1060	1070	1080	1090	1100	1110	1120
LGPAAEIDHV	IPLISKHLEQ	KEAFLKACTL	ARRNAEVFLK	YIHRNNVSMP	SVASHTRGPE	QQVKAILSEL	LQRENRVLHF
1130	1140	1150	1160	1170	1180	1190	1200
WTLKKRRLDQ	CQQYVVFERS	AKQALDWIQE	TGEFYLSTHT	STGETTEETQ	ELLKEYGEFR	VPAKQTKEKV	KLLIQLADSF
1210	1220	1230	1240	1250	1260	1270	1280
VEKGHIHATE	IRKWVTTVDK	HYRDFSLRMG	KYRYSLEKAL	GVNTEDNKDL	ELDIIPASLS	DREVKLRDAN	HEVNEEKRKS
1290	1300	1310	1320	1330	1340	1350	1360
ARKKEFIMAE	LLQTEKAYVR	DLHECLETYL	WEMTSGVEEI	PPGILNKEHI	IFGNIQEIYD	FHNNIFLKEL	EKYEQLPEDV
1370	1380	1390	1400	1410	1420	1430	1440
GHCFVTWADK	FQMYVTYCKN	KPDSNQLILE	HAGTFFDEIQ	QRHGLANSIS	SYLIKPVQRI	TKYQLLLKEL	LTCCEEGKGE
1450	1460	1470	1480	1490	1500	1510	1520
LKDGLEVMLS	VPKKANDAMH	VSMLEGFDEN	LDVQGELILQ	DAFQVWDPKS	LIRKGRERHL	FLFEISLVFS	KEIKDSSGHT
1530	1540						
KYVYKNKLLP							

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	1429-1438	K.ELLTCCEEGK.G		QD:QU 0.50

Detailed Protein Report

Protein 1176: metaxin-3 isoform 1 [Homo sapiens]

Accession:	gi|267844828	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.6
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVSQPAKILN	FLRKQKYNAD	YELSAKQGAD	TLAYIALLEE	KLLPAVLHTF	WVESDNYFTV	TKPWFASQIP	FPLSLILPGR
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
MSKGALNRIL	LTRGQPPLYH	LREVEAQIYR	DAKECLNLLS	NRLGTSQFFF	GDTPSTLDAY	VFGFLAPLYK	VRFPKVQLQE
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
HLKQLSNLCR	FCDDILSSYF	RLSLGGISPA	GQETVDANLQ	KLTQLVNKES	NLIEKMDDNL	RQSPQLPPRK	LPTLKLTPAE
250	**260**						
EENNSFQRLS	P						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
54	1	796.8016	-102.05	2	30.6	10.4	1	209-221	K.ESNLIEKMDDNLR.Q	Oxidation: 8

Detailed Protein Report

Protein 1177: 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	

Detailed Protein Report

Protein 1178: 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

QD:QU **Median:** 1.06 **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	EEEIIHEDNE	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	QD:QU 1.06

Detailed Protein Report

Protein 1179: 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

```
         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
1711	1	648.2267	-186.12	2	51.7	10.4	0	2-14	M.SISTSAIISSAMK.W	

Detailed Protein Report

Protein 1180: PREDICTED: sialate O-acetylesterase isoform X1 [Homo sapiens]

Accession:	gi|530398206	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	29.7
Database Date:	2015-11-30	**pI:**	9.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVAPGLVLGL	VLPLILWADR	SAGIGFRFAS	YINNDMVLQK	EPAGAVIWGF	GTPGATVTVT	LRQGQETIMK	KVTSVKAHSD
90	100	110	120	130	140	150	160
TWMVVLDPMK	PGGPFEVMAQ	QTLEKINFTL	RVHDVLFGDV	WLCSGQSNMQ	MTVLQIFNAT	RELSNTAAYQ	SVRILSVSPI
170	180	190	200	210	220	230	240
QAEQELEDLV	AVDLQWSKPT	SGFFPRLPTN	LPSCCGEMSL	PSTSSVKISR	PFGMGSASIS	RRCLHSKSSL	LSSLVSVSVD
250	260	270	280				
NWSLFRANSD	LGSPFSRAFF	NPLGTVVFPS	VHSA				

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	223-227	R.CLHSK.S	Carbamidomethyl: 1

Detailed Protein Report

Protein 1181: protein FAM214B [Homo sapiens]

Accession: gi|33636717
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.4
MW [kDa]: 56.7
pI: 10.0
Sequence Coverage [%]: 2.8
No. of unique Peptides: 1

Quantitation

QD:QU **Median:** 0.47 **CV:** 0.00 % **No. of Peptides:** 1

Alias proteins:

Accession	Name	Description
gi|578816745	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM214B isoform X12 [Homo sapiens]
gi|530390168	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM214B isoform X4 [Homo sapiens]
gi|530390166	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM214B isoform X3 [Homo sapiens]
gi|530390164	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM214B isoform X2 [Homo sapiens]
gi|530390162	refseq_human (refseq_human_20140103.fasta)	PREDICTED: protein FAM214B isoform X1 [Homo sapiens]

10	20	30	40	50	60	70	80
MRHVQAEPSP	SSEPEAGPSQ	PPVRQGALQG	GLLMGYSPAG	GATSPGVYQV	SIFSPPAGTS	EPHRALKRQA	PSTEGPRELK
90	100	110	120	130	140	150	160
RGPGLGAREG	LPPEEPSTVG	LLGPEGPGLG	LGVASQHFSH	RGLCVVEQRS	SVTSSWTSGA	WSPPCPPSNA	SCNTLHTRDW
170	180	190	200	210	220	230	240
ASPDPGGQGS	LGESPGPAPP	GQLHTLDTDL	HSLAQIGGKS	PVAGVGNGGS	LWPRESPGTA	NGHSPEHTPP	GPGPPGPCPT
250	260	270	280	290	300	310	320
KRRLLPAGEA	PDVSSEEEGP	APRRRRGSLG	HPTAANSSDA	KATPFWSHLL	PGPKEPVLDP	TDCGPMGRRL	KGARRLKLSP
330	340	350	360	370	380	390	400
LRSLRKGPGL	LSPPSASPVP	TPAVSRTLLG	NFEESLLRGR	FAPSGHIEGF	TAEIGASGSY	CPQHVTLPVT	VTFFDVSEQN
410	420	430	440	450	460	470	480
APAPFLGIVD	LNPLGRKGYS	VPKVGTVQVT	LFNPNQTVVK	MFLVTFDFSD	MPAAHMTFLR	HRLFLVPVGE	EGNANPTHRL
490	500	510	520	530	540		
LCYLLHLRFR	SSRSGRLSLH	GDIRLLFSRR	SLELDTGLPY	ELQAVTEAPH	NPRYSPLP		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	Ratios
1734	1	727.3981	23.60	2	50.2	10.4	0	200-214	K.SPVAGVGNGGSLWPR.E		QD:QU 0.47

Detailed Protein Report

Protein 1182: segment polarity protein dishevelled homolog DVL-3 [Homo sapiens]

Accession: gi|41406097
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.4
MW [kDa]: 78.0
pI: 6.2
Sequence Coverage [%]: 2.4
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MGETKIIYHL	DGQETPYLVK	LPLPAERVTL	ADFKGVLQRP	SYKFFFKSMD	DDFGVVKEEI	SDDNAKLPCF	NGRVVSWLVS
90	100	110	120	130	140	150	160
AEGSHPDPAP	FCADNPSELP	PPMERTGGIG	DSRPPSFHPH	AGGGSQENLD	NDTETDSLVS	AQRERPRRRD	GPEHATRLNG
170	180	190	200	210	220	230	240
TAKGERRREP	GGYDSSSTLM	SSELETTSFF	DSDEDDSTSR	FSSSTEQSSA	SRLMRRHKRR	RRKQKVSRIE	RSSSFSSITD
250	260	270	280	290	300	310	320
STMSLNIITV	TLNMEKYNFL	GISIVGQSNE	RGDGGIYIGS	IMKGGAVAAD	GRIEPGDMLL	QVNEINFENM	SNDDAVRVLR
330	340	350	360	370	380	390	400
EIVHKPGPIT	LTVAKCWDPS	PRGCFTLPRS	EPIRPIDPAA	WVSHTAAMTG	TFPAYGMSPS	LSTITSTSSS	ITSSIPDTER
410	420	430	440	450	460	470	480
LDDFHLSIHS	DMAAIVKAMA	SPESGLEVRD	RMWLKITIPN	AFIGSDVVDW	LYHNVEGFTD	RREARKYASN	LLKAGFIRHT
490	500	510	520	530	540	550	560
VNKITFSEQC	YYIFGDLCGN	MANLSLHDHD	GSSGASDQDT	LAPLPHPGAA	PWPMAFPYQY	PPPPHPYNPH	PGFPELGYSY
570	580	590	600	610	620	630	640
GGGSASSQHS	EGSRSSGSNR	SGSDRRKEKD	PKAGDSKSGG	SGSESDHTTR	SSLRGPRERA	PSERSGPAAS	EHSHRSHHSL
650	660	670	680	690	700	710	720
ASSLRSHHTH	PSYGPPGVPP	LYGPPMLMMP	PPPAAMGPPG	APPGRDLASV	PPELTASRQS	FRMAMGNPSE	FFVDVM

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2710	1	937.4704	-22.97	2	62.8	10.4	1	686-702	R.DLASVPPELTASRQSFR.M	

Detailed Protein Report

Protein 1183: PREDICTED: dedicator of cytokinesis protein 6 isoform X5 [Homo sapiens]

Accession:	gi|578833406	**Score:**	10.4
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

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
2956	1	753.3925	-14.65	2	66.1	10.4	0	986-998	K.TLLSTDHAFPYIK.T	

Detailed Protein Report

Protein 1184: PREDICTED: lactosylceramide alpha-2,3-sialyltransferase isoform X1 [Homo sapiens]

Accession:	gi|530368252	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.4
Database Date:	2015-11-30	**pI:**	9.6
		Sequence Coverage [%]:	4.4
		No. of unique 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	DPDHVKRAQK	YAQQVLQKEC	RPKFAKTSMA	LLFEHRYSVD	LLPFVQKAPK	DSEAESKYDP
170	180	190	200	210	220	230	240
PFGFRKFSSK	VQTLLELLPE	HDLPEHLKAK	TCRRCVVIGS	GGILHGLELG	HTLNQFDVVI	RLNSAPVEGY	SEHVGNKTTI
250	260	270	280	290	300	310	320
RMTYPEGAPL	SDLEYYSNDL	FVAVLFKSVD	FNWLQAMVKK	ETLNVPTIGV	IAVVLATHLC	DEVSLAGFGY	DLNQPRTPLH
330	340	350	360	370			
YFDSQCMAAM	NFQTMHNVTT	ETKFLLKLVK	EGVVKDLSGG	IDREF			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1485	1	850.8758	-46.71	2	48.7	10.4	0	222-237	R.LNSAPVEGYSEHVGNK.T	

Detailed Protein Report

Protein 1185: PREDICTED: triadin isoform X4 [Homo sapiens]

Accession:	gi|578812314	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.5
Database Date:	2015-11-30	**pI:**	9.9
		Sequence Coverage [%]:	1.9
		No. of unique Peptides:	1

Quantitation

QD:QU **Median:** 1.12 **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		QD:QU 1.12

Detailed Protein Report

Protein 1186: UBX domain-containing protein 7 [Homo sapiens]

Accession:	gi|149944496	**Score:**	10.4
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	54.8
Database Date:	2015-11-30	**pI:**	4.9
		Sequence Coverage [%]:	3.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAHGGSAAS	SALKGLIQQF	TTITGASESV	GKHMLEACNN	NLEMAVTMFL	DGGGIAEEPS	TSSASVSTVR	PHTEEEVRAP
90	100	110	120	130	140	150	160
IPQKQEILVE	PEPLFGAPKR	RRPARSIFDG	FRDFQTETIR	QEQELRNGGA	IDKKLTTLAD	LFRPPIDLMH	KGSFETAKEC
170	180	190	200	210	220	230	240
GQMQNKWLMI	NIQNVQDFAC	QCLNRDVWSN	EAVKNIIREH	FIFWQVYHDS	EEGQRYIQFY	KLGDFPYVSI	LDPRTGQKLV
250	260	270	280	290	300	310	320
EWHQLDVSSF	LDQVTGFLGE	HGQLDGLSSS	PPKKCARSES	LIDASEDSQL	EAAIRASLQE	THFDSTQTKQ	DSRSDEESES
330	340	350	360	370	380	390	400
ELFSGSEEFI	SVCGSDEEEE	VENLAKSRKS	PHKDLGHRKE	ENRRPLTEPP	VRTDPGTATN	HQGLPAVDSE	ILEMPPEKAD
410	420	430	440	450	460	470	480
GVVEGIDVNG	PKAQLMLRYP	DGKREQITLP	EQAKLLALVK	HVQSKGYPNE	RFELLTNFPR	RKLSHLDYDI	TLQEAGLCPQ
490							
ETVFVQERN							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1751	1	916.3102	-155.02	2	52.2	10.4	1	106-120	R.SIFDGFRDFQTETIR.Q	

Detailed Protein Report

Protein 1187: 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	

Detailed Protein Report

Protein 1188: 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	

Detailed Protein Report

Protein 1189: PREDICTED: DBIRD complex subunit ZNF326 isoform X1 [Homo sapiens]

Accession:	gi|530362445	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	43.1
Database Date:	2015-11-30	**pI:**	4.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.0
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|530362447	refseq_human (refseq_human_20140103.fasta)	PREDICTED: DBIRD complex subunit ZNF326 isoform X2 [Homo sapiens]

10	20	30	40	50	60	70	80
MGDFGSIHRP	GIVVDYQNKS	TNVTVAAARG	IKRKMMQPFN	KPSGTFIKKP	KLAKPMEKIS	LSKSPTKTDP	KNEEEEKRRI
90	100	110	120	130	140	150	160
EARREKQRRR	REKNSEKYGD	GYRMAFTCSF	CKFRTFEEKD	IELHLESSSH	QETLDHIQKQ	TKFDKVVMEF	LHECMVNKFK
170	180	190	200	210	220	230	240
KTSIRKQQTN	NQTEVVKIIE	KDVMEGVTVD	DHMMKVETVH	CSACSVYIPA	LHSSVQQHLK	SPDHIKGKQA	YKEQIKRESV
250	260	270	280	290	300	310	320
LTATSILNNP	IVKARYERFV	KGENPFEIQD	HSQDQQIEGD	EEDEEKIDEP	IEEEEDEDEE	EEAEEVGEVE	EVEEVEEVRE
330	340	350	360	370	380		
GGIEGEGNIQ	GVGEGGEVGV	VGEVEGVGEV	EEVEELEEET	AKEEPADFPV	EQPEEN		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2131	1	955.8582	-116.90	2	55.2	10.3	1	146-160	K.VVMEFLHECMVNKFK.K	Carbamidomethyl: 9

Detailed Protein Report

Protein 1190: PREDICTED: calcyphosin-like protein isoform X2 [Homo sapiens]

Accession:	gi|578809847	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	23.1
Database Date:	2015-11-30	**pI:**	8.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	10.6
		No. of unique Peptides:	1

```
        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
71	1	1205.0469	-41.61	2	29.6	10.3	0	107-127	K.DGNGTIDFNEFLLTLRPPMSR.A	Oxidation: 19

Detailed Protein Report

Protein 1191: 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 1192: 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 1193: transmembrane protein 165 precursor [Homo sapiens]

Accession:	gi|32189371	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.9
Database Date:	2015-11-30	**pI:**	6.7
		Sequence Coverage [%]:	5.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAAAPGNGR	ASAPRLLLLF	LVPLLWAPAA	VRAGPDEDLS	HRNKEPPAPA	QQLQPQPVAV	QGPEPARVEK	IFTPAAPVHT
90	100	110	120	130	140	150	160
NKEDPATQTN	LGFIHAFVAA	ISVIIVSELG	DKTFFIAAIM	AMRYNRLTVL	AGAMLALGLM	TCLSVLFGYA	TTVIPRVYTY
170	180	190	200	210	220	230	240
YVSTVLFAIF	GIRMLREGLK	MSPDEGQEEL	EEVQAELKKK	DEEFQRTKLL	NGPGDVETGT	SITVPQKKWL	HFISPIFVQA
250	260	270	280	290	300	310	320
LTLTFLAEWG	DRSQLTTIVL	AAREDPYGVA	VGGTVGHCLC	TGLAVIGGRM	IAQKISVRTV	TIIGGIVFLA	FAFSALFISP
330							
DSGF							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2323	1	953.2249	122.58	2	57.7	10.3	0	16-32	R.LLLLFLVPLLWAPAAVR.A	

Detailed Protein Report

Protein 1194: epithelial discoidin domain-containing receptor 1 isoform 4 precursor [Homo sapiens]

Accession:	gi|321400059	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	56.1
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	4.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MGPEALSSLL LLLLVASGDA DMKGHFDPAK CRYALGMQDR TIPDSDISAS SSWSDSTAAR HSRLESSDGD GAWCPAGSVF
        90        100        110        120        130        140        150        160
PKEEEYLQVD LQRLHLVALV GTQGRHAGGL GKEFSRSYRL RYSRDGRRWM GWKDRWGQEV ISGNEDPEGV VLKDLGPPMV
       170        180        190        200        210        220        230        240
ARLVRFYPRA DRVMSVCLRV ELYGCLWRDG LLSYTAPVGQ TMYLSEAVYL NDSTYDGHTV GGLQYGGLGQ LADGVVGLDD
       250        260        270        280        290        300        310        320
FRKSQELRVW PGYDYVGWSN HSFSSGYVEM EFEFDRLRAF QAMQVHCNNM HTLGARLPGG VECRFRRGPA MAWEGEPMRH
       330        340        350        360        370        380        390        400
NLGGNLGDPR ARAVSVPLGG RVARFLQCRF LFAGPWLLFS EISFISDVVN NSSPALGGTF PPAPWWPPGP PPTNFSSLEL
       410        420        430        440        450        460        470        480
EPRGQQPVAK AEGSPTAILI GCLVAIILLL LLIIALMLWR LHWRRLLSKA ERRVLEEELT VHLSVPGDTI LINNRPGPRE
       490        500        510
PPPYQEPRPR GNPPHSAPCV PNGSGAPV
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
165	1	1239.6313	46.44	2	30.8	10.3	1	308-330	R.GPAMAWEGEPMRHNLGGNLGDPR.A	Oxidation: 4

Detailed Protein Report

Protein 1195: tyrosine-protein kinase Fgr [Homo sapiens]

Accession:	gi|4885235	**Score:**	10.3
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	59.4
Database Date:	2015-11-30	**pI:**	5.3
		Sequence Coverage [%]:	3.6
		No. of unique Peptides:	1

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
2074	1	682.6660	-32.64	3	56.3	10.3	2	8-26	K.KLEPVATAKEDAGLEGDFR.S	

Detailed Protein Report

Protein 1196: 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

QD:QU **Median:** 0.70 **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	QD:QU 0.70

Detailed Protein Report

Protein 1197: 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 1198: 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

Detailed Protein Report

Protein 1199: 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 1200: 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	

Detailed Protein Report

Protein 1201: UPF0687 protein C20orf27 isoform 1 [Homo sapiens]

Accession:	gi|85362737	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	21.6
Database Date:	2015-11-30	**pI:**	7.1
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	10.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MAAANKGKCL	PGVVGLAQAL	PVGPGRRAIA	AGNKPRVRSI	RFAAGHDAEG	SHSHVHFDEK	LHDSVVMVTQ	ESDSSFLVKV
90	100	110	120	130	140	150	160
GFLKILHRYE	ITFTLPPVHR	LSKDVREAPV	PSLHLKLLSV	VPVPEGYSVK	CEYSAHKEGV	LKEEILLACE	GGTGTCVRVT
170	180	190	200				
VQARVMDRHH	GTPMLLDGVK	CVGAELEYDS	EHSDWHGFD				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2677	1	973.4960	-59.36	2	62.4	10.2	1	7-26	K.GKCLPGVVGLAQALPVGPGR.R	Carbamidomethyl: 3

Detailed Protein Report

Protein 1202: PREDICTED: cysteine and glycine-rich protein 2 isoform X2 [Homo sapiens]

Accession:	gi|578823362	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	26.7
Database Date:	2015-11-30	**pI:**	10.1
		Sequence Coverage [%]:	7.8
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578823364	refseq_human (refseq_human_20140103.fasta)	PREDICTED: cysteine and glycine-rich protein 2 isoform X3 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MPVWGGGNKC GACGRTVYHA EEVQCDGRSF HRCCFLCMVC RKNLDSTTVA IHDEEIYCKS CYGKKYGPKG YGYGQGAGTL
        90        100        110        120        130        140        150        160
NMDRGERLGI KPESIPSCIK ESCSQKQVIC IYFNFTAPWR PDVMKLNGRE MCCVNHERCF SCAIVQPHRP TTNPNTSKFA
       170        180        190        200        210        220        230        240
QKYGGAEKCS RCGDSVYAAE KIIGAGKPWH KNCFRCAKCG KSLESTTLTE KEGEIYCKGC YAKNFGPKGF GYGQGAGALV
       250
HAQ
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1993	1	1023.9055	-123.30	2	55.3	10.2	1	88-106	R.LGIKPESIPSCIKESCSQK.Q	

Detailed Protein Report

Protein 1203: proteasome subunit alpha type-3 isoform 2 [Homo sapiens]

Accession:	gi|23110939	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	27.6
Database Date:	2015-11-30	**pI:**	5.1
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MSSIGTGYDL	SASTFSPDGR	VFQVEYAMKA	VENSSTAIGI	RCKDGVVFGV	EKLVLSKLYE	EGSNKRLFNV	DRHVGMAVAG
90	100	110	120	130	140	150	160
LLADARSLAD	IAREEASNFR	SNFGYNIPLK	HLADRVAMYV	HAYTLYSAVR	PFGCSVNDGA	QLYMIDPSGV	SYGYWGCAIG
170	180	190	200	210	220	230	240
KARQAAKTEI	EKLQMKEMTC	RDIVKEVAKI	IYIVHDEVKD	KAFELELSWV	GELTNGRHEI	VPKDIREEAE	KYAKESLKEE
250							
DESDDDNM							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2036	1	698.7830	-127.26	2	54.0	10.2	0	73-86	R.HVGMAVAGLLADAR.S	Oxidation: 4

Detailed Protein Report

Protein 1204: PREDICTED: putative uncharacterized protein CXorf49-like [Homo sapiens]

Accession:	gi|410170282	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	53.2
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.4
		No. of unique 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
1182	1	662.2009	-171.93	2	44.9	10.2	0	479-490	R.QQQPPGAQGCPR.V	Carbamidomethyl: 10

Detailed Protein Report

Protein 1205: zinc finger protein 611 isoform b [Homo sapiens]

Accession:	gi|239787086	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	73.4
Database Date:	2015-11-30	**pI:**	10.3
		Sequence Coverage [%]:	1.4
		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 1206: rho GTPase-activating protein 7 isoform 4 [Homo sapiens]

Accession: gi|256017153
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.2
MW [kDa]: 114.1
pI: 8.7
Sequence Coverage [%]: 1.0
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MKLEISPHRK	RSDDSDEDEP	CAISGKWTFQ	RDSKRWSRLE	EFDVFSPKQD	LVPGSPDDSH	PKDGPSPGGT	LMDLSERQEV
90	100	110	120	130	140	150	160
SSVRSLSSTG	SLPSHAPPSE	DAATPRTNSV	ISVCSSSNLA	GNDDSFGSLP	SPKELSSFSF	SMKGHEKTAK	SKTRSLLKRM
170	180	190	200	210	220	230	240
ESLKLKSSHH	SKHKAPSKLG	LIISGPILQE	GMDEEKLKQL	NCVEISALNG	NRINVPMVRK	RSVSNSTQTS	SSSSQSETSS
250	260	270	280	290	300	310	320
AVSTPSPVTR	TRSLSACNKR	VGMYLEGFDP	FNQSTFNNVV	EQNFKNRESY	PEDTVFYIPE	DHKPGTFPKA	LTNGSFSPSG
330	340	350	360	370	380	390	400
NNGSVNWRTG	SFHGPGHISL	RRENSSDSPK	ELKRRNSSSS	MSSRLSIYDN	VPGSILYSSS	GDLADLENED	IFPELDDILY
410	420	430	440	450	460	470	480
HVKGMQRIVN	QWSEKFSDEG	DSDSALDSVS	PCPSSPKQIH	LDVDNDRTTP	SDLDSTGNSL	NEPEEPSEIP	ERRDSGVGAS
490	500	510	520	530	540	550	560
LTRSNRHRLR	WHSFQSSHRP	SLNSVSLQIN	CQSVAQMNLL	QKYSLLKLTA	LLEKYTPSNK	HGFSWAVPKF	MKRIKVPDYK
570	580	590	600	610	620	630	640
DRSVFGVPLT	VNVQRTGQPL	PQSIQQAMRY	LRNHCLDQVG	LFRKSGVKSR	IQALRQMNEG	AIDCVNYEGQ	SAYDVADMLK
650	660	670	680	690	700	710	720
QYFRDLPEPL	MTNKLSETFL	QIYQYVPKDQ	RLQAIKAAIM	LLPDENREVL	QTLLYFLSDV	TAAVKENQMT	PTNLAVCLAP
730	740	750	760	770	780	790	800
SLFHLNTLKR	ENSSPRVMQR	KQSLGKPDQK	DLNENLAATQ	GLAHMIAECK	KLFQVPEEMS	RCRNSYTEQE	LKPLTLEALG
810	820	830	840	850	860	870	880
HLGNDDSADY	QHFLQDCVDG	LFKEVKEKFK	GWVSYSTSEQ	AELSYKKVSE	GPPLRLWRSV	IEVPAVPEEI	LKRLLKEQHL
890	900	910	920	930	940	950	960
WDVDLLDSKV	IEILDSQTEI	YQYVQNSMAP	HPARDYVVLR	TWRTNLPKGA	CALLLTSVDH	DRAPVVGVRV	NVLLSRYLIE
970	980	990	1000	1010	1020		
PCGPGKSKLT	YMCRVDLRGH	MPEWYTKSFG	HLCAAEVVKI	RDSFSNQNTE	TKDTKSR		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
701	1	564.6838	-245.09	2	37.3	10.2	1	741-750	R.KQSLGKPDQK.D	

Detailed Protein Report

Protein 1207: tripartite motif-containing protein 3 isoform 1 [Homo sapiens]

Accession:	gi|32454737	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	80.8
Database Date:	2015-11-30	**pI:**	9.1
Modification(s):	Carbamidomethyl, Oxidation	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|351721563	refseq_human (refseq_human_20140103.fasta)	tripartite motif-containing protein 3 isoform 1 [Homo sapiens]
gi|32454739	refseq_human (refseq_human_20140103.fasta)	tripartite motif-containing protein 3 isoform 1 [Homo sapiens]

10	20	30	40	50	60	70	80
MAKREDSPGP	EVQPMDKQFL	VCSICLDRYQ	CPKVLPCLHT	FCERCLQNYI	PAQSLTLSCP	VCRQTSILPE	QGVSALQNNF
90	100	110	120	130	140	150	160
FISSLMEAMQ	QAPDGAHDPE	DPHPLSVVAG	RPLSCPNHEG	KTMEFYCEAC	ETAMCGECRA	GEHREHGTVL	LRDVVEQHKA
170	180	190	200	210	220	230	240
ALQRQLEAVR	GRLPQLSAAI	ALVGGISQQL	QERKAEALAQ	ISAAFEDLEQ	ALQQRKQALV	SDLETICGAK	QKVLQSQLDT
250	260	270	280	290	300	310	320
LRQGQEHIGS	SCSFAEQALR	LGSAPEVLLV	RKHMRERLAA	LAAQAFPERP	HENAQLELVL	EVDGLRRSVL	NLGALLTTSA
330	340	350	360	370	380	390	400
TAHETVATGE	GLRQALVGQP	ASLTVTTKDK	DGRLVRTGSA	ELRAEITGPD	GTRLPVPVVD	HKNGTYELVY	TARTEGELLL
410	420	430	440	450	460	470	480
SVLLYGQPVR	GSPFRVRALR	PGDLPPSPDD	VKRRVKSPGG	PGSHVRQKAV	RRPSSMYSTG	GKRKDNPIED	ELVFRVGSRG
490	500	510	520	530	540	550	560
REKGEFTNLQ	GVSAASSGRI	VVADSNNQCI	QVFSNEGQFK	FRFGVRGRSP	GQLQRPTGVA	VDTNGDIIVA	DYDNRWVSIF
570	580	590	600	610	620	630	640
SPEGKFKTKI	GAGRLMGPKG	VAVDRNGHII	VVDNKSCCVF	TFQPNGKLVG	RFGGRGATDR	HFAGPHFVAV	NNKNEIVVTD
650	660	670	680	690	700	710	720
FHNHSVKVYS	ADGEFLFKFG	SHGEGNGQFN	APTGVAVDSN	GNIIVADWGN	SRIQVFDSSG	SFLSYINTSA	EPLYGPQGLA
730	740	750					
LTSDGHVVVA	DAGNHCFKAY	RYLQ					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1313	1	946.1922	94.03	3	44.9	10.2	1	5-28	R.EDSPGPEVQPMDKQFLVCSICLDR.Y	Carbamidomethyl: 18, 21; Oxidation: 11

Detailed Protein Report

Protein 1208: 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 1209: PREDICTED: uncharacterized protein LOC102725509 [Homo sapiens]

Accession:	gi|578796799	**Score:**	10.2
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
1393	1	955.6039	52.35	2	46.0	10.2	1	149-169	R.INMVGLGLVGGAGAGLVRGAK.W	

Detailed Protein Report

Protein 1210: PREDICTED: choriogonadotropin subunit beta variant 1 isoform X1 [Homo sapiens]

Accession:	gi|530415623	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	15.3
Database Date:	2015-11-30	**pI:**	10.7
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	16.1
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MGGTWASKEP	LRPRCRPINA	TLAVEKEGCP	VCITVNTTIC	AGYCPTMTRV	LQGVLPALPQ	VVCNYRDVRF	ESIRLPGCPR
90	**100**	**110**	**120**	**130**	**140**	**150**	
GVNPVVSYAV	ALSCQCALCR	RSTTDCGGPK	DHPLTCDDPR	FQDSSSSKAP	PPSLPSPSRL	PGP	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
175	1	1302.5158	-43.75	2	30.9	10.2	0	27-49	K.EGCPVCITVNTTICAGYCPTMTR.V	Carbamidomethyl: 3, 14, 18

Protein 1211: PREDICTED: histone deacetylase 11 isoform X4 [Homo sapiens]

Accession:	gi|578806599	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	30.2
Database Date:	2015-11-30	**pI:**	8.9
		Sequence Coverage [%]:	3.7
		No. of unique 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
653	1	564.6821	-229.40	2	38.2	10.2	0	132-141	R.GWAINVEAIR.R	

Detailed Protein Report

Protein 1212: homeobox protein engrailed-2 [Homo sapiens]

Accession:	gi|7710121	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	34.2
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	4.5
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MEENDPKPGE AAAAVEGQRQ PESSPGGGSG GGGGSSPGEA DTGRRRALML PAVLQAPGNH QHPHRITNFF IDNILRPEFG

        90        100        110        120        130        140        150        160
RRKDAGTCCA GAGGGRGGGA GGEGGASGAE GGGGAGGSEQ LLGSGSREPR QNPPCAPGAG GPLPAAGSDS PGDGEGGSKT

       170        180        190        200        210        220        230        240
LSLHGGAKKG GDPGGPLDGS LKARGLGGGD LSVSSDSDSS QAGANLGAQP MLWPAWVYCT RYSDRPSSGP RSRKPKKKNP

       250        260        270        280        290        300        310        320
NKEDKRPRTA FTAEQLQRLK AEFQTNRYLT EQRRQSLAQE LSLNESQIKI WFQNKRAKIK KATGNKNTLA VHLMAQGLYN

       330        340
HSTTAKEGKS DSE
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2047	1	698.7972	-93.59	2	54.1	10.2	1	170-184	K.GGDPGGPLDGSLKAR.G	

Detailed Protein Report

Protein 1213: N-terminal EF-hand calcium-binding protein 1 [Homo sapiens]

Accession:	gi|24308279	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.5
Database Date:	2015-11-30	**pI:**	4.7
		Sequence Coverage [%]:	4.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MEDSQETSPS SNNSSEELSS ALHLSKGMSI FLDILRRADK NDDGKLSFEE FKAYFADGVL SGEELHELFH TIDTHNTNNL
        90        100        110        120        130        140        150        160
DTEELCEYFS QHLGEYENVL AALEDLNLSI LKAMGKTKKD YQEASNLEQF VTRFLLKETL NQLQSLQNSL ECAMETTEEQ
       170        180        190        200        210        220        230        240
TRQERQGPAK PEVLSIQWPG KRSSRRVQRH NSFSPNSPQF NVSGPGLLEE DNQWMTQINR LQKLIDRLEK KDLKLEPPEE
       250        260        270        280        290        300        310        320
EIIEGNTKSH IMLVQRQMSV IEEDLEEFQL ALKHYVESAS SQSGCLRISI QKLSNESRYM IYEFWENSSV WNSHLQTNYS
       330        340        350        360
KTFQRSNVDF LETPELTSTM LVPASWWILN N
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2070	1	977.3619	-145.82	2	54.4	10.2	1	232-248	K.DLKLEPPEEEIIEGNTK.S	

Detailed Protein Report

Protein 1214: beta-defensin 108B precursor [Homo sapiens]

Accession:	gi|50344744	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	8.3
Database Date:	2015-11-30	**pI:**	10.5
		Sequence Coverage [%]:	28.8
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MRIAVLLFAI FFFMSQVLPA RGKFKEICER PNGSCRDFCL ETEIHVGRCL NSQPCCLPLG HQPRIESTTP KKD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
713	1	824.1368	3.71	3	37.5	10.2	1	1-21	-.MRIAVLLFAIFFFMSQVLPAR.G	

Detailed Protein Report

Protein 1215: **PREDICTED: probable cysteine--tRNA ligase, mitochondrial isoform X6 [Homo sapiens]**

Accession:	gi|578825266	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	50.0
Database Date:	2015-11-30	**pI:**	6.6
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	2.9
		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 1216: **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 1217: **PREDICTED: dual specificity mitogen-activated protein kinase kinase 6 isoform X1 [Homo sapiens]**

Accession:	gi|530412539	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	31.3
Database Date:	2015-11-30	**pI:**	6.7
Modification(s):	Oxidation	**Sequence Coverage [%]:**	5.0
		No. of unique Peptides:	1

Alias proteins:

Accession	**Name**	**Description**
gi|578831139	refseq_human (refseq_human_20140103.fasta)	PREDICTED: dual specificity mitogen-activated protein kinase kinase 6 isoform X4 [Homo sapiens]
gi|530412543	refseq_human (refseq_human_20140103.fasta)	PREDICTED: dual specificity mitogen-activated protein kinase kinase 6 isoform X3 [Homo sapiens]
gi|530412541	refseq_human (refseq_human_20140103.fasta)	PREDICTED: dual specificity mitogen-activated protein kinase kinase 6 isoform X2 [Homo sapiens]

```
        10         20         30         40         50         60         70         80
MELGRGAYGV VEKMRHVPSG QIMAVKRIRA TVNSQEQKRL LMDLDISMRT VDCPFTVTFY GALFREGDVW ICMELMDTSL
        90        100        110        120        130        140        150        160
DKFYKQVIDK GQTIPEDILG KIAVSIVKAL EHLHSKLSVI HRDVKPSNVL INALGQVKMC DFGISGYLVD SVAKTIDAGC
       170        180        190        200        210        220        230        240
KPYMAPERIN PELNQKGYSV KSDIWSLGIT MIELAILRFP YDSWGTPFQQ LKQVVEEPSP QLPADKFSAE FVDFTSQCLK
       250        260        270        280
KNSKERPTYP ELMQHPFFTL HESKGTDVAS FVKLILGD
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2791	1	813.3853	-67.23	2	64.0	10.2	2	14-27	K.MRHVPSGQIMAVKR.I	Oxidation: 10

Detailed Protein Report

Protein 1218: 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

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	m/z meas.	Δ m/z	z	Rt	Score	P	Range	Sequence	Modification

	Cmpds.		[ppm]		[min]					
2608	1	913.4638	-3.43	2	63.3	10.2	1	304-319	K.TALYWAVEKGNATMVR.D	Oxidation: 14

Detailed Protein Report

Protein 1219: 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

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
185	1	896.4274	-19.41	3	32.3	10.2	1	521-544	K.SLRYAGYGEGFDDVIIQGDLEELK.F	

Detailed Protein Report

Protein 1220: 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

Protein 1221: zinc finger protein 585B [Homo sapiens]

Accession:	gi|289547716	**Score:**	10.2
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	88.0
Database Date:	2015-11-30	**pI:**	10.2
		Sequence Coverage [%]:	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MPASWTSPQK	SSALAPEDHG	SSYEGSVSFR	DVAIDFSREE	WRHLDLSQRN	LYRDVMLETY	SHLLSVGYQV	PKPEVVMLEQ
90	100	110	120	130	140	150	160
GKEPWALQGE	RPRHSCPGEK	LWDHNQHRKI	IGYKPASSQD	QKIYSGEKSY	ECAEFGKSFT	WKSQFKVHLK	VPTGEKLYVC
170	180	190	200	210	220	230	240
IECGRAFVQK	PEFITHQKTH	MREKPYKCNE	CGKSFFQVSS	LFRHHRIHTG	EKLYECSECG	KGFPYNSDLS	IHEKIHTGER
250	260	270	280	290	300	310	320
HHECTDCGKA	FTQKSTLKIH	QKIHTGERSY	ICIECGQAFI	QKTQLIAHRR	IHSGEKPYEC	NNCGKSFISK	SQLQVHQRVH
330	340	350	360	370	380	390	400
TRVKPYICTE	YGKVFSNNSN	LITHEKIQSR	EKSSICTECG	KAFTYRSELI	IHQRIHTGEK	PYECSDCGRA	FTQKSALTVH
410	420	430	440	450	460	470	480
QRIHTGEKSY	ICMKCGLAFI	RKAHLITHQI	IHTGEKPYKC	GHCGKLFTSK	SQLHVHKRIH	TGEKPYVCNK	CGKAFTNRSN
490	500	510	520	530	540	550	560
LITHQKTHTG	EKSYICSKCG	KAFTQRSDLI	THQRIHTGEK	PYECNTCGKA	FTQKSNLNIH	QKIHTGERQY	ECHECGKAFN
570	580	590	600	610	620	630	640
QKSILIVHQK	IHTGEKPYVC	TECGRAFIRK	SNFITHQRIH	TGEKPYECSD	CGKSFTSKSQ	LLVHQPVHTG	EKPYVCAECG
650	660	670	680	690	700	710	720
KAFSGRSNLS	KHQKTHTGEK	PYICSECGKT	FRQKSELITH	HRIHTGEKPY	ECSDCGKSFT	KKSQLQVHQR	IHTGEKPYVC
730	740	750	760	770			
AECGKAFSNR	SNLNKHQTTH	TGDKPYKCGI	CGKGFVQKSV	FSVHQSSHA			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2900	1	753.8854	27.29	2	65.4	10.2	0	222-234	K.GFPYNSDLSIHEK.I	

Detailed Protein Report

Protein 1222: sodium/potassium/calcium exchanger 3 precursor [Homo sapiens]

Accession: gi|31563526

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Modification(s): Oxidation

Score: 10.1

MW [kDa]: 71.9

pI: 5.1

Sequence Coverage [%]: 1.6

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MRPSGDEDRA	RRRRRRRRRR	DLLLSQLCFL	ASVALLLWSL	SSLREQKELD	LMDLVGEDRK	WMMARKLMQV	NDTLTSEDAG
90	100	110	120	130	140	150	160
LRNSKNCTEP	ALHEFPNDIF	TNEDRRQGAV	VLHVLCAIYM	FYALAIVCDD	FFVPSLEKIC	ERLHLSEDVA	GATFMAAGSS
170	180	190	200	210	220	230	240
APELFTSVIG	VFITKGDVGV	GTIVGSAVFN	ILCIIGVCGL	FAGQVVALSS	WCLLRDSIYY	TLSVIALIVF	IYDEKVSWWE
250	260	270	280	290	300	310	320
SLVLVLMYLI	YIVIMKYNAC	IHQCFERRTK	GAGNMVNGLA	NNAEIDDSSN	CDATVVLLKK	ANFHRKASVI	MVDELLSAYP
330	340	350	360	370	380	390	400
HQLSFSEAGL	RIMITSHFPP	KTRLSMASRM	LINERQRLIN	SRAYTNGESE	VAIKIPIKHT	VENGTGPSSA	PDRGVNGTRR
410	420	430	440	450	460	470	480
DDVVAEAGNE	TENENEDNEN	DEEEEEDEDD	DEGPYTPFDT	PSGKLETVKW	AFTWPLSFVL	YFTVPNCNKP	RWEKWFMVTF
490	500	510	520	530	540	550	560
ASSTLWIAAF	SYMMVWMVTI	IGYTLGIPDV	IMGITFLAAG	TSVPDCMASL	IVARQGMGDM	AVSNSIGSNV	FDILIGLGLP
570	580	590	600	610	620	630	640
WALQTLAVDY	GSYIRLNSRG	LIYSVGLLLA	SVFVTVFGVH	LNKWQLDKKL	GCGCLLLYGV	FLCFSIMTEF	NVFTFVNLPM
650							
CGDH							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1276	1	593.6730	-244.29	2	44.5	10.1	0	332-341	R.IMITSHFPPK.T	Oxidation: 2

Detailed Protein Report

Protein 1223: 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

QD:QU **Median:** 1.32 **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; Oxidation: 11	QD:QU 1.32

Detailed Protein Report

Protein 1224: IQ domain-containing protein D [Homo sapiens]

Accession:	gi|19923981	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.1
Database Date:	2015-11-30	**pI:**	9.9
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.6
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MALDILAMAP	LYQAPAINRI	GPKTDPSKRP	ADPLKPLVLS	RTKLTTIEAK	RIMSILDEAI	YKVELVTLLS	YVASNREDME
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
GMLGEDVMRA	VREHEDLCQV	LLENVRCLKE	KERQLQEQKE	AEEEGWLRDR	LLSIELQKSS	LSPLMQQIKD	STKNVLRLLL
170	**180**	**190**	**200**	**210**	**220**	**230**	**240**
SNPQAARLLQ	MQTQGRSAEA	QNFIDSLIEL	RGFLFEKLLT	SPMEARDKAQ	FLQDISRQNS	NNQQIIDTLE	KELAERMKNR
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**
NAEEELEDLD	AVHREEKISL	EELRRRHKVL	VGEFAQIREE	REINSKKRME	AEQEMVRMVR	AATLIQALWK	GYLVRSLLRS
330	**340**	**350**					
KKKRGKGKAK	DKEKGKQKGK	EKGKGKK					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
550	1	581.8032	-0.54	2	36.9	10.1	2	232-240	K.ELAERMKNR.N	Oxidation: 6

Detailed Protein Report

Protein 1225: cytochrome c oxidase assembly factor 5 [Homo sapiens]

Accession:	gi|56118949	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	8.4
Database Date:	2015-11-30	**pI:**	10.0
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	20.3
		No. of unique Peptides:	1

```
        10         20         30         40         50         60         70         80
MPKYYEDKPQ GGACAGLKED LGACLLQSDC VVQEGKSPRQ CLKEGYCNSL KYAFFECKRS VLDNRARFRG RKGY
```

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2682	1	958.4638	44.34	2	62.4	10.1	1	44-58	K.EGYCNSLKYAFFECK.R	Carbamidomethyl: 4, 14

Detailed Protein Report

Protein 1226: diacylglycerol kinase zeta isoform 7 [Homo sapiens]

Accession:	gi|313102999	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	101.2
Database Date:	2015-11-30	**pI:**	8.5
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.2
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MEPRDGSPEA	RSSDSESASA	SSSGSERDAG	PEPDKAPRRL	NKRRFPGLRL	FGHRKAITKS	GLQHLAPPPP	TPGAPCSESE
90	100	110	120	130	140	150	160
RQIRSTVDWS	ESATYGEHIW	FETNVSGDFC	YVGEQYCVAR	MLQKSVSRRK	CAACKIVVHT	PCIEQLEKIN	FRCKPSFRES
170	180	190	200	210	220	230	240
GSRNVREGFQ	QKFTFHSKEI	VAISCSWCKQ	AYHSKVSCFM	LQQIEEPCSL	GVHAAVVIPP	TWILRARRPQ	NTLKASKKKK
250	260	270	280	290	300	310	320
RASFKRKSSK	KGPEEGRWRP	FIIRPTPSPL	MKPLLVFVNP	KSGGNQGAKI	IQSFLWYLNP	RQVFDLSQGG	PKEALEMYRK
330	340	350	360	370	380	390	400
VHNLRILACG	GDGTVGWILS	TLDQLRLKPP	PPVAILPLGT	GNDLARTLNW	GGGYTDEPVS	KILSHVEEGN	VVQLDRWDLH
410	420	430	440	450	460	470	480
AEPNPEAGPE	DRDEGATDRL	PLDVFNNYFS	LGFDAHVTLE	FHESREANPE	KFNSRFRNKM	FYAGTAFSDF	LMGSSKDLAK
490	500	510	520	530	540	550	560
HIRVVCDGMD	LTPKIQDLKP	QCVVFLNIPR	YCAGTMPWGH	PGEHHDFEPQ	RHDDGYLEVI	GFTMTSLAAL	QVGGHGERLT
570	580	590	600	610	620	630	640
QCREVVLTTS	KAIPVQVDGE	PCKLAASRIR	IALRNQATMV	QKAKRRSAAP	LHSDQQPVPE	QLRIQVSRVS	MHDYEALHYD
650	660	670	680	690	700	710	720
KEQLKEASVP	LGTVVVPGDS	DLELCRAHIE	RLQQEPDGAG	AKSPTCQKLS	PKWCFLDATT	ASRFYRIDRA	QEHLNYVTEI
730	740	750	760	770	780	790	800
AQDEIYILDP	ELLGASARPD	LPTPTSPLPT	SPCSPTPRSL	QGDAAPPQGE	ELIEAAKRND	FCKLQELHRA	GGDLMHRDEQ
810	820	830	840	850	860	870	880
SRTLLHHAVS	TGSKDVVRYL	LDHAPPEILD	AVEENGETCL	HQAAALGQRT	ICHYIVEAGA	SLMKTDQQGD	TPRQRAEKAQ
890	900	910					
DTELAAYLEN	RQHYQMIQRE	DQETAV					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
800	2	451.4498	-220.69	3	38.5	10.1	0	179-189	K.EIVAISCSWCK.Q	Carbamidomethyl: 7, 10

Protein 1227: PREDICTED: zinc finger CCCH domain-containing protein 4 isoform X3 [Homo sapiens]

Accession: gi|530416049

Database: refseq_human(refseq_human_20140103.fasta)

Database Date: 2015-11-30

Score: 10.1

MW [kDa]: 135.2

pI: 5.9

Sequence Coverage [%]: 1.8

No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MLRGREDGEL	EEGELEDDGA	EETQDTSGGP	ERSRKEKGEK	HHSDSDEEKS	HRRLKRKRKK	EREKEKRRSK	KRRKSKHKRH
90	100	110	120	130	140	150	160
ASSSDDFSDF	SDDSDFSPSE	KGHRKYREYS	PPYAPSHQQY	PPSHATPLPK	KAYSKMDSKS	YGMYEDYENE	QYGEYEGDEE
170	180	190	200	210	220	230	240
EDMGKEDYDD	FTKELNQYRR	AKEGSSRGRG	SRGRGRGYRG	RGSRGGSRGR	GMGRGSRGRG	RGSMGGDHPE	DEEDFYEEEM
250	260	270	280	290	300	310	320
DYGESEEPMG	DDDYDEYSKE	LNQYRRSKDS	RGRGLSRGRG	RGSRGRGKGM	GRGRGRGGSR	GGMNKGGMND	DEDFYDEDMG
330	340	350	360	370	380	390	400
DGGGGSYRSR	DHDKPHQQSD	KKGKVICKYF	VEGRCTWGDH	CNFSHDIELP	KKRELCKFYI	TGFCARAENC	PYMHGDFPCK
410	420	430	440	450	460	470	480
LYHTTGNCIN	GDDCMFSHDP	LTEETRELLD	KMLADDAEAG	AEDEKEVEEL	KKQGINPLPK	PPPGVGLLPT	PPRPPGPQAP
490	500	510	520	530	540	550	560
TSPNGRPMQG	GPPPPPPPPP	PPPGPPQMPM	PVHEPLSPQQ	LQQQDMYNKK	IPSLFEIVVR	PTGQLAEKLG	VRFPGPGGPP
570	580	590	600	610	620	630	640
GPMGPGPNMG	PPGPMGGPMH	PDMHPDMHPD	MHPDMHADMH	ADMPMGPGMN	PGPPMGPGGP	PMMPYGPGDS	PHSGMMPPIP
650	660	670	680	690	700	710	720
PAQNFYENFY	QQQEGMEMEP	GLLGDAEDYG	HYEELPGEPG	EHLFPEHPLE	PDSFSEGGPP	GRPKPGAGVP	DFLPSAQRAL
730	740	750	760	770	780	790	800
YLRIQQKQQE	EEERARRLAE	SSKQDRENEE	GDTGNWYSSD	EDEGGSSVTS	ILKTLRQQTS	SRPPASVGEL	SSSGLGDPRL
810	820	830	840	850	860	870	880
QKGHPTGSRL	ADPRLSRDPR	LTRHVEASGG	SGPGDSGPSD	PRLARALPTS	KPEGSLHSSP	VGPSSSKGSG	PPPTEEEEGE
890	900	910	920	930	940	950	960
RALREKAVNI	PLDPLPGHPL	RDPRSQLQQF	SHIKKDVTLS	KPSFARTVLW	NPEDLIPLPI	PKQDAVPPVP	AALQSMPTLD
970	980	990	1000	1010	1020	1030	1040
PRLHRAATAG	PPNARQRPGA	STDSSTQGAN	LPDFELLSRI	LKTVNATGSS	AAPGSSDKPS	DPRVRKAPTD	PRLQKPTDST
1050	1060	1070	1080	1090	1100	1110	1120
ASSRAAKPGP	AEAPSPTASP	SGDASPPATA	PYDPRVLAAG	GLGQGGGGGQ	SSVLSGISLY	DPRTPNAGGK	ATEPAADTGA
1130	1140	1150	1160	1170	1180	1190	1200
QPKGAEGNGK	SSASKAKEPP	FVRKSALEQP	ETGKAGADGG	TPTDRYNSYN	RPRPKAAAAP	AATTATPPPE	GAPPQPGVHN
1210	1220	1230	1240	1250	1260		
LPVPTLFGTV	KQTPKTGSGS	PFAGNSPARE	GEQDAASLKD	VFKGFDPTAS	PFCQ		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
924	1	712.6415	-45.15	3	40.0	10.1	1	821-842	R.LTRHVEASGGSGPGDSGPSDPR.L	

Detailed Protein Report

Protein 1228: growth arrest-specific protein 1 precursor [Homo sapiens]

Accession:	gi|167466169	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	35.7
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	4.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MVAALLGGGG	EARGGTVPGA	WLCLMALLQL	LGSAPRGSGL	AHGRRLICWQ	ALLQCQGEPE	CSYAYNQYAE	ACAPVLAQHG
90	100	110	120	130	140	150	160
GGDAPGAAAA	AFPASAASFS	SRWRCPSHCI	SALIQLNHTR	RGPALEDCDC	AQDENCKSTK	RAIEPCLPRT	SGGGAGGPGA
170	180	190	200	210	220	230	240
GGVMGCTEAR	RRCDRDSRCN	LALSRYLTYC	GKVFNGLRCT	DECRTVIEDM	LAMPKAALLN	DCVCDGLERP	ICESVKENMA
250	260	270	280	290	300	310	320
RLCFGAELGN	GPGSSGSDGG	LDDYYDEDYD	DEQRTGGAGG	EQPLDDDDGV	PHPPRPGSGA	AASGGRGDLP	YGPGRRSSGG
330	340	350					
GGRLAPRGAW	TPLASILLLL	LGPLF					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1959	1	660.8945	-58.20	3	53.0	10.1	1	121-137	R.RGPALEDCDCAQDENCK.S	Carbamidomethyl: 8, 16

Detailed Protein Report

Protein 1229: **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 1230: 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 1231: 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 1232: **PREDICTED: ribosome biogenesis methyltransferase WBSCR22 isoform X2 [Homo sapiens]**

Accession:	gi|578813903	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	28.2
Database Date:	2015-11-30	**pI:**	9.5
Modification(s):	Oxidation	**Sequence Coverage [%]:**	2.8
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MIDIQTRMAG	RALELLYLPE	NKPCYLLDIG	CGTGLSGSYL	SDEGHYWVGL	DISPAMLDEA	VDREIEGDLL	LGDMGQGIPF
90	100	110	120	130	140	150	160
KPGTFDGCIS	ISAVQWLCNA	NKKSENPAKR	LYCFFASLFS	VLVRGSRAVL	QLYPENSEQL	ELITTQATKA	GFSGGMVVDY
170	180	190	200	210	220	230	240
PNSAKAKKFY	LCLFSGPSTF	IPEGLSENQD	EVEPRESVFT	NERFPLRMSR	RGMVRKSRAW	VLEKKERHRR	QGREVRPDTQ
250	260						
YTGRKRKPRF							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2741	1	922.4990	6.80	1	63.2	10.1	1	204-210	R.FPLRMSR.R	Oxidation: 5

Detailed Protein Report

Protein 1233: **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 1234: 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 1235: **PREDICTED: steroidogenic acute regulatory protein, mitochondrial isoform X4 [Homo sapiens]**

Accession: gi|578815478
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30
Modification(s): Oxidation

Score: 10.1
MW [kDa]: 19.5
pI: 9.6
Sequence Coverage [%]: 6.9
No. of unique Peptides: 1

10	20	30	40	50	60	70	80
MLLATFKLCA	GSSYRHMRNM	KGLRQQAVMA	ISQELNRRAL	GGPTPSTWIN	QVRRRSSLLG	SRLEETLYSD	QELAYLQQGE
90	**100**	**110**	**120**	**130**	**140**	**150**	**160**
EAMQKALGIL	SNQEGWKKES	QQDNGDKVMS	KVVPDVGKVF	RLEVVVDQPM	ERLYEELVER	MEAMGEWNPN	VKEIKGGARS
170	**180**						
HLHGASPVGW	KSL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
1893	1	719.2685	-58.42	2	52.2	10.1	0	141-152	R.MEAMGEWNPNVK.E	Oxidation: 1, 4

Detailed Protein Report

Protein 1236: 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

Protein 1237: PREDICTED: zinc finger protein 532 isoform X14 [Homo sapiens]

Accession:	gi|578832581	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	114.0
Database Date:	2015-11-30	**pI:**	9.7
		Sequence Coverage [%]:	0.9
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTMGDMKTPD	FDDLLAAFDI	PDMVDPKAAI	ESGHDDHESH	MKQNAHGEDD	SHAPSSSDVG	VSVIVKNVRN	IDSSEGGEKD
90	100	110	120	130	140	150	160
GHNPTGNGLH	NGFLTASSLD	SYSKDGAKSL	KGDVPASEVT	LKDSTFSQFS	PISSAEEFDD	DEKIEVDDPP	DKEDMRSSFR
170	180	190	200	210	220	230	240
SNVLTGSAPQ	QDYDKLKALG	GENSSKTGLS	TSGNVEKNKA	VKRETEASSI	NLSVYEPFKV	RKAEDKLKES	SDKVLENRVL
250	260	270	280	290	300	310	320
DGKLSSEKND	TSLPSVAPSK	TKSSSKLSSC	IAAIAALSAK	KAASDSCKEP	VANSRESSPL	PKEVNDSPRA	ADKSPESQNL
330	340	350	360	370	380	390	400
IDGTKKPSLK	QPDSPRSISS	ENSSKGSPSS	PAGSTPAIPK	VRIKTIKTSS	GEIKRTVTRV	LPEVDLDSGK	KPSEQTASVM
410	420	430	440	450	460	470	480
ASVTSLLSSP	ASAAVLSSPP	RAPLQSAVVT	NAVSPAELTP	KQVTIKPVAT	AFLPVSAVKT	AGSQVINLKL	ANNTTVKATV
490	500	510	520	530	540	550	560
ISAASVQSAS	SAIIKAANAI	QQQTVVVPAS	SLANAKLVPK	TVHLANLNLL	PQGAQATSEL	RQVLTKPQQQ	IKQAIINAAA
570	580	590	600	610	620	630	640
SQPPKKVSRV	QVVSSLQSSV	VEAFNKVLSS	VNPVPVYIPN	LSPPANAGIT	LPTRGYKCLE	CGDSFALEKS	LTQHYDRRSV
650	660	670	680	690	700	710	720
RIEVTCNHCT	KNLVFYNKCS	LLSHARGHKE	KGVVMQCSHL	ILKPVPADQM	IVSPSSNTST	STSTLQSPVG	AGTHTVTKIQ
730	740	750	760	770	780	790	800
SGITGTVISA	PSSTPITPAM	PLDEDPSKLC	RHSLKCLECN	EVFQDETSLA	THFQQAADTS	GQKTCTICQM	LLPNQCSYAS
810	820	830	840	850	860	870	880
HQRIHQHKSP	YTCPECGAIC	RSVHFQTHVT	KNCLHYTRRV	GFRCVHCNVV	YSDVAALKSH	IQGSHCEVFY	KCPICPMAFK
890	900	910	920	930	940	950	960
SAPSTHSHAY	TQHPGIKIGE	PKIIYKCSMC	DTVFTLQTLL	YRHFDQHIEN	QKVSVFKCPD	CSLLYAQKQL	MMDHIKSMHG
970	980	990	1000	1010	1020	1030	1040
TLKSIEGPPN	LGINLPLSIK	PATQNSANQN	KEDTKSMNGK	EKLEKKSPSP	VKKSMETKKV	ASPGWTCWEC	DCLFMQRDVY
1050	1060	1070					
ISHVRKEHGK	FGSGKRNHIL						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
633	1	537.6446	-266.88	2	36.5	10.1	2	1046- 1055	R.KEHGKFGSGK.R	

Detailed Protein Report

Protein 1238: 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 1239: PREDICTED: L-fucose kinase isoform X3 [Homo sapiens]

Accession:	gi|578828897	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	81.7
Database Date:	2015-11-30	**pI:**	6.4
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	1.7
		No. of unique Peptides:	1

10	20	30	40	50	60	70	80
MTSSASEFLL	SLTLPGAPGA	QIVHSQVEEQ	QLLAAGSSVV	SCLLEGPVQL	GPGSVLQHCH	LQGPIHIGAG	CLVTGLDTAH
90	100	110	120	130	140	150	160
SKALHGRELR	DLVLQGHHTR	LHGSPGHAFT	LVGRLDSWER	QGAGTYLNVP	WSEFFKRTGV	RAWDLWDPET	LPAEYCLPSA
170	180	190	200	210	220	230	240
RLFPVLHPSR	ELGPQDLLWM	LDHQEDGGEA	LRAWRASWRL	SWEQLQPCLD	RAATLASRRD	LFFRQALHKA	RHVLEARQDL
250	260	270	280	290	300	310	320
SLRPLIWAAV	REGCPGPLLA	TLDQVAAGAG	DPGVAARALA	CVADVLGCMA	EGRGGLRSGP	AANPEWMRPF	SYLECGDLAA
330	340	350	360	370	380	390	400
GVEALAQERD	KWLSRPALLV	RAARHYEGAG	QILIRQAVMS	AQHFVSTEQV	ELPGPGQWVV	AECPARVDFS	GGWSDTPPLA
410	420	430	440	450	460	470	480
YELGGAVLGL	AVRVDGRRPI	GARARRIPEP	ELWLAVGPRQ	DEMTVKIVCR	CLADLRDYCQ	PHAPGALLKA	AFICAGIVHV
490	500	510	520	530	540	550	560
HSELQLSEQL	LRTFGGGFEL	HTWSELPHGS	GLGTSSILAG	TALAALQRAA	GRVVGTEALI	HAVLHLEQVL	TTGGGWQDQV
570	580	590	600	610	620	630	640
GGLMPGIKVG	RSRAQLPLKV	EVEEVTVPEG	FVQKLNDHLL	LVYTGKTRLA	RNLLQDVLRS	WYARLPAVVQ	NAHSLVRQTE
650	660	670	680	690	700	710	720
ECAEGFRQGS	LPLLGQCLTS	YWEQKKLMAP	GCEPLTVRRM	MDVLAPHVHG	QSLAGAGGGG	FLYLLTKEPQ	QKEALEAVLA
730	740	750	760				
KTEGLGNYSI	HLVEVDTQGL	SLKLLGTEAS	TCCPFP				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2561	1	698.1910	-181.61	2	60.7	10.1	0	744-756	K.LLGTEASTCCPFP.-	Carbamidomethyl: 9

Detailed Protein Report

Protein 1240: beta-defensin 125 preproprotein [Homo sapiens]

Accession:	gi|76563936	**Score:**	10.1
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	17.5
Database Date:	2015-11-30	**pI:**	5.2
Modification(s):	Carbamidomethyl	**Sequence Coverage [%]:**	6.4
		No. of unique 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
973	1	637.3502	98.48	2	42.2	10.1	1	27-36	K.CWKNNVGHCR.R	Carbamidomethyl: 1

Detailed Protein Report

Protein 1241: 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 1242: **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	

Detailed Protein Report

Protein 1243: 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	

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Detailed Protein Report

Protein 1244: zona pellucida sperm-binding protein 3 isoform 2 [Homo sapiens]

Accession:	gi|38327649	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	41.2
Database Date:	2015-11-30	**pI:**	5.7
Modification(s):	Oxidation	**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 1245: PREDICTED: transportin-1 isoform X2 [Homo sapiens]

Accession: gi|530379292
Database: refseq_human(refseq_human_20140103.fasta)
Database Date: 2015-11-30

Score: 10.0
MW [kDa]: 98.6
pI: 4.7
Sequence Coverage [%]: 1.5
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 1246: 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 1247: PREDICTED: transcriptional adapter 2-alpha isoform X4 [Homo sapiens]

Accession:	gi|578831320	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	40.0
Database Date:	2015-11-30	**pI:**	9.4
Modification(s):	Oxidation	**Sequence Coverage [%]:**	3.2
		No. of unique Peptides:	1

Alias proteins:

Accession	Name	Description
gi|578840385	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transcriptional adapter 2-alpha isoform X4 [Homo sapiens]
gi|578840383	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transcriptional adapter 2-alpha isoform X3 [Homo sapiens]
gi|578840381	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transcriptional adapter 2-alpha isoform X2 [Homo sapiens]
gi|578831324	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transcriptional adapter 2-alpha isoform X6 [Homo sapiens]
gi|578831322	refseq_human (refseq_human_20140103.fasta)	PREDICTED: transcriptional adapter 2-alpha isoform X5 [Homo sapiens]

10	20	30	40	50	60	70	80
MCTKTKEECE	KHYMKHFINN	PLFASTLLNL	KQAEEAKTAD	TAIPFHSTDD	PPRPTFDSLL	SRDMAGYMPA	RADFIEEFDN
90	100	110	120	130	140	150	160
YAEWDLRDID	FVEDDSDILH	ALKMAVVDIY	HSRLKERQRR	KKIIRDHGLI	NLRKFQLMER	RYPKEVQDLY	ETMRRFARIV
170	180	190	200	210	220	230	240
GPVEHDKFIE	SHALEFELRR	EIKRLQEYRT	AGITNFCSAR	TYDHLKKTRE	EERLKRTMLS	EVLQYIQDSS	ACQQWLRRQA
250	260	270	280	290	300	310	320
DIDSGLSPSI	PMASNSGRRS	APPLNLTGLP	GTEKLNEKEK	ELCQMVRLVP	GAYLEYKSAL	LNECNKQGGL	RLAQARALIK
330	340	350					
IDVNKTRKIY	DFLIREGYIT	KG					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
2592	1	673.3616	101.24	2	63.1	10.0	2	1-11	-.MCTKTKEECEK.H	Oxidation: 1

Detailed Protein Report

Protein 1248: 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 1249: uncharacterized protein C7orf72 [Homo sapiens]

Accession:	gi|332634960	**Score:**	10.0
Database:	refseq_human(refseq_human_20140103.fasta)	**MW [kDa]:**	49.6
Database Date:	2015-11-30	**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	